



هفدهمین کنگره بین المللی

میکروب شناسی ایران

۲ تا ۴ شهریورماه ۱۳۹۵

دانشکده پزشکی دانشگاه علوم پزشکی تهران

The 17th International and Iranian Congress of
Microbiology

23-25 August 2016, Tehran - Iran





يا من اسمه دواء و ذكره شفاء



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دانشگاه علوم پزشکی اردبیل



سازمان نظام دامپزشکی جمهوری اسلامی ایران



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به کوشش : محمد رضا آشتیانی
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پست الکترونیکی : Rasane_takhassosi@yahoo.com وب سایت: Rasanetakhassosi.ir



فهرست مطالب

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پیام رئیس انجمن علم میکروب‌شناسی ایران

دکتر محمد مهدی فیض آبادی

همکاران گرامی، اساتید و دانشجویان عزیز

مقدم شما را به هفدهمین کنگره بین‌المللی میکروب‌شناسی گرامی می‌داریم. به لطف و حمایت شما اعضای گرامی، انجمن میکروب‌شناسی ایران توانسته است قدم‌هایی را در جهت شکل‌گیری همکاری‌ها و هم‌اندیشی‌های علمی بین اعضای خود و نیز سازمان‌های مختلف کشور برقرار نماید. انجمن محل برخورد اندیشه‌های علمی اعضای آن جدای از نگاه‌های شخصی و سلیقه‌ای بوده و خوشبختانه توانسته است قدم‌های موفق‌تری در این زمینه بردارد. تعامل علمی بین اعضا، جلوگیری از ایجاد هرگونه سوء تفاهم و حفظ وحدت وظیفه تمامی اعضای انجمن بویژه هیئت مدیره آن می‌باشد. این امر در شرایطی که شاهد تلاش‌های نابردان و سودجویان در کنار گذاشتن متخصصین علوم بیومدیکال و از جمله رشته میکروب‌شناسی از مراکز تشخیصی می‌باشیم بسیار ضروری است. عدم توجه به این مسئله از بین رفتن حقوق بیماران، شدت گرفتن بیماری‌های صعب‌العلاج (مقاومت میکروب‌ها نسبت به آنتی‌بیوتیک‌ها و افزایش هرچه بیشتر عفونت‌های بیمارستانی) را در پی خواهد داشت. از عوارض دیگر سهل‌انگاری نسبت به دانش میکروب‌شناسی در شرایط فعلی سست شدن پایه‌های فناوری‌های مبتنی بر میکروب‌شناسی از جمله ساخت واکسن‌ها و پیشگیری از بیماری‌هاست. انجمن میکروب‌شناسی با داشتن گروه‌های تخصصی توانسته است در مواردی به حوزه‌های درمانی و پژوهشی مساعدت‌هایی نماید. انتظار می‌رود که مسئولین آموزشی وزارت متبوع به توانایی‌های برنامه‌ریزی آموزشی این انجمن نیز توجه نمایند.

فرصت را مغتنم شمرده و مراتب تشکر خود را از حمایت ارزشمند موسسه تحقیقات واکسن و سرم‌سازی رازی که همچون سال‌های گذشته با دعوت از سخنرانان خارجی به محتوای علمی کنگره افزودند اعلام نمایم. هیئت مدیره انجمن از مساعدت جناب آقای دکتر امامی ریاست محترم دانشکده پزشکی و هیئت رئیسه دانشکده پزشکی تشکر فراوان دارد.



پیام دبیر علمی کنگره

دکتر پژواک خاکی

با نام و یاد خدا و استعانت از درگاه بی‌کرانش، ضمن آرزوی توفیقات روزافزون خدمت تمامی پژوهشگران، اساتید و دانشجویان، از صمیم قلب حضور سبزتان را در هفدهمین کنگره بین‌المللی میکروب‌شناسی ایران که به همت و همکاری تیم‌های اجرایی، علمی، حامیان کنگره و حضور ارزشمند نخبگان و اصحاب اندیشه در حوزه علوم میکروبی، امسال نیز طبق روال سالیان گذشته در تاریخ ۲ تا ۴ شهریور ماه در محل دانشکده پزشکی دانشگاه علوم پزشکی تهران برگزار می‌گردد، را ارج می‌نهم.

کنگره هفدهم در کنار سرفصل‌های متعدد و متنوع، اهداف اختصاصی نظیر پرداختن به اهمیت عفونت‌های بیمارستانی و مقاومت‌های میکروبی و آخرین اطلاعات مربوط به مقاومت دارویی در ایران و سایر نقاط جهان و جستجوی اهداف جدید جهت استفاده از آنتی‌بیوتیک‌های جدید و موثر و آشنایی با متابولیت‌های جدید میکروبی و موارد استفاده از آنها در درمان می‌باشد. همچنین مباحث مربوط به نانوتکنولوژی در میکروب‌شناسی پزشکی، مشکلات بیماری‌های ریوی سل و غیر سلی در ایران و جهان، روش‌های نوین تشخیص و تایپینگ میکروب‌های بیماری‌زا و اپیدمیولوژی بیماری‌های عفونی بازپدید و نوپدید در ایران و مقایسه آنها با گزارشات جهانی از دیگر محورهای اختصاصی کنگره پیش‌رو می‌باشد.

امید است با برگزاری این کنگره بستری فراهم شود تا پژوهشگران و دانشجویان عزیز نتایج آخرین فعالیت‌های پژوهشی و آموخته‌های نوین خود را ارائه نموده و از یافته‌های سایرین در قالب کارگاه‌های آموزشی، پوسترها و سخنرانی‌ها بویژه محققین خارجی حاضر، بهره کافی را ببرند.

برای دستیابی به این امر تلاش کمیته علمی بر انتخاب موضوعات و سخنرانان مجرب در حیطه علمی و کاربردی علوم پایه قرار گرفته است. همچنین برگزاری کارگاه‌های متعدد در کنار سخنرانی‌ها برای شرکت‌کنندگان و دانشجویان عزیز فراهم می‌کند که بتواند مهارت‌های عملی خود را نیز افزایش دهند. در پایان کمیته برنامه‌ریزی علمی کنگره و انجمن میکروب‌شناسی ایران حضور ارزشمند تمامی شرکت‌کنندگان، مدعوین گرامی داخل و خارج از کشور را غنیمت شمرده و همواره در صدد بهره‌گیری از تجارب و نظرات ارزشمند همه بزرگواران در جهت هر چه بهتر برگزار شدن این کنگره می‌باشیم.

ارکان هفدهمین کنگره بین‌المللی میکروپزشناسی ایران

۲ تا ۴ شهریور ماه ۱۳۹۵ / دانشکده پزشکی دانشگاه علوم پزشکی تهران



دکتر عباسعلی ایمانی فولادی
دبیر اجرایی کنگره



دکتر پژواک خاکی
دبیر علمی کنگره



دکتر محمد مهدی فیض آبادی
رئیس کنگره

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- هنگامه زندی / دانشگاه علوم پزشکی یزد
- تقی زهرائی صالحی / دانشگاه تهران
- محمد زینلی / انستیتو پاستور ایران
- مریم ساده / دانشگاه علوم پزشکی یزد
- محمد حسین سالاری / دانشگاه علوم پزشکی تهران
- ستاره سروش / دانشگاه علوم پزشکی لرستان
- سید داور سیادت / انستیتو پاستور ایران
- فرشته شاهچراغی / انستیتو پاستور ایران
- سید ابوالحسن شاهزاده فاضلی / هیئت علمی جهاد دانشگاهی
- حسن شجاعی / دانشگاه علوم پزشکی اصفهان
- اصغر شریفی / دانشگاه علوم پزشکی یاسوج
- مسعود شریفی / دانشگاه علوم پزشکی قزوین
- علی اکبر شعبانی / دانشگاه علوم پزشکی سمنان
- محمد شناگری
- شهرام شهرکی / دانشگاه علوم پزشکی همدان

- محمد حسن شیرازی / دانشگاه علوم پزشکی تهران
- حوریه صادری / دانشگاه علوم پزشکی شاهد
- نور خدا صادقی فرد / دانشگاه علوم پزشکی ایلام
- بهزاد صالحی / دانشگاه آزاد اسلامی واحد کرج
- غلامرضا صالحی جوزانی / انستیتو بیوتکنولوژی کشاورزی
- میترا صالحی سیرجان / دانشگاه آزاد اسلامی واحد تهران شمال
- محمد رضا صعودی / دانشگاه الزهراء
- محمود صفاری / دانشگاه علوم پزشکی کاشان
- پروانه صفاریان / دانشگاه علوم پزشکی آزاد اسلامی-واحد تهران پزشکی
- حسین صمدی کفیل / دانشگاه علوم پزشکی تبریز
- سنبل طارمیان / دانشگاه علوم پزشکی گیلان
- مروت طاهری کلانی / دانشگاه علوم پزشکی لرستان
- بهمن عابدی کیاسری / موسسه تحقیقات واکسن و سرم سازی رازی
- عباس عبدالهی / دانشگاه علوم پزشکی فسا
- احیا عابدی عالی / دانشگاه الزهراء
- رامین عبیری / دانشگاه علوم پزشکی کرمانشاه
- محمدرضا عربستانی / دانشگاه علوم پزشکی همدان
- عزت عسگرانی / دانشگاه الزهراء
- رمضانعلی عطایی / دانشگاه علوم پزشکی بقیه الله
- سید محمد علوی / علوم پزشکی اهواز
- آتوسا علی احمدی / مرکز تحقیقات گیاهان دارویی دانشگاه شهید بهشتی
- محمد یوسف علیخانی / دانشگاه علوم پزشکی همدان
- حمید عمادی کوچک / دانشگاه علوم پزشکی تهران
- محمد جواد غروی / دانشگاه علوم پزشکی البرز
- احسان غزنوی / دانشگاه علوم پزشکی اراک
- سبجان غفوریان / دانشگاه علوم پزشکی ایلام
- حسین فاضلی / دانشگاه علوم پزشکی اصفهان
- بهرام فتح اله زاده / دانشگاه علوم پزشکی تهران
- شهره فرشاد / دانشگاه علوم پزشکی شیراز
- کامبیز فرقان پرست / دانشگاه علوم پزشکی گیلان
- هما فروهش تهرانی / دانشگاه علوم پزشکی ایران

- جمشید فقری / دانشگاه علوم پزشکی اصفهان
- طاهره فلسفی / دانشگاه الزهرا
- جمشید فولادی / دانشگاه الزهراء
- فرزانه فیروزه / دانشگاه علوم پزشکی کاشان
- رایناک قادری / موسسه تحقیقات واکسن و سرم سازی رازی
- علیرضا قاسم پور / مرکز تحقیقات گیاهان دارویی دانشگاه شهید بهشتی
- کیارش قزوینی / دانشگاه علوم پزشکی مشهد
- ابوالفضل قلی پور / دانشگاه علوم پزشکی شهرکرد
- روحا کسری کرمانشاهی / دانشگاه الزهرا
- عنایت اله کلانتر / دانشگاه علوم پزشکی البرز
- داود کلانتر نیستانی / دانشگاه علوم پزشکی کرمان
- حمید کهرام / موسسه تحقیقات واکسن و سرم سازی رازی
- غلامرضا گودرزی / دانشگاه علوم پزشکی لرستان
- محسن لطفی / موسسه تحقیقات واکسن و سرم سازی رازی
- پرویز مالک نژاد / دانشگاه علوم پزشکی تهران
- علی مجتهدی / دانشگاه علوم پزشکی گیلان
- اشرف محبتی مبارز / دانشگاه تربیت مدرس
- محمد رضا محزونیه / دانشکده دامپزشکی - دانشگاه شهرکرد
- مرجان محمدی / انستیتو پاستور ایران
- فاطمه محمدی پناه / دانشگاه تهران - دانشکده علوم
- حمیده محمود زاده حسینی / دانشگاه علوم پزشکی بقیه الله (عج)
- سهیلا مرادی بیدهندی / موسسه تحقیقات واکسن و سرم سازی رازی
- احسان مصطفوی / انستیتو پاستور ایران
- نادر مصوری / موسسه تحقیقات واکسن و سرم سازی رازی
- حسین معتمدی / دانشگاه علوم پزشکی شیراز
- نسرين معظمی / سازمان پژوهشهای علمی و صنعتی ایران
- شهلا منصوری / دانشگاه علوم پزشکی کرمان
- سید حمید رضا منوری / دانشگاه علوم پزشکی ایران
- رضوان منیری / دانشگاه علوم پزشکی کاشان
- پرویز مهاجری / دانشگاه علوم پزشکی کرمانشاه
- علی مهرابی توانا / دانشگاه علوم پزشکی بقیه الله

- سید فضل الله موسوی / انستیتو پاستور ایران
- زهره مومنی / دانشگاه آزاد اسلامی واحد کرج
- مهدی میرزائی / دانشگاه علوم پزشکی شاهرود
- مهدی میرسعیدی / دانشگاه شیکاگو
- اکبر میر صالحیان / دانشگاه علوم پزشکی تهران
- شیوا میرکلانتری / دانشگاه علوم پزشکی سمنان
- رضا میرنژاد / دانشگاه علوم پزشکی بقیه الله
- محبوبه نادری نسب / دانشگاه علوم پزشکی مشهد
- مهشید ناصحی / مرکز مدیریت بیماریهای وزارت بهداشت
- شهین نجار بیرایه / دانشگاه تربیت مدرس
- صمد نژاد ابراهیمی / مرکز تحقیقات گیاهان دارویی دانشگاه شهید بهشتی
- بیژن نعمان پور / دانشگاه علوم پزشکی کرمانشاه
- مصطفی نعمتی
- محمد حسن نمایی / دانشگاه علوم پزشکی بیرجند
- محمد رضا نهایی / دانشگاه علوم پزشکی تبریز
- جمیله نوروزی / دانشگاه آزاد اسلامی واحد علوم تحقیقات
- مهدی نوروزی / دانشگاه علوم پزشکی تهران
- محمد نیاکان / دانشگاه علوم پزشکی شاهد
- ایرج نیکوکار / دانشگاه علوم پزشکی گیلان
- غلامرضا هاشمی تبار / دانشگاه فردوسی
- عبدالرزاق هاشمی شهرکی / انستیتو پاستور ایران
- ناصر هرزندی / دانشگاه آزاد اسلامی واحد کرج
- زویا هژبری ماهانی / دانشگاه علوم پزشکی سمنان
- فرزاد وزیری / انستیتو پاستور ایران
- جلیل وند یوسفی / موسسه تحقیقات واکسن و سرم سازی رازی
- امیر هوشنگ الوندی / دانشگاه علوم پزشکی کرمانشاه
- عباس یادگار / تربیت مدرس
- یوسف یحیی پور / دانشگاه علوم پزشکی بابل
- سمیه یسلیانی فرد / دانشگاه علوم پزشکی البرز
- صابر یوسفی / دانشگاه علوم پزشکی ارومیه
- رسول یوسفی مشعوف / دانشگاه علوم پزشکی همدان

اعضای کمیته اجرایی (بر اساس حروف الفبای فارسی)

شهربانو کشاورز	حسینعلی راهدار	فاطمه اتحاد مروستی
رضوان محراب	الهام رضوانی	آزاده احمدی
رقیه محمدزاده	ریحانه روشن	نجمه اردشیری
نیما محمدزاده	عباس زارعی	سمانه استاد محمدی
حمیده محمودزاده حسینی	فتانه سبزیعلی	سهیلا استاد محمدی
فهیمة مرتضی	آذین ستاری	پریسا اسدالهی
مریم مهره کش حقیقت	محمد کامران سرکندی	مژگان اسماعیلی
آرزو میرزایی	پرдіس سعیدی	سجاد اشتیاقی
مریم میرشکار	سید علی میرحسینی	شیما افراسیابی
رضا نجف پور	نرگس شهبازی	کیانا امیری
زهره نجفی علیا	شها شهبازی	سپهر بوذری
محمد جواد نصیری	عارفه شهریاری	سمانه بوربور
مجتبی هدایتی	علی شیوائی	سمیرا بهرامی
منصوره هوشیار	حمیدرضا صادق	الهام بهزادی
سجاد یزدان ستاد	فریده صادق خانی	الهه تاکی
	حمید صدیقیان راد	سمیرا تراشی
	سیده رحیمه صنیع خانی	مینا سادات تقوی
	رضا عزیزیان	الهام تقی نیا
	زینب عزیزیان	سمیه جاسمی
	نرگس فراهانی	مارال چاووشی
	الیکا فرج تبریزی	شادی حبیب نیا
	محمد امین فسونگر	زهره حسینی توسل
	افروز فهیمی پور	سپیده حق نظری
	مهدی قره خانی	پروانه خیابانی
	رویا قنواتی	مسعود داداشی
	جلیل کاردان	مصیب دالوند
	حسین کاظمیان	عطیه دربندی
	مرتضی کرمی	راحله حلبیان

حامیان کنگره

- دانشگاه علوم پزشکی تهران
- وزارت بهداشت، درمان و آموزش پزشکی
- موسسه تحقیقات واکسن و سرم سازی رازی
- انستیتو پاستور ایران
- مرکز ملی ذخایر ژنتیکی و زیستی ایران
- سازمان نظام دامپزشکی جمهوری اسلامی ایران
- دانشگاه علوم پزشکی ایلام
- شرکت باریج اسانس
- سازمان صنایع شیر ایران (پگاه)
- مرکز مدیریت بیماریهای واگیر
- **FEMS**(FEDERATION OF EUROPEAN MICROBIOLOGICAL SOCIETIES)

برنامه روزانه

هفدهمین کنگره بین المللی
میکروب شناسی ایران

برنامه سخنرانی‌ها در سالن ابن سینا

سه شنبه ۱۳۹۵/۶/۲

زمان	عنوان سخنرانی	سخنرانان	تخصص
۸:۰۰ الی ۸:۴۵	افتتاحیه		
	قرائت قرآن و سرود ملی جمهوری اسلامی ایران		
	سخنرانی و خوشامدگویی رییس انجمن میکروب شناسی ایران		
	دکتر محمد مهدی فیض آبادی		
	سخنرانی و خوشامدگویی رییس محترم دانشکده پزشکی- دانشگاه علوم پزشکی تهران		
۸:۴۵ الی ۹:۱۰	دکتر سید امیر حسین امامی		
	سخنرانی دبیر علمی کنگره		
	دکتر پژواک خاکی		
۹:۴۵ الی ۱۰:۱۰	HIV vaccine. State of Art	Prof. Joan Joseph Munne	Barcelona University, Spain
۹:۱۰ الی ۹:۳۵	World and European epidemiology (molecular/traditional) of Botulism and tetanus, a review	Prof. Michel-Robert Popoff	Director Anaerobic Bacteria and Botulism (Reference Center) Pasteur Institute, France
۹:۳۵ الی ۱۰:۰۰	Actinomycetes in Antibiotica Research at the Helmholtz Centre for Infection Research	Prof. Joachim Wink	Microbial Strain Collection (MISG), Helmholtz Centre for Infection Research, Braunschweig, Germany
۱۰:۰۰ الی ۱۰:۳۰	پذیرایی و بازدید از پوسترها		
۱۰:۳۰ الی ۱۰:۵۰	اپیدمیولوژی سل در ایران	خانم دکتر مهشید ناصحی	
۱۰:۵۰ الی ۱۱:۱۰	کنترل سل در شرایط کنونی	دکتر محمد رضا مسجدی	
۱۱:۱۰ الی ۱۲:۳۰	پانل مایکوباکتریوم توبرکولوزیس؛ اپیدمیولوژی، تشخیص، مقاومت دارویی TB-HIV		
رئیس پانل: دکتر مهشید ناصحی (دانشیار اپیدمیولوژی، رییس اداره سل و جذام، مرکز مدیریت بیماری‌ها)			
اعضاء پانل: دکتر محمد مهدی فیض آبادی (استاد میکروب شناسی پزشکی، دانشگاه علوم پزشکی تهران)، دکتر عباسعلی ایمانی فولادی (استاد باکتری شناسی پزشکی، دانشگاه علوم پزشکی بقیه الله (عج)، دکتر پیام طبرسی (دانشیار عفونی، دانشگاه علوم پزشکی شهید بهشتی)، دکتر محمدرضا مسجدی (فوق تخصص ریه، استاد دانشگاه علوم پزشکی شهید بهشتی)، دکتر احسان آرین (استادیار، میکروپزشناسی پزشکی، دانشگاه علوم پزشکی مشهد)، دکتر سیامک میراب سمیعی (دکتری بیوتکنولوژی- رییس اداره امور آزمایشگاههای وزارت بهداشت، درمان و آموزش پزشکی)، دکتر نادر مصوری (دانشیار، میکروپزشناسی پزشکی، موسسه رازی کرج)، دکتر شهلا فارسی (آزمایشگاه مرجع سلامت وزارت بهداشت، درمان و آموزش پزشکی)، دکتر کیارش قزوینی (دانشیار میکروپزشناسی پزشکی، دانشگاه علوم پزشکی مشهد)، دکتر سید داور سیادت (استاد، باکتری شناسی پزشکی، انستیتو پاستور ایران)، دکتر پرویز مهاجری (دانشیار میکروب شناسی پزشکی، دانشگاه علوم پزشکی کرمانشاه)			
۱۱:۱۰ الی ۱۱:۲۰	دکتر پیام طبرسی	Mycobacterial infection in HIV infected patients	
۱۱:۲۰ الی ۱۱:۳۰	دکتر کیارش قزوینی	اپیدمیولوژی مولکولی سل	

زمان	عنوان سخنرانی	سخنرانان	تخصص
۱۱:۳۰ الی ۱۱:۴۰	دکتر احسان آربین	روشهای جدید تشخیص سل در آزمایشگاه	
۱۱:۴۰ الی ۱۱:۵۰	دکتر سیامک میراب سمیعی	اعتبار بخشی آزمایشگاه‌های سل کشور	
۱۱:۵۰ الی ۱۲:۰۰	دکتر شهلا فارسی	ایمنی و بهداشت در آزمایشگاههای دید مستقیم و کشت سل	
۱۲:۰۰ الی ۱۲:۱۰	دکتر نادر مصوری	بیماری‌های مایکوباکتریوم در دامپزشکی	
۱۲:۱۰ الی ۱۲:۲۰	دکتر پرویز مهاجری	Distribution of non tuberculous mycobacteria isolated from clinical specimens and identified by PCR-Sequencing method in west of Iran	
۱۲:۲۰ الی ۱۲:۴۰	بحث و تبادل نظر		
۱۲:۴۰ الی ۱۴:۰۰	نماز، نهار و استراحت		
۱۴:۰۰ الی ۱۴:۱۵	An up-dating on sepsis	Dr. Jean-Marc Cavaillon	Director Department of Infection and Epidemiology Pasteur Institute, France
۱۴:۱۵ الی ۱۴:۳۰	نقش ناقلین در ظهور مقاومت آنتی بیوتیکی	دکتر فرشته شاهچراغی	استاد، باکتری شناسی پزشکی، انستیتو پاستور ایران
۱۴:۳۰ الی ۱۶:۰۰	پانل مقاومت های میکروبی و عفونت های بیمارستانی		
رئیس پانل: دکتر فرشته شاهچراغی(استاد، باکتری شناسی پزشکی، انستیتو پاستور ایران) اعضای پانل: Dr. Jean-Marc Cavaillon، دکتر فرشته جبل عاملی (استادیار میکروبیشناسی دانشگاه علوم پزشکی تهران)، دکتر مروت طاهری کلانی (دانشیار باکتری شناسی پزشکی، دانشگاه علوم پزشکی لرستان)، دکتر احمد خورشیدی مال احمدی (استاد، متخصص میکروب شناسی، دانشگاه علوم پزشکی کاشان)، دکتر حسن شجاعی(استاد میکروبیشناسی پزشکی، دانشگاه علوم پزشکی اصفهان)، دکتر داوود یادگاری (استاد متخصص بیماریهای عفونی، استاد دانشگاه علوم پزشکی شهید بهشتی)، دکتر مینوش شعبانی(عضو هیئت علمی بیمارستان لقمان،دانشگاه علوم پزشکی شهید بهشتی)، دکتر مرجان فرزانی(آزمایشگاه مرجع سلامت،وزارت بهداشت)، دکتر طاهرا موسوی(مرکز مدیریت بیماریها ، اداره مقاومت میکروبی،وزارت بهداشت)			
۱۴:۳۰ الی ۱۴:۴۰	دکتر داوود یادگاری	مقاومت آنتی بیوتیکی در عفونت های بیمارستانی	
۱۴:۴۰ الی ۱۴:۵۰	دکتر مینوش شعبانی برزگر	Resistance to antibiotics in N.gonorrhoeae in Iran	
۱۴:۵۰ الی ۱۵:۰۰	دکتر احمد خورشیدی	How can we prevent antibiotic resistance	
۱۵:۰۰ الی ۱۵:۱۰	دکتر مروت طاهری کلانی	Resistance to Acinetobacteria	

عنوان سخنرانی		سخنرانان	تخصص	زمان
Primary Report Of AMR Surveillance In Iran		دکتر طاهای موسوی		۱۵:۲۰ الی ۱۵:۳۰
Drug Resistances in NTM (Non tuberculosis Mycobacterium)		دکتر حسن شجاعی		۱۵:۳۰ الی ۱۵:۴۰
برنامه کشوری مراقبت مقاومت ضد میکروبی، ظرفیت سازی و تقویت شبکه آزمایشگاهی		دکتر مرجان فرزانی		۱۵:۴۰ الی ۱۵:۵۰
بحث و تبادل نظر				۱۶:۰۰ الی ۱۵:۳۰
پذیرایی و بازدید از پوسترها				۱۶:۰۰ الی ۱۶:۳۰
General Manager of Hygiena International Ltd, United Kingdom	Dr. Martin Easter	Rapid Objective Monitoring of Hygiene and Sanitation for Infection Prevention and Control: The Novel ATP Bioluminescence Technology		۱۶:۴۵ الی ۱۶:۳۰
دکترای اپیدمیولوژی رئیس اداره عفونتهای بیمارستانی مرکز مدیریت بیماریهای واگیر وزارت بهداشت	دکتر بابک عشرتی	اپیدمیولوژی عفونتهای بیمارستانی		۱۶:۴۵ الی ۱۷:۰۰
پانل عفونت در بیماران با نقص ایمنی				۱۷:۰۰ الی ۱۸:۳۰
رئیس پانل: دکتر شیرین افهمی (متخصص بیماریهای عفونی، دانشگاه علوم پزشکی تهران، بیمارستان دکتر شریعتی) اعضاء پانل: دکتر آرش سیفی (متخصص بیماریهای عفونی، دانشگاه علوم پزشکی تهران، بیمارستان امام خمینی)، دکتر سید علی دهقان منشادی (متخصص بیماریهای عفونی، استادیار دانشگاه علوم پزشکی تهران)، Dr. Martin Easter، دکتر پیام طبرسی (متخصص بیماریهای عفونی، دانشگاه علوم پزشکی شهید بهشتی، بیمارستان مسیح دانشوری)، دکتر کورس آقازاده (متخصص بیماریهای عفونی دانشگاه علوم پزشکی ارتش)، دکتر محمدرضا صالحی (متخصص بیماریهای عفونی، دانشگاه علوم پزشکی تهران، بیمارستان امام خمینی)				
دکتر شیرین افهمی		اصول پیشگیری از عفونتهای بیمارستانی		۱۷:۰۰ الی ۱۷:۱۰
دکتر علی دهقان منشادی		عفونت در HIV/AIDS		۱۷:۱۰ الی ۱۷:۲۰
دکتر آرش سیفی		میکروبهای شایع در عفونتهای بیمارستانی		۱۷:۲۰ الی ۱۷:۳۰
دکتر محمدرضا صالحی		عفونت های بعد از شیمی درمانی		۱۷:۳۰ الی ۱۷:۴۰
دکتر پیام طبرسی		عفونت در پیوند ارگان solid		۱۷:۴۰ الی ۱۷:۵۰
دکتر کورس آقازاده		عفونت در پیوند مغز استخوان		۱۷:۵۰ الی ۱۸:۰۰
بحث و تبادل نظر				۱۸:۰۰ الی ۱۸:۳۰

زمان	عنوان سخنرانی	سخنرانان	تخصص
چهارشنبه ۱۳۹۵/۶/۳			
هیئت رئیسه: دکتر گیتا اسلامی(استاد- دکترای تخصصی میکروبیولوژی، دانشگاه علوم پزشکی شهید بهشتی)، دکتر فاضل پور احمد (دانشگاه علوم پزشکی ایلام)، دکتر نور امیر مظفری(استاد- دکترای تخصصی میکروپزشکی، دانشگاه علوم پزشکی ایران)، دکتر محمد رهبر(دکتری میکروپزشکی- آزمایشگاه مرجع سلامت)، دکتر روحا کسری کرمانشاهی(استاد، دکترای میکروپزشکی- دانشگاه الزهراء)، دکتر فرامرز مسجدیان (استادیار دانشگاه علوم پزشکی ایران)، دکتر رامین عبیری (دانشیار- دکترای میکروپزشکی پزشکی دانشگاه علوم پزشکی کرمانشاه)			
۸:۳۰ الی ۸:۵۰	Zataria Multiflora Oil As Alternative Herbal Treatment In Management Of Vaginitis In Women	Mohaddese mabhoubi PhD of Microbiology, Barij Essense Pharmaceutical Company	
۸:۵۰ الی ۹:۰۵	Toward the semi-synthesis of new plant-derived antibacterial compounds	Professor Peyman Salehi Professor of Organic Chemistry, Medicinal Plants and Drugs Research Institute, Shahid Beheshti University	
۹:۰۵ الی ۹:۲۰	Nanotechnology approaches for development of novel natural antibacterial products; pros and cons	Dr. Hassan Rafati, Associate Professor of Pharmaceutics, Medicinal Plants and Drugs Research Institute, Shahid Beheshti University	
۹:۲۰ الی ۹:۳۰	How to produce a product from natural sources?	Dr. Mahdi Vazirian, Assistant Professor of Pharmacognosy, school of Pharmacy, Tehran University of Medical Sciences	
۹:۳۰ الی ۹:۴۰	Nanoliposomal Meropenem Enhances Antimicrobial Activity Against Pseudomonas Aeruginosa Isolates	Morteza Milani	
۹:۴۰ الی ۹:۵۰	Ag/Sio2 Co-Doped Fullerene As A Novel Nanosystem For Efficient Photodynamic Inactivation Of Pseudomonas Aeruginosa Biofilm	Esmail Darabpour	
۹:۵۰ الی ۱۰:۰۰	بحث و تبادل نظر		
۱۰:۰۰ الی ۱۰:۳۰	پذیرایی و بازدید از پوسترها		
۱۰:۳۰ الی ۱۰:۴۵	Occurrence of Pasteurellaceae in domestic/wildlife animals in Europe and the potential raised risks to human population	Prof Anders Miki Bojesen	Head of Section for Clinical Veterinary Microbiology, Faculty of Health and Medical Sciences, University of Copenhagen, Denmark
۱۰:۴۵ الی ۱۱:۰۰	Role of molecular diagnostic in medical bacteriology	دکتر امیر هوشنگ الوندی	دانشگاه علوم پزشکی کرمانشاه

زمان	عنوان سخنرانی	سخنرانان	تخصص
۱۱:۰۰ الی ۱۲:۳۰	پانل تشخیص ، تایپینگ و اپیدمیولوژی بیماریهای عفونی		
رئیس پانل: دکتر سهیلا مرادی بید هندی (دانشیار، متخصص میکروب شناسی، موسسه تحقیقات واکسن و سرم سازی) اعضاء پانل: Prof Anders Miki Bojesen، دکتر غلامرضا ایرجیان (دانشیار، دانشگاه علوم پزشکی ایران) ، دکتر امیر هوشنگ الوندی (استاد دانشگاه علوم پزشکی کرمانشاه)، دکتر نورخدا صادقی فرد (استاد دانشگاه علوم پزشکی ایلام)، دکتر مجید زارع بیدکی (میکروب شناسی، استاد دانشگاه علوم پزشکی بیرجند) ، دکتر احسان الله غزنوی راد (استاد دانشگاه علوم پزشکی اراک)، دکتر رایناک قادری (هیئت علمی موسسه تحقیقات واکسن و سرم سازی رازی)، دکتر رضا رنجبر (استاد دانشگاه علوم پزشکی بقیة الله (عج))			
۱۱:۰۰ الی ۱۱:۱۰	دکتر ایرج پاکزاد	تشخیص بروسلوز	
۱۱:۱۰ الی ۱۱:۲۰	دکتر احسان الله غزنوی راد	Frequency of bacterial agents associated with dysentery at central iran:its time to seek the campylobacter	
۱۱:۲۰ الی ۱۱:۳۰	دکتر فرامرز مسجدیان	بروسلوز در ایران	
۱۱:۳۰ الی ۱۱:۴۰	دکتر نورخدا صادقی فرد	Applications of MALDI-TOF mass spectrometry for identification of pathogenic bacteria and detection of antibiotic resistance	
۱۱:۴۰ الی ۱۱:۵۰	دکتر رایناک قادری	Genotyping schemes in "Evolutionary Studies" & "Epidemiological Surveillance" of Salmonella enterica; present and future	
۱۱:۵۰ الی ۱۲:۰۰	دکتر کامبیز ورمیرا	کاربرد اپتامرها در تشخیص بیماری های عفونی	
۱۲:۰۰ الی ۱۲:۱۰	دکتر مجید زارع بیدکی	یادگیری الکترونیکی میکروپزشناسی پزشکی: از کتاب الکترونیکی تا آزمایشگاه مجازی	
۱۲:۱۰ الی ۱۲:۲۰	دکتر رضا رنجبر	ملاحظات،الزامات و چالش های پیش رو در مسیر استفاده و بکارگیری صحیح روش های تایپینگ ملکولی باکتری ها	
۱۲:۲۰ الی ۱۲:۴۰	بحث و تبادل نظر		
۱۲:۴۰ الی ۱۴:۰۰	نماز، نهار و استراحت		
۱۴:۰۰ الی ۱۴:۱۵	Pre-clinical development of recombinant BCG based HIV-TB pediatric vaccine: Challenges and failures	Prof. Joan Joseph Munne	Barcelona University, Spain
۱۴:۱۵ الی ۱۴:۳۰	Leptospiral vaccines	Prof. Yung-Fu Chang	Director, Infectious Disease Research Laboratory Department of Population Medicine and Diagnostic Sciences, New York, USA

زمان	عنوان سخنرانی	سخنرانان	تخصص
۱۴:۳۰ الی ۱۶:۰۰	پانل واکسن های باکتریایی		
رئیس پانل: دکتر سید داور سیادت (استاد، باکتری شناسی پزشکی، انستیتو پاستور ایران) اعضاء پانل: Prof. Yung-Fu Chang، دکتر پرویز اولیا (استاد متخصص میکروب شناسی، دانشگاه شاهد)، Prof. Joan Joseph Munne، دکتر مجتبی نوفلی (استادیار، موسسه سرم سازی رازی)، دکتر سیما رافتی (استاد، انستیتو پاستور ایران)، دکتر حسین ذوالفقاریان (دانشیار، موسسه تحقیقات واکسن و سرم سازی رازی)، دکتر احمد رضا جباری (دانشیار، موسسه تحقیقات واکسن و سرم سازی رازی)، دکتر فرزاد وزیری (استادیار ، باکتری شناسی، انستیتو پاستور ایران)			
۱۴:۴۰ الی ۱۴:۴۰	دکتر سید داور سیادت	Outer membrane vesicle or extra membrane vesicle: vaccine or adjuvant	
۱۴:۴۰ الی ۱۴:۵۰	دکتر مجتبی نوفلی	A novel vaccine candidate against B.pertussis	
۱۴:۵۰ الی ۱۵:۰۰	دکتر حسین ذوالفقاریان	Humoral Immune response to Nanoparticle containing diphtheria and tetanus toxoids by internasal administration	
۱۵:۰۰ الی ۱۵:۱۰	دکتر احمد رضا جباری	Current status of conventional and molecular vaccines against Pasteurella infections in animals	
۱۵:۱۰ الی ۱۵:۲۰	دکتر آرش قلیانچی لنگرودی	Full-length characterization of S1 gene of three types of 793/B Avian infectious Bronchitis commercial vaccines	
۱۵:۲۰ الی ۱۵:۳۰	دکتر فرزاد وزیری	Review on the novel vaccine candidates for tuberculosis	
۱۵:۳۰ الی ۱۶:۰۰	بحث و تبادل نظر		
۱۶:۰۰ الی ۱۶:۳۰	پذیرایی و بازدید از پوسترها		
۱۶:۳۰ الی ۱۶:۴۵	Clostridial diseases and vaccines, a veterinary perspective	Prof. Michel-Robert Popoff	Director Anaerobic Bacteria and Botulism (Reference Center) Pasteur Institute, France
۱۶:۴۵ الی ۱۷:۰۰	Fusion of Clostridiumperfringens type D epsilon toxin gene and Clostridium septicum alpha toxin gene and its cloning in E. coli	دکتر رضا پیله چیان لنگرودی	استادیار، متخصص ژنتیک ملکولی ، عضو هیات علمی موسسه تحقیقات واکسن و سرم سازی

زمان	عنوان سخنرانی	سخنرانان	تخصص
۱۷:۰۰ الی ۱۸:۳۰	پانل باکتری های بی هوازی		
رئیس پانل: دکتر رضا پیله چیان (استادیار، متخصص میکروب شناسی، عضو هیات علمی موسسه تحقیقات واکسن و سرم سازی) اعضاء پانل: Prof. Michel-Robert Popoff, دکتر اشرف محبتی مبارز (میکروب شناسی، دانشیار دانشگاه تربیت مدرس) ، دکتر مهرداد شمس الدینی (متخصص کلینیکال پاتولوژی، عضو هیات علمی موسسه تحقیقات واکسن و سرم سازی رازی) ، دکتر محمد تقی اخی (مرکز تحقیقات ایمنو لوژی، دانشگاه علوم پزشکی تبریز)، دکتر عباس بهادر (دانشیار، میکروب شناسی پزشکی، دانشگاه علوم پزشکی تهران)، دکتر فیروز ابراهیمی (استادیار بیوشیمی پزشکی، دانشگاه امام حسین(ع))، دکتر بهرام گلستانی ایمانی (استادیار دانشگاه آزاد اسلامی واحد ارومیه)			
۱۷:۱۰ الی ۱۷:۲۰	دکتر اشرف مبارز	The application of anaerobic bacteria in cancer therapy	
۱۷:۲۰ الی ۱۷:۳۰	دکتر محمد تقی اخی	Detection of enterotoxigenic and antibiotic susceptibility of Bacteroides fragilis isolates in diarrheic feces of children	
۱۷:۳۰ الی ۱۷:۴۰	دکتر مهرداد شمس الدینی	Molecular survey of Clostridium perfringens type Atoxins	
۱۷:۴۰ الی ۱۷:۴۵	دکتر فیروز ابراهیمی	Overview of the one decay study on botulinum neurotoxin vaccines in Iran	
۱۷:۴۵ الی ۱۷:۵۰	سپیده خداپرست	Detection Of Toxigenic Clostridium difficile In Colitis Patients Stool By Real Time PCR	
۱۷:۵۰ الی ۱۸:۰۰	دکتر بهرام گلستانی ایمانی	An investigation of the effect of copper oxide and silver nanoparticles on anaerobic bacteria genome by RAPD molecular markers	
۱۸:۰۰ الی ۱۸:۱۰	معصومه عظیمی راد	Evaluation And Comparison Of Concentration And Cultivation Methods For Detection Of Clostridium perfringens Spores In Water Samples	
۱۸:۱۰ الی ۱۸:۲۰	دکتر کسری اسماعیل نیا	Fasciolidosis and Cysticercosis, necrotic parasites of sheep liver and their relation with Black Disease due to Clostridium novyi	
۱۸:۲۰ الی ۱۸:۳۰	بحث و تبادل نظر		
پنج شنبه ۱۳۹۵/۶/۴			
۸:۰۰ الی ۸:۱۵	The current state of important zoonotic disease in human in IRAN	دکتر محمد شیرزادی	متخصص عفونی، مرکز مدیریت بیماری های واگیر وزارت بهداشت و درمان
۸:۱۵ الی ۸:۳۵	Gallibacterium anatis in poultry and other potential hosts, a review	Prof Anders Miki Bojesen	Head of Section for Clinical Veterinary Microbiology, Faculty of Health and Medical Sciences, University of Copenhagen, Denmark

زمان	عنوان سخنرانی	سخنرانان	تخصص
۸:۳۵ الی ۱۰:۰۰	پانل بیماری های مشترک انسان و دام (زئونوز ها)		
رئیس پانل: دکتر تقی زهرایی صالحی(استاد، متخصص میکروب شناسی دامپزشکی ، دانشگاه تهران) اعضاء پانل:دکتر محمد شیرزادی (متخصص عفونی، مرکز مدیریت بیماری‌های واگیر وزارت بهداشت و درمان)، دکتر محمدرضا محزونیه(استاد میکروب شناسی، دانشکده دامپزشکی دانشگاه علوم پزشکی شهرکرد)، Prof Anders Miki Bojesen ، دکتر نادر مصوری (دانشیار، متخصص میکروب شناسی، موسسه تحقیقات واکسن و سرم سازی)، دکتر داریوش جهان پیمان (دکتری دامپزشکی، مدیر کل دفتر بهداشت و مدیریت بیماریهای دامی سازمان دامپزشکی کشور) ، دکتر کسری اسماعیل نیا (استادیار، انگل شناسی ، موسسه تحقیقات واکسن و سرم سازی) ، دکتر ناصر هرزندی (دانشیار میکروب شناسی، دانشگاه آزاد اسلامی ، واحد کرج)، دکتر حسام الدین اکبرین (استادیار اپیدمیولوژی دانشکده دامپزشکی دانشگاه تهران)			
۸:۳۵ الی ۸:۴۵	دکتر داریوش جهان پیمان	The current state of important zoonotic disease in animals in IRAN	
۸:۴۵ الی ۸:۵۵	دکتر نادر مصوری	Glanders in IRAN, new strategies in control and eradication schemes	
۸:۵۵ الی ۹:۰۵	دکتر کسری اسماعیل نیا	Canine Leishmaniasis: a spreading disease in Alborz province and necessity of a fast detection method	
۹:۰۵ الی ۹:۱۵	دکتر سامد برومند فر	An overview of current state and recent outbreaks of Glanders in IRAN	
۹:۱۵ الی ۹:۲۵	دکتر پیمان کیهانی	Molecular Detection and Genotyping of Chlamydia psittaci in Captive Psittacines and their owners from Isfahan (Iran)	
۹:۲۵ الی ۹:۳۵	دکتر روح الله کشاورز	Development and optimization a high sensitive and specific ELISA system for rapid detection of Brucella in cattle	
۹:۳۵ الی ۹:۴۵	دکتر رامین باقری نژاد	"Extraction and Characterization of Brucella abortus Strain RB51 Rough Lipopolysaccharide"	
۹:۴۵ الی ۱۰:۰۰	بحث و تبادل نظر		
۱۰:۰۰ الی ۱۰:۳۰	پذیرایی و بازدید از پوستر ها		
۱۰:۳۰ الی ۱۰:۴۵	بیماری های نوپدید و بازپدید و اهمیت آن ها در دنیا	دکتر محمد مهدی گويا	متخصص بیماری‌های عفونی، مرکز مدیریت بیماری‌های واگیر
۱۰:۴۵ الی ۱۱:۰۰	Lumpy Skin Disease in South Africa: Current outbreaks, diagnoses, control and research	Dr. Baratang Alison Lubisi	Onderstepoort Veterinary Institute

زمان	عنوان سخنرانی	سخنرانان	تخصص
۱۱:۰۰ الی ۱۲:۳۰	پانل بیماری های نو پدید و باز پدید		
رئیس پانل: محمد مهدی گویا (متخصص بیماری های عفونی، مرکز مدیریت بیماری های واگیر) اعضاء پانل: دکتر طلعت مختاری آزاد (استاد، متخصص ویروس شناسی دانشگاه علوم پزشکی تهران)، Dr. Baratang Alison Lubisi، دکتر آرش آرش کیا (دانشیار، متخصص ویروس شناسی، رئیس بخش ویروس شناسی انستیتو پاستور ایران) ، دکتر قاسم رضائیان زاده (دامپزشک، متخصص طیور، معاون بهداشتی سازمان دامپزشکی کشور)، دکتر سیامک مسعودی (کارشناس سازمان حفاظت محیط زیست)، دکتر احسان مصطفوی (دانشیار، متخصص اپیدمیولوژی، رئیس پایگاه تحقیقاتی بیماری های نوپدید و بازپدید، انیستیتو پاستور ایران) ، دکتر محمد خلیلی (دامپزشک، میکروب شناس، دانشکده دامپزشکی دانشگاه کرمان) ، دکتر مصطفی صالحی وزیری (متخصص ویروس شناسی، رئیس بخش آروبیرویس انستیتو پاستور ایران)			
۱۱:۰۰ الی ۱۱:۱۰	دکتر طلعت مختاری آزاد	مروری بر آخرین وضعیت بیماری آنفلوانزا در ایران	
۱۱:۱۰ الی ۱۱:۲۰	دکتر احسان مصطفوی	مروری بر آخرین وضعیت بیماری های نوپدید و بازپدید مهم در ایران	
۱۱:۲۰ الی ۱۱:۳۰	دکتر آرش آرش کیا	مروری بر آخرین وضعیت زیکاویروس در ایران	
۱۱:۳۰ الی ۱۱:۴۰	دکتر قاسم رضائیان زاده	مخاطرات و ارزیابی بیماری های دامپزشکی فرامرزی	
۱۱:۴۰ الی ۱۱:۵۰	دکتر مصطفی صالحی وزیری	مروری بر آخرین وضعیت بیماری تب خونریزی دهنده کریمه کنگو در ایران	
۱۱:۵۰ الی ۱۲:۰۰	دکتر محمد خلیلی	مروری بر مطالعات انجام شده تب کیو در ایران	
۱۲:۰۰ الی ۱۲:۱۰	دکتر سیامک مسعودی	مروری بر وضعیت طاعون نشخوارکنندگان و تب برفکی در حیات وحش کشور	
۱۲:۱۰ الی ۱۲:۳۰	بحث و تبادل نظر		
۱۲:۳۰	اختتامیه		
۱۲:۳۰ الی ۱۲:۴۰	گزارش دبیر اجرایی پیرامون نحوه انجام کنگره هفدهم		

سالن فرعی (عزالت)

سه شنبه ۱۳۹۵/۶/۲

زمان	عنوان سخنرانی	سخنران	تخصص
۱۰:۳۰ الی ۱۰:۴۵	An update on human epidemiology of anthrax in the Iranian territory	دکتر محمد شیرزادی	مرکز مدیریت بیماریهای واگیر وزارت بهداشت و درمان
۱۱:۰۰ الی ۱۰:۴۵	Bacillus anthracis Sterne 34F2, the Max Sterne heritage for the world	Dr. Baratang Alison Lubisi	Onderstepoort Veterinary Institute
پانل باسیلوس آنتراسیس و سیاه زخم			۱۱:۰۰ الی ۱۲:۳۰
رئیس پانل: دکتر کیوان تدین (دانشیار، میکروپزشکی، موسسه تحقیقاتی واکسن و سرم سازی رازی)			
اعضاء پانل: Dr. Baratang Alison Lubisi، دکتر تقی محمد پور فرامی (کمیسیون خلع سلاح وزارت امور خارجه)، دکتر مراد مرادی گراوند (سازمان دامپزشکی ایران)، دکتر مسعود غفاری (وزارت امور خارجه)، دکتر ابوالفضل خفری (استادیار، میکروپزشکی، موسسه تحقیقاتی واکسن و سرم سازی رازی)، دکتر بیتا بخشی (استاد، دانشگاه تربیت مدرس)			
۱۱:۱۰ الی ۱۱:۳۰	دکتر کیوان تدین	Population genetic of Bacillus anthracis in Iran	
۱۱:۳۰ الی ۱۱:۴۰	دکتر تقی محمد پور	The Biological Weapons Convention (BWC) , Past, present and future of an international treaty succeeding the 1925 Geneva protocol	
۱۱:۴۰ الی ۱۱:۵۰	دکتر مراد مرادی گراوند	Epizootological Survey of Anthrax in Persia, an OIE-expert's perspective	
۱۱:۵۰ الی ۱۲:۰۰	دکتر مسعود غفاری	Biological Weapons and weaponization of biologicals, the Iranian stand	
۱۲:۰۰ الی ۱۲:۱۰	دکتر ابوالفضل خفری	Razi Anthrax spore vaccine, how a good vaccine brings a monster under control	
۱۲:۱۰ الی ۱۲:۳۰	دکتر بیتا بخشی	Microbiology of B. anthracis, what makes Ba a perfect killer	
۱۲:۳۰ الی ۱۲:۴۰	دکتر سید رضا بنی هاشمی	Non-spore vaccines against Anthrax	
بحث و تبادل نظر			۱۲:۴۰ الی ۱۳:۳۰
نماز ، نهار و استراحت			
۱۳:۳۰ الی ۱۴:۰۰	ارتقاء کیفیت در آزمایشگاههای کنترل غذا، استانداردها و منابع خطا	دکتر ناهید رحیمی فرد	دکتری تخصصی میکروپزشکی
۱۴:۰۰ الی ۱۴:۳۰	تغییرات در نتایج آزمون و عدم قطعیت در روشهای شمارش میکروپزشکی	دکتر شیلا صفائیان	دکتری تخصصی میکروپزشکی

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۱۴:۳۰ الی ۱۶:۰۰	پانل میکروب شناسی مواد غذایی و آشامیدنی		
رئیس پانل: دکتر ناهید رحیمی فرد (دانشیار، دکتری تخصصی میکروب شناسی، سازمان غذا و دارو و رئیس بخش میکروبیولوژی مرکز آزمایشگاه‌های مرجع کنترل غذا و دارو ، وزارت بهداشت درمان آموزش پزشکی)			
اعضاء پانل: دکتر مسعود آل بویه (استادیار، دکتری میکروب شناسی پزشکی، پژوهشکده گوارش و کبد، مرکز تحقیقات بیماری های منتقله از آب و غذا، تهران)، دکتر سهیل اسکندری (دانشیار، دکترای تخصصی بهداشت و کنترل مواد غذایی، سازمان غذا و دارو)، دکتر شهریار دبیریان (استادیار، دکترای تخصصی کنترل کیفیت و بهداشت مواد غذایی، صنایع شیر ایران)، دکتر شیلا صفانیان (دانشیار، دکترای تخصصی میکروبی‌شناسی، دانشگاه آزاد اسلامی تهران واحد شمال)، دکتر بابک پوراکبری (استادیار، دکتری تخصصی میکروب شناسی، مرکز تحقیقات بیماری‌های عفونی دانشگاه علوم پزشکی تهران)، دکتر نسرين حاجی سیدجوادی (دکترای علوم آزمایشگاهی، انستیتو تحقیقات تغذیه ای و صنایع غذایی کشور، دانشگاه علوم پزشکی شهید بهشتی)، دکتر مهدی رئیسی (دانشیار، دکترای تخصصی بهداشت، دانشگاه آزاد اسلامی شهرکرد)، دکتر امیر رحیمی راد (دکترای تخصصی بهداشت مواد غذایی، دانشگاه علوم پزشکی آذربایجان غربی)، دکتر مریم تاج آبادی ابراهیمی (دانشیار، رئیس انجمن پروبیوتیک ،دانشگاه آزاد اسلامی تهران واحد مرکز)			
۱۴:۳۰ الی ۱۴:۴۰	دکتر امیر رحیمی راد	بررسی آلودگی میکروبی فرآورده‌های غذایی تهیه شده به روش سنتی در طی سالهای ۱۳۹۴ و ۱۳۹۵	
۱۴:۴۰ الی ۱۴:۵۰	دکتر مهدی رئیسی	شناسایی ژنهای ویروالانس <i>آئروموناس هیدروفیلا</i> جدا شده از ماهی و میگو	
۱۴:۵۰ الی ۱۵:۰۰	دکتر شهریار دبیریان	شناسایی فلور کپکی در شیر خام دامداری های استان تهران	
۱۵:۰۰ الی ۱۵:۱۰	دکتر ناهید رحیمی فرد	استانداردهای ملی ایران در زمینه میکروبیولوژی مواد غذایی و آشامیدنی	
۱۵:۱۰ الی ۱۵:۲۰	دکتر بابک پوراکبری	روشهای استاندارد کنترل فرآورده های پروبیوتیک	
۱۵:۲۰ الی ۱۵:۳۰	دکتر مریم تاج آبادی ابراهیمی	کاربرد باکتریهای اسیدلاکتیک در کاهش آفاتوکسین	
۱۵:۳۰ الی ۱۶:۰۰	بحث و تبادل نظر		
پذیرایی و بازدید از پوسترها			
چهارشنبه ۱۳۹۵/۶/۳			
هیئت رئیسه: دکتر آذر دخت خسروی (دانشیار -دکتری تخصصی میکروبی‌شناسی بالینی دانشگاه علوم پزشکی جندی شاپور)، دکتر هادی پیری دوگاهه (دانشیار - دکتری باکتری شناسی دانشگاه علوم پزشکی اردبیل)، دکتر علیشاکیا (دانشیار - دکتری میکروب شناسی دانشگاه علوم پزشکی کرمانشاه)، دکتر علی مجتهدی (استادیار - دکتری تخصصی میکروب شناسی دانشگاه علوم پزشکی گیلان)، دکتر ایرج نیکوکار (دانشیار - دکتری میکروب شناسی دانشگاه علوم پزشکی گیلان)، دکتر غلامرضا هاشمی تبار (دانشیار -دانشگاه فردوسی)، دکتر حسین دبیری (دانشیار - دکتری میکروب شناسی - دانشگاه علوم پزشکی شهید بهشتی)، دکتر سمیه یسلیانی (فرد) (استادیار - دکتری تخصصی باکتری شناسی دانشگاه علوم پزشکی البرز)			
۸:۳۰ الی ۸:۴۰	Genetic Analysis Of Plasmodium Falciparum Thrombospondin Related Adhesive Protein As A Malaria Vaccine Candidate Antigen	Azadeh Jafaryzadeh	
۸:۴۰ الی ۸:۵۰	Cloning, Expression And Purification Of Recombinant Hmw1, Hmw2, And Hia As A Fusion Protein For Vaccine Candidate Of Nontypeable Haemophilus Influenzae	Ghasem Abbaszadeh-Goudarzi	

زمان	عنوان سخنرانی	سخنران	تخصص
۹:۰۰ تا ۸:۵۰	Enhancement Of Hiv-1 Protein Vaccination Using Cell Penetrating Peptides	Somayeh Kadkhodayan	
۹:۱۰ الی ۹:۰۰	Il 27,Il12,Tgf-Beta,Vegf Genes Analysis Of Canser Bearing C57bl/6mice After Vaccination With Flic_E7d &E7d Vaccines	Behazin Aria	
۹:۲۰ الی ۹:۱۰	Clonig Of Mutant Escherichia Coli Phytase(R92k)By Site Directed Mutagenesis	Zeinab Alssadat Ahmadi	
۹:۳۰ الی ۹:۲۰	Construction Of Recombinant Fusion Fimch Protein As Immunogen Candidate Against Urinary Tract Infection	Robab Mollamehalizade	
۹:۴۰ الی ۹:۳۰	Genomic Characterization Of Bordetella Pertussis 0134, A Vaccine Strain With Historic Values	Farnaz Boroumand	
۹:۵۰ الی ۹:۴۰	Immunological Effect Of Recombinant Protein Of Helicobacter Pylori In Functional Of Peritoneal Macrophages	Neda Soleimani	
۹:۵۰ الی ۱۰:۰۰	بحث و تبادل نظر		
۱۰:۰۰ الی ۱۰:۳۰	پذیرایی و بازدید از پوسترها		
۱۰:۳۰ الی ۱۰:۴۵	اثر <i>Porphyromonas gingivalis</i> در به انحراف کشاندن سیستم ایمنی میزبان	دکتر ماندانا ستاری	استاد، دانشگاه علوم پزشکی شهید بهشتی
۱۱:۰۰ الی ۱۰:۴۵	میکروبیولوژی در اندودنتیکس	دکتر هنگامه اخوان	استادیار اندودانتیکس، دانشگاه آزاد اسلامی
۱۱:۰۰ الی ۱۲:۳۰	پانل میکروبیولوژی دهان		
رئیس پانل:دکتر ماندانا ستاری (استاد، دانشگاه علوم پزشکی شهید بهشتی)			
اعضاء پانل:دکتر هنگامه اخوان (استادیار اندودانتیکس، دانشگاه آزاد اسلامی)، دکتر محسن افکار (استادیار اندودانتیکس، دانشگاه آزاد اسلامی)، دکتر شیده مهرمفخم (عضو هیأت علمی، دانشگاه علوم پزشکی شهید بهشتی)			
۱۱:۱۰ الی ۱۱:۰۰	دکتر محسن افکار	بررسی نقش درجات مختلف پوسیدگی دندان و میکروارگانیسمهای مربوطه در بیان TLR4 و TLR2 در پالپ دندان	
۱۱:۲۰ الی ۱۱:۱۰	دکتر شیده مهرمفخم	بررسی رابطه میان CD14 محلول دهان به عنوان یکی از پذیرنده های LPS با مرگ نوتروفیل ها	
۱۱:۳۰ الی ۱۱:۲۰	دکتر سریرا شهنواز	بررسی رابطه میان حاصل از پاتوژن های پرپروتئوپاتییک TLR2 و Cross talk و CXCL4 با پرپروتئیت مزمن	
۱۱:۴۰ الی ۱۱:۳۰	آناهیتا فولاد زاده	مقایسه پرپروتئیت مزمن و لته سالم از نظر بیان ژن HSP70	
۱۱:۵۰ الی ۱۱:۴۰	دکتر علی سعیدی	بررسی رابطه میان میزان بیان ژن TLR5 به عنوان مهمترین گیرنده فمبری و RANKL در بافت لته با بیماری پرپروتئال	
۱۱:۵۰ الی ۱۲:۰۰	دکتر شقایق پزشکی	Moesin، مولکول جدید در شناسایی LPS	
۱۲:۰۰ الی ۱۲:۳۰	بحث و تبادل نظر		
۱۲:۳۰ الی ۱۴:۰۰	نماز، نهار و استراحت		

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۱۴:۰۰ الی ۱۴:۲۰	نقش انترتوکسین B در درمان سرطان ها	دکتر عباسعلی ایمانی فولادی	استاد باکتری شناسی پزشکی ، مرکز تحقیقات میکروبیولوژی کاربردی، دانشگاه علوم پزشکی بقیه الله (عج)
۱۴:۲۰ الی ۱۴:۴۰	کاربرد اگزوزوم های میکروبی در طراحی واکسن	دکتر حمیده محمودزاده حسینی	استادیار، مرکز تحقیقات میکروبیولوژی کاربردی، دانشگاه علوم پزشکی بقیه الله (عج)
پانل نقش متابولیت های میکروبی در درمان			۱۴:۴۰ الی ۱۶:۰۰
رئیس پانل: دکتر عباسعلی ایمانی فولادی(استاد باکتری شناسی پزشکی، مرکز تحقیقات میکروبیولوژی کاربردی، دانشگاه علوم پزشکی بقیه الله (عج))			
اعضاء پانل: دکتر حمیده محمودزاده حسینی (استادیار، مرکز تحقیقات میکروبیولوژی کاربردی، دانشگاه علوم پزشکی بقیه الله) ، دکتر راحله حلبیان (استادیار، مرکز تحقیقات میکروبیولوژی کاربردی، دانشگاه علوم پزشکی بقیه الله) ، دکتر پروانه صفاریان (استادیار تهران، دانشگاه علوم پزشکی آزاد اسلامی، واحد پزشکی)، دکتر جعفر سلیمیان (دانشیار، مرکز تحقیقات آسیب های شیمیایی، دانشگاه علوم پزشکی بقیه الله (عج)، دکتر الناز مهدی زاده اقدم (استادیار، دانشکده داروسازی، دانشگاه علوم پزشکی تبریز)			
۱۴:۴۰ الی ۱۴:۵۰	دکتر راحله حلبیان	مقاوم سازی سلول های بنیادی با استفاده از متابولیت های میکروبی به منظور سلول درمانی	
۱۴:۵۰ الی ۱۵:۰۰	دکتر جعفر سلیمیان	واکنش سیستم ایمنی به داروهای با پایه متابولیت های میکروبی در درمان	
۱۵:۰۰ الی ۱۵:۱۰	دکتر الناز مهدی زاده اقدم	رایوسوئیچ ها هدفی جدید برای طراحی آنتی بیوتیک ها	
۱۵:۱۰ الی ۱۵:۲۰	دکتر پروانه صفاریان	کاربرد متابولیت های میکروبی، تحول در محصولات آرایشی	
۱۵:۲۰ الی ۱۵:۳۰	دکتر جعفر سلیمیان	نقش درمانی توکسین بوتولینوم (ساختمان و عملکرد)	
۱۵:۳۰ الی ۱۶:۰۰	بحث و تبادل نظر		
پذیرایی و بازدید از پوسرها			۱۶:۰۰ الی ۱۶:۳۰
پنج شنبه ۹۵/۶/۴			
۸:۰۰ الی ۸:۲۰	نظام مراقبت منزلت در کشور	دکتر محسن زهرایی	دانشیار مرکز مدیریت بیماریهای وزارت بهداشت و درمان
۸:۲۰ الی ۸:۴۰	Clinical Aspects of Acute Bacterial Meningitis	دکتر سید علیرضا فهیم زاد	دانشیار مرکز تحقیقات عفونی اطفال دانشگاه علوم پزشکی شهید بهشتی

زمان	عنوان سخنرانی	سخنران	تخصص
۱۸:۴۰ الی ۱۰:۰۰	پانل مننژیت میکروبی		
رئیس پانل: دکتر سید فضل ا... موسوی(دانشیار انستیتو پاستور ایران) اعضاء پانل: دکتر محسن زهرایی (دانشیار مرکز مدیریت بیماریهای وزارت بهداشت و درمان)، دکتر سید علیرضا فهیم زاد(دانشیار مرکز تحقیقات عفونی اطفال دانشگاه علوم پزشکی شهید بهشتی)، دکتر عبدا... کریمی (استاد دانشگاه علوم پزشکی ایران) دکتر سید علیرضا سید صیام دوست (استادیار دانشگاه علوم پزشکی ایران)دکترمحمد درویشی(دانشیاردانشگاه علوم پزشکی ارتش)، دکترسیروس جعفری (دانشیار بخش عفونی بیمارستان امام خمینی، دانشگاه علوم پزشکی تهران)، دکتر افرا خسروی(استاد دانشگاه علوم پزشکی ایلام) ، دکتر رمضانعلی عطایی کچویی (استاد ،گروه میکروب شناسی، دانشگاه علوم پزشکی بقیه الله (عج)			
۸:۴۰ الی ۸:۵۰	دکترسیروس جعفری	Treatment of acute bacterial meningitis	
۸:۵۰ الی ۹:۰۰	دکترمحمد درویشی	Meningitis and meningococcal vaccines	
۹:۰۰ الی ۹:۱۰	دکتر افرا خسروی	Interaction of Meningitis and Immunity	
۹:۱۰ الی ۹:۲۰	دکتر سید علیرضا سید صیام دوست	“Timing and Decision Making in Secured Air way Establishment of patients with Meningitis Admitted to ICU”	
۹:۲۰ الی ۹:۳۰	دکتر رمضانعلی عطایی کچویی	Post Antibiotic world: What we need for?	
۹:۳۰ الی ۱۰:۰۰	بحث و تبادل نظر		
۱۰:۰۰ الی ۱۰:۳۰	پذیرایی و بازدید از پوستر ها		

سالن فرعی (طب تجربی)

سه شنبه ۱۳۹۵/۶/۲

زمان	عنوان سخنرانی	سخنرانان	تخصص
۱۰:۳۰ الی ۱۰:۴۵	نقش پپتید های زیست فعال تولید شده توسط پروبیوتیک ها در غذاهای تخمیری	دکتر سید سعید میردامادی	رییس پژوهشکده زیست فناوری سازمان پژوهش های علمی و صنعتی
۱۰:۴۵ الی ۱۱:۰۰	کاربرد و مکانیسم اثر پروبیوتیک ها در درمان چاقی	دکتر محمد هادی اسکندری	دانشیار دانشگاه علوم پزشکی شیراز
۱۱:۰۰ الی ۱۲:۳۰	پانل پروبیوتیک		
رئیس پانل: دکتر شهریار دبیریان (دکترای تخصصی کنترل کیفیت و بهداشت مواد غذایی، صنایع شیر ایران) اعضا پانل: دکتر میردامادی (رییس پژوهشکده زیست فناوری سازمان پژوهش های علمی و صنعتی)، دکتر محمد هادی اسکندری (دانشیار دانشگاه علوم پزشکی شیراز)، دکتر ناهید رحیمی فرد (دانشیار، دکتری تخصصی میکروپزشناسی، سازمان غذا و دارو و رئیس بخش میکروبیولوژی مرکز آزمایشگاه های مرجع کنترل غذا و دارو، وزارت بهداشت درمان آموزش پزشکی)، دکتر مریم تاج آبادی (دکتری میکروبیولوژی، استادیار دانشگاه آزاد اسلامی، دپارتمان بیولوژی)، دکتر ناهید مژگانی (دانشیار موسسه تحقیقات واکنش و سرم سازی رازی)، دکتر سهیل اسکندری (معاونت فنی مدیر کل نظارت بر مواد غذایی اشامیدنی و بهداشتی سازمان غذا و دارو)			
۱۱:۰۰ الی ۱۱:۱۰	دکتر ناهید رحیمی فرد	Probiotic effects on cancer stages	
۱۱:۱۰ الی ۱۱:۲۰	مهندس مژگان حیدرپور	مروری بر استاندارد های ملی و بین المللی پروبیوتیک ها و چالش های موجود در تولید محصولات	
۱۱:۲۰ الی ۱۱:۳۰	دکتر مجتبی زاغری	نقش و اهمیت پروبیوتیک ها در هضم خوراک	
۱۱:۳۰ الی ۱۱:۴۰	دکتر پروانه جعفری	نقش پروبیوتیک در کنترل حملات صرعی القا شده توسط PTZ	
۱۱:۴۰ الی ۱۱:۵۰	دکتر ناهید مژگانی	Virulence genes and invivo safety analysis of probiotic bacteria	
۱۱:۵۰ الی ۱۲:۰۰	دکتر مهدی شکرابی	نقش میکروبیوتا در ایمون تولرانس لوله گوارشی (از پاتوژن تا کاربرد بالینی)	
۱۲:۰۰ الی ۱۲:۳۰	بحث و تبادل نظر		
۱۲:۳۰ الی ۱۴:۰۰	نماز، نهار و استراحت		
۱۴:۰۰ الی ۱۴:۱۵	جدیدترین پرتکل تشخیص و درمان بیماریهای منتقله از راه تماسجنسی وزارت بهداشت	دکتر حمید عمادی کوچک	دانشیار بیماریهای عفونی و گرمسیری، دانشگاه علوم پزشکی تهران ،عضو کمیته کشوری وزارت بهداشت و درمان
۱۴:۱۵ الی ۱۴:۳۰	اپیدمیولوژی ایدز و بیماریهای منتقله از راه جنسی در ایران	دکتر پروین افسر کازرونی	متخصص پزشکی اجتماعی ، مسئول اداره ایدز و بیماریهای آمیزشی وزارت بهداشت و درمان

زمان	عنوان سخنرانی	سخنرانان	تخصص
۱۴:۳۰ الی ۱۶:۰۰	پانل بیماری‌های منتقله از راه تماس جنسی (STD)		
رئیس پانل: دکتر مهرانگیز زنگنه (دانشیار بیماری‌های عفونی و گرمسیری، واحد پزشکی تهران، دانشگاه علوم پزشکی آزاد اسلامی، پژوهشگاه درمان ناباروری رویان)			
اعضاء پانل: دکتر حمید عمادی کوچک (دانشیار بیماری‌های عفونی و گرمسیری، دانشگاه علوم پزشکی تهران، عضو کمیته کشوری وراثت بهداشت و درمان)، دکتر پروین افسر کازرونی (متخصص پزشکی اجتماعی، مسئول اداره ایدز و بیماری‌های آمیزشی وراثت بهداشت و درمان)، دکتر محمد درویشی (دانشیار بیماری‌های عفونی و گرمسیری، دانشگاه علوم پزشکی ارتش، بیمارستان بعثت)، دکتر رشید رمضانزاده (استاد دانشگاه علوم پزشکی کردستان)، دکتر منیژه دزفولینژاد (استاد یار بیماری‌های عفونی و گرمسیری، واحد پزشکی تهران، دانشگاه علوم پزشکی آزاد اسلامی)، دکتر سهیلا ابوالقاسمی (استاد یار بیماری‌های عفونی و گرمسیری، واحد پزشکی تهران، دانشگاه علوم پزشکی آزاد اسلامی)، دکتر محسن علیجانی (استاد یار بیماری‌های عفونی و گرمسیری، واحد پزشکی تهران، دانشگاه علوم پزشکی آزاد اسلامی)، دکتر بهنام فرهودی (دانشیار بیماری‌های عفونی و گرمسیری، واحد پزشکی تهران، دانشگاه علوم پزشکی آزاد اسلامی)			
۱۴:۳۰ الی ۱۴:۴۰	ارتباط عفونت کلامیدیا تراکوماتیس با زایمان زودرس	دکتر رشید رمضانزاده	
۱۴:۴۰ الی ۱۴:۵۰	اپیدمیولوژی بیماری‌های منتقله از راه تماس جنسی در ایران و جهان	دکتر منیژه دزفولی نژاد	
۱۴:۵۰ الی ۱۵:۰۰	پیشگیری در بیماری‌های منتقله از راه تماس جنسی	دکتر بهنام فرهودی	
۱۵:۰۰ الی ۱۵:۱۰	علائم بالینی در بیماری‌های منتقله از راه تماس جنسی	دکتر سهیلا ابوالقاسمی	
۱۵:۱۰ الی ۱۵:۲۰	ارتباط بیماری‌های منتقله از راه تماس جنسی با نازایی در مردان و زنان	دکتر مهرانگیز زنگنه	
۱۵:۲۰ الی ۱۵:۳۰	نقش واکسیناسیون در بیماری‌های منتقله از راه تماس جنسی	دکتر محمد درویشی	
۱۵:۳۰ الی ۱۵:۴۰	تشخیص و مقاومت دارویی در بیماری‌های منتقله از راه تماس جنسی	دکتر محسن علیجانی	
۱۵:۴۰ الی ۱۶:۰۰	بحث و تبادل نظر		
۱۶:۰۰ الی ۱۶:۳۰	پذیرایی و بازدید از پوسترها		
چهارشنبه ۱۳۹۵/۶/۳			
هیئت رئیسه: دکتر مژده حاکمی والا (دانشیار - دکتری میکروبیولوژی و شناسایی، دانشگاه علوم پزشکی شهید بهشتی)، دکتر سیدسجاد خرم روز (دکتری باکتری شناسی پزشکی، دانشگاه علوم پزشکی یاسوج)، دکتر محبوبه نادری نسب (دکتری تخصصی باکتری شناسی، دانشگاه علوم پزشکی مشهد)، دکتر حسین صمدی کفیل (دکتری باکتری شناسی پزشکی دانشگاه علوم پزشکی تبریز)، دکتر احیا عبدی عالی (دانشیار، دکترای میکروبیولوژی دانشگاه الزهراء)، دکتر صدیقه جوادپور (دکتری باکتری شناسی پزشکی دانشگاه علوم پزشکی هرمزگان)، دکتر رمضان رجب نیا (دانشیار باکتری شناسی دانشگاه علوم پزشکی بابل)، دکتر رضا میر نژاد (دانشیار باکتری شناسی، دانشگاه علوم پزشکی بقیه‌الله (عج))			
۸:۳۰ الی ۸:۴۰	Genotyping Of Mycobacterium Tuberculosis Strais Directly On Clinical Samples By 24 Locus Miru-Vntr Method	Hamidreza Sadegh	
۸:۴۰ الی ۸:۵۰	Comparison Of Proportional Direct And Indirect Methods In Antibiotic Resistance In Mycobacterium Tuberculosis Detection	Sirus Amini	
۸:۵۰ الی ۹:۰۰	Study Of Molecular Epidemiology Of Mycobacterium Tuberculosis Complex Isolated From Patiants In The Northeast Of Iran In 2014 Using Miru-Vntr And Spoligotyping To Assess Genetic Diversity Of Strains	Hassan Ravansalar	
۹:۰۰ الی ۹:۱۰	Evaluating The Expression Of Mexab-Oprm Efflux Pump Genes In Resistant Clinical Isolates Of Pseudomonas Aeruginosa Using Quantitative Real-Time Pcr Method.	Iman Bahrami Abdehghah ¹	
۹:۱۰ الی ۹:۲۰	First Detection Of Oxa-48 Producing Carbapenemase Escherichia Coli In Iran	Hamid Solgi	

زمان	عنوان سخنرانی	سخنرانان	تخصص
۹:۲۰ الی ۹:۳۰	Molecular Detection And Genotyping Of Chlamydia Psittaci In Captive Psittacines And Their Owners From Isfahan (Iran)	Mehdi Moradi Sarmeidani	
۹:۳۰ الی ۹:۴۰	Molecular Identification Of Drug Resistant Mutation Of Tetracyclines In Mycoplasma Spp Isolated From Patients With Multiple Sclerosis (Ms) In Kerman Province.	Maryam Naghib	
۹:۴۰ الی ۹:۵۰	Development Of A Semi Nested Polymerase Chain Reaction Method For Detection And Amplification Of Hepatitis B Virus Core Gene	Zahraa Mohammadali	
۹:۵۰ الی ۱۰:۰۰	بحث و تبادل نظر		
۱۰:۰۰ الی ۱۰:۳۰	پذیرایی و بازدید از پوسترها		
۱۰:۳۰ الی ۱۰:۴۵	جایگاه طب سنتی در مقابله با عفونت ها	دکتر رجا رحیمی	استادیار فارماکونوزی، دانشگاه علوم پزشکی تهران
۱۰:۴۵ الی ۱۱:۰۰	اهمیت استفاده از ترکیبات طبیعی در مقابله با باکتری ها	دکتر ویدا کاظمی	دکتری داروسازی، دانشگاه علوم پزشکی تهران
۱۱:۰۰ الی ۱۲:۳۰	پانل گیاهان دارویی		
رئیس پانل: دکتر آتوسا علی احمدی (استادیار میکروبیولوژی، پژوهشکده گیاهان و مواد اولیه دارویی دانشگاه شهید بهشتی) اعضای پانل: دکتر فرشته افتخار (استاد میکروبیولوژی، دانشکده علوم زیستی دانشگاه شهید بهشتی)، دکتر مهدی رزاقی ابیانه (استاد قارچ شناسی، انستیتو پاستور ایران)، دکتر ناهید رحیمی فرد (دانشیار، دکتري تخصصی میکروب شناسی، سازمان غذا و دارو و رئیس بخش میکروبیولوژی مرکز آزمایشگاه های مرجع کنترل غذا و دارو، وزارت بهداشت درمان آموزش پزشکی)، دکتر محدثه محبوبی (استادیار میکروبیولوژی، شرکت بارپچ اسانس)، دکتر مهدی وزیریان (استادیار فارماکونوزی، دانشکده داروسازی دانشگاه علوم پزشکی تهران)، دکتر رجا رحیمی (استادیار فارماکونوزی، گروه داروسازی سنتی، دانشکده طب سنتی، دانشگاه علوم پزشکی تهران)، دکتر سیده نرگس سادات لمروودی (استادیار فارماکونوزی، گروه داروسازی سنتی، دانشکده طب سنتی دانشگاه علوم پزشکی تهران)، دکتر زهرا توفیقی (استادیار فارماکونوزی، گروه فارماکونوزی، دانشکده دارو سازی، دانشگاه علوم پزشکی تهران)			
۱۱:۰۰ الی ۱۱:۱۰	دکتر ناهید رحیمی فرد	روش های بررسی اثرات ضد میکروبی اسانس و عصاره های گیاهی	
۱۱:۱۰ الی ۱۱:۲۰	دکتر نرگس ساداتی لمروودی	Efflux pump inhibitors derived from plants: a promising approach to interfere efflux-mediated drug resistance in bacteria	
۱۱:۲۰ الی ۱۱:۳۰	دکتر الهه مهدی زاده	The anti-dermatophyte and anti-elastase activity of Zataria multiflora essential oils	
۱۱:۳۰ الی ۱۱:۴۰	دکتر زهرا توفیقی	Natural products can be introduced as new generation of antibiotics in future	
۱۱:۴۰ الی ۱۱:۵۰	دکتر حنا نه کر دیچه	Anti-quorum sensing activity of Pistacia atlantica methanolic extract against Pseudomonas aeruginosa PAO1	
۱۱:۵۰ الی ۱۲:۰۰	دکتر مرضیه سبحانی	Discovery of active compounds from Iranian plants against Candida albicans by HPLC-base activity profiling	
۱۲:۰۰ الی ۱۲:۱۰	دکتر مریم صدرنیا	Evaluation of growth inhibitory effect of microemulsion produced from aqueous extract of hypericum on gram-negative clinical strains	
۱۲:۱۰ الی ۱۲:۳۰	بحث و تبادل نظر		

فهرست پوسترهای

هفدهمین کنگره بین المللی
میکروب شناسی ایران

برنامه زمانبندی پوسترها

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۸:۰۰-۹:۱۵ شماره پوستر ۱۰۱۰-۱۱۱۰	۸:۰۰-۹:۱۵ شماره پوستر ۴۰۴-۵۰۴	۹:۰۰-۱۰:۱۵ شماره پوستر ۱-۱۰۰
۹:۲۵-۱۰:۴۰ شماره پوستر ۱۱۱۱-۱۲۱۱	۹:۲۵-۱۰:۴۰ شماره پوستر ۵۰۵-۶۰۵	۱۰:۲۵-۱۱:۴۰ شماره پوستر ۱۰۱-۲۰۱
	۱۰:۵۰-۱۲:۰۵ شماره پوستر ۶۰۶-۷۰۶	۱۴:۰۰-۱۵:۱۵ شماره پوستر ۲۰۲-۳۰۲
	۱۴:۰۰-۱۵:۱۵ شماره پوستر ۷۰۷-۸۰۷	۱۵:۲۵-۱۶:۴۰ شماره پوستر ۳۰۳-۴۰۳
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Row	Title	Submission Author	Session
روز اول ساعت ۱۰:۱۵-۹:۰۰ شماره پوستر ۱-۱۰			
1	ANTIMICROBIAL ACTIVITY OF DIFFERENT LACTOBACILLUS ISOLATES FROM TRADITIONAL YOGURTS RURAL AND TRIBAL AREAS OF KOHILUYEH& BOYERAHMAD AGAINST CLINICAL ISOLATES OF CLOSTRIDIUM DIFFICILE	Asgarian Shahrbanoo	Anaerobic Bacteria
2	STRAIN IMPROVEMENT AND OPTIMIZATION STUDIES FOR ENHANCED PRODUCTION OF ERYTHROMYCIN IN SACCHAROPOLYSPORA ERYTHRAEA BY UV MUTAGENESIS	Falahpoor Narges	Applied (industrial and agricultural) Microbiology
3	ISOLATION AND CHARACTERIZATION OF HEAVY METAL RESISTANT ACINETOBACTER SP. AND ITS POTENTIAL FOR CU BIOSORPTION	Ashrafi gerdeh Maryam	Applied (industrial and agricultural) Microbiology
4	THE EFFECT OF PLANT GROWTH PROMOTING RHIZOBACTERIA ON SEEDLING STAGE OF SUN FLOWER	Saadatnasri Fatemeh	Applied (industrial and agricultural) Microbiology
5	CLONING OF A CHROMOSOME- ENCODED CATECHOL 2, 3- DIOXYGENASE(METAPYROCATECHASE) GENE FROM ACINETOBACTER OLEIVORANS GSN15	Babazadeh Fatemeh	Applied (industrial and agricultural) Microbiology
6	SCREENING SALT ADAPTED PLANT GROWTH PROMOTING RHIZOBACTERIA FROM AGRICULTURAL FIELDS IN KERMAN, IRAN	Riazi Vali	Applied (industrial and agricultural) Microbiology
7	IN VITRO PLANT GROWTH PROMOTING ACTIVITIES OF PHOSPHATE AND ZINC SOLUBILIZING RHIZOBACTERIA ISOLATED FROM A FIELD IN KERMAN, IRAN.	Jalali rigi Nooshin	Applied (industrial and agricultural) Microbiology
8	ENHANCEMENT OF TYLOSIN PRODUCTION BY TRANSFORMATION OF BLDD GENE FROM S. ERYTHRAEA IN S. FRADIEA	Maleki Fatemeh	Applied (industrial and agricultural) Microbiology
9	PRODUCTION OF CLAVULANIC ACID BY STREPTOMYCES CLAVULIGERUS WITH USING NATIVE NITROGEN SOURCE RAPESEED MEAL BY MICROBIAL FERMENTATION METHOD	Shahrad Ramin	Applied (industrial and agricultural) Microbiology
10	ISOLATION AND MOLECULAR IDENIFICATION OF LEAD(PB) RESISTANT BACTERIA FROM SEWAGE OF SEVERAL INDUSTRIAL FACTORIES IN ISFAHAN PROVINCE.	Mirsafaei Marzieh sadat	Applied (industrial and agricultural) Microbiology

Row	Title	Submission Author	Session
11	IMPROVEMENT OF ACTINOMYCIN PRODUCTION BY TRANSFORMATION OF DRRRA, DRRB, DNRI AND AFSR GENES FROM S. PEUCETIUS IN S. ANTIBIOTICUS BY PCR CLONING	Rassi Hossein	Applied (industrial and agricultural) Microbiology
12	ISOLATION OF PROTEASE PRODUCING MODERATELY HALOPHILIC BACTERIA FROM SALINE SOIL	Ghorbani Nilufar	Applied (industrial and agricultural) Microbiology
13	COMPARATIVE PROTEASE ACTIVITY OF ARCHANGIUM GEPHYRA UTM 4007 WITH OTHER POTENT SERINE PROTEASE PRODUCERS	Roohi zohrab Nasim	Applied (industrial and agricultural) Microbiology
14	ISOLATION OF AMYLASE PRODUCING HALOPHILIC BACTERIA FROM SEDIMENTS OF SALINE RIVER IN ESHTEHARD	Saryazdi Mojgan	Applied (industrial and agricultural) Microbiology
15	ISOLATION AND IDENTIFICATION OF PHOSPHATE SOLUBILIZING RHIZOBACTERIA WITH PLANT GROWTH PROMOTING ACTIVITIES	Parvan Zohreh	Applied (industrial and agricultural) Microbiology
16	THE ISOLATION AND IDENTIFICATION OF ENDOPHYTIC BACTERIUM, ENTEROBACTER ASBURIAE, FROM CACTUS IN IRAN	Emamy Parisa	Applied (industrial and agricultural) Microbiology
17	THE ISOLATION AND IDENTIFICATION OF PANTOEIA COFFEIPHILA ASSOCIATED WITH SUMMER SQUASH WATER-SOAKED SYMPTOM IN IRAN	Emamy Parisa	Applied (industrial and agricultural) Microbiology
18	NITROGEN FIXATION AND PHOSPHATE SOLUBILIZATION BY A RHIZOBACTERIUM STRAIN IAU3001 ISOLATED FROM A FIELD IN KERMAN, IRAN.	Molaie Elnaz	Applied (industrial and agricultural) Microbiology
19	PLANT GROWTH PROMOTING ACTIVITY OF RHIZOBACTERIUM STRAIN IAU3001	Molaie Elnaz	Applied (industrial and agricultural) Microbiology
20	AMMONIA PRODUCTION AND ZINC SOLUBILIZATION BY IAU3005 STRAIN RHIZOBACTERIUM ISOLATED FROM A FIELD IN KERMAN, IRAN.	Molaie Elnaz	Applied (industrial and agricultural) Microbiology
21	OPTIMIZATION OF BACILLUS PASTEURII GROWTH CONDITION FOR ENHANCED UREASE ACTIVITY	Dilmaghani Azita	Applied (industrial and agricultural) Microbiology
22	ISOLATION AND IDENTIFICATION OF BACILLUS CEREUS FROM PETROLEUM PIPELINES	Pedramfar Arezo	Applied (industrial and agricultural) Microbiology
23	ISOLATION AND IDENTIFICATION OF GOLD NANOPARTICLE EXTRA CELLULAR PRODUCING BACILLUS FROM SOIL SAMPLE IN FARS PROVINCE	Ebrahimi Fard Sepide	Applied (industrial and agricultural) Microbiology

Row	Title	Submission Author	Session
24	ISOLATION AND IDENTIFICATION OF CELLULOLYTIC BACTERIA FROM SOIL AND LEAVE IN KERMAN - IRAN	Khosravi Farshid	Applied (industrial and agricultural) Microbiology
25	BIODESULFURIZATION OF DIBENZOTHIOPHENE WITH ENTROBACTER BAB3164 ISOLATED FROM OIL CONTAMINATED SOIL IN ABADAN RIFINERY	Shantiaee Shima	Applied (industrial and agricultural) Microbiology
26	EVALUATION OF MICROBIAL CONTAMINATION IN WATERS (DISPOSAL, DRINKING AND NATURAL) IN URMIA	Abbasi ghaznag Maryam	Applied (industrial and agricultural) Microbiology
27	OPTIMIZATION OF COLD-ACTIVE PROTEASE PRODUCTION BY THE COLD TOLERANT BACTERIUM STENOTROPHOMONAS SP. WITH ONE FACTOR AT A TIME METHODOLOGY	Nikbakhti Reihaneh	Applied (industrial and agricultural) Microbiology
28	ISOLATION AND SCREENING OF PIGMENT PRODUCING ACTINOBACTERIA FROM SOIL	Ranjbari Mahdieh	Applied (industrial and agricultural) Microbiology
29	COMPARISON OF DIFFERENT METHODS IN PROTEIN A IMMOBILIZATION	Qafari Seyed Mehdi	Applied (industrial and agricultural) Microbiology
30	INTRODUCTION OF SAROCLADIUM SP. AS A POTENT OLEAGINOUS YEAST STRAIN FOR PRODUCTION OF BIOFUEL	Nikbakhtad Mahzad	Applied (industrial and agricultural) Microbiology
31	DETECTION OF PETROLEUM CONTAMINATION USING BIOLOGICAL SYSTEM BASED ON BIOLUMINESCENCE PRODUCTION BY VIBRIO FISCHERI	Naghavi Nafiseh Sadat	Applied (industrial and agricultural) Microbiology
32	EVALUATION OF ERMSF TRANSFORMATION IN SACCHAROPOLYSPORA ERYTHRAEA FOR ENHANCEMENT OF ERYTHROMYCIN	Adnani Forghani Sanam	Applied (industrial and agricultural) Microbiology
33	ISOLATION OF RESISTANT BACTERIA TO SELENATE, COPPER, MERCURY AND LEAD	Yaghoobizadeh Fatemeh	Applied (industrial and agricultural) Microbiology
34	INVESTIGATION OF DIFFERENT SALINITY EFFECTS ON THE BIOMASS PRODUCTION OF SPIRULINA PLATENSIS	Yaghoobizadeh Fatemeh	Applied (industrial and agricultural) Microbiology
35	BIOFIXATION OF CO ₂ WITH ISOLATED MICROALGAE IN PHOTOTROPHIC CONDITION	Sheykhinejad Ali	Applied (industrial and agricultural) Microbiology

Row	Title	Submission Author	Session
36	THE AMOUNT OF COLIFORM CONTAMINATION OF SURROUNDING WATERS IN THE SOUTH BASIN OF THE CASPIAN SEA PROVINCE OF MAZANDARAN IN DIFFERENT SEASONS (SPRING, SUMMER, AUTUMN AND WINTER)	Sadeghpour Majid	Applied (industrial and agricultural) Microbiology
37	STUDYING THE EFFECT OF AERATION ON GROWTH AND DECOMPOSITION OF MINERAL SULFUR COMPOUNDS BY ISOB 14 A NEW BACTERIA ISOLATED	Nazari Fatemeh	Applied (industrial and agricultural) Microbiology
38	THE MEDIUM PH AND TEMPERATURE OPTIMIZATION OF ISOB 14 A NEW BACTERIA ISOLATED	Nazari Fatemeh	Applied (industrial and agricultural) Microbiology
39	BIOTREATMENT OF INDUSTRIAL CATTLE POLLUTANT GASES BY BIOFILTRATION	Karami rubati Sahar	Applied (industrial and agricultural) Microbiology
40	WHETHER MICROBES HAVE THE ABILITY TO CLEAN UP POLLUTED AIR ASALUYEH?	Heydari Mohammad	Applied (industrial and agricultural) Microbiology
41	PRODUCTION ENHANCEMENT OF EPIDERMAL GROWTH FACTOR (EGF) IN E. COLI BATCH CULTURE	Babaeipour Valiollah	Applied (industrial and agricultural) Microbiology
42	THE COMPUTATIONAL EVALUATION OF ACTIVITY OF SIMULATED BACILLUS SUBTILIS A-AMYLASE (PDB: 1UA7(	Eslamifar Zahra	Applied (industrial and agricultural) Microbiology
43	ISOLATION OF AN UREOLYTIC BACTERIUM FROM HOUSEFLY FOR IMPROVEMENT OF COMPRESSIVE STRENGTH OF MORTAR	Sohrabi Mahlagha	Applied (industrial and agricultural) Microbiology
44	ISOLATION OF INDIGENOUS SIDEROPHORE-PRODUCING BACTERIA AND DETECTION OF A VARIETY OF SIDEROPHORES	ESHAGHI EBRAHIM	Applied (industrial and agricultural) Microbiology
45	STUDING THE SALT STRESS EFFECTS ON SOME PHYSIOLOGICAL AND MORPHOLOGICAL RESPONSES OF CYANOBACTERIUM NOSTOC SP.FS77 WITH EMPHASIZE ON POTENTIALITY IN AGRICULTURAL BIOTECHNOLOGY	Badeli Zynab	Applied (industrial and agricultural) Microbiology
46	EVALUATION OF SIMPLE CARBON SOURCES IN MICROBIAL FUEL CELL USING URMIA LAKE SEDIMENT	Mohammadi Shahnaz	Applied (industrial and agricultural) Microbiology
47	ISOLATION OF DIFFERENT RHIZOBACTERIA FROM RHIZOSPHERIC SOILS WITH DIFFERENT PLANT GROWTH PROMOTING TRAITS	Sharifi Fakhreh	Applied (industrial and agricultural) Microbiology
48	EFFECTS OF PHOSPHATE AND ZINC SOLUBILIZING RHIZOBACTERIA ON TEPARY BEAN	Sharifi Fakhreh	Applied (industrial and agricultural) Microbiology

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49	THE USE OF RECOMBINANT LACCASE OF YARROWIA LIPOLYTICA FOR DECOLORIZATION OF ENVIRONMENTAL POLLUTANT DYES	Moradi Marzie	Applied (industrial and agricultural) Microbiology
50	LACCASE PRODUCTION FROM SUCROSE BY RECOMBINANT YARROWIA LIPOLYTICA	Moradi Marzie	Applied (industrial and agricultural) Microbiology
51	INFLUENCE OF PERMEABILITY OF MICROBIAL CELLS ON THEBAINE BIOTRANSFORMATION	Ataee Nazanin	Applied (industrial and agricultural) Microbiology
52	INFLUENCE OF PHYSIOLOGICAL CELL STAGES ON THEBAINE BIOTRANSFORMATION	Ataee Nazanin	Applied (industrial and agricultural) Microbiology
53	DECOLORIZATION OF FOUR TEXTILE AZO DYES BY NEUROSPORA SP. UTM 5041 UNDER SALINE CONDITIONS	Moayed Rad Setareh	Applied (industrial and agricultural) Microbiology
54	EVALUATION OF KINETIC OF DIFFERENTIAL FACTORS IN ARCHAEA HALOBACTERIUM SALINARUM	Najafabadi samani Akram	Applied (industrial and agricultural) Microbiology
55	OPTIMIZATION OF SACCHAROMYCES CEREVISIAE FOR TOLERANCE OF FURFURAL DENSITY BY IMMOBILIZATION IN ALGINATE-CHITOSAN MICROCAPSULE.	Gerami Parmida	Applied (industrial and agricultural) Microbiology
56	SCREENING OF NATIVE MICROALGAE FOR LIPID PRODUCTION	Dani Nafise	Applied (industrial and agricultural) Microbiology
57	ISOLATION AND CHARACTERIZATION OF MESOPHILIC ALPHA-AMYLASE FROM UFM29 BACTERIUM	Afrisham Saideh	Applied (industrial and agricultural) Microbiology
58	STUDY ON AZO DYES BIODEGRADATION BY ISOLATED BACTERIA FROM TEXTILE EFFLUENT	Pourkazem Husein	Applied (industrial and agricultural) Microbiology
59	SCREENING AND ISOLATION OF EXTRACELLULAR PROTEASE PRODUCING HALOPHILIC BACTERIA FROM BADAB-SOURT	Satari Faghihi Leila	Applied (industrial and agricultural) Microbiology
60	EVALUATION SOME OF SANITIZATION METHODS FOR BACTERIA ELIMINATION IN OCIMUM AND MENTHA GENUS	Danaeipour Reyhaneh	Applied (industrial and agricultural) Microbiology
61	DIPHTheria TOXOID PRECIPITATION BY AMMONIUM SULPHATE IN TWO CONDITIONS DRY AND LIQUID FORMS	Akrami Meisam	Applied Microbiology
62	PURIFICATION OF DIPHTheria TOXIN BY SEPHACRYL SIZE EXCLUSION CHROMATOGRAPHY	Akrami Meisam	Applied Microbiology
63	OPTIMIZATION OF PURIFICATION DIPHTheria TOXOID USING DIFFERENT RESEN	Akrami Meisam	Applied Microbiology

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64	BACTERIAL DEGRADATION OF WASTEWATER CONTAINING CYANIDE AND ITS EVALUATION USING BIOLUMINESCENCE	Asadi Ali	Applied Microbiology
65	TRIM69 AS A SUITABLE CANDIDATE FOR IMMUNOTOXINS DESIGNING WITH WIDE RANGE TARGETS AS WELL AS OVARIAN CANCER	Sabagh Razieh	Applied Microbiology
66	EVALUATION OF EXTREMOZYMES IN COLD TOLERANT BACTERIAL ISOLATES FROM OSHTORANKUH MOUNTAINS	Lashani Elham	Applied Microbiology
67	THE COMPARATIVE INVESTIGATION OF THE ANTIMICROBIAL EFFECTS OF THE HEN EGG LYSOZYME ENZYME IN WILD AND MUTANT STRAINS	Mirzabayati Vahid	Applied Microbiology
68	THE EFFECT OF HEAVY METALS IN THE PRODUCTION OF PIGMENTS IN RHODOCOCCLUS RHODOCHROUS	Haddad mahdieh sadat	Applied Microbiology
69	STUDY OF BIOFILM FORMATION OF RHODOCOCCLUS SP. USING MICROPLATE METHOD	Adhami Elham	Applied Microbiology
70	CULTURE OPTIMIZATION OF ANTIFUNGAL METABOLITE PRODUCTION IN THE BACTERIUM BACILLUS LICHENIFORMIS	Beigi saki Athar	Applied Microbiology
71	OVEREXPRESSION OPTIMIZATION OF AN ANTI-EPCAM EXTRACELLULAR DOMAIN SINGLE CHAIN VARIABLE FRAGMENT IN ESCHERICHIA COLI	Najafi Soulari Reyhaneh	Applied Microbiology
72	ACTINOMYCETES IN ANTIBIOTICA RESEARCH AT THE HELMHOLTZ CENTRE FOR INFECTION RESEARCH	Wink Joachim	Applied Microbiology
73	CONSTRUCTION OF EXPRESSION PLASMID BASED ON THE ARABINOSE PROMOTER CAREERING THE IPAB GENE IN THE E.COLI	Nasrollahi boroujeni Fateme	Applied Microbiology
74	ISOTHERMS AND KINETICS STUDIES FOR BIOSORPTION OF CADMIUM FROM AQUEOUS SOLUTION BY COCHLIOBOLUS AUSTRALIENSIS UTM 5042	Khajeh mohammadilar Fatemeh sadat	Applied Microbiology
75	EFFECT OF PRETREATMENT ON THE BIOSORPTION OF CADMIUM BY COCHLIOBOLUS AUSTRALIENSIS UTM 5042	Khajeh mohammadilar Fatemeh sadat	Applied Microbiology
76	DETECTION AND ISOLATION OF L-ASPARAGINASE AND LIPASE PRODUCING BACTERIA FROM SOIL	Gholami Nasrin	Applied Microbiology

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77	SCREENING AND ISOLATION OF ASPARAGINASE PRODUCING BACTERIA FROM CONTAMINATE SOIL OF SLAUGHTER HOUSE WASTE.	Gholami Nasrin	Applied Microbiology
78	ISOLATION AND IDENTIFICATION BACTERIA RHIZOBIUM OF ROOT NODULE PLANTS.	ESHAGHI EBRAHIM	Applied Microbiology
79	PURIFICATION AND EVALUATION OF POLYSACCHARIDE INTERCELLULAR ADHESION (PIA) ANTIGEN FROM STAPHYLOCOCCUS EPIDERMIDIS.	Mirzaei Bahman	Applied Microbiology
80	A STUDY OF PECTINASE ENZYME GENE IN HALOPHILIC BACTERIA FROM SALT LAKE IRAN	Nasrollahzade Zohre	Applied Microbiology
81	DEGRADATION OF 2,4,6-TRINITROTOLUENE BY TWO NATIVE ISOLATED BACTERIA	Ali begloui Mehdi	Applied Microbiology
82	INCREASED BIOLOGICAL REMOVAL OF PETROLEUM HYDROCARBONS BY YEAST MIX-CULTURES OF SAROCLADIUM SP. AND CRYPTOCCUS SP.	Kamyabi Aliyeh	Applied Microbiology
83	MYCOSORPTION OF DIFFERENT AZO DYES BY SAROCLADIUM SP. FOR BIODECOLORIZATION OF TEXTILE EFFLUENTS	Kamyabi Aliyeh	Applied Microbiology
84	OVERPRODUCTION OF RECOMBINANT HUMAN GROWTH HORMONE IN BATCH CULTURE IN E.COLI USING PLACKET-BURMAN STATISTICAL METHODS	Babaeipour Valiollah	Applied Microbiology
85	GENERATION OF ELECTRICITY USING MICROBIAL FUEL CELL	Afshari Elnaz	Applied Microbiology
86	EVOLUTIONARY ENGINEERING OF NATIVE CITROBACTER STRAIN TO IMPROVE THE PERFORMANCE ON ORGANOPHOSPHORUS PESTICIDES DEGRADATION BY GENOME SHUFFLING	Beikverdi Mohammad Sadegh	Applied Microbiology
87	ENHANCEMENT OF DEGRADATION ORGANOPHOSPHORUS PESTICIDES BY INTRASPECIFIC PROTOPLAST FUSION OF NATIVE CITROBACTER BACTERIA MUTANT STRAINS.	Beikverdi Mohammad Sadegh	Applied Microbiology
88	EVALUATION OF THE ANTIMICROBIAL ACTIVITY OF PROBIOTIC BACTERIA ESCHERICHIA COLI ISOLATED FROM DIFFERENT NATURAL SOURCES HEMORRHAGIC E.COLI O157H7	Sahar Karami	Applied Microbiology

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89	COMPARISON OF PRODUCTION OF HYALURONIC ACID FROM STREPTOCOCCUS SALIVARIUS SUBSP. THERMOPHILUS AND ISOLATED STREPTOCOCCUS THERMOPHILUS SAMPLES FROM YOGHURT AND OPTIMIZATION OF THE GROWTH CONDITIONS	Tabatabaei Diba	Applied Microbiology
90	STRUCTURAL MINIATURIZATION OF THE EXOTOXIN A OF THE PSEUDOMONAS FOR IMMUNOTOXINS DEVELOPMENT	Hoseinian Seyyed ali	Applied Microbiology
91	AN IN SILICO COMPARATIVE INVESTIGATION OF THE ANTIMICROBIAL ACTIVITY OF THE AMYLOIDOGENIC MUTANTS AND WILD TYPE OF HUMAN LYSOZYME	Hoseinian Seyyed ali	Applied Microbiology
92	A STUDY ON THE EFFECT OF CALCIUM PEROXIDE NANOPARTICLES AND FE (II) IONS ON MICROBIAL POPULATION OF GROUNDWATER IN MODIFIED FENTON REACTION	Gholami Fatemeh	Applied Microbiology
93	BIOREMEDIATION OF NAPHTHALENE CONTAMINATED GROUNDWATER BY MAGNESIUM PEROXIDE (MGO2) NANOPARTICLE	Gholami Fatemeh	Applied Microbiology
94	THE EFFECT OF BURN GEL NAMED "BURNOGEL" AGAINST BIOFILM OF P. AERUGINOSA ISOLATED FROM BURN PATIENTS	Shafiei Morvarid	Applied Microbiology
95	INTRODUCING NEW METHODS FOR SELECTIVE ISOLATION OF STREPTOMYCES AND NON-STREPTOMYCES ACTINOBACTERIA FROM MARINE SAMPLES	Almasi Faezeh	Applied Microbiology
96	INTRODUCING AN ATRAZINE DEGRADING BACTERIUM ISOLATED FROM SOIL OF SUGARCANE FIELD	Motamedi Hossein	Applied Microbiology
97	TETRACOSANE DEGRADATION BY NATIVE STRAINS ISOLATED FROM OIL CONTAMINATED SOILS	Motamedi Hossein	Applied Microbiology
98	PHYSIOLOGICAL CHARACTERIZATION OF CHLORELLA AND SELENASTRUM SP. AS PROTEIN AND LIPID SOURCE IN VARIOUS CULTURES	Baftehchi Ladan	Applied Microbiology
99	PROPOSAL OF NEW METHODS FOR LONG-TERM PRESERVATION OF SALT-LOVING MICROORGANISMS IN IBRC	Harirchi Sharareh	Applied Microbiology

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100	BIOINFORMATICS STUDIES, CLONING AND EXPRESSION OF FUSION PROTEIN MRPA.FLIC OF PROTEUS MIRABILIS AS A NEW TARGET AGAINST URINARY TRACT INFECTION	Habibi Mehri	Applied Microbiology
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101	INVESTIGATION BIOREMOVAL ORGANIC SULFUR OF COAL BY PERCOLATION LEACHING AND BACTERIA ISOLATED	Kouchaki Mohammadreza	Applied Microbiology
102	INVESTIGATION ON NAPHTHALENE BIODEGRADATION ABILITY IN A BACILLUS SP. CONSORTIUM	Mousavi Mahshid	Applied Microbiology
103	TEMPERATURE EFFECT ON A-LUFFIN EXPRESSION AND SOLUBILITY RATE IN ESCHERICHIA COLI BACTERIA AS A HOST	Namvar Shaghayegh	Applied Microbiology
104	ANTI-MRSA METABOLITES PRODUCED BY CO-CULTURED ACTINOMYCETES ISOLATED FROM HOZ-SULTAN SALT LAKE, QOM	Taheri Fatemeh	Applied Microbiology
105	COMPARISON OF PROTEIN PROFILES OF ISOLATES STRAINS OF BURKHOLDERIAMALEI IN IRAN'S AND MALEIN PRODUCING STRAINS OF RAZI INSTITUTE	Babaie Mahdi	Applied Microbiology
106	THE INFLUENCE OF MINERALS ON ANTIBACTERIAL SECONDARY METABOLITE PRODUCTION BY STREPTOMYCES SP.ACS 116 ISOLATED FROM OMAN SEA	Zargari Orozaki Razieh	Applied Microbiology
107	THE EFFECT OF DIFFERENT CARBON AND NITROGEN SOURCES ON ANTIBACTERIAL PRODUCTION BY STREPTOMYCES SP.ACS 116 ISOLATED FROM OMAN SEA	Zargari Orozaki Razieh	Applied Microbiology
108	EXPRESSION OF EPCAM EXTRACELLULAR DOMAIN AS A CANDIDATE VACCINE IN COLORECTAL CANCER IN E.COLI	Rasouli kery bozorg Farideh	Applied Microbiology
109	PRODUCTION OF FIBROLYTIC ENZYMES BY A LOCAL YEAST STRAIN OF CONICHAETA SP.	Barati Fateme	Applied Microbiology
110	BIODEGRADATION OF 2,4-DICHLOROPHENOXY ACETIC ACID USING BACTERIA ISOLATED FROM SOIL	Khojamli Khadije	Applied Microbiology
111	ISOLATION OF EXOELECTROGENIC SHEWANELLA SP. FROM NATURAL ENVIRONMENTS FOR THE GENERATION OF ELECTRICITY IN MICROBIAL FUEL CELLS	Ekrami Seyedeh maryam	Applied Microbiology

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112	EXTRACELLULAR SYNTHESIS OF SILVER NANOPARTICLES USING SULFATE REDUCING BACTERIUM ISOLATED FROM SEDIMENTS OF THE CASPIAN SEA	Ekrami Seyedeh maryam	Applied Microbiology
113	AUTO INDUCTION; A SIMPLE PROTOCOL FOR EXPRESSION OF RECOMBINANT PROTEIN IN E. COLI.	Mirzaiee Masoomeh	Applied Microbiology
114	DSBA SIGNAL PEPTIDE DIRECTS RECOMBINANT HUMAN GROWTH HORMONE TO PERIPLASMIC SPACE OF E. COLI	Mirzaiee Masoomeh	Applied Microbiology
115	ISOLATION & SCREENING OF - TOLERANT BACTERIA SOIL CONTAMINATED BY OIL	Rostami Parimah	Applied Microbiology
116	ISOLATION & SCREENING OF ORGANIC SOLVENT- TOLERANT BACTERIA SOIL OF ZANJAN CONTAMINATED BY OIL	Rostami Parimah	Applied Microbiology
117	MAGNETIC PROPERTIES OF MAGNETOSPIRILLUM GRYPHISWALDENSE IN MAGNETIC FIELD	Jeddi Shima	Applied Microbiology
118	ISOLATION AND CHARACTERIZATION OF HALOTOLERANT PURPLE NON SULFUR BACTERIA, FROM KARAJ SOILS	Jalilvand Mehrdad	Applied Microbiology
119	MICROCIN TYPING AND EVALUATION OF PROBIOTIC POTENTIAL OF DIARRHEAGENIC E. COLI	Etehad Asnaf Sheida	Applied Microbiology
120	DESIGN, CLONING AND EXPRESSION OF A CYSTEINE CONTAINING MUTANT OF STREPTOKINASE	Rezaei Mahsa	Applied Microbiology
121	EVALUATION OF THE ISFAHAN COMPOST SAMPLES AFTER PROCESSING IN TERMS OF COLIFORMS	Fathi Elham	Applied Microbiology
122	ISOLATION AND IDENTIFICATION OF LIPASE PRODUCING BACTERIA FROM OILY WASTEWATER	DIBANEZHAD NEDA	Applied Microbiology
123	PRODUCTION OF BIOPLASTIC FROM RHIZOBIUM LEGUMINOSARUM ISOLATED FROM CLOVER	Ghanaat Momeneh	Applied Microbiology
124	ISOLATION OF HALOPHILIC BACTERIA PRODUCING ANTIFUNGAL AGENTS FROM SEMNAN PROVINCES (IRAN)	Dilmaghani Azita	Applied Microbiology
125	OPTIMIZATION OF INDUCER CONCENTRATION FOR RECOMBINANT ACTIVIN A EXPRESSION	Biroonro Nahid	Applied Microbiology
126	RELATION BETWEEN ALKANE HYDROXYLASE GENE AND DEGRADATION OF CRUDE OIL BY SOME MARINE BACTERIA	Mehdipour Ziba	Applied Microbiology

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127	GENETIC DIVERSITY OF RHIZOSPHERE BACTERIA ASSOCIATED WITH DIFFERENT CHICKPEA CULTIVARS	Azizpour Nadia	Applied Microbiology
128	PAENIBACILLUS POLYMYXA A RHIZOSPHER BACTERIA OF CHICKPEA AS ANTAGONIST AGAINST ASCOCHYTA RABIEI	Azizpour Nadia	Applied Microbiology
129	DESIGN OF FR3 SYNTHETIC PEPTIDE AND EVALUATION OF ITS ANTIBACTERIAL AND CYTOTOXIC EFFECTS.	Ghahari Seyed Mohammad Mahdi	Applied Microbiology
130	OPTIMIZATION OF ENVIRONMENTAL CONDITION FOR BIO-PLASTIC (PHB) PRODUCTION BY ALCALIGENES EUTROPHA PTCC1615	Rasoli Mahasti	Applied Microbiology
131	DNA SHUFFLING OF A FAMILY OF ORGANOPHOSPHORUS HYDROLASE ENZYME	Rahimizadeh Rasool	Applied Microbiology
132	CLONING AND EXPRESSION OF RECOMBINANT GENE OF ORGANOPHOSPHORUS HYDROLASE ENZYME	Rahimizadeh Rasool	Applied Microbiology
133	SECRETORY POLYSACCHARIDE DEGRADING ENZYMES IN CERTAIN LOCAL YEAST SPECIES	Azadmard Azadeh	Applied Microbiology
134	ANTAGONISTIC ACTIVITIES OF TRICHODERMA SPP. ON SCLEROTINIA SCLEROTIORUMT ROT OF SUNFLOWER	Safari Seyed Majid	Applied Microbiology
135	MOLECULAR CLONING OF HYALURONAN SYNTHASE AND ITS EXPRESSION IN E. COLI BL21 (DE3)	Parsian Parsa	Applied Microbiology
136	CLONING AND EXPRESSION OF THE RECOMBINANT EPEX IN PICHIA PASTORIS	Zamani Mozhdeh	Applied Microbiology
137	AN INVESTIGATION ON THE STABILITY OF THE CATALYTIC DOMAIN OF DIPHTHERIA TOXIN IN SEPARATED SITUATION	Fatehi abdol abadi Mohammad	Applied Microbiology
138	ISOLATION AND IDENTIFICATION OF OIL- PRODUCING NOSTOC AS A POTENTIAL FOR BIODIESEL PRODUCTION	Solati Susan	Applied Microbiology
139	ISOLATION AND IDENTIFICATION OF PHB PRODUCING BACTERIA FROM WASTE OF FACTORY	Gholam veisi Nazila	Applied Microbiology
140	ISOLATION AND CLONING OF ASPERGILLUS NIGER GLUCOSE OXIDASE IN YARROWIA LIPOLYTICA EXPRESSION MONOCOPY VECTOR	Khadivi derakhshan Fatemeh	Applied Microbiology

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141	OPTIMIZATION OF CARBON AND NITROGEN SOURCES AND THEIR CONCENTRATION FOR ANTIMICROBIAL METABOLITES PRODUCTION BY STREPTOMYCES ACS135	Sadeghzadeh Mahsa	Applied Microbiology
142	THE EFFECT OF MINERAL PARAMETERS ON PRODUCTION OF BIOACTIVE COMPOUNDS BY STREPTOMYCES ACS 135	Sadeghzadeh Mahsa	Applied Microbiology
143	EVALUATION OF TOPICAL THERAPEUTIC EFFECTS OF EUCALYPTUS ESSENTIAL OIL ON EXPERIMENTAL MASTITIS CAUSED BY STREPTOCOCCUS AGALACTIAE	Jafari Hasan	Clinical Microbiology
144	ANTIBIOTIC RESISTANCE OF CLINICAL ISOLATES OF ACINETOBACTER BAUMANNII ISOLATED FROM PATIENTS IN A HOSPITAL IN ZAHEDAN, IRAN. نه	Sabbaghi Mahnaz	Clinical Microbiology
145	GENOTOXIC EFFECTS OF OUTER MEMBRANE VESICLES FROM A CLINICAL ISOLATE OF PSEUDOMONAS AERUGINOSA ON HUMAN PERIPHERAL BLOOD LYMPHOCYTES USING MICRONUCLEUS ASSAY	Aboutalebi Faezeh	Clinical Microbiology
146	ISOLATION AND CHARACTERIZATION OF OUTER MEMBRANE VESICLES FROM A CLINICAL ISOLATE OF PSEUDOMONAS AERUGINOSA	Aboutalebi Faezeh	Clinical Microbiology
147	EVALUATION OF ANITIBIOTICAL RESISTANCE PATTERN IN ESCHERICHIA COLI ISOLATED FROM URINARY TRACT CAUSING INFECTION REFERRED TO CURE CENTERS OF LAHIJAN CITY	Simaei Mehdi	Clinical Microbiology
148	DETERMINATION OF CORRELATION BETWEEN BIOFILM AND EXTENDED SPECTRUM B LACTAMASES PRODUCERS OF URINARY ESCHERICHIA	Ahmadi Ailin	Clinical Microbiology
149	DETECTION OF HELICOBACTER PYLORI IN PATIENTS WITH HYPERLIPIDEMIA BY PCR	Khodabakhshi Simin	Clinical Microbiology
150	BACTERIOLOGY OF URINARY TRACT INFECTION AND ANTIMICROBIAL SENSITIVITY AMONG DIABETIC PATIENTS AT SARLIRAN	Hejazi Fatemeh	Clinical Microbiology
151	DISSEMINATION OF MULTIDRUG-RESISTANT ACINETOBACTER BAUMANNII IN THE HOSPITAL ENVIRONMENT	Esmaeilee Torkanpoory Nasrin	Clinical Microbiology

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152	COMPARISON OF PSEUDOMONAS AERUGINOSA VIRULENT GENES(EXO,PHZ,LASA,LASB) IN CLINICAL SAMPLES	Ghobadi saki Bahareh	Clinical Microbiology
153	EFFECT OF SUB-INHIBITORY VANCOMYCIN AND LINEZOLID ON CLFA AND CLFB GENES EXPRESSION AND ADHESION OF METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS	Asadi Fatemeh	Clinical Microbiology
154	A CASE OF HUMAN WRIST SYNOVIAL INFECTION CAUSED BY ACCIDENTAL INJECTION OF ANIMAL VACCINE	Abad Mohsen	Clinical Microbiology
155	STUDYING THE OUTBREAK OF ANTIBIOTIC RESISTANCE GENES OF QUINOLONES IN ISOLATED BACTERIA OF URINARY TRACT INFECTION.	Monavari Atousa	Clinical Microbiology
156	DETECTION OF DIFFERENT SEROVARES OF SALMONELLA ENTRICA BY MULTIPLEX PCR IN DIARRHEA REFERED TO HOSPITALS OF SABZEVAR	Hosseini Fatemi Seyyed Mostafa	Clinical Microbiology
157	IDENTIFICATION OF ACNE RESONATOR BACTERIAL FACTORS AND CHECK THE ANTIBIOTIC RESISTANCE OF ISOLATED STRAINS	Dehghani champiri Iman	Clinical Microbiology
158	O-SEROTYPING OF ESCHERICHIA COLI ISOLATES COLLECTED FROM BROILERS WITH COLIBACILLOSIS IN ZABOL	Mirzayi Fateme	Clinical Microbiology
159	EVALUTION OF ANTILEISHMANIAL ACTIVITY OF THE ESSENTIAL OIL OF MEDICAGO LUPULINA' LEAVES AGAINST LEISHMANIA MAJOR (MHOM/IR/75/ER) PROMASTIGOTES BY USING MTT ASSAY	Gharirvand eskandari Elham	Clinical Microbiology
160	DESIGN, CONSTRUCTION AND EXPRESSION OF RECOMBINANT VECTOR CONTAINING THE RABIES VIRUS NUCLEOPROTEIN IN PROKARYOTIC EXPRESSION SYSTEM	Fadajan Zohreh	Clinical Microbiology
161	Isolation and identification of Bacteroides fragilis from chronic tonsillitis, Iraq	Yousif Maitham ghaly	Clinical Microbiology
162	AN ASSOCIATION STUDY BETWEEN LEWIS BLOOD GROUP PHENOTYPE AND IL-6 PRODUCTION BY P. AERUGINOSA STIMULATED PBMK	Alinezhad monfared Samaneh	Clinical Microbiology
163	BACTERIAL CONTAMINATION OF TOOTH BRUSH	Rigi Zeinab	Clinical Microbiology

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164	RESISTANCE AND ANTIBIOTIC SUSCEPTIBILITY PATTERN KLEBSIELLA PNEUMONIAE STRAINS ISOLATED FROM CLINICAL SPECIMENS IN EDUCATIONAL HOSPITAL IN ZAHEDAN	Ghaedi Maryam	Clinical Microbiology
165	IDENTIFICATION OF CAMPYLOBACTER JEJUNI, AND C. COLI IN URBAN DUCKS FECES IN THE NORTH OF IRAN	Saberi nik Elham	Clinical Microbiology
166	PREVALENCE OF SEASONAL CAMPYLOBACTER COLI IN DIARRHEIC SAMPLES BY USING PCR FROM KAZEROUN CITY	Fattahi Hossein	Clinical Microbiology
167	STAPHYLOCOCCUS AUREUS BURN WOUND INFECTION AMONG PATIENTS ATTENDING IMAM REZA HOSPITAL, MASHHAD, IRAN	Sedaghat Alireza	Clinical Microbiology
168	EVALUATION OF DIFFERENT DEGRESS OF DENTAL CARIES REGARDING TLR2 AND TLR4	Afkar Mohsen	Clinical Microbiology
169	IDENTIFICATION AND CHARACTERIZATION OF MUTACIN AND PUTATIVE BACTERIOCIN GENES IN ISOLATED STREPTOCOCCUS MUTANS AND ITS ANTIMICROBIAL ACTIVITY AGAINST GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA	Salehizadeh Mandana	Clinical Microbiology
170	A CLUE TO FIND THE NEW ANTIMICROBIAL PEPTIDES IN IRANIAN HONEYS.	Mahmoodi Khaledi Elahe	Clinical Microbiology
171	IS HYDROGEN PEROXIDE A CONSIDERABLE ANTIMICROBIAL AGENT OF ALL HONEY TYPES?	Mahmoodi Khaledi Elahe	Clinical Microbiology
172	RAPID DETECTION OF LEGIONELLA PNEUMOPHILA IN CLINICAL SPECIMENS OF PATIENTS WITH RESPIRATORY SYMPTOMS REFERING TO AHVAZ TEACHING HOSPITALS BY URINARY ANTIGEN AND PCR OF 16SRRNA GENE.	Khoshkholgh Sima Mahtab	Clinical Microbiology
173	IDENTIFICATION OF OQXAB EFFLUX PUMPS IN EXTENDED SPECTRUM-B-LACTAMASE- PRODUCING ENTEROBACTERIACEAE ISOLATES OF PATIENTS REFERING TO TEACHING HOSPITALS IN AHVAZ, IRAN.	Khoshkholgh Sima Mahtab	Clinical Microbiology
174	ANTIBIOTIC RESISTANCE OR MICROBIAL ANTAGONISM	Astaneh Mohammad Ebrahim	Clinical Microbiology

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175	SURVEYING THE PREVALENCE OF VARIOUS VIRULENCE FACTORS (ANTIBIOTIC RESISTANCE, BIOFILM FORMATION, COLONIZATION FACTORS) IN ACINETOBACTER BAUMANNII ISOLATES RECOVERED FROM CLINICAL SOURCES, BY PHENOTYPIC AND GENOTYPIC METHODS	Babapour Ebrahim	Clinical Microbiology
176	ISOLATION AND IDENTIFICATION OF NOCARDIA ASTEROIDS COMPLEX FROM A PATIENT WITH KERATITIS	Ahani Azin	Clinical Microbiology
177	IDENTIFICATION CAPSULAR GENES AS A SPECIFIC MARKER FOR THE DIFFERENTIATION OF STREPTOCOCCUS PNEUMONIA STRAINS FROM VIRIDANS GROUP	Asgari Ali	Clinical Microbiology
178	MUTATION SURVAY IN GYR (A) OF UREAPLASMA UREALYTICUM ISOLATED FROM WOMEN WITH PCR AND SEQUENCING, SANANDAJ CITY, IRAN	Safari Amir	Clinical Microbiology
179	AN INVESTIGATION INTO DRUG RESISTANCE AND BIOFILM FORMATION IN ESCHERICHIA COLI SEPARATED FROM PATIENTS AFFLICTED WITH URINARY TRACT INFECTION IN MARAGHEH.	Davari narj abad Elnaz	Clinical Microbiology
180	THE CAUSES OF BACTERIAL AND ANTIMICROBIAL RESISTANCE OF URINARY TRACT INFECTION IN CHILDREN REFERRED TO CHILDREN'S HOSPITAL OF TABRIZ	Ahmadizadeh Changiz	Clinical Microbiology
181	PREVALENCE OF EXFOLIATIVE TOXIN GENES IN STAPHYLOCOCCUS AUREUS ISOLATED FROM CLINICAL SPECIMENS	Rafiei Fariba	Clinical Microbiology
182	PREVALENCE OF BACTERIAL VAGINOSIS IN WOMEN REFERRED TO HEALTH CENTERS IN AHAR CITY AND ITS ANTIBIOTIC SUSCEPTIBILITY PATTERN	Azizi Arezoo	Clinical Microbiology
183	EVALUATION OF UPEC BIOFILM FORMATION AMONG ISOLATES FORM PATIENTS WITH UTI IN MILAD HOSPITAL, TEHRAN	Nosrati Sadaghiani Nafise	Clinical Microbiology
184	PREVALENCE AND ANTIMICROBIAL RESISTANCE PATTERNS OF NOSOCOMIAL INFECTIONS IN SAMPLES ABADAN WOUNDS AT TALEGHANI HOSPITAL IN 2015	Ghasemnezhad Masoumeh	Clinical Microbiology

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185	PREVALENCE AND ANTIMICROBIAL RESISTANCE OF STAPHYLOCOCCI ISOLATED FROM BLOOD CULTURES OF NEONATES ADMITTED IN PEDIATRIC WARD IN ABADAN HOSPITALS, 2015	Ghasemnezhad Masoumeh	Clinical Microbiology
186	EVALUATION OF INVA AND TTRC GENES IN CLINICAL SALMONELLA TYPHIMURIUM STRAINS BY MULTIPLEX-PCR METHOD AND DETERMINATION OF THEIR ANTIBIOTIC RESISTANCE PROFILE	Amiri Sareh	Clinical Microbiology
187	IDENTIFICATION OF ANTIMICROBIAL RESISTANCE GENES IN SALMONELLA SPECIES ISOLATED FROM CHILDREN WITH ACUTE INFECTIOUS DIARRHEA BY MULTIPLEX-PCR AND THEIR ANTIBIOTIC RESISTANCE PROFILE	Amiri Sareh	Clinical Microbiology
188	PREVALENCE OF INTESTINAL PARASITIC INFECTIONS IN MENTALLY/PHYSICALLY DISABLED CHILDREN AND ADOLESCENTS AND THEIR CAREGIVERS "SABZEVARAN" BOARDING CARE CENTER IN JIROFT CITY, IRAN	Ghasemi Nejad Almani Pooya	Clinical Microbiology
189	FREQUENCY OF AAC(3)-IIA GENE IN UROPATHOGENIC STRAINS OF ESCHERICHIA COLI IN WOMENS WHIT UTI IN SHAHREKORD TEACHING HOSPITALS USEAING PCR METHOD-2015	Miraliakbarian Seyed Alireza	Clinical Microbiology
190	ANTIMICROBIAL RESISTANCE AND MOLECULAR PREVALENCE OF EFFLUX PUMP ENCODING GENES (ADER, ADEB) IN ACINETOBACTER BAUMANNII STRAINS ISOLATED FROM HOSPITALIZED PATIENTS IN TEHRAN	Shabani Samaneh	Clinical Microbiology
191	STUDY THE ANTIMICROBIAL ACTIVITY OF SEA ANEMONE AGAINST ACINETOBACTER	Hamayeli Homa	Clinical Microbiology
192	MICROTITER PLATE ASSAY FOR ASSESSMENT OF LISTERIA MONOCYTOGENES BIOFILM FORMATION	Parvin Seyede sara	Clinical Microbiology
193	ISOLATION AND IDENTIFICATION OF ACINETOBACTER STRAINS WITH WIDESPREAD RESISTANCE TO VARIOUS ANTIBIOTIC FROM SPUTUM IN SHAHID RAJAEI HOSPITAL IN SHIRAZ	Baoosh Azadeh	Clinical Microbiology

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194	COMPARISON BETWEEN CAPSULAR POLYSACCHARIDE (PRP) EXTRACTED FROM HAEMOPHILUS INFLUENZA TYPE-B FROM CULTURE SUPERNATANT AND PELLET	Salahi Arezoo	Clinical Microbiology
195	MEASUREMENT OF ANTI BODY AGAINST HAEMOPHILUS INFLUENZA TYPE B (HIB) CAPSULAR POLYSACCHARIDE CONJUGATED WITH TETANUS TOXOID BY ELISA	Salahi Arezoo	Clinical Microbiology
196	EPIDEMIOLOGY OF HEALTH CARE ASSOCIATED CONJUNCTIVITIS AMONG NEONATES IN AN IRANIAN HOSPITAL 1000 BED-TERTIARY CARE HOSPITAL.	Mirjafari tafti Zahra sadat	Clinical Microbiology
197	ALTERATION IN CYTOKINES RESPONSE MAY PREDICT RELAPSE IN BRUCELLOSIS	AsriRezaei Siamak	Clinical Microbiology
198	DESIGN AND EXPRESSION OF RECOMBINANT CHIMERIC ANTIGEN SEQUENCE AS POLY TROPHIC UROPATHOGENIC ESCHERICHIA COLI	Sadeghi Niloufar	Clinical Microbiology
199	DETECTION OF VIRULENCE GENES PRODUCING URINARY TRACT INFECTION IN UROPATHOGENIC E. COLI ISOLATED FROM HUMAN SAMPLES	Salami khaneshan Elaheh	Clinical Microbiology
200	PREVALENCE OF PBP2B AND ALY GENES AMONG STREPTOCOCCUS PNEUMONIAE ISOLATED FROM CHILDREN BELOW 6 YEARS OF AGE	Karimy Elnaz	Clinical Microbiology
201	ANTIBACTERIAL ACTIVITY OF ZATARIA MULTIFLORA BOISS ESSENCE OIL AGAINST ESBL PRODUCING ISOLATES OF ESCHERICHIA COLI	Pourramezan Nasrin	Clinical Microbiology
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202	ANTIBACTERIAL ACTIVITY OF ZIZIPHORA CLINOPODIODES ESSENTIAL OIL AGAINST CLINICAL ISOLATES OF METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS (MRSA)	Pourramezan Nasrin	Clinical Microbiology
203	INCIDENCE OF CHLAMYDIA TRACHOMATIS INFECTION AND TNFA - 308 G/A POLYMORPHISM IN MISCARRIAGE.	DARVISHI KOLOR FATEMEH	Clinical Microbiology
204	DISCRIMINATION BETWEEN L.MONOCYTOGENES STRAINS ISOLATED FROM DIFFERENT CLINICAL AND FOOD SOURCES USING RAPD-PCR	Hemmati Azar	Clinical Microbiology

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205	EVALUATION THE RATE OF ANTIBIOTIC SUSCEPTIBILITY AND THE ANTIBIOTIC RESISTANCE OF ISOLATED ESCHERIA.COLI OF URINARY TRACT INFECTION OF THE TEHRAN MAHDIE HOSPITAL 'S IN MEHR MONTH 1394.	Akhlaghikia Amirreza	Clinical Microbiology
206	EVALUATION OF THE PREVALENCE OF THE HYA ,IUCD AND PAPE GENES AMONG ISOLATED UROPATHOGENIC STAINS OF ESCHERIACHOLI FROM THE PATIENTS OF TEHRAN MAHDIE HOSPITAL IN MEHR OF 1394.	Akhlaghikia Amirreza	Clinical Microbiology
207	PRODUCTION OF ANTI-BREAST CANCER DNA THERAPY VECTOR USING TOP10S	Hashemi Zahra Sadat	Clinical Microbiology
208	DETERMINATION OF ANTIBIOTIC RESISTANCE PATTERN AND PRODUCTION OF EXTENDED-SPECTRUM BETA-LACTAMASES AMONG DIARRHEAGENIC ESCHERICHIA COLI ISOLATES	Mahdavi Broojerdi Sanaz	Clinical Microbiology
209	MOLECULAR DETECTION OF BACTERIAL CAUSING URINARY TRACT INFECTION IN DIABETIC PATIENTS IN KERMANSHAH, IRAN	Yadollahi Farshad	Clinical Microbiology
210	E.COLI SECRETS RECOMBINANT HUMAN GROWTH HORMONE TO PERIPLASM BY MEANS OF XYLA SIGNAL PEPTIDE	AKBARI VAJIHE	Clinical Microbiology
211	FREQUENCY OF ANTIBIOTIC RESISTANCE IN PSEUDOMONAS AERUGINOSA ISOLATED FROM URINARY TRACT INFECTIONS (UTIS) IN RAJAEI HOSPITAL PATIENTS IN WINTER SEASON	Bonyanpour Elnaz	Clinical Microbiology
212	FREQUENCY OF TEM EXTENDED SPECTRUM BETA LACTAMASE PRODUCING ESCHERICHIA COLI IN URINE SPECIMENS BY PHENOTYPIC AND MOLECULAR METHODS IN KARAJ	Hamzeloo Shima	Clinical Microbiology
213	ISOLATION OF ANTIBIOTIC-RESISTANT STAPHYLOCOCCUS ARGENTEUS FROM SPUTUM SAMPLE	Fatehfard Pantea	Clinical Microbiology
214	DIAGNOSIS OF PULMONARY AND EXTRAPULMONARY TUBERCULOSIS WITH THE XPERT MTB/RIF ASSAY AND COMPARING ACCURACY WITH THE STANDARD CONVENTIONAL METHODS	Khoshkhoo Afsaneh	Clinical Microbiology

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215	CROSS SECTIONAL STUDY OF ESBL PRODUCER E. COLI ISOLATES FROM UTI PATIENTS OF PAYVAND'S LAB DURING 2014-15	Poopak Behzad	Clinical Microbiology
216	LACTAMASE GENE CODING FOR THE ENZYME AMPC IN CLINICAL ISOLATES OF KLEBSIELLA PNEUMONIAE	Dahmardeh Javad	Clinical Microbiology
217	MOLECULAR CHARACTERIZATION OF ESBLs KLEBSIELLA PNEUMONIAE ISOLATES COLLECTED FROM HOSPITALS IN ZAHEDAN	Dahmardeh Javad	Clinical Microbiology
218	MOLECULAR IDENTIFICATION OF MYCOPLASMA SPP ISOLATED FROM PATIENTS WITH MULTIPLE SCLEROSIS (MS) IN KERMAN PROVINCE.	Naghib Maryam	Clinical Microbiology
219	A SURVEY ON THE OCCURRENCE OF VANCOMYCIN RESISTANCE IN THE STAPHYLOCOCCUS AUREUS STRAINS ISOLATED FROM CLINICAL SPECIMENS	Alekhamis Vedad	Clinical Microbiology
220	ENTEROCOCCUS FAECALIS INFECTION AND BURN WOUND INFECTION	Khodadad Motlagh Mohammad	Clinical Microbiology
221	DESIGN OF AN INTERNAL POSITIVE CONTROL FOR MOLECULAR DETECTION OF YERSINIA PESTIS	Kabiri Khatereh	Clinical Microbiology
222	DESIGN AND DEVELOPMENT OF A COMPETITIVE INTERNAL POSITIVE CONTROL FOR THE DETECTION PLA AND CAF1 GENES OF YERSINIA PESTIS USING REAL TIME PCR	Kabiri Khatereh	Clinical Microbiology
223	EVALUATE PATIENT'S REFERRING TO THE MASSOUD LABORATORY FOR DIAGNOSIS MYCOBACTERIUM TUBERCULOSIS THROUGH 2013	Azizian Reza	Clinical Microbiology
224	COMPARISON BETWEEN TRADITIONAL AND MOLECULAR DIAGNOSTIC ORDERS FOR PATIENT WHO REFER TO THE MASSOUD LABORATORY FOR DIAGNOSIS MYCOBACTERIUM TUBERCULOSIS THROUGH 2014	Azizian Reza	Clinical Microbiology
225	DETECTION OF IINT-1,INT-2 AND CTX BETA-LACTAMASE GENES IN ESCHERICHIA COLI ISOLATED FROM URINARY TRACT INFECTION USING POLYMERASE CHAIN REACTION	Ahanjan Mohammad	Clinical Microbiology
226	THE PREVALENCE OF CHLAMYDIA AND GONOCOCCI CERVICAL INFECTION IN SYMPTOMATIC AND ASYMPTOMATIC WOMEN IN KASHAN-IRAN	Afrasiabi Shima	Clinical Microbiology

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227	PREVALENCE OF THE BLACTX-M-1 GENES GROUP AND THEIR TRANSFERABILITY IN CLINICAL ISOLATES OF SHIGELLA SEROGROUPS FROM HOSPITALS IN TEHRAN	Salimian rizi Kobra	Clinical Microbiology
228	COMPARISON OF ANTIBIOTIC RESISTANCE PATTERN OF BACTERIA CAUSING URINARY TRACT INFECTIONS IN OUTPATIENT AND INPATIENT OF SHAHIDMOHAMMADI HOSPITAL IN BANDARABBAS	Dehghan Farzaneh	Clinical Microbiology
229	COMPARISON OF ZNO NANOPARTICLE ANTIBACTERIAL EFFECT AGAINST CLINICAL ISOLATED STREPTOCOCCUS MUTANS AND STREPTOCOCCUS MUTANS PTCC 1683 USING SERIAL DILUTION METHOD	Esmaeilee Sarvenaz	Clinical Microbiology
230	FIRST REPORT OF DIVERSITY LEVELS AMONG ESCHERICHIA COLI ISOLATED FROM PATIENTS WITH DIFFERENT CLINICAL SYMPTOMS OF URINARY TRACT INFECTIONS IN TEHRAN, IRAN	Tabasi Mohsen	Clinical Microbiology
231	AN EVALUATION OF ASSOCIATION BETWEEN DENTAL PRACTICE AND COLONIZATION OF CANDIDA ALBICANS IN DENTISTS' MOUTHS	Zare Bidaki Majid	Clinical Microbiology
232	ANTIMICROBIAL EFFECTS OF PLANT EXTRACTS ON TEUCRIUM POLIUM RESISTANT STRAIN OF KLEBSIELLA PNEUMONIA	Gholizadeh Roqieh	Clinical Microbiology
233	THE FREQUENCY OF BLA VIM GENES IN CLINICAL ISOLATES OF PSEUDOMONAS AERUGINOSA AND BLO IMP CENTERS IN ZAHEDAN	Gholizadeh Roqieh	Clinical Microbiology
234	INVESTIGATION OF THE PRESENCE PSTS AND BLA OXA -50 RESISTANCE GENES TO ANTIBIOTICS IN P. AERUGINOSA STRAINS ISOLATED FROM DIFFERENT PARTS OF SHAHID TALEGHANI HOSPITAL OF CHALLUS USING PCR TECHNIQUE	Eiri Abdoljalil	Clinical Microbiology
235	MOLECULAR STUDY OF THE PREVALENCE OF CTX-M1, CTX-M2, CTX-M3 IN PSEUDOMONAS AERUGINOSA ISOLATED FROM CLINICAL SAMPLES IN TABRIZ TOWN, IRAN	Jafari sales Abolfazl	Clinical Microbiology
236	INTEGRONS ASSAY IN KLEBSIELLA STRAINS ISOLATED FROM URINARY TRACT INFECTIONS	Haddadi Azam	Clinical Microbiology

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237	PREVALENCE DETERMINATION OF ESBL-PRODUCING KLEBSIELLA ISOLATES AND THEIR ANTIMICROBIAL SUSCEPTIBILITY PATTERNS ISOLATED FROM KARAJ, IRAN	Haddadi Azam	Clinical Microbiology
238	DETECTION OF KLEBSIELLA PNEUMONIAE PRODUCING CARBAPENEMASE BY MODIFIED HODGE TEST FROM CLINICAL SAMPLES OF TOHID HOSPITAL IN SANANDAJ	SHAKIB PEGAH	Clinical Microbiology
239	PREVALENCE OF VIRULENCE FACTORS AND VANCOMYCIN-RESISTANT GENES AMONG ENTEROCOCCUS FAECALIS AND ENTEROCOCCUS FAECIUM ISOLATED FROM CLINICAL SPECIMENS	Hosseini Seyed mostafa	Clinical Microbiology
240	INFECTIONS AND INCREASED RATE OF DIABETES MELLITUS: IS THERE A LINK?	Zahedi Abed	Clinical Microbiology
241	BRAIN ENCEPHALITIS DUE TO MELANIZED FUNGI; HOW COME WE ARE ALIVE?	Badali Hamid	Clinical Microbiology
242	EVALUATION OF AMINOGLYCOSIDES RESISTANCE GENES AMONG BETA LACTAMASE PRODUCING ESCHERICHIA COLI	Sorayaei Vida	Clinical Microbiology
243	COMPARISON OF RT-PCR AND NESTED-PCR ASSAYS AND VIRUS ISOLATION FOR DETECTION OF INFECTIOUS BRONCHITIS VIRUS IN BROILER FLOCKS WITH RESPIRATORY TRACT SYNDROME	Azizpour Aidin	Clinical Microbiology
244	THE PREVALENCE OF ANAPLASMA IN SHEEP AND CATTLE IN KURDISTAN PROVINCE, IRAN	Khezri Mohammad	Clinical Microbiology
245	THE PREVALENCE OF THEILERIA OVIS IN SHEEP IN KURDISTAN PROVINCE, IRAN	Khezri Mohammad	Clinical Microbiology
246	THE PREVALENCE OF HELCOBACTER PYLORI GENOTYPES ACCORDNG TO CAGA, CAGM AND CAGE GENES IN IRANIAN PATIENTS WITH GASTRIC ADENOCARCINOMA	Bahadori Ali	Clinical Microbiology
247	EFFICACY OF DDAC ON EXTEND – SPECTRUM – BETA LACTAMASE (ESBL) ARE PRODUCING BY E.COLI STRAINS	Mirlahiji Syedeh golchereh	Clinical Microbiology
248	EPIDEMIOLOGICAL SURVEY OF MENINGITIS IN SOUTH KHORASAN PROVINCE IN 2011-2015	Bijari Bita	Clinical Microbiology

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249	EVALUATION OF SERUM C-REACTIVE PROTEIN AND ITS RELATIONSHIP WITH CAUSATIVE FACTOR IN URINARY TRACT INFECTION	Naghmachi Mohsen	Clinical Microbiology
250	MOLECULAR DETECTION AND ANTIMICROBIAL RESISTANCE OF INTESTINAL PATHOTYPES OF ESCHERICHIA COLI IN KHUZESTAN PROVINCE	Mashhadikarimdarbandi Atieh	Clinical Microbiology
251	THE PREVALENCE OF ESBL-PRODUCING PSEUDOMONAS AERUGINOSA ISOLATED FROM CLINICAL SAMPLES IN TABRIZ TOWN	Shadi Dizaji Azizeh	Clinical Microbiology
252	A STUDY OF THE INHIBITION OF BIOSURFACTANT ON IN VITRO BIOFILM FORMATION BY BACTERIAL PATHOGENS: APPLICATION OF MALDI-TOF MS IN STRAIN IDENTIFICATION AND CHARACTERISATION OF THE LIPOPEPTIDES	Khonsari Shadi	Clinical Microbiology
253	DIAGNOSIS OF ACUTE Q FEVER IN THREE PATIENTS WITH A HISTORY OF CONSUMING UNPASTEURIZED DAIRY BY NESTED-PCR IN KHORRAMABAD CITY	Ferdosi Farnaz	Clinical Microbiology
254	MOLECULAR DIAGNOSIS OF ACUTE Q FEVER IN TWO PATIENTS WITH POSITIVE WRIGHT TEST IN KHORRAMABAD CITY	Ferdosi Farnaz	Clinical Microbiology
255	ISOLATION AND ANTIBIOTIC SUSCEPTIBILITY PATTERNS OF SHIGELLA AND SALMONELLA SPECIES AMONG CHILDREN WITH ACUTE DIARRHEA	Amiri Kiana	Clinical Microbiology
256	PREVALENCE OF UROPATHOGENS BACTERIA AND THEIR ANTIMICROBIAL SUSCEPTIBILITY PATTERNS ISOLATED FROM CHILDREN	Amiri Kiana	Clinical Microbiology
257	RELATIONSHIP BETWEEN BIOFILM PRODUCTION AND FREQUENCY OF VIRULENCE GENES IN CLINICAL ISOLATES OF PSEUDOMONAS AERUGINOSA AT A UNIVERSITY HOSPITAL IN URMIA, IRAN	Yousefi Saber	Clinical Microbiology
258	EVALUATION OF THE RELATIONSHIP BETWEEN PATIENTS' AGE AND PHENOTYPIC/GENOTYPIC CHARACTERISTICS OF UROPATOGENIC E. COLI ISOLATES DERIVED FROM HOSPITALIZED WOMEN WITH URINARY TRACT INFECTION	Ghazvini Zohreh	Clinical Microbiology

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259	EFFECTS OF CENTRAL RECEPTOR OF H1 AND H2 ON THE AMOUNT OF BROILER WATHER AND FOOD USAGE	Salahi Safoura	Clinical Microbiology
260	HEMAGGLUTINATION PROPERTIES OF PROTEUS MIRABILIS ISOLATED FROM URINARY TRACT INFECTIONS	Mirzaei Arezoo	Clinical Microbiology
261	DETECTION OF ARMA,TET(39),AND THE INSERTION SEQUENCE ISABA4 GENES AMONG ACINETOBACTER BAUMANNII CLINICAL STRAINS ISOLATED FROM THE UNIVERSITY HOSPITAL IN TEHRAN BY PCR AND SEQUENCING TECHNIQUES.	Khiabani rad Parvaneh	Clinical Microbiology
262	PREVALENCE OF CTX-M 1 EXTENDED-SPECTRUM -LACTAMASE-PRODUCING ESCHERICHIA COLI AND KLEBSIELLA PNEUMONIAE IN PATIENTS WITH LUKEMIA	Roshani Mahdane	Clinical Microbiology
263	THE PREVALENCE OF URINARY AND ENTERIC INFECTIONS IN IMAM-KHOMEINI HOSPITAL IN SHIRVAN IN NORTH-KHORASAN PROVINCE IN 2015	Hamidi hesari Moein	Clinical Microbiology
264	CONSTRUCTION OF A RECOMBINANT BACMID DNA CONTAINING INFLUENZA A VIRUS HEMAGGLUTININ GENE USING A SITE-SPECIFIC TRANSPOSITION MECHANISM	Shafaati Mohammadreza	Clinical Microbiology
265	PREVALENCE OF BACTERIAL VAGINOSIS AND SENSITIVITIES TO DIFFERENT ANTIBIOTICS IN FERTILE/INFERTILE WOMEN REFERRING TO ARDABIL HEALTH CENTERS	Baezzat Elnaz	Clinical Microbiology
266	GENETIC ANALYSIS OF PERTUSSIS TOXIN SUBUNIT3 AMONG BORDETELLA PERTUSSIS ISOLATES IN IRAN	Shahbazi Tayebe	Clinical Microbiology
267	POLYMORPHISM OF FIMBRIAE AND PERTACTIN GENES AMONG BORDETELLA PERTUSSIS CLINICAL ISOLATES ON 2014-2016	Shahbazi Tayebe	Clinical Microbiology
268	INVESTIGATING THE INCIDENCE OF BLOODSTREAM INFECTIONS IN KHATAM-OL-ANBIA HOSPITAL IN GONBAD IN 2015	Samiei Mahdi	Clinical Microbiology
269	CONSIDERATION THE REASONS OF SUPPURATION IN PEDUNCLE DORSAL IN RAINBOW TROUT IN KERMAN	Yazdanpanah Laleh	Clinical Microbiology
270	PREVALENCE OF TEM AND PER TYPE EXTENDED SPECTRUM B-LACTAMASES IN ACINETOBACTER BAUMANNII CLINICAL ISOLATES BY PCR	Shams Nasim	Clinical Microbiology

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271	EVALUATION OF ANTIMICROBIAL ACTIVITY OF (5-NITRO-2-FURYL)& (5-NITRO-2-IMIDAZOLYL)-1,3,4-THIADIAZOLE DERIVATIVES	Moshafi Mohammad Hassan	Clinical Microbiology
272	PREVALENCE OF CNA, FNBA, FNBB AND PVL AS SPREADING FACTORS RELATED GENES IN CLINICAL ISOLATED STAPHYLOCOCCUS AUREUS BY MULTIPLEX COLONY PCR	Mirzaei Bahman	Clinical Microbiology
273	COMPARISON BETWEEN PHENOTYPIC AND GENOTYPIC FEATURES IN CLINICAL ISOLATED STAPHYLOCOCCUS EPIDERMIDIS.	Mirzaei Bahman	Clinical Microbiology
274	KELEBSIELLA RHINOSCLEROMA: A DIAGNOSTIC CHALLENGE FOR NASAL/UPPER RESPIRATORY TRACT GRANULOMATOUS INFECTION REPORT OF TWO CASES AND REVIEW OF THE LITERATURE	Shafaeian Bahman	Clinical Microbiology
275	DETECTION OF ENTEROPATHOGENIC ESCHERICHIA.COLI STRAINS ISOLATED FROM CHILDREN WITH DIARRHEA IN AHVAZ	Sirous Mehrandokht	Clinical Microbiology
276	EVALUATING HEPATITIS B VACCINE EFFICACY IN IRANIAN MEDICAL STUDENTS AND HEALTHCARE WORKERS- A META-ANALYSIS STUDY	Azami Milad	Clinical Microbiology
277	COMPARISON OF DOMVS AND NOMVS IMMUNIZATION AS A NEW CHOLERA VACCINE	Rezaei Razieh	Clinical Microbiology
278	RAPID DIAGNOSIS OF LEPTOSPIROSIS BY PCR BASED ON LIGA GENE	Salahedin Seyed mohsen	Clinical Microbiology
279	FATAL GASTROINTESTINAL AND SEPTICEMIC ANTHRAX AFTER EATING THE CONTAMINATED GOAT MEAT, NORTH EASTERN IRAN, BOJNURD	Nojoomi Sara	Clinical Microbiology
280	DETECTION OF CAMPYLOBACTER IN STOOL SAMPLES OF CHILDREN AND OTHER DIARRHEIC SAMPLES IN PASTEUR MEDICAL LABORATORY FROM ARAK-IRAN	Salehi Marjan	Clinical Microbiology
281	BIODEGRADATION AND DECOLORIZATION (DAYS CONGO RED INDIGOCARMINE) BY SOME SPECIES OF THE BACTERIA (BACILLUS AND ACINETOBACTER)	Chalabzardi Mitra	Clinical Microbiology
282	MOLECULAR STUDY OF PER, VEB AND FOC GENS IN ACINETOBACTER BAUMANNI ISOLATED FROM PATIENS IN HOSPITAL MOSTAFA KHOMEINI IN ILAM CITY	Chalabzardi Mitra	Clinical Microbiology

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283	ISOLATION AND IDENTIFICATION OF MOLECULAR CHLAMYDIA TRACHOMATIS FROM GENITAL TRACT OF FERTILE WOMEN REFERRING TO AFZALIPOUR INFERTILITY HOSPITAL IN KERMAN	Rafati Samaneh	Clinical Microbiology
284	EVALUATION OF ANTI-BACTERIAL EFFECTS OF COLLOIDAL SILVER NANOPARTICLES ON BIOFILM PRODUCTION OF HOSPITAL ASSOCIATED METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS WITH MULTIDRUG RESISTANT	Ghahremany Maryam	Clinical Microbiology
285	IMMUNOTHERAPY EFFECTS ON ENTEROCOCCUS FAECALIS (A MICROFLORA BACTERIA) VIRULENCE GENES IN PROSTATE CANCER PATIENTS	Talebzadeh Tayebbeh	Clinical Microbiology
286	THE ACTIVITY OF FOSFOMYCIN AGAINST ESCHERICHIA COLI ISOLATES FROM URINARY TRACT INFECTIONS	Aris Parisa	Clinical Microbiology
287	COMPARATIVE EVALUATION OF THE ANTIBACTERIAL SUSCEPTIBILITY TEST OF RESAZURIN-PLATE AND QUICOLOR COLORIMETRIC METHODS	Siamaki Shahla	Clinical Microbiology
288	COMBINED EFFECT OF PHOSPHOMYCIN AND B-CHLORO-L-ALANINE ON BIOFILM PRODUCTION BY METHICILLIN RESISTANT S.AUREUS	Akbari ayezloy ELHAM	Clinical Microbiology
289	PREVALENCE OF ESP, CYLA GENES IN CLINICAL ISOLATES OF ENTEROCOCCUS FAECALIS	Malekei Naeim	Clinical Microbiology
290	DETECTION OF BORRELIA MICRITI INFECTION IN MICE BY WESTERN BLOT ANALYSIS	Naeimi Sabah	Clinical Microbiology
291	ASSOCIATION OF HELICOBACTER PYLORI INFECTION WITH THE ABO AND RH BLOOD GROUPS IN IN MILITARY STUDENTS AND SOLDIERS	Naimi Adel	Clinical Microbiology
292	DISCUSSING THE ANTIBIOTIC RESISTANCE OF ESCHERICHIA COLI BACTERIA FOUND IN URINAL INFECTION OF WOMEN	Rahbarei Kamran	Clinical Microbiology
293	PHENOTIPIC AND GENOTIPIC SCREENING OF VIRULENCE FACTORS OF ENTEROCOCCUS FAECIUM AND ENTEROCOCCUS FAECALIS ISOLATED FROM ZANJAN HOSPITALS	Lohrasbi Vahid	Clinical Microbiology

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294	DESIGN AND EVALUATION OF A NOVEL KIT FOR RAPID DETECTION OF STREPTOCOCCUS PYOGENES FROM PHARYNGEAL SPECIMENS	Rahimi moghaddam Akram	Clinical Microbiology
295	THE RELATIONSHIP OF HELICOBACTER PYLORI INFECTION AND SERUM LEVEL OF FERRITIN, TIBC, TRANSFERRIN AND IL-17 IN INFECTED AND HEALTHY CHILDREN	Salehi Mohammad	Clinical Microbiology
296	PREVALENCE OF HELICOBACTER PYLORI INFECTION IN NEYSHABUR, IRAN DURING 2010-2014	Salehi Mohammad	Clinical Microbiology
297	RELATIONSHIP BETWEEN HELICOBACTER PYLORI CAGE GENE AND CAGA STATUS AND RISK OF HISTOLOGIC SUBTYPE GASTRIC ADENOCARCINOMAS IN IRAN	Gholizade tobnagh Shokufe	Clinical Microbiology
298	RELEVANCE OF CAGA, AND CAGE GENOTYPES OF HELICOBACTER PYLORI CAG PATHOGENICITY ISLAND TO CARDIA- AND NON-CARDIA-CANCER	Gholizade tobnagh Shokufe	Clinical Microbiology
299	OCCURRENCE OF SEA, SEP AND SCN GENES IN METHICILIN-RESISTANT STAPHYLOCOCCUS AUREUS ISOLATES	Ariyarad Simin	Clinical Microbiology
300	ANTIMICROBIAL RESISTANCE PATTERN OF PATHOGENIC BACTERIA ISOLATED FROM CLINICAL SAMPLES (ROUHHANI AND YAHYANEJAD HOSPITALS)	Sadighian Farahnaz	Clinical Microbiology
301	THE SERO-EPIDEMIOLOGY OF INFECTIOUS MONONUCLEOSIS IN NEYSHABUR DURING 2010-2014	Salehi Mohammad	Clinical Microbiology
302	PHENOTYPIC DETECTION OF ESBL AND AMPC BETA-LACTAMASE IN CLINICAL ISOLATES OF ESCHERICHIA COLI	Dehghani Maryam	Drug Resistance
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303	ANTIBIOTIC RESISTANCE IN YERSINIA ENTEROCULITICA ISOLATED FROM BROILER MEAT IN ARDABIL	Shekari Somayeh	Drug Resistance
304	AdeABC efflux pump genes in multidrug resistant Acinetobacter baumannii isolated from patients in Baghdad, Iraq	Kassim Kais	Drug Resistance
305	AdeABC efflux pump genes in multidrug resistant Acinetobacter baumannii isolated from patients in Baghdad, Iraq	Kassim Kais	Drug Resistance
306	EVALUATION OF PLASMID MEDIATED ANTIBIOTIC RESISTANT PATTERN IN LACTOBACILLUS SPP ISOLATED FROM DRUG PRODUCTS AVAILABLE IN IRAN	Shafiei seifabadi Fatemeh	Drug Resistance

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307	INCREASING TREND OF IMPENEM-RESISTANCE AMONG ACINETOBACTER BAUMANNII ISOLATED FROM HOSPITAL ACQUIRED PNEUMONIA IN NORTHEAST OF IRAN	Ghazvini Kiarash	Drug Resistance
308	DESIGN AND DISCOVERY OF ANTIBACTERIALS TARGETING RIBOSWITCHES: BACKGROUND AND PERSPECTIVES	Mehdizadeh Aghdam Elnaz	Drug Resistance
309	FLORA BACTERIAL CONTAMINATION OF ANNUAL STOOL SAMPLES IN ZAHEDAN TEACHING HOSPITALS TO COMPARE THE DISTRIBUTION OF THE SAMPLES SHIGELLA, SALMONELLA, ANTIBIOTIC SENSITIVITY AND ANTIBODY TITER	Hosseini Hadi	Drug Resistance
310	FREQUENCY OF VANC GENE IN VANCOMYCIN-RESISTANT ENTEROCOCCUS ISOLATED FROM CLINICAL SAMPLES	Lohrasbi Vahid	Drug Resistance
311	IDENTIFICATION OF DRUG RESISTANT ACINETOBACTER BAUMANNII AMONG BURN PATIENTS	Shoja Saeed	Drug Resistance
312	THE PREVALENCE SURVEY AND ANTIBIOTIC RESISTANT IN ENTEROCOCCI SPP. ISOLATED FROM DELIVERY ROOMS OF TWO UNIVERSITY HOSPITAL IN QOM, IRAN IN 2015	Kabiri Faezeh	Drug Resistance
313	HIGH PREVALENCE OF MULTIPLE DRUG RESISTANCE (MDR) AMONG ESBLs-PRODUCING KLEBSIELLA PNEUMONIAE ISOLATED FROM HOSPITALIZED PATIENTS IN ISFAHAN, IRAN	Tahanasab Zahra	Drug Resistance
314	EVALUATION OF ANTIBIOTIC RESISTANCE PATTERN AND SEROTYPING OF UROPATHOGENIC ESCHERICHIA COLI ISOLATED FROM HOSPITALIZED PATIENT IN BASHT, IRAN	Pooransari Razieh	Drug Resistance
315	DETECTION OF BLA NDM -1, BLA VIM AND BLA IMP GENES IN ACINETOBACTER BAUMANNII AT TEHRAN HOSPITALS BY PCR AND GENE SEQUENCING	Erfani Yousef	Drug Resistance
316	EMERGING OF A NEW ANTIBIOTIC RESISTANCE BACTERIA PATHOGEN, ACINETOBACTER LWOFII IN WATER ENVIRONMENTS AND THEIR PATHOGENIC EFFECTS	Dadar Maryam	Drug Resistance

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317	PREVALENCE AND SUSCEPTIBILITY PATTERNS OF VANCOMYCIN RESISTANT ENTEROCOCCUS FAECIUM ISOLATES IN UNIVERSITY HOSPITALS IN AHWAZ	Arshadi Maniya	Drug Resistance
318	GENOTYPING OF MULTIDRUG-RESISTANT STRAINS OF PSEUDOMONAS AERUGINOSA ISOLATED FROM BURN AND WOUND INFECTIONS BY ERIC-PCR	Hoveizavi Hajar	Drug Resistance
319	EVALUATION OF SALMONELLA ENTERITIDIS RESISTANCE TO BETA-LACTAM DRUGS IN KHUZESTAN PROVINCE	Zandi Sedighe	Drug Resistance
320	INVESTIGATION OF ANTIBACTERIAL EFFECT OF POTENTILLA ANSERINA AGAINST STAPHYLOCOCCUS AUREUS STRAINS RESISTANT TO ANTIBIOTICS OF CHOICE	Vaseghi kale daragh Samad	Drug Resistance
321	EVALUATION OF ANTIBIOTIC RESISTANCE IN E. COLI STRAINS ISOLATED FROM URINARY TRACT INFECTIONS	Vaseghi kale daragh Samad	Drug Resistance
322	INVESTIGATION OF ANTIBACTERIAL EFFECT OF NATIVE BLACK PEPPER HYDRO-ALCOHOLIC EXTRACTS ON ANTIBIOTIC-RESISTANT STREPTOCOCCUS PNEUMONIAE	Vaseghi kale daragh Samad	Drug Resistance
323	IN VITRO ACTIVITY OF GENTAMICIN IN COMBINATION WITH IMIPENEM AND PIPERACILLIN AGAINST RESISTANT ISOLATES OF PSEUDOMONAS AERUGINOSA .	BAHRAMI ABDEHGAH IMAN	Drug Resistance
324	DETERMINATION ANTIBIOTIC RESISTANCE PROFILE OF PSEUDOMONAS AERUGINOSA STRAINS ISOLATED FROM HOSPITALIZED PATIENTS IN SOUTHWEST HOSPITALS OF IRAN.	BAHRAMI ABDEHGAH IMAN	Drug Resistance
325	A INVESTIGATION ON CLASS 3 INTEGRON BETWEEN ESCHERICHIA COLI CLINICAL SAMPLES, KURDISTAN PROVINCE, IRAN	Akhdar Sako	Drug Resistance
326	FREQUENCY OF EXO Y GENE IN ISOLATES OF PSEUDOMONAS AERUGINOSA WITH MULTI-DRUG RESISTANCE	Nazaraliyan Shima	Drug Resistance
327	DETERMINATION OF ANTIMICROBIAL RESISTANCE PATTERN OF ACINETOBACTER BAUMANII ISOLATED FROM TEHRAN HOSPITALS	Mousavi sani Akram sadat	Drug Resistance

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328	PREVALENCE OF OXA-TYPE B-LACTAMASES GENES AMONG ACINETOBACTER BUMANNII ISOLATED FROM TEHRAN HOSPITALS	Mousavi sani Akram sadat	Drug Resistance
329	STUDY OF DRUG-RESISTANT STAPHYLOCOCCUS AUREUS IN RAW MILK AND CHEESE SAMPLES IN KERMAN PROVINCE	Heydari gharaei Hamid	Drug Resistance
330	PREVALENCE AND DRUG RESISTANCE PATTERNS IN PSEUDOMONAS AERUGINOSA ISOLATED FROM PATIENTS REFERRING TO HOSPITALS IN KERMAN PROVINCE	Heydari gharaei Hamid	Drug Resistance
331	EVALUATION OF THE ISOLATED BACTERIAL DIVERSITY FROM PATIENTS WITH DIABETIC FOOT INFECTION AND DETERMINATION OF THEIR ANTIBIOTIC RESISTANCE PATTERNS	Nahid Noushin	Drug Resistance
332	A COMPARATIVE STUDY OF VARIOUS METHODS FOR DETECTION OF DRUG SUSCEPTIBILITY TEST IN PATIENTS WITH SUSPECTED TB REFERRED TO PASTEUR INSTITUTE OF IRAN	Sakhaee Fatemeh	Drug Resistance
333	MOLECULAR ANALYSIS OF METALLO BETA-LACTAMASE RESISTANCE GENES AMONG UROPATHOGENIC ESCHERICHIA COLI ISOLATED FROM URINE OF PATIENTS WITH URINARY TRACT INFECTION	Shahbazi Shahla	Drug Resistance
334	ANTIMICROBIAL RESISTANCE OF SALMONELLA SPP. AND ESCHERICHIA COLI ISOLATED FROM TABLE EGGS	Ghadiri Amirhossein	Drug Resistance
335	ANTIBIOTIC RESISTANCE PATTERN OF E. COLI O157:H7/NM ISOLATES FROM FECAL SAMPLES OF HEALTHY OSTRICH IN LORESTAN PROVINCE	Shams Nemat	Drug Resistance
336	METALLO-BETA-LACTAMASE BLAVIM AND BLAIMP GENES AMONG KLEBSIELLA PNEUMONIAE ISOLATED FROM HOSPITALS OF KHORRAMABAD, IRAN	Goudarzi Gholamreza	Drug Resistance
337	ANTIBIOTIC RESISTANCE OF KLEBSIELLA PNEUMONIA ISOLATES IN URINARY TRACT INFECTIONS IN IMAM KHOMEINI HOSPITAL, SHIRVAN, IRAN, 2015	Hamidi hesari Moein	Drug Resistance

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338	ASSESSMENT OF ANTIBIOTIC RESISTANCE OF STAPHYLOCOCCUS SPECIES ISOLATED OF NEONATAL INTENSIVE CARE UNIT (NICU) OF MOBINI HOSPITAL IN SABZEVAR.	Haghighi Faezeh	Drug Resistance
339	DETERMINATION OF ANTIBIOTIC SUSCEPTIBILITY PATTERNS AMONG ESBL PRODUCING UROPHATOGENIC E.COLI	Mirkalantari Shiva	Drug Resistance
340	CLASS 1 INTEGRON DISTRIBUTION IN S.MALTOPHILIA CLINICAL AND ENVIRONMENTAL ISOLATES	Nemati Amir Hesam	Drug Resistance
341	ANTIMICROBIAL SUSCEPTIBILITY ASSAY AND PFGE TYPING OF S.MALTOPHILIA CLINICAL AND ENVIRONMENTAL ISOLATES FROM BLOOD SAMPLES	Nemati Amir Hesam	Drug Resistance
342	PREVALENCE AND ANTIBIOTIC SUSCEPTIBILITY IN KLEBSIELLA PNEUMONIAE ISOLATES FROM PATIENTS WITH URINARY TRACT INFECTION, ISFAHAN, IRAN.	Maleki Nafiseh	Drug Resistance
343	DETERMINATION OF ANTIBIOTIC RESISTANCE PATTERN AND CHECK AMINOGLYCOSIDE RESISTANCE IN PSEUDOMONAS AERUGINOSA	Mahdiun Faeze	Drug Resistance
344	HIGH PREVALENCE OF MACROLID RESISTANCE AMONG CAMPYLOBACTERS ISOLATED FROM DYSENTERY PATIENTS IN MARKAZI PROVINCE - 2015	Abbasi Elnaz	Drug Resistance
345	HIGH ANTIBIOTIC SUSCEPTIBILITY OF LACTOBACILLUS SPP. ISOLATED FROM DAIRY PRODUCTS	Yekani Mina	Drug Resistance
346	ANTIBIOTIC SUSCEPTIBILITY PATTERN OF MRSA FROM HOSPITALIZED NASAL CARRIAGE IN CARDIOTHORACIC CENTER	Yekani Mina	Drug Resistance
347	FREQUENCY AND ANTIBIOTIC SUSCEPTIBILITY PATTERN OF STAPHYLOCOCCUS AUREUS ISOLATED FROM WOUND INFECTIONS	Yekani Mina	Drug Resistance
348	HIGH LEVEL DISINFECTANT RESISTANCE IN CLINICALLY ISOLATED ESBL POSITIVE E. COLI IN A TERTIARY CARE HOSPITAL	Shafaati Maryam	Drug Resistance
349	CORRELATION BETWEEN QACE AND QACEΔ1 EFFLUX PUMP GENES, ANTIBIOTIC AND DISINFECTANT RESISTANT AMONG CLINICAL ISOLATES OF E.COLI	Shafaati Maryam	Drug Resistance

Row	Title	Submission Author	Session
350	HIGH PREVALENCE OF TRIMETHOPRIM RESISTANCE IN E. COLI ISOLATES FROM THALASSEMIA INFECTED PATIENTS IN KERMAN, IRAN	Alizade Hesam	Drug Resistance
351	SURVEY OF RESISTANT TO AMINOGLYCOSIDE IN ESCHERICHIA COLI ISOLATES FROM HIV PATIENTS IN SOUTHEAST OF IRAN (KERMAN)	Alizade Hesam	Drug Resistance
352	FREQUENCY AND ANTIBIOGRAM PATTERN OF PSEUDOMONAS AERUGINOSA SPECIES ISOLATED FROM CLINICAL SPECIMENS IN SHAHID MOHAMMADI HOSPITAL	Javadpour Sedigheh	Drug Resistance
353	MRSA IN SURGICAL SITE INFECTIONS; FREQUENCY AND VANCOMYCIN MIC	Memar Mohammad yousef	Drug Resistance
354	PREVALENCE AND ANTIMICROBIAL SUSCEPTIBILITY PATTERNS OF BACTERIA ISOLATED FROM URINARY TRACT INFECTIONS IN FULAD-SHAHR, IRAN	Ghanbari Fahimeh	Drug Resistance
355	ANTIMICROBIAL RESISTANCE PATTERNS OF ESCHERICHIA COLI ISOLATES FROM BROILER FLOCKS IN ARDABIL PROVINCE TO SIX ANTIBACTERIAL AGENTS COMMONLY USED IN THE IRANIAN POULTRY INDUSTRY	Azizpour Aidin	Drug Resistance
356	FAECAL CARRIAGE OF ESBL AND PLASMID-MEDIATED AMPC B-LACTAMASE GENES IN KLEBSIELLA SPP. AND SHIGELLA SPP. ISOLATED FROM INPATIENT AND OUTPATIENT CARRIERS IN TABRIZ, IRAN	Zahedi Abed	Drug Resistance
357	EPIDEMIOLOGY OF DRUG-RESISTANT KLEBSIELLA PNEUMONIAE IN IRAN: A SYSTEMATIC REVIEW	Heidary Mohsen	Drug Resistance
358	PREVALENCE OF DRUG-RESISTANT PSEUDOMONAS AERUGINOSA IN IRANIAN BURNED PATIENTS: SYSTEMATIC REVIEW AND META-ANALYSIS	Heidary Mohsen	Drug Resistance
359	SIMPLE METHOD FOR ASSESSMENT MDR ACINETOBACTER BAUMANNII BY AGAR ETHIDIUM BROMIDE CARTWHEEL METHOD	Sepehr Amin	Drug Resistance
360	HIGH PREVALENCE OF CLINICAL AND ENVIRONMENTAL TRIAZOLE RESISTANT ASPERGILLUS FUMIGATUS IN IRAN: IS IT A CHALLENGING ISSUE?	Badali Hamid	Drug Resistance

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361	STUDY OF ANTIBIOTIC RESISTANCE PATTERNS IN KLEBSIELLA PNEUMONIA ISOLATED FROM PATIENTS REFERRED TO HOSPITALS OF SEMNAN	Bineshian Farahnaz	Drug Resistance
362	RESISTANCE TO NALIDIXIC ACID AND AZITHROMYCIN IN SALMONELLA ENTERIC STRAINS ISOLATED FROM BLOOD STREAM INFECTION	Mardaneh Jalal	Drug Resistance
363	THE BLACK SEED MINIMAL BACTERICIDAL CONCENTRATION AGAINST GRAM POSITIVE BACTERIA	Mardaneh Jalal	Drug Resistance
364	DETECTION CARBAPENEM-RESISTANT PSEUDOMONAS AERUGINOSA ISOLATES BY PHENOTYPIC METHODS	Mardaneh Jalal	Drug Resistance
365	SURVEY OF DISTRIBUTION RATES AND ANTIBIOTIC RESISTANCE PATTERN OF GROUP B STREPTOCOCCI (STREPTOCOCCUS AGALACTIAE) STRAINS ISOLATED FROM CLINICAL SPECIMENS	Hosseini Seyed mostafa	Drug Resistance
366	PHENOTYPIC HODGE TEST APPLICATION FOR GRAM POSITIVE AND GRAM NEGATIVE BACILLI BACTERIA CARBAPENEMASE ENZYME PRODUCER ISOLATED FROM NON-BIOLOGICAL ENVIRONMENTS OF HOSPITAL	Rouhi Samaneh	Drug Resistance
367	CHARECTERIZATION CARBAPENEM RESISTANT PSEUDOMONAS AERUGINOSA STRAINS ISOLATED FROM HOSPITALIZED PATIENTS IN GONABAD, IRAN	Mardaneh Jalal	Drug Resistance
368	PREVALENCE OF MULTI-DRUG RESISTANCE(MDR)PSEUDOMONAS IN PATIENTS WITH URINARY TRACT INFECTION IN GORGAN, NORTH OF IRAN	Bagheri Hanieh	Drug Resistance
369	COMPARISON THE EFFECT OF STEVIA EXTRACT WITH GLUCOSE AND FRUCTOSE ON DENTAL ENAMEL CARIES FORMATION	Hosseini Seyed mostafa	Drug Resistance
370	ANTIBIOTIC RESISTANCE PROFILE OF H. PYLORI IN PATIENTS WITH UPPER GASTROINTESTINAL IN KASHAN, IRAN	Keshavarz azizi raftar Shahrbanoo	Drug Resistance
371	STUDY OF ANTIBACTERIAL PROPERTIES OF SNAKE VENOM AGAINST SOME BACTERIAL STRAINS	Zayerzadeh Ehsan	Drug Resistance

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372	SENSITIVITY TO DOXYCYCLINE AND NITAZOXANIDE AMONG METRONIDAZOLE RESISTANT HELICOBACTER PYLORI STRAINS IN PATIENTS WITH GASTRITIS	Baradaran Ali	Drug Resistance
373	MOLECULAR CHARACTERIZATION OF NDM-1 PRODUCING GRAM NEGATIVE BACILLI ISOLATED FROM DIFFERENT HOSPITALS, IRAN	Mobaiyen Haedeh	Drug Resistance
374	MOLECULAR STUDY OF ENCODING GENES OF PER-1 AND VIM-1 TYPES B-LACTAMASES ENZYMES IN PSEUDOMONAS AERUGINOSA AND ACINTOBACTER BAUMANII ISOLATES	Mobaiyen Haedeh	Drug Resistance
375	IN VITRO ACTIVITY OF CEFOPRAZONE AND CEFTRIAZONE IN VANCOMYCIN RESISTANT ENTEROCOCCI	HASANI ALKA	Drug Resistance
376	MULTIDRUG RESISTANCE IN CLOSTRIDIUM ISOLATES FROM BROILER CHICKENS	Alimolaei Mojtaba	Drug Resistance
377	MIC DETERMINATION AND QUALITATIVE ASSESSMENT OF ANTIBIOTIC SUSCEPTIBILITY AMONG CLINICAL, FOOD AND CATTLE BASED L.MONOCYTOGENES ISOLATES.	Lotfollahi Lida	Drug Resistance
378	CHARACTERIZATION OF ANTIMICROBIAL RESISTANT UROPATHOGENIC ESCHERICHIA COLI ISOLATED FROM IRAN	Mirzaee Mohsen	Drug Resistance
379	FREQUENCY OF MULTI-DRUG RESISTANCE AND MORE RAISED ESBLs IN SALMONELLA ISOLATES FROM HUMANS , LIVESTOCK AND POULTRY	Gharekhani Mehdi	Drug Resistance
380	STUDY OF EXTENDED SPECTRUM BETA-LACTAMASE (ESBL) E.COLI ISOLATED FROM PATIENTS WITH URINARY TRACT INFECTION BY DOUBLE DISC SYNERGY TEST IN MASHHAD	Hashemi Tabar Gholamreza	Drug Resistance
381	SURVEY OF ANTIBIOTIC-RESISTANCE PATTERNS IN E.COLI ISOLATED FROM PATIENTS WITH URINARY TRACT INFECTION IN MASHHAD	Hashemi Tabar Gholamreza	Drug Resistance
382	BLOODSTREAM BACTERIAL PATHOGENS AND THEIR ANTIMICROBIAL RESISTANCE PATTERN IN RASHT, IRAN	Kazemi Samaneh	Drug Resistance
383	COMPARISON STUDY OF ANTIMICROBIAL AGENT ON BACTERIAL ISOLATED FROM HOSPITALIZED PATIENTS IN QOM	Khodadad Motlagh Mohammad	Drug Resistance

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384	ANTIBIOTIC RESISTANT BACTERIA ISOLATED FROM YOLK SACCULITIS OF OSTRICH EGGS	Nabinejad Abdolreza	Drug Resistance
385	INVESTIGATION OF ANTIBACTERIAL EFFECTS OF SPIRULINA PLATENSIS EXTRACTS	Yaghoobizadeh Fatemeh	Drug Resistance
386	THE BLAKPC AND BLAGES CARBAPENEMASE GENES AND INTEGRON CLASS 1 IN KLEBSIELLA PNEUMONIAE ISOLATES IN KASHAN	Firoozeh Farzaneh	Drug Resistance
387	RECA GENE EXPRESSION IN CIPROFLOXACIN RESISTANT ESCHERICHIA COLI DINI- MUTANTS	Mohammadi Sareh	Drug Resistance
388	IN VITRO INHIBITORY EFFECT OF PYRAN NANOPARTICLES ON AMPC BETA-LACTAMASE PRODUCING ESCHERICHIA COLI STRAINS	Noormohammadi Azadeh	Drug Resistance
389	CORRELATION OF ANTIBIOTIC RESISTANCE PROFILE AND BIOFILM PRODUCTION LEVEL AMONG CLINICAL ISOLATES OF PSEUDOMONAS AERUGINOSA IN URMIA, IRAN	Shojadel Ehsan	Drug Resistance
390	ANTIBIOGRAM PATTERN OF PROTEUS MIRABILIS STRAINS RETRIEVED FROM DIGESTIVE TRACT OF LUCILIA SERICATA	Ahmadi Nahid	Drug Resistance
391	DETERMINATION OF RESISTANCE PATTERN IN KLEBSIELLA PNEUMONIA ISOLATED FROM URINARY TRACT INFECTIONS IN QOM	Shahbazi Saghar	Drug Resistance
392	ANTIBIOTIC RESISTANCE PATTERN OF KLEBSIELLA PNEUMONIA STRAINS ISOLATED FROM URINE SAMPLES OF CHILDREN WITH URINARY TRACT INFECTIONS IN TABRIZ CHILDREN HOSPITAL	Leisy azar Sevda	Drug Resistance
393	AN OVERVIEW ON CARBAPENAMASE ENZYMES	Aghamali Mina	Drug Resistance
394	AVIBACTAM AS A B-LACTAMASE INHIBITOR	Aghamali Mina	Drug Resistance
395	OCCURENCE OF HIGH LEVEL AMINOGLYCOSIDE RESISTANCE (HLAR) AMONG THE CLINICAL ENTEROCOCCUS FAECIUM AND ENTEROCOCCUS FAECALIS ISOLATES IN NORTH-WEST OF IRAN	Jahansepas Ali	Drug Resistance
396	IDENTIFICATION OF GLYCOPEPTIDE RESISTANCE ENTEROCOCCUS(GRE) SPECIES FROM CLINICAL SPECIMENS OF PATIENTS IN AHWAZ TEACHING HOSPITALS	HAMIDI HAJAR	Drug Resistance

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397	PREVALENCE OF VANCOMYCIN RESISTANT STAPHYLOCOCCUS STRAINS ISOLATED FROM URINARY TRACT INFECTIONS	Abbasi Fatemeh	Drug Resistance
398	THE EFFECT FE2NIO4 NANOPARTICLES ON GRAM NEGATIVE BACTERIA CAUSE URINARY TRACT INFECTIONS RESISTANT TO MULTIPLE ANTIBIOTICS	SEYEDGHALEHJOUZDANI NASRIN ALSADAT	Drug Resistance
399	ANTIBIOTIC RESISTANCE PATTERNS OF E.COLI ISOLATES COLLECTED FROM UTI, IN SHOHADA HOSPITAL, TAKAB.	Aliakbari Hadis	Drug Resistance
400	DETECTION OF CLASS 1 AND 2 INTEGRONS AND GENE CASSETTES AMONG MULTIDRUG-RESISTANT (MDR) ESCHERICHIA COLI UROPATHOGENIC STRAINS ISOLATED FROM CLINICAL SPECIMENS IN SOUTH OF IRAN	Tootoonsaz Sara	Drug Resistance
401	FREQUENCY STUDY OF DNA TOPOISOMERASE II MUTATION IN FLUOROQUINOLONES RESISTANCE PSEUDOMONAS AERUGINOSA STRAINS ISOLATED FROM PATIENT REFERRING TO THE IMAM REZA HOSPITAL	Cheshmenoushi Bahareh	Drug Resistance
402	DETERMINING ANTIBIOTIC RESISTANCE OF CLINICAL ISOLATES OF PSEUDOMONAS AERUGINOSA TEACHING HOSPITALS IN PARS ABAD	Farhoomand Hilda	Drug Resistance
403	PHENOTYPIC AND GENOTYPIC STUDY OF BIOFILM FORMATION IN STAPHYLOCOCCUS AUREUS ISOLATED FROM URINARY TRACT INFECTIONS	Yousefi Masoud	Drug Resistance
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404	STUDY OF ANTIMICROBIAL SUSCEPTIBILITY PROFILES OF GRAM-NEGATIVE BACTERIA CAUSING URINARY TRACT INFECTION IN TABRIZ, IRAN	Nemati Ahmad Abad Saba	Drug Resistance
405	DETERMINATION OF ANTIMICROBIAL RESISTANCE PATTERN AND PHENOTYPIC DETECTION OF ESBL AMONG CLINICAL ISOLATES OF KLEBSIELLA PNEUMONIAE	Saki Hiva	Drug Resistance
406	ANTI- MICROBIAL RESISTANCE STAPHYLOCOCCUS EPIDERMIDIS	Bitaraf Hamid Reza	Drug Resistance
407	VIRULENCE GENOTYPE AND ANTIMICROBIAL SUSCEPTIBILITY PATTERN IN CLINICAL PSEUDOMONAS AERUGINOSA ISOLATES	Malek mohamad Somayeh	Drug Resistance

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408	CORRELATION BETWEEN VIRULENCE GENOTYPE AND SPECIMEN TYPE IN MULTIDRUG RESISTANCE PSEUDOMONAS AERUGINOSA	Malek mohamad Somayeh	Drug Resistance
409	NOVEL SYNTHETIC DERIVATIVES WITH ANTISTAPHYLOCOCCAL ACTIVITY AGAINST MRSA	Salehi Maryam	Drug Resistance
410	DETECTION OF MACROLID, LINCOSAMIDE AND STREPTOGRAMIN RESISTANCE GENES IN STAPHYLOCOCCUS EPIDERMIDIS STRAINS ISOLATED FROM CLINICAL SAMPLES IN ISFAHAN	Mousavi Mahtabossadat	Drug Resistance
411	FREQUENCY OF TETRACYCLINE RESISTANCE GENES (TET K, TETM, TETL AND TETO) IN STAPHYLOCOCCUS AUREUS ISOLATED FROM TWO TEACHING HOSPITAL IN SOUTHWEST OF IRAN.	Alipoor Samin	Drug Resistance
412	MOLECULAR CHARACTERIZATION OF THREE CATIONIC RW-RICH ANTIMICROBIAL PEPTIDES DERIVED FROM IRANIAN SCORPION VENOM	Baradaran Masoumeh	Drug Resistance
413	THE RATIONALE BEHIND ANTIBIOTIC RESISTANCE PATTERN IN KLEBSIELLA PNEUMONIAE	Malekshahian Sara	Drug Resistance
414	THE PREVALENC OF ACRA AND ACRB GENES AMONG MULTIPLE-DRUG RESISTANCE OF UROPATHOGENIC ESCHERICHIA COLI ISOLATED FROM PATIENTS WITH UTI IN MILAD HOSPITAL, TEHRAN	Maleki Davood	Drug Resistance
415	PREVALENCE AND ANTIBIOTIC-RESISTANT BACTERIA CAUSING URINARY TRACT INFECTIONS (UTI) AMONG LABORATORIES, HOSPITALIZED PATIENTS AND OUTPATIENTS IN SHAHREZA, ISFAHAN, IRAN	Tayebi Mahdiye Sadat	Drug Resistance
416	INVESTIGATION OF THE REMAINING ASSESS DIAGNOSTIC ACCURACY OF TETRACYCLINE IN GARMSAR CITY MILK AND PASTEURIZED MILK FARMS WITH DIFFERENT BRANDS OF MILK COLLECTION CENTERS WITH HIGH PERFORMANCE LIQUID CHROMATOGRAPHY	Kherghepoush Zahra	Drug Resistance
417	DETECTION OF SERINE HYDROLASE EXPRESSION AMONG METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS BY CDNA-AFLP	Hoorijani Mohammad Neshvan	Drug Resistance

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418	DETECTION AND CLONING OF A HYPOTHETICAL PROTEIN GENE FROM MRSA IN PRESENCE OF OXACILLIN	Hoorijani Mohammad Neshvan	Drug Resistance
419	DRUG RESISTANT BACTERIA IN UNCOMPLICATED URINARY TRACT INFECTIONS RAISES CONCERN: SHOULD NITROFURANTOIN BE OPTED AS FIRST LINE THERAPY	Noie oskouie Arezoo	Drug Resistance
420	UTILITY OF BLOOD CULTURES AND ANTIBIOTIC RESISTANCE IN PATIENTS ADMITTED TO INTENSIVE CARE UNITS	Soltani Elghar	Drug Resistance
421	ANTIBACTERIAL EFFECTS OF VANCOMYCIN/METHICILIN COMBINATIONS AGAINST METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS(MRSA)	Abdolahi Ali	Drug Resistance
422	FREQUENCY OF STAPHYLOCOCCUS AUREUS NASAL CARRIAGE IN HEALTHY STUDENTS OF URMIA UNIVERSITY	Abroo Solyman	Drug Resistance
423	COLONIZATION OF METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS (MRSA) STRAINS IN PATIENTS OF WOMEN SURGICAL WARD IN BENTOLHODA HOSPITAL IN BOJNURD	Gholami Sepideh	Drug Resistance
424	ANTIBIOTIC RESISTANCE OF UROPATHOGENS	Pooyan Sima	Drug Resistance
425	PREVALENCE OF EXTENDED SPECTRUM BETA-LACTAMASE (SHV) PRODUCING ESCHERICHIA COLI IN POULTRY COLIBACILLOSIS BY POLYMERASE CHAIN REACTION	Alie Sara	Drug Resistance
426	THE INACTIVATION EFFECT OF CSPA GENE ON RESISTANCE TO CIPROFLOXACIN IN ESCHERICHIA COLI CSPA-	Akhavan armaki Hoda	Drug Resistance
427	ANTIBIOTIC RESISTANCE PATTERNS OF UROPATHOGENIC KLEBSIELLA PNEUMONIA STRAINS ISOLATED FROM PREGNANT WOMEN IN KERMAN HOSPITALS	Rajabi pour Atefe	Drug Resistance
428	DETERMINATION OF TETRACYCLINE RESISTANCE GENES IN FECAL ESCHERICHIA COLI ISOLATED FROM PIGEON (COLUMBA LIVIA)	Shobeiri Sajad	Drug Resistance
429	PHYLOGROUPS DETERMINATION OF ESCHERICHIA COLI ISOLATED FROM PIGEON (COLUMBA LIVIA)	Shobeiri Sajad	Drug Resistance
430	ANTIBACTERIAL EFFECTS OF LOCAL ANALGESICS AND ANESTHETICS	Noori Mehri	Drug Resistance

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431	IDENTIFICATION MRSA AND MSSA STRAINS AND THEIR ANTIBIOTIC SENSITIVITY PATTERN	Shahmohammadi Saeed	Drug Resistance
432	GREEN SYNTHESIS OF SILVER NANOPARTICLES USING EXTRACT OF ECHIUM AMOENUM CAPPED WITH L-CYSTEINE	Mirabi Najme	Drug Resistance
433	PHENOTYPIC EVALUATION OF EFFLUX PUMPS ACTIVITY OF UPEC AND KLEBSIELLA MDR ISOLATES BY CARTWHEEL METHOD	Gooyandeh Shervin	Drug Resistance
434	THE PATTERN OF DRUG RESISTANCE IN ESCHERICHIA COLI STRAINS ISOLATED FROM PATIENTS REFERRED TO THE HOSPITAL, ALI IBN ABI TALIB (AS) ZAHEDAN	Mazaheri Masomeh	Drug Resistance
435	DETERMINE ANTIBIOTIC SUSCEPTIBILITY RATE OF STAPHYLOCOCCUS AUREUS (MRSA) BACTERIA ISOLATED FROM CLINICAL INFECTIONS OF PATIENTS IN EMAM HOSSEIN HOSPITAL	Ghobadi saki Bahareh	Drug Resistance
436	PHENOTYPIC AND MOLECULAR CHARACTERIZATION OF TEM EXTENDED SPECTRUM BETA LACTAMASE IN URINARY E.COLI ISOLATES.	Adham Fariba	Drug Resistance
437	STUDY THE DEPENDENCE OF CIPROFLOXACIN-INDUCED MUTAGENESIS ON UMUC IN ESCHERICHIA COLI	Nourbakhsh rezaei Sayyede Marzieh	Drug Resistance
438	PATTERN OF ANTIBIOTIC RESISTANCE IN PSEUDOMONAS AERUGINOSA STRAINS ISOLATED FROM BURN PATIENTS IN TALEGHANI BURN HOSPITAL OF AHVAZ, IRAN	Motahar Moloudsadat	Drug Resistance
439	ANTIMICROBIAL RESISTANCE PATTERN OF URINARY TRACT INFECTIONS PATHOGENS IN HOSPITALIZED PATIENTS FROM SHAHID MADANI HOSPITAL OF KHORRAMABAD, IRAN	Omidimajd Sakineh	Drug Resistance
440	EVALUATION OF ANTIBIOTICAL SENSIVITY OF URINARY TRACT PATHOGENS IN CHILDREN REFERRED TO PEDIATRIC CLINICS IN ZAHEDAN IN YEAR 94	Jahantigh Mojde	Drug Resistance
441	ANTIBIOGRAM AND VIRULENCE GENES PROFILE OF E. COLI ISOLATED FROM HEALTHY CAT'S FECAL	Shakeri khamseh Shima	Drug Resistance

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442	ANTIBIOTIC RESISTANCE PROFILE OF MULTIDRUG RESISTANT GRAM NEGATIVE BACTERIA ISOLATED FROM AND PLASMID HOSPITAL EFFLUENTS	Khanpoor zarengye Raziye	Drug Resistance
443	THE INCREASING EMERGENCE OF VANCOMYCIN RESISTANCE IN METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS	Shekarabi Marjan	Drug Resistance
444	ISOLATION AND CHARACTERIZATION OF PHAGE AGAINST SALMONELLA TYPHIMURIUM IN RASHT	Panahi Pegah	Drug Resistance
445	IN VITRO INHIBITORY EFFECT OF ALCOHOLIC EXTRACT OF PHYSALIS ALKEKengi ON AMPC BETA-LACTAMASE PRODUCING ESCHERICHIA COLI STRAINS ISOLATED FROM DIFFERENT CLINICAL SPECIMENS IN KARAJ	Zafari Ziba	Drug Resistance
446	THE PREVALENCE OF RESISTANCE GENES BETA-LACTAMASE CTX / PER / AMPC (CMY 2) IN ESCHERICHIA COLI ISOLATED FROM URINARY TRACT INFECTIONS IN KARAJ	Hosseini Sansz	Drug Resistance
447	THE PREVALENCE OF RESISTANCE GENES BETA-LACTAMASETEM/VEB/SHV IN ESCHERICHIA COLI ISOLATED FROM URINARY TRACT INFECTIONS IN KARAJ	Hosseini Sansz	Drug Resistance
448	INVESTIGATION ANTIFUNGAL ACTIVITIES OF THE EXTRACT ALGAE SARGASSUM GLAUDESCENS AGAINST HUMAN PATHOGENS	Amirsharifi Maryam	Drug Resistance
449	THE RELATIONSHIP BETWEEN MASTITIS FREQUENCY WITH TOTAL COUNT ,SOMATIC CELL COUNT AND MILK PRODUCTION CITY ANDIMESHK	Khataminia Ali	Food and Water Microbiology
450	SALMONELLA AND FOOD HYGIENE A REVIEW	Amini pooya Salia	Food and Water Microbiology
451	ANTIMICROBIAL EFFECTS KEFIR FERMENTATION AT DIFFERENT TIMES E.COLI	Sarabandy Farideh	Food and Water Microbiology
452	KEFIR ANTIMICROBIAL EFFECTS ON SHIGELLA FLEXNERI	Sarabandy Farideh	Food and Water Microbiology
453	SURVEY ON MICROBIAL POLLUTION OF SOY YOGURT IN IRAN FOR DETESURVEY ON MICROBIAL POLLUTION OF SOY YOGURT IN IRAN FOR DETERMINATION OF MICROBIOLOGICAL CHARACTERISTICS IN NATIONAL STANDARD	Ghobadi dana Maryam	Food and Water Microbiology

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454	SURVEY ON MICROBIAL POLLUTION OF SOY DOUGH IN IRAN FOR DETERMINATION OF MICROBIOLOGICAL CHARACTERISTICS IN NATIONAL STANDARD	Ghobadi dana Maryam	Food and Water Microbiology
455	MOLECULAR IDENTIFICATION VIRULENCE GENES (STX1, STX2,FLICH7, EAEA, HLY)OF E. COLI STEC PATHOVARS ISOLATED FROM UNSTERILE MILK BY MULTIPLEX PCR	Aghamir mojtahed Reyhaneh	Food and Water Microbiology
456	EVALUATION OF BACTERIAL QUALITY AND ANTIBIOTIC RESISTANCE PROFILES OF ISOLATED BACTERIAL FROM AVICULTURES WELL WATER IN SAQQEZ CITY WEST OF IRAN IN 2014-2015	Alizadeh mamaghani Hojjat	Food and Water Microbiology
457	FREQUENCY OF ASPERGILLUS FUMIGATUS , ASPERGILLUS FLAVUS AND AFLATOXIN LEVEL IN HONEYBEE AND PRODUCED HONEY IN SAQQEZ AND BANEH, WEST OF IRAN IN 2014 - 2015.	Alizadeh mamaghani Hojjat	Food and Water Microbiology
458	BACTERIAL CONTAMINATION OF SHAHRCHAY RIVERS IN URMIA WITH THE INDICATOR OF E.COLI AND COLIFORMS	Jafari Shabnam	Food and Water Microbiology
459	MULTILAYERED ANTIMICROBIAL EDIBLE COATING AND ITS EFFECT ON LACTIC ACID BACTERIA ON RAINBOW TROUT (ONCORHYNCHUS MYKISS) FILLETS DURING REFRIGERATED STORAGE	Tabatabaei moradi Leila	Food and Water Microbiology
460	PREVALENCE OF E.COLI O157:H7 FROM FROZEN CHICKEN SAMPLES USING CULTURE AND MULTIPLEX PCR IN SLAUGHTERHOUSES OF KERMANSHAH PROVINCE	Seifi Sonya	Food and Water Microbiology
461	ASSESSMENT OF AFLATOXIN IN CULTURED RICE OF KHOZESTAN PROVINCE	Ranjbar Razie	Food and Water Microbiology
462	EVALUATION OF VIRULENCE GENES IN ENTEROCOCCUS SPECIES WITH PROBIOTIC POTENTIALS	Khatibi Mahzad	Food and Water Microbiology
463	MOLECULAR SURVEY, SEROTYPING AND ANTIBIOGRAM PATTERN IN MARKETED LOCAL, INDUSTRIAL AND BREEDER POULTRY EGG IN TABRIZ CITY	Daneshgohar Soniya	Food and Water Microbiology

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464	STUDY OF THE ANTIMICROBIAL ACTIVITY OF THE BACTERIOCIN AGAINST SOME OF THE PATHOGENS	Kheirollahi Fatemeh	Food and Water Microbiology
465	ANTIMICROBIAL ACTIVITY, ANTIBIOTIC SENSITIVITY AND VIRULENCE FACTORS OF LOCALLY ISOLATED BACILLUS SPECIES INTENDED FOR USE AS PROBIOTICS	Rezvanian Nazanin	Food and Water Microbiology
466	MOLECULAR DETECTION OF CAMPYLOBACTER JEJUNI IN RAW MILK BY PCR	Hamrahi Hengameh	Food and Water Microbiology
467	MOLECULAR DIAGNOSIS OF CAMPYLOBACTER JEJUNI IN TRADITIONAL ICE CREAM USING PCR METHOD	Hamrahi Hengameh	Food and Water Microbiology
468	RAPID MOLECULAR DETECTION OF LISTERIA MONOCYTOGENES, IN IRAN INDUSTRIAL FRUIT JUICES BY PCR	Samie zafarghandi Newsha	Food and Water Microbiology
469	ANTIMICROBIAL PROPERTIES OF AQUEOUS AND ALCOHOLIC EXTRACTS OF RED AND WHITE SUMAC (RHUS CORIARIA) ON SOME FOOD BORN BACTERIA	Saghaoghli Neda	Food and Water Microbiology
470	DETECTION OF BACILLUS COAGULANS IN PROBIOTIC PRODUCTS BY PCR MOLECULAR METHOD	Motazedi Farima	Food and Water Microbiology
471	THE INCIDENCE OF VIRULENCE FACTORS IN ENTEROCOCCUS FAECALIS AND ENTEROCOCCUS FAECIUM ISOLATED FROM TRADITIONAL CHEESES IN NORTH-WEST OF IRAN	Jahansepas Ali	Food and Water Microbiology
472	ENRICHMENT, ISOLATION AND IDENTIFICATION OF INDIGENOUS SACCHAROMYCES CEREVISIAE STRAINS AND THEIR QUALIFICATION AS BAKER'S YEAST	Mohamadinasab Pouya	Food and Water Microbiology
473	EVALUATION OF ESCHERICHIA .COLI CONTAMINATION IN LIQUID SUGAR PALM BY USING LS+	Atharinia Masomeh	Food and Water Microbiology
474	ASSESSMENT OF FECAL COLIFORM CONTAMINATION OF THE WASTEWATER TREATMENT PLANT (WWTP) IN INDUSTRIAL FACTORIES OF HAMADAN WITH MOST PROBABLE NUMBER TEST, IRAN IN 2016	Noroozi Somayeh	Food and Water Microbiology
475	POLYMORPHISM OF COAGULASE GEN IN STAPHYLOCOCCUS AREUES ISOLATED FROM COW MILK AND CHEESE IN TABRIZ CITY	Sadeghi Zali Mohammadhossein	Food and Water Microbiology

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476	A STUDY ON THE MICROBIAL QUALITY AND ANTIBIOTIC RESISTANCE OF KARUN RIVER	Motamedi Hossein	Food and Water Microbiology
477	MICROBIAL ANALYSIS OF IRANIAN SAFFRON	Elikaei Ameneh	Food and Water Microbiology
478	PRESENCE OF VIRULENCE FACTORS AND ANTIBIOTIC RESISTANCES IN ENTEROCOCCUS SP	Hosseini Seyed mostafa	Food and Water Microbiology
479	MOLECULAR DETECTION OF SALMONELLA ENTERICA SEROTYPE INFANTIS STRAINS USING MLST	Rahmati Hedieh	Food and Water Microbiology
480	PREVALENCE OF LIVER FLUKE INFECTIONS IN SLAUGHTERED ANIMALS IN JAVANRUD CITY, KERMANSHAH PROVINCE, IRAN	Nazari Naser	Food and Water Microbiology
481	ANTIMICROBIAL AND ANTI-BIOFILM FORMATION ACTIVITIES OF ZINC OXIDE NANOPARTICLES ON STAPHYLOCOCCUS AUREUS	Abbasvali Maryam	Food and Water Microbiology
482	ANTIBACTERIAL ACTIVITY AND INHIBITORY EFFECT OF ZINC OXIDE NANOPARTICLE ON ESCHERICHIA COLI BIOFILM FORMATION	Abbasvali Maryam	Food and Water Microbiology
483	THE EFFECTS OF NISIN ,STORAGE TIME AND TEMPERATURE ON TOXIN PRODUCTION OF STAPHYLOCOCCUS AUREUS BY ELIZA METHOD.	Mashak Zohreh	Food and Water Microbiology
484	EVALUATION OF ANTIBACTERIAL EFFECTS OF AQUEOUS EXTRACT OF BARBERRY FRUITS ON METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS	Hassani Mina	Food and Water Microbiology
485	MICROBIAL FUEL CELL TECHNOLOGY, AS A NEW TECHNOLOGY IN WASTEWATER TREATMENT AND ENERGY PRODUCTION	Kanani Behzad	Food and Water Microbiology
486	THE STUDY OF EFFECT AEROMONAS HYDROPHILA ON SWIM FIN CORRSION AND NECROSIS IN CAPOETA DAMASCINA	Yazdanpanah Laleh	Food and Water Microbiology
487	EVALUATION OF CHITOSAN MODIFIED ZEOLITE AS AN ADSORBENT FOR NITRATE REMOVAL AND ITS ANTIBACTERIAL CHARACTERISTICS	Yazdian Fatemeh	Food and Water Microbiology
488	PSEUDOMONAS AERUGINOSA IN PUBLIC HOT SPRING POOLS OF MESHGHINSHAHR	Movassagh gharamaleki Leyla	Food and Water Microbiology
489	DETECTION OF ZOITES AND MICROSCOPIC TISSUE CYSTS OF SARCOCYSTIS IN MEAT USING DIGESTION METHOD AND DOB SMEAR IN RASHT, IRAN	Ahady Mohammad Taghi	Food and Water Microbiology

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490	THE INFECTION RATE OF ESCHERICHIA COLI O157: H7 IN RAW MILK OF URMIA CITY DURING 2014-2015 YEARS	Hajilouyan Elham	Food and Water Microbiology
491	ANTIBIOTIC SUSCEPTIBILITY PROFILE OF E. COLI SEROTYPE O157:H7 IN URMIA, IRAN	Hajilouyan Elham	Food and Water Microbiology
492	SURVEILLANCE OF DAIRY PRODUCTION HOLDINGS SUPPLYING RAW MILK TO FARMHOUSE CHEESE MAKERS FOR VEROCYTOTOXIN PRODUCING E. COLI O157 AND OTHER VTEC.	Hajilouyan Elham	Food and Water Microbiology
493	PREVALENCE RATE AND ANTIBIOTIC RESISTANT PATTERN OF E.COLI O157 ISOLATES FROM CONSUMED MINCED MEAT OF URMIA CITY (IRAN) DURING 2015	Abdolah pori hosseine Mahmoud	Food and Water Microbiology
494	DETECTION OF PATHOGENICITY GENES IN CURTOBACTERIUM FLACCUMFACIENS, THE CAUSAL AGENT OF BACTERIAL WILT OF DRY BEANS	Fazliarab Amal	Food and Water Microbiology
495	BACTERIOCIN PRODUCTION IN CURTOBACTERIUM FLACCUMFACIENS STRAINS ISOLATED FROM IRAN	Fazliarab Amal	Food and Water Microbiology
496	EFFECT OF BENZALKONIUM CHLORIDE AND PERACETIC ACID ON LISTERIA MONOCYTOGENES BIOFILM IN RAW MILK	Baghery Naser	Food and Water Microbiology
497	DETERMINATION OF FREQUENCY VIBRIO SPP. IN FISHES DISTRIBUTED IN SHIRAZ	Sharifzadeh Ali	Food and Water Microbiology
498	THE EFFECTS OF THE HERBAL ESSENCES(URTICA DIOICA) ON THE CLOSTRIDIUM AND E.COLI	Sharifzadeh Ali	Food and Water Microbiology
499	INVESTIGATING THE MICROBIAL CONTAMINATION OF TRADITIONAL ICE CREAMS IN RAFSANJAN CITY IN 2015	Hosseininavh Ozra	Food and Water Microbiology
500	TEST OF CHEMICAL TOXICITY OF A NEUROTOXIN, COLCHICINE, ON SAVAGE WATER LIVING MICROORGANISM PARAMECIUM CAUDATUM	Mohammadi Robabeh	Food and Water Microbiology
501	STUDY OF OXYTETRACYCLINE ANTIBIOTIC RESIDUES IN RAW, PASTEURIZED AND STERILIZED COW MILK IN DAMGHAN CITY AND EFFECT OF THERMAL PROCESS ON LEVEL ANTIBIOTIC RESIDUE BY ELISA METHOD	Pouya Rezvan allah	Food and Water Microbiology

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502	INVESTIGATION OF PSEUDOMONAS AERUGINOSA, AS A SOURCE OF NOSOCOMIAL INFECTIONS, IN DRINKING WATER DISTRIBUTION SYSTEM OF SELECTED HOSPITALS IN TEHRAN CITY	Kashi Giti	Food and Water Microbiology
503	RAPID MOLECULAR DETECTION OF LISTERIA MONOCYTOGENES IN IRAN INDUSTRIAL SAUCE	Shahhosseiny Atefeh	Food and Water Microbiology
504	RAPID MOLECULAR DETECTION OF CAMPYLOBACTER JEJUNI IN IRAN INDUSTRIAL SAUCE	Shahhosseiny Atefeh	Food and Water Microbiology
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505	THE USE OF PROBOTIC LACTOBACILLI AS A PROPER CANDIDATE TO TREAT URINARY TRACT INFECTION CAUSED BY UPEC	Arbab Soleimani Nazila	Food and Water Microbiology
506	THE PREVALENCE OF YERSINIA ENTEROCOLITICA IN BROILER MEAT SUPPLIED IN ARDABIL	Shekari Somayeh	Food and Water Microbiology
507	SPECIES IDENTIFICATION OF STAPHYLOCOCCI ISOLATED FROM PASTRIES USING PARTIAL 16S RRNA SEQUENCING AND CONVENTIONAL METHODS	Hoveyda Laleh	Food and Water Microbiology
508	THE EPIDEMIOLOGY OF CANDIDA SPECIES RELATED TO VULVOVAGINAL CANDIDIASIS IN NEYSHABUR DURING 2013-2015	Salehi Mohammad	Fungi
509	EFFECT OF POLYSACCHARIDE ANTIGEN OF ASPERGILLUS NIGER CELL WALL ON SOME IMMUNOLOGICAL PARAMETER IN RABBITS	Abd Frial	Fungi
510	IN VITRO ACTIVITIES OF FLUCONAZOLE AND AMPHOTERICIN B ALONE AND IN COMBINATION AGAINST CANDIDA ALBICANS	Khezrian Fatemeh	Fungi
511	INVESTIGATION AND IDENTIFICATION SKIN FUNGAL INFECTION OF SALMONIDS FISH OF FARMS ARDABIL PROVINCE	Eslamkhah Mirsajjad	Fungi
512	BIOREMEDIATION OF CRUDE OIL AND PYRENE BY HALOTOLERANT FUNGUS EMBELLISIA PHRAGMOSPORA ISOLATED FROM SALINE SOIL	Jenab Kian	Fungi
513	EVALUATION OF SATUREJA RECHINGERI ESSENTIAL OILS ON GROWTH AND AFLATOXIN B1 PRODUCTION BY ASPERGILLUS FLAVUS PICC-AF39	Zergani najad Roghieh	Fungi

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514	COMPARISON OF IN-VITRO ANTIFUNGAL ACTIVITY OF OLIVE LEAF EXTRACT, BERBERIS VULGARIS AND BLACKBERRY ON STANDARD STRAIN OF CANDIDA ALBICANS PTCC 5027	Abolhasannezhad Maryam	Fungi
515	ETHNOMEDICINAL PLANTS: SCREENING OF IN VITRO ANTIFUNGAL EFFECT OF PISTACIA KHINJUKS ESSENTIAL OIL (COMBINED WITH THE DOMINANCE Γ -TERPINENE) WITH AGAR DISK DIFFUSION METHOD ON CANDIDA ALBICANS.	Zangeneh Mohammad mahdi	Fungi
516	ONYCHOMYCOSIS DUE TO FUSARIUM SPP. IN PATIENT WITH SQUAMOUS CELL CARCINOMA	Shokri Hojjatollah	Fungi
517	THE DISTRIBUTION AND IDENTIFICATION OF MYCOFLORA FROM GENITAL SYSTEM OF HEALTHY SHEEP	Shokri Hojjatollah	Fungi
518	THE ANTIFUNGAL ACTIVITY OF IRANIAN PROPOLIS AGAINST AZOLE-RESISTANT CANDIDA ALBICANS STRAINS ISOLATED FROM HIV+ PATIENTS WITH OROPHARYNGEAL CANDIDIASIS	Shokri Hojjatollah	Fungi
519	ELUCIDATION OF RISK GROUP , RADIOLOGICAL SIGNS, TREATMENT OF PRIMARY PULMONARY COCCIDIOIDOMYCOSIS AND SURVEY ABOUT COCCIDIOIDOMA	Mirsane Sayed alireza	Fungi
520	EVALUATION OF ANTIFUNGAL ACTIVITY OF NYSTATIN AGAINST VARIOUS CANDIDA ISOLATES	Salari Samira	Fungi
521	SEROPREVALENCE OF LISTERIA MONOCYTOGENES IN WOMEN WITH RECURRENT SPONTANEOUS ABORTION	Talebi Somayeh	Fungi
522	INVESTIGATION OF ANTIFUNGAL EFFECT OF PLANT EXTRACTS ON CANDIDA ALBICANS	Talebi Somayeh	Fungi
523	ISOLATION AND ENUMERATION OF GEOTRICUM CANDIDUM IN UNPASTEURIZED DAIRY PRODUCTS MARKETING IN TABRIZ BY PCR	Homeyni Elnaz	Fungi
524	NECROTIZING FUNGAL OTITIS EXTERNA IN A DIABETIC IMMUNOCOMPROMISED PATIENT	Gholinejad Nahid	Fungi
525	EVALUATION AND COMPARISON THE EXPRESSION OF THE ENZYME GLUCOSE OXIDASE RECOMBINANT EXPRESSION IN YEAST SYSTEMS PICHIA PASTORIS	Belyad Fakhry	Fungi

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526	CULTURE MEDIA SELECTION FOR CHITIN-GLUCAN COMPLEX PRODUCTION BY GANODERMA LUCIDUM	Moradi tanha Akram	Fungi
527	CAUSAL AGENTS IDENTIFICATION OF THOMSON NAVEL ORANGE FRUITS DECAY IN CONVENTIONAL AND STANDARD STORAGES IN EAST OF MAZANDARAN	Falaki Faezeh	Fungi
528	THE STUDY OF PREVALENCE OF (OTOMYCOSIS) IN PATIENTS REFERRING TO THE REFERENCE LABORATORY OF MYCOLOGY OF KASHAN DURING THE YEARS 1390 TO 1394.	Anvari Mahdis	Fungi
529	REPETITIVE SEQUENCES BASED ON GENOTYPING OF CANDIDA ALBICANS ISOLATES OBTAINED FROM IRANIAN PATIENTS WITH HUMAN IMMUNODEFICIENCY VIRUS	Yahyaraeyat Ramak	Fungi
530	CHARACTERIZATION OF FUNGI ISOLATED FROM THE SUNFLOWER (HELIANTHUS ANNUUS L.) RHIZOSPHERE IN WEST AZARBAYJAN	Safari Seyed Majid	Fungi
531	THE EFFECT OF ETHANOL EXTRACT DERACOCEPHALUM KOTSCHYI OF THE LEVEL OF SERUM PROTEINS IN MICE INFECTED WITH CANDIDA ALBICANS	Zareiyan jahromi Razieh	Fungi
532	A SURVEY OF THE EFFECT OF CAMPHOR ON INT1 AND EFG1 GENES EXPRESSION OF CANDIDA ALBICANS IN THREE TIME POINTS OF TREATMENT, 24 HOURS, 48 HOURS AND 72 HOURS VIA REAL-TIME PCR	Ghaffaripour Reza	Fungi
533	THE EFFECT OF ETHANOL EXTRACT DRACOCEPHALUM KOTSCHYI BOISS. ON CELLULAR DEFENSE IN MICE INFECTED BY CANDIDA ALBICANS INVIVO	Zareiyan jahromi Razieh	Immunology
534	IL-35 IS A NEW ANTI-INFLAMMATORY CYTOKINE IN THE DEVELOPMENT OF SEPSIS	Chatrabnous Nazanin	Immunology
535	DEVELOPMENT OF ANTI- ETEC IGY ANTIBODY IN QUAIL	Ghuryani khervi Khalil	Immunology
536	FMD FORMULATION IN MONTANIDE ISA-201 VG : ROBUST TH1 PATTERN	Sarkeshik zadeh moghadas Fatemeh sadat	Immunology
537	SELECTION OF ANTI-HUMAN PD-1 SINGLE-CHAIN VARIABLE FRAGMENT ANTIBODY FROM A HUMAN PHAGE LIBRARY	Safaie Sepideh	Immunology

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538	EVALUATION OF RABBIT HUMORAL IMMUNE RESPONSES AFTER ADMINISTRATION OF FRACTIONATED AND CRUDE SNAKE VENOM	Kashkool koluee Shiva	Immunology
539	CORRELATION BETWEEN EXPRESSION OF GINGIVAL TLR5 AS THE MOST IMPORTANT RECEPTOR FOR BACTERIAL FIMBRIA AND RANKL IN TISSUES AND PERIODONTAL DISEASES	Saeedi Ali	Immunology
540	COMPARISON OF HEALTHY AND CHRONIC PERIODONTITIS REGARDING GINGIVAL EXPRESSION OF HSP70	Fooladzadeh Anahita	Immunology
541	CORRELATION BETWEEN CXCR4 AND TLR2 AND CHRONIC PERIODONTITIS	Shahnavaz Sarira	Immunology
542	CORRELATION BETWEEN THE LEVEL OF SOLUBLE CD14 AS A RECEPTOR FOR BACTERIAL LPS AND NEUTROPHIL DEATH	Mehrmofakham Shideh	Immunology
543	MOESIN, A NOVEL MOLECULE, IN RECOGNIZING LPS AND PERIODONTITIS	Pezeshki Shaghayegh	Immunology
544	STUDY OF SOME HEMATOLOGICAL AND BIOCHEMICAL PARAMETERS IN VACCINATED CHICKEN WITH COMBINED INACTIVATED NEWCASTLE-INFLUENZA VACCINE	Ezdiyadi Mahdi	Immunology
545	PRODUCTION OF NANOPARTICLE CONTAINING ENTEROTOXIGENIC ESCHERICHIA COLI MAJOR PILIN SUBUNIT RECOMBINANT PROTEIN, CFAB, FROM COLONIZATION FACTOR ANTIGEN I (CFA/I) FIMBRIAE, AND ITS IMMUNOLOGICAL EVALUATION AFTER ORAL ADMINISTRATION IN MICE MODEL	Hoseinpour Samaneh	Immunology
546	DEVELOPMENT OF ANTI-BOVINE IGG IMMUNOGLOBULIN Y (IGYS) IN QUAIL	Attari roodi Yoones	Immunology
547	THE EFFECT OF GENE POLYMORPHISMS TUMOR NECROSIS FACTOR (TNF) PRODUCTION OF ACUTE PHASE PROTEINS IN THE LIVER IN PATIENTS WITH HEPATITIS B	Jahan tigh Soheila	Immunology
548	INCREASED SYNTHESIS OF IL-8 BY MONONUCLEAR CELLS OF NON-SECRETOR INDIVIDUALS WITH A BLOOD GROUP AFTER CULTIVATION AND STIMULATION WITH ANTIGENS EXTRACTED FROM PSEUDOMONAS AERUGINOSA	Farshidfar Soheila	Immunology

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549	THE EFFECT OF AQUEOUS EXTRACT OF ELAEAGNUS ANGUSTIFOLIA ON SERUM TNF LEVEL IN MICE WERE RECEIVED BRUCELLA ABORTUS LPS	Pandooneh Ali	Immunology
550	THE EFFECTS OF CYTHOLETHAL DISTENDING TOXIN- ENCODING SALMONELLA ENTERICA ON EXPRESSION OF TLR2, TLR4 AND TLR5 IN HT-29 CELLS	Ganji Leila	Immunology
551	POLYMORPHISMS OF INTERLEUKIN IMPACT ON HEPATITIS	Motevalli Mahrokh	Immunology
552	IMPACT OF HSA-MIR-590-5P, HSA-MIR-520F, HSA-MIR-338-5P, HAS-MIR942 TO JURKAT CELL SIGNALING PHATWAYS UNDER INDUCTION WITH IL-2	Mapar Maryam	Immunology
553	THE PHYLOGENIC STUDY OF HIV IN KHORASAN RAZAVI	Fakour Faeze	Immunology
554	PRODUCING AND EVALUATION QUANTITY AND QUALITY OF POLYCLONAL ANTIBODY AGAINST EXOTOXIN A PSEUDOMONAS AERUGINOSA IN RABBITS	Saeidvafa Shabnam	Immunology
555	ANTIBACTERIAL EFFECT OF SILVER NANOPARTICLES USING EXTRACT OF OLIVE LEAF	Shirkhani Somayeh	Medicinal Plants
556	SANITIZING AND ANTIBIOFILM PROPERTIES OF ZATARIAMULTIFLORA ESSENTIAL OIL AGAINST STAPHYLOCOCCUS AUREUS	Shirdel Maryam	Medicinal Plants
557	DEVELOPMENT OF A SYMBIOTIC IRANIAN WHITE CHEESE ADDED WITH BIFIDOBACTERIUM BIFIDUM AND ALLIUM AMPELOPRASUM	Mehdizadeh Tooraj	Medicinal Plants
558	PREVALENCE OF POSITIVE SAMPLES OF TUBERCULOSIS IN PATIENTS REFERRED TO BOOALI HOSPITAL IN ZAHEDAN IN 2011	Hosseini Hadi	Medicinal Plants
559	GREEN TEA EXTRACT INHIBITS BIOFILM FORMATION BY CANDIDA ALBICANS (IN VITRO STUDY)	Raei Parisa	Medicinal Plants
560	ANTIMICROBIAL ACTIVITIES OF ESSENTIAL OIL OF SOME PHLOMIS SPECIES	Nikan Marjan	Medicinal Plants
561	ESSENTIAL OIL OF TRACHYSPERMUM AMMI LINK EFFECTIVE ANTIBACTERIAL AGENT AGAINST ISOLATED AND STANDARD BACTERIA	Omidpanah Sahar	Medicinal Plants
562	ANTIBACTERIAL ACTIVITY OF SOME MEDICINAL PLANTS AGAINST ISOLATED ESCHERICHIA COLI FROM DISEASED LAYING HENS	Omidpanah Sahar	Medicinal Plants

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563	ANTIMICROBIAL ACTIVITY OF LEAF EXTRACT OF A NATIVE PLANT FROM SOUTHWEST OF MARIVAN	Yazdani Morteza	Medicinal Plants
564	ANTIMICROBIAL ACTIVITY OF A NATIVE PLANT EXTRACT FROM SOUTH WEST OF MARIVAN	Yazdani Morteza	Medicinal Plants
565	ANTIMICROBIAL ACTIVITY OF THE PLANT EXTRACT FROM ZYGOPHYLLACEAE FAMILY FROM SOUTHWEST OF MARIVAN	Yazdani Morteza	Medicinal Plants
566	A REVIEW OF HERBAL REMEDIES LEISHMANIASIS IN IRAN: SYSTEMATIC REVIEW	Mahmoodi kouhi Ahmad	Medicinal Plants
567	THE ANTIBACTERIAL EFFECTS ON PATHOGENIC BACTERIA METHANOL EXTRACT OF LEMON GRASS	Nezamdoost shadbad Nader	Medicinal Plants
568	THE EFFECT OF POMEGRANATE, CASTOR AND GARLIC EXTRACTS ON CLINICAL MULTI-DRUG RESISTANT E. COLI ISOLATES	Kermani jamkarani Somaye	Medicinal Plants
569	ANTIOXIDANT AND ANTIBACTERIAL PROPERTIES OF SAFFRON LEAVES	Rismanbaf Ali	Medicinal Plants
570	ANTIBACTERIAL ACTIVITY OF LAVANDULA ANGUSTIFALIE ALCHOLI AND WATER EXTRACT ON PATHOGENIC BACTERIA	Najafi farid Mojtaba	Medicinal Plants
571	ETHNOMEDICINAL PLANTS: THE ANTIBACTERIAL ACTIVITY OF ESSENTIAL OIL OF CORIANDRUM SATIVUM ON STAPHYLOCOCCUS AUREUS.	Zangeneh Mohammad mahdi	Medicinal Plants
572	MEDICINAL PLANTS: ANTIBACTERIAL ACTIVITY OF ESSENTIAL OIL OF ROSMARINUS OFFICINALIS AGAINST PSEUDOMONAS AERUGINOSA BACTERIA.	Zangeneh Mohammad mahdi	Medicinal Plants
573	SCREENING OF A IRANIAN MEDICINAL PLANT (ESSENTIAL OIL OF TRACHYSpermum AMMI) FOR ITS ANTIBACTERIAL ACTIVITY ON BACILLUS SUBTILIS.	Zangeneh Mohammad mahdi	Medicinal Plants
574	STUDY ON ANTIBACTERIAL ACTIVITY OF ESSENTIAL OIL OF CINNAMOMUM ZEYLANICUM ON ESCHERICHIA COLI O157:H7.	Zangeneh Mohammad mahdi	Medicinal Plants
575	ETHNOMEDICINAL PLANTS: SCREENING OF IN VITRO ANTIBACTERIAL ACTIVITY OF ESSENTIAL OIL OF PISTACIA KHINJUK (COMBINED WITH THE DOMINANCE Γ -TERPINENE) ON BACILLUS SUBTILIS.	Zangeneh Mohammad mahdi	Medicinal Plants

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576	CHEMICAL COMPOSITION AND IN VITRO ANTIBACTERIAL EFFECT OF ESSENTIAL OIL OF PISTACIA KHINJUK (COMBINED WITH THE DOMINANCE Γ -TERPINENE) ON PSEUDOMONAS AERUGINOSA.	Zangeneh Mohammad mahdi	Medicinal Plants
577	ANTIMICROBIAL ACTIVITY OF PHOENIX DACTYLIFERA ON ISOLATED VIBRIO SPP. FROM SHRIMP AQUACULTURE IN BUSHEHR PROVINCE, IRAN	Baseri Somaye	Medicinal Plants
578	PHYTOCHEMICAL EVALUATION OF METHANOLIC EXTRACT OF LEAVES OF STEVIA REBAUDIANA BERTONI FROM GUILAN	Ojani Shahab	Medicinal Plants
579	INHIBITORY EFFECT OF SALVIA RHYTIDEA BENTH. (LAMIACEAE) EXTRACT AGAINST VARIOUS CANDIDA ISOLATES	Salari Samira	Medicinal Plants
580	EVALUATION OF ANTIFUNGAL PROPERTY OF METHANOLIC EXTRACT OF SALVIA RHYTIDEA AGAINST C. TROPICALIS ISOLATES	Salari Samira	Medicinal Plants
581	EVALUATION ANTIFUNGAL EFFECT OF SALVIA RHYTIDEA AGAINST C. GLABRATA ISOLATES	Salari Samira	Medicinal Plants
582	EVALUATION OF ANTIFUNGAL ACTIVITY OF ASTRAGALUS HAMOSUS	Shojaii Asie	Medicinal Plants
583	THE ANTI-DERMATOPHYTE AND ANTI-ELASTASE ACTIVITY OF ZATARIA MULTIFLORA ESSENTIAL OILS	Heidary tabar Rezvan	Medicinal Plants
584	ANTIBACTERIAL ACTIVITIES OF ROSEMARY (ROSMARINUS OFFICINALIS) AND ITS INTRACTION IN COMBINATION WITH CONVENTIONAL ANTIMICROBIAL, AGAINST GRAM POSITIVE AND NEGATIVE BACTERIA	Afshari Elnaz	Medicinal Plants
585	COMPARISON OF QUANTITATIVE DIAGNOSTIC KIT AND GAS CHROMATOGRAPHY TECHNIQUE FOR DETERMINATION OF METHANOL AT TRACE LEVELS IN HERBACEOUS DISTILLATES	Rahati noveir Maliheh	Medicinal Plants
586	THE EFFECTS OF MENTHA SPICATA L., CUMINUM CYMINUM L. AND MENTHA LONGIFOLIA L. ESSENTIAL OILS INDIVIDUALLY AND COMBINED WITH SODIUM BENZOATE AGAINST ESCHERICHIA COLI O157:H7	Ekhtelat Maryam	Medicinal Plants

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587	ANTIBACTERIAL ACTIVITY OF CURCUMA LONGA EXTRACT AGAINST STAPHYLOCOCCUS AUREUS ISOLATED FROM DIFFERENT INFECTIONS	Attarpour Yazdi Mohammad Mehdi	Medicinal Plants
588	ANTIBACTERIAL ACTIVITY OF PUNICA GRANATUM PEEL EXTRACTS AGAINST ESCHERICHIA COLI ISOLATED FROM URINARY TRACT INFECTIONS	Attarpour Yazdi Mohammad Mehdi	Medicinal Plants
589	بررسی فعالیت ضد باکتریایی عصاره های مختلف گل بهار نارنج (AURANTIUM L CITRUS) بر روی گونه های میکروبی در شرایط آزمایشگاهی	Ahanjan Mohammad	Medicinal Plants
590	USING BOILED BEET FOR IMPROVING THE YOLK QUALITY AND PREVENTION OF MAREK DISEASE OUTBREAK IN LAYER	Nabinejad Abdolreza	Medicinal Plants
591	ANTIBACTERIAL AND ANTIFUNGAL PROPERTIES OF THYME	Hadavand Masoume	Medicinal Plants
592	THE STUDY EFFECTS ANTIMICROBIAL OF FOENICULUM VULGARE MILL AND ACHILLES MILLE FOLIUM PLANT ON BACTERIAL PATHOGENS CAUSING URINARY TRACT INFECTIONS AND NOSOCOMIAL INFECTION	Mahmoudi Hassan	Medicinal Plants
593	ANTIMICROBIAL ACTIVITIES OF ISOLATED BACTERIAL ENDOPHYTES FROM PETROSELINUM CRISPUM ON SOME FIELD ISOLATES OF VETERINARY BACTERIAL PATHOGENS	Amidi Masoumeh	Medicinal Plants
594	ANTIBACTERIAL ACTIVITY OF ISOLATED BACTERIAL ENDOPHYTES OF SUPERNATANT CULTURE BROTH AND CHLOROFORM INACTIVATED BACTERIAL COLONIES FROM ACHILLEA MILLEFOLIUM ON SOME FIELD ISOLATES OF BACTERIAL PATHOGENS	Amidi Masoumeh	Medicinal Plants
595	ANTIBACTERIAL ACTIVITY OF LEAVES HYDROALCOHOLIC EXTRACT OF CHAEROPHYLLUM MACROPODUM(APIACEAE)	Bineshian Farahnaz	Medicinal Plants
596	COMBINATION EFFECT OF CINAMON AND CLOVE EXTRACTS AGAINST EXTENDED EXPECTRUM BETALACTAMASE PRODUCING ESCHERICHIA COLI	Kafshdouzan Khatereh	Medicinal Plants
597	EVALUATION OF GROWTH INHIBITORY EFFECT OF MICROEMULSION PRODUCED FROM AQUEOUS EXTRACT OF HYPERICUM ON GRAM-NEGATIVE CLINICAL STRAINS	Sadrnia Maryam	Medicinal Plants

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598	EVALUATION OF ANTIBACTERIAL ACTIVITY OF ESSENTIAL OIL OF ZIZIPHORA CLINOPODIODES AND ACHILLEA WILHELMSII ON ANTIBIOTIC-RESISTANT STRAINS OF STAPHYLOCOCCUS AUREUS	Jafari sales Abolfazl	Medicinal Plants
599	ANTI LEISHMANIA EFFECT OF NANO CURCUMIN: IN VITRO ANALYSIS	Razavinia Abazar	Medicinal Plants
600	THE STUDY OF PASTEURIZATION DIFFERENT TEMPERATURES OF CHICORY DISTILLATE	Pourhosseini Mehri	Medicinal Plants
601	THE STUDY OF PASTEURIZATION DIFFERENT TEMPERATURES OF DILL DISTILLATE	Pourhosseini Mehri	Medicinal Plants
602	ANTIMICROBIAL ACTIVITY OF METHANOL EXTRACT OF SALVIA LIMBATA C. A. MEY FROM KASHAN-GHAZAAAN	Iravani Maryam	Medicinal Plants
603	ANTIMICROBIAL ACTIVITY OF SALVIA GLOTINOSA L. METHANOL EXTRACT FROM GILAN-MASAL	Iravani Maryam	Medicinal Plants
604	EXPRESSION OF RECOMBINANT A-LUFFIN IN ESCHERIACHIA COLI	Namvar Shaghayegh	Medicinal Plants
605	فعالیت ضد باکتریایی عصاره متانولی چهار گیاه لاوند، ریحان، صعتر و اکلیل کوهی	Beigizadeh Narges	Medicinal Plants
روز دوم ساعت ۱۲:۰۵-۱۰:۰۵ شماره پوستر ۶۰۶-۷۰۶			
606	ANTIBACTERIAL ACTIVITY OF 4 METHANOL EXTRACTS OF LAVANDULA STOECHAS, OCIMUM BASILICAM, THYMUS VULGARIS AND ROSMARINUS OFFICINALIS	Beigizadeh Narges	Medicinal Plants
607	ANTIBACTERIAL ACTIVITIES OF PLARGONIUM GRAVEOLENS IN COMBINATION WITH CONVENTIONAL ANTIMICROBIAL, AGAINST GRAM POSITIVE AND NEGATIVE BACTERIA	Koluei Ziba	Medicinal Plants
608	COMPARATIVE STUDY OF THE ANTIMICROBIAL EFFECTS OF AQUEOUS AND ORGANIC EXTRACTS OF NETTLE ON MEMBERS OF THE GENUS KLEBSIELLA, AND THEIR COMPARISON WITH COMMONLY USED ANTIBIOTICS	Azizi alidoust Fatemeh	Medicinal Plants
609	ANTIMICROBIAL EFFECTS OF ETHANOL EXTRACTS OF PLANTS STALKS CENTAUREA CYANUS AND FLOWERS CENTAUREA CYANUS ON A NUMBER OF GRAM POSITIVE AND NEGATIVE BACTERIA IN VITRO	Khaledi Mansoor	Medicinal Plants

Row	Title	Submission Author	Session
610	ANTIBACTERIAL EFFECT OF FRACTIONS OF POLAR AND SEMI-POLAR, NONPOLAR WORMWOOD EXTRACT THE BACTERIA STAPHYLOCOCCUS AUREUS, ESCHERICHIA COLI, PSEUDOMONAS AERUGINOSA	Ahmadizadeh Changiz	Medicinal Plants
611	THE SURVEY OF ANTIBACTERIAL EFFECT OF HYPERICUM PERFORATUM L. EXTRACT POLAR, SEMI-POLAR AND NON-POLAR FRACTIONS ON STAPHYLOCOCCUS AUREUS, BACILLUS CEREUS ESCHERICHIA COLI AND PSEUDOMONAS AERUGINOSA BACTERIA	Ahmadizadeh Changiz	Medicinal Plants
612	THE VIEW OF TRADITIONAL PERSIAN MEDICINE ABOUT MICROBE AND ANTIMICROBIAL AGENTS	Rahimi Roja	Medicinal Plants
613	NATURAL MEDICINE, AN OLD BUT NEW APPROACH TO ANTIMICROBIAL RESISTANCE	Vazirian Mahdi	Medicinal Plants
614	EFFLUX PUMP INHIBITORS DERIVED FROM PLANTS: A PROMISING APPROACH TO INTERFERE EFFLUX-MEDIATED DRUG RESISTANCE IN BACTERIA	Sadati Lamardi Seyede Nargess	Medicinal Plants
615	ANTIBACTERIAL ACTIVITY OF EXTRACT AND PURE COMPOUNDS OF LEUTEAE AVICENNIA MOZAFF.	Sabernavaei Mahsa	Medicinal Plants
616	IN VITRO ANTIBACTERIAL EFFECTS OF THE GARLIC CRUDE EXTRACT AGAINST ISOLATES OF PSEUDOMONAS AERUGINOSA.	JAFARPOUR AKRAM	Medicinal Plants
617	GENE EXPRESSION ANALYSIS OF THE EFECCT OF GARLIC- CRUDE EXTRACT AGAINST PSEUDOMONAS AERUGINOSA BIOFILM FORMATION	JAFARPOUR AKRAM	Medicinal Plants
618	ANTIMICROBIAL EFFECTS OF AQUEOUS AND METHANOL EXTRACTS OF ORANGE PEEL AND ITS EFFECT ON THE SHELF-LIFE OF FLAVORED MILK	Razmjoo Maryam	Medicinal Plants
619	THE ANTIBACTERIAL EFFECT OF ETHANOLIC EXTRACT OF SAFFRON ON GROUP A BETA-HEMOLYTIC STREPTOCOCCUS (A GRAM-POSITIVE BACTERIA)	Asadallahi Hanieh	Medicinal Plants

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620	STUDY OF ANTIBACTERIAL ACTIVITY OF ETHYLACETAT TOTAL EXTRACT AND ITS ALKALOID FRACTION FROM FLOWERING AERIAL PARTS OF GLAUCIUM VITELLINUM BOISS.ET BUHSE AGAINST CLINICAL ESCHERICHIA COLI STRAINS ISOLATED FROM UTI	Tavaflangeroudi Shohreh	Medicinal Plants
621	THE ROLE OF PEGANUM HARMALA ETHANOLIC EXTRACT AND TYPE II TOXIN ANTITOXIN SYSTEM IN BIOFILM FORMATION	Aalipour Bitra	Medicinal Plants
622	COMPARISON OF THE ANTIBACTERIAL EFFECT OF ROSA DAMASCENA AND ALOEVERA EXTRACTS ON E.COLI	Besharati Reza	Medicinal Plants
623	ANTIMICROBIAL ACTIVITY OF ALCOHOLIC EXTRACT FROM BLACKBERRY GROWN IN SHIRAZ (IRAN)	Homayoon Maryam	Medicinal Plants
624	INHIBITORY EFFECT OF SCROPHULARIA STRIATA ON AFLATOXINS B1 AND B2 PRODUCTION BY ASPERGILLUS FLAVUS	Moradi Leila	Medicinal Plants
625	IN VITRO ANTI FUNGAL EFFECTS OF SHALLOT CRUDE EXTRACT AGAINST ISOLATES OF CANDIDA ALBICANS .	Sherafati Negin	Medicinal Plants
626	GENE EXPRESSION ANALYSIS THE EFFECT OF SHALLOT CRUDE EXTRACT AGAINST CANDIDA ALBICANS HYPHAE FORMATION.	Sherafati Negin	Medicinal Plants
627	THE ANTIMICROBIAL ACTIVITY OF MALVA SYLVESTRIS EXTRACT AGAINST UROPATHOGENIC ISOLATES OF ESCHERICHIA COLI	Zadeh Hosseingholi Elaheh	Medicinal Plants
628	ANTIMICROBIAL EFFECTS OF VERBASCUM SP. EXTRACT	Bahonar Bitra	Medicinal Plants
629	ANTIMICROBIAL EFFECTS RED LENTILS ON SOME BACTERIA CAUSING WOUND INFECTIONS	Khataminia Ali	Medicinal Plants
630	SURVEY OF ANTIBACTERIAL PROPERTIES OF GINGER EXTRACT ON ISOLATED BACTERIA FROM PATIENTS WITH URINARY TRACT INFECTIONS	Simaei Mehdi	Medicinal Plants
631	EVALUATION OF ANTIBACTERIAL ACTIVITY AND ANTI BIOFILM FORMATION OF METHANOL EXTRACT OF RUMEX ALVEOLLATUS LEAVES AGAINST STAPHYLOCOCCUS AUREUS AND PSEUDOMONAS AERUGINOSA	Korkorian Neda	Medicinal Plants

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632	COMPARISON OF ANTIMICROBIAL ACTIVITY OF FENNEL ESSENTIAL OIL AGAINST STAPHYLOCOCCUS AUREUS WITH SOME ANTIBACTERIAL DRUGS	Shokri Mahsa	Medicinal Plants
633	INVESTIGATION EFFECT OF SATUREJA KHUZESTANICA AGAINST SOME GRAM NEGATIVE AND POSITIVE BACTERIA	Shahpari Mona	Medicinal Plants
634	EVALUATION EFFECT OF DANDELION EXTRACT ON SOME NEGATIVE AND POSITIVE GRAM BACTERIA	Shahpari Mona	Medicinal Plants
635	INTESTINAL INFECTIONS IN CHILDREN REFERRED TO ABUZAR HOSPITAL IN AHVAZ	Khorasanizadeh Ali	Microbial infections in Surgical, metabolic and Burns Wounds
636	DETECTION OF GENES ENCODING FNBP AND CLFA ADHESIONS AMONG STAPHYLOCOCCUS AUREUS ISOLATED FROM CLINICAL SAMPLE OF PATIENTS	Shafaei Elmira	Microbial infections in Surgical, metabolic and Burns Wounds
637	MANIPULATION OF MESENCHYMAL STEM CELLS WITH ENZYBIOTICS TO ENHANCE ANTIBACTERIAL ACTIVITY IN WOUND HEALING	Saeedi Pardis	Microbial infections in Surgical, metabolic and Burns Wounds
638	DETERMINATION OF TEM GENE IN ESCHERICHIA COLI STRAINS PRODUCING EXTENDED-SPECTRUM BETA-LACTAMASE ISOLATED FROM URINARY TRACT INFECTIONS IN ESLAMABADGHARB CITY	Chalabzardi Mitra	Microbial infections in Surgical, metabolic and Burns Wounds
639	DRUG RESISTANCE AND STATUS OF INFECTION OF ACINETOBACTER BAUMANNII IN BURN INTENSIVE CARE	Roham Maryam	Microbial infections in Surgical, metabolic and Burns Wounds
640	EFFECT ANTIBACTERIAL OF METHANOL AND ASETON EXTRACT LICHENS PROTOPARMELIOPSIS MURALIS, PHYSCONIA DISTORTA ON SOME PATHOGENIC BACTERIA ISOLATED NFECTIONS HOSPITAL MOSTFA KHOMINI IN ILAM CITY	Chalabzardi Mitra	Microbial infections in Surgical, metabolic and Burns Wounds
641	THE PREVALENCE OF CTXM1 –CTX15 GENES IN ESCHERICHIA COLI STRAINS PRODUCING EXTENDED-SPECTRUM BETA-LACTAMASE ISOLATED FROM URINARY TRACT INFECTIONS INHOSPITAL IMAM KHOMEINI ESLAMABADGHARB CITY	Chalabzardi Mitra	Microbial infections in Surgical, metabolic and Burns Wounds
642	EVALUATING THE EFFECTS OF INACTIVE IMMUNIZATION WITH POLYCLONAL EXOTOXIN A ANTIBODY OF PSEUDOMONAS AERUGINOSA IN BURNED MOUSE MODEL	Saeidvafa Shabnam	Microbial infections in Surgical, metabolic and Burns Wounds

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643	PREVALENCE OF ESBLs AND BLACTX-M-I, BLASHV AND BLATEM GENES AMONG UROPATHOGENIC ESCHERICHIA COLI ISOLATES	Salehi Mohammad	Microbial infections in Surgical, metabolic and Burns Wounds
644	EVALUATION THE PREVALENCE AND OF ANTIBIOTIC RESISTAN PATTERN IN AEROMONAS ISOLATED FROM BURN PATIENS IN HOSPITAL TALEGHANI ILAM CITY	Chalabzardi Mitra	Microbial Metabolite and Therapy
645	SURVEY ANTIMICROBIAL EFFECT OF BOILING WATER AND ALCOHOLIC EXTRACT OF SCROPHULARIA STRIATA ON ESCHERICHIA COLI	Chalabzardi Mitra	Microbial Metabolite and Therapy
646	EFFECT OF LINOLEIC ACID ON ASTAXANTHIN PRODUCTION IN MICROALGAE	Khalili Zahra	Microbial Metabolite and Therapy
647	DESIGNING AND EVALUATION A NEW IMMUNOTOXIN CONSTRUCT FOR TARGETING GASTRIC CANCER	Neyestani Zohreh	Microbial Metabolite and Therapy
648	EFFECT OF BACILLUS THURINGIENSIS TOXIN ON TRICHOMONAS VAGINALIS IN VITRO CONDITION	Roghani Negin	Microbial Metabolite and Therapy
649	EVALUATION OF ANTICANCER ACTIVITIES OF LACTOBACILLI ISOLATED FROM TRADITIONAL CHEESES OF IRAN	Rabiei Ghermezgoli Mitra	Microbial Metabolite and Therapy
650	ANTIBACTERIAL ACTIVITIES OF SYMBIOTIC ACTINOBACTERIA ISOLATED FROM INVERTEBRATES IN MAZANDARAN	Dehghan Khadijeh	Microbial Metabolite and Therapy
651	THE EFFECT OF BACILLUS ATROPHAEUS HNSQJYH170 LIPOPEPTIDES ON GERMTUBE PRODUCTION IN CANDIDA ALBICANS	Moghtadi pisheh Solmaz	Microbial Metabolite and Therapy
652	THE EFFECT OF BACILLUS AMYLOLIQUEFACIENS M13RW01 METABOLITES ON GERM TUBE FORMATION IN CANDIDA ALBICANS	Aghaali Marnani Mahsa	Microbial Metabolite and Therapy
653	USING PEPTIDE PHAGE LIBRARY FOR ISOLATION OF PEPTIDES TARGETING KLEBSIELLA PNEUMONIAE	Moqaddqm Tallieh	Microbial Metabolite and Therapy
654	USING PEPTIDE PHAGE LIBRARY FOR ISOLATION OF PEPTIDES TARGETING ACINETOBACTER BAUMANNII	Irani Nazanin	Microbial Metabolite and Therapy
655	EFFECTS OF EXTRACELLULAR LECTINS OF BACILLUS SUBTILIS ON BLOOD CANCER CELL LINE	Mohamadnejad Reyhaneh	Microbial Metabolite and Therapy
656	ANTIBACTERIAL ACTIVITY OF PIGMENTS PRODUCED FROM NATIVE ISOLATED MICROORGANISMS	Alihosseini Mitra sadat	Microbial Metabolite and Therapy

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657	DESIGNING A GENETICS CONSTRUCT BASED ON A-SARCIN APPLICATION FOR TARGETING COLON CANCER VIA IN-SILICO EVALUATION	Moghimi kakhki Mozhdeh	Microbial Metabolite and Therapy
658	ANTIBACTERIAL PROPERTY OF A CAMEL RECOMBINANT PEPTIDE (LACTOFAMPYN- LACTOFERRIN) - AN IN-VITRO STUDY	Sayadi Mahdie	Microbial Metabolite and Therapy
659	EVALUATION OF THE EFFECT OF SOMATIC ANTIGENS OF MARSHALLAGIA MARSHALI ON THE EXPRESSION OF TLR4 IN SPLENOCYTES OF ASTHMATIC MICE BY QUANTITATIVE PCR METHOD	Zakeri Amin	Microbial Metabolite and Therapy
660	SCREENING AND ISOLATION OF PHENYLALANINE AMMONIA LYASE FROM IRANIAN CYANOBACTER ANABAENA90	Baradaran ghaffary Reyhaneh	Microbial Metabolite and Therapy
661	THE MONITORING OF STRUCTURAL AND FUNCTIONAL CHARACTERISTICS OF COMBOTOX IN ORDER TO DEVELOP A NEW GENERATION OF MEDICINE EFFECTIVE FOR LYMPHOMA.	Ahmadpour moghaddam Seyyede fatemeh	Microbial Metabolite and Therapy
662	IDENTIFICATION AND ASSESS THE GENETIC DIVERSITY OF AGROBACTERIUM STRAINS ISOLATED FROM DIFFERENT HOST PLANTS IN WEST AZARBAYJAN	Khezzinejad Nabi	Molecular Detection
663	ISOLATION, IDENTIFICATION AND HOST RANGE DETERMINATION OF THE CAUSAL AGENT OF CROWN GALL DISEASE ON STONE FRUIT CULTIVARS	Khezzinejad Nabi	Molecular Detection
664	USE OF MULTI LOCUS SEQUENCE TYPING METHOD FOR MOLECULAR DETECTION OF SALMONELLA ENTERICA SEROTYPE ENTERITIDIS	Sarfi Faegheh	Molecular Detection
665	DETECTION OF THE BOVINE VIRAL DIARRHEA VIRUS IN POOLED BOVINE SERUM BY RT- PCR	Najafi mosleh Sajjad	Molecular Detection
666	DETECTION OF PAP, AFA AND FIM GENES IN UROPATHOGENIC ESCHERICHIA COLI ISOLATES FROM PATIENTS WITH URINARY TRACT INFECTION IN SHAHREKORD	Kherghepoush Zahra	Molecular Detection
667	MOLECULAR DETECTION OF G1691A MUTATION AND ITS RELATION WITH TNF A -308 G /A POLYMORPHISM IN ABORTION HUMAN	Kehani Samaneh	Molecular Detection

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668	MOLECULAR DIAGNOSIS OF CHLAMYDIA TRACHOMATIS IN SUSPECTED PSEUDOMONAS AERUGINOSA KERATITIS BY PCR	Dalirgoli zeynab	Molecular Detection
669	STUDY THE PRESENCE OF REGULATORY SEQUENCE OF FHLA PROTEIN IN GYRB UPSTREAM REGION	Akhavan armaki Hoda	Molecular Detection
670	Real-time PCR Analysis of p21 Gene Expression in Jurkat E6.1 T-lymphocyte Leukemia Cell Line Irradiated with Low Power Laser Irradiation (635nm and 780nm)	Alamery Layla	Molecular Detection
671	CORRELATION BETWEEN HELICOBACTER PYLORI AND MBL RS1800450 POLYMORPHISM IN COLORECTAL CANCER	Ajdamfekr Somaye	Molecular Detection
672	ASSOCIATION OF CHLAMYDIA TRACHOMATIS CT681 AND CT135 GENES, IN INFERTILITY INDUCTION IN INFERTILE PATIENTS OF TEHRAN CITY	Sabouri Akram	Molecular Detection
673	IDENTIFICATION OF THERMOPHILIC STRAINS NATIVE TO MOLECULAR METHODS TO IDENTIFY DNA POLYMERASE GENE CODER	Emami Zahra	Molecular Detection
674	MOLECULAR INVESTIGATION OF COMMON TNF A -308 G /A POLYMORPHISM AND HELICOBACTER PYLORI IN TYPE II DIABETES	Rassi Hossein	Molecular Detection
675	PREVALENCE OF HUMAN PAPILLOMAVIRUS GENOTYPES ASSOCIATED WITH CERVICAL CANCERS AND ITS RELATION WITH TNF A -308 G /A POLYMORPHISM IN IRAN	Rassi Hossein	Molecular Detection
676	MOLECULAR INVESTIGATION OF MBL RS1800450 POLYMORPHISM AND HELICOBACTER PYLORI IN TYPE II DIABETES	Rassi Hossein	Molecular Detection
677	INVESTIGATION OF CHLAMYDIA TRACHOMATIS IN PATIENTS REFERRED TO URMIA SHAHID MOTAHHARI HOSPITAL BY PCR	Ebrahimzadeh Amir	Molecular Detection
678	TOXINOTYPING OF CLOSTERIDIUM PERFRINGENS ISOLATED FROM HEALTHY BROILERS AND BROILERS WITH MILD NECROTIC ENTERITIS IN EAST NORKH OF IRAN	Yousefi Mohammad	Molecular Detection
679	WOLBACHIA ENDOBACTERIA IN NATURAL POPULATION OF PAEDERUS FUSCIPES: THE AGENT OF HUMAN DERMATITIS	Akhavan Niloofar	Molecular Detection

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680	DISTRIBUTION OF ALKANE HYDROXYLASE GENES INTO CRUDE-OIL DEGRADING BACTERIAL POPULATION IN PERSIAN GULF	Mehdipour Ziba	Molecular Detection
681	RAPID DETECTION OF ENTEROCOCCUS FAECALIS USING PCR BY AMPLIFICATION OF EF0737, A NOVEL GENE	Sabzi Samira	Molecular Detection
682	PHYLOGENETIC STUDY OF E.COLI IN COW MEAT	Alivandi Azadeh	Molecular Detection
683	HETEROGENEITY OF ESCHERICHIA COLI ISOLATES WITHIN DIFFERENT AGE GROUPS OF PATIENTS WITH URINARY TRACT INFECTIONS IN MASHHAD	Iman panah Zakieyh	Molecular Detection
684	MOLECULAR TYPING OF ESCHERICHIA COLI ISOLATES FROM URINARY TRACT INFECTIONS BY USING ENTEROBACTERIAL REPETITIVE INTERGENIC CONSENSUS (ERIC-PCR) IN MASHHAD	Iman panah Zakieyh	Molecular Detection
685	MOLECULAR IDENTIFICATION OF A GDSL FAMILY OF LIPASE-ENCODING GENES IN NATIVE LACTIC ACID BACTERIA ISOLATED FROM IRANIAN DAIRY PRODUCTS	Pirmanesh Samira	Molecular Detection
686	THE USEFULNESS OF HYPERVARIABLE REGIONS OF 16S rRNA GENE FOR IDENTIFICATION OF BACTERIAL MICROFLORA OF LUCILIA SERICATA	Soroushzadeh Zahra	Molecular Detection
687	DETECTION OF MYCOPLASMA PNEUMONIAE IN BRONCHOALVEOLAR LAVAGE (BAL) SUSPECTED WITH TUBERCULOSIS	AMERI MAHNAZ	Molecular Detection
688	THE RECA INTERACTION WITH COMPETITIVE MODULATORS DINI AND RECX	Mohammadi Sareh	Molecular Detection
689	COMPARISON OF 16S rRNA TARGET GENE PRIMERS IN DETECTION OF MYCOPLASMA SPP	Farhoudinasab Naeimeh	Molecular Detection
690	BIOINFORMATICS ANALYSIS OF SORTASES OF CLOSTRIDIUM PERFRINGENS PUTATIVE	Qafari Seyed Mehdi	Molecular Detection
691	PREVALENCE OF EXFOLIATIVE TOXIN A GENE AND ANTIMICROBIAL RESISTANCE PATTERNS IN STAPHYLOCOCCUS AUREUS STRAINS ISOLATED FROM PATIENTS AND HEALTHY INDIVIDUALS IN NORTHERN IRAN	Abbasi Pegah	Molecular Detection

Row	Title	Submission Author	Session
692	MULTIPLEX PCR ASSAY TARGETING THE MECA AND SPA GENE FOR RAPID DETECTION OF METHICILLIN RESISTANCE STAPHYLOCOCCUS AUREUS	Kashani Sara	Molecular Detection
693	DIAGNOSIS OF CANDIDA ALBICANS SINUSITIS BY PCR	Fardi Fatemeh	Molecular Detection
694	MOLECULAR DETECTION OF MYCOPLASMA SPP. IN SERUM OF MULTIPLE SCLEROSIS (MS) PATIENTS	Kobra Ghasempur	Molecular Detection
695	BIOINFORMATIC AND IN-VITRO CHARACTERIZATION OF SCAF AS A NOVEL GENE FOR IDENTIFICATION OF STAPHYLOCOCCUS AUREUS ISOLATES	Salimi Elaheh	Molecular Detection
696	ISOLATION AND MOLECULAR IDENTIFICATION (SEROTYPING) NEISSERIA SPECIES ISOLATED FROM CHILDREN UNDER 5 YEARS	Vosough Mehrad	Molecular Detection
697	MOLECULAR STUDY OF THE P40 GENE OF MYCOPLASMA AGALACTIAE ISOLATES FROM 13 PROVINCES OF IRAN	Babazadeh Maedeh	Molecular Detection
698	RAPID DETECTION OF STAPHYLOCOCCUS AUREUS BY PCR IN SYNOVIAL FLUID OF PATIENTS WITH ARTHRITIS	Gomarian Zahra	Molecular Detection
699	MLVA MOLECULAR TYPING OF HAEMOPHILUS INFLUENZAE ISOLATED FROM TWO IRANIAN UNIVERSITY HOSPITALS	Nejati Faranak	Molecular Detection
700	IN-HOUSE, QUALITATIVE BASED MULTIPLE PCR: DIAGNOSIS OF PAPILLOMA VIRUS TYPES 16 & 18 IN SUSPECTED SAMPLE	Shafaati Mohammadreza	Molecular Detection
701	THE MULTI LOCUS SEQUENCE TYPING (MLST) OF PASTEURELLA MULTOCIDA, A TECHNICAL APPROACH	TADAYON KEYVAN	Molecular Detection
702	EVALUATE AND COMPARE TECHNIQUES OF DIAGNOSIS HELICOBACTER PYLORI AND INTRODUCT SUITABLE METHODS THAT HAVE RESULTS OF FAST AND ACCURATE LABORATORY	Nourizadeh Ezzat	Molecular Detection
703	MOLECULAR DETECTION OF FUNGI IN SYNOVIAL FLUID BY PCR METHOD	Batoei Azam	Molecular Detection
704	SINGLE-COPY AND MULTIPLE-COPY TARGET GENES FOR DETECTION OF MYCOBACTERIUM TUBERCULOSIS COMPLEX: COMPARISON OF ANALYTICAL AND DIAGNOSTIC SENSITIVITIES OF NESTED PCR	Mirbagheri Seyede zohre	Molecular Detection

Row	Title	Submission Author	Session
705	UNCONCEIVABLE PREVALENCE OF TOXIN ANTI -TOXIN SYSTEMS IN ACINETOBACTER BAUMANNII	Hematian Ali	Molecular Detection
706	MOLECULAR TYPING OF METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS ISOLATES BASED ON COAGULASE GENE BY PCR-RFLP	Motamedi Hossein	Molecular Detection
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707	DEVELOPMENT OF A TAQMAN REAL TIME PCR ASSAY FOR RAPID DETECTION OF HAEMOPHILUS INFLUENZAE	Taghinezhad Saroukalaei Sedigheh	Molecular Detection
708	IDENTIFICATION OF MOLLUSCUM CONTAGIOSUM VIRUS (MCV) FROM VAGINAL SWAB SAMPLES BY USING TAQMAN REAL TIME PCR	Taghinezhad Saroukalaei Sedigheh	Molecular Detection
709	DETECTION OF CTX-M GENES IN ESBL-PRODUCING ESCHERICHIA COLI CLINICAL ISOLATES BY COMBINED DISC TEST AND REAL-TIME POLYMERASE CHAIN REACTION	Rouhi Samaneh	Molecular Detection
710	DESIGN OF A MULTIPLEX REAL TIME PCR WITH INTERNAL CONTROL METHOD TO DETECT YERSINIA PESTIS	Kabiri Khatereh	Molecular Detection
711	ANALYSIS OF SALMONELLA ENTERICA BY USING TWO DIFFERENT METHODS	Golab Narges	Molecular Detection
712	DETERMINATION OF THE PREVALENCE OF THE GENES ENCODING OUTER MEMBRANE SIDEROPHORE RECEPTORS IN UROPATHOGENIC ESCHERICHIA COLI ISOLATED FROM URINARY TRACT INFECTIONS AS NEW VACCINE CANDIDATES	Asadi Karam Mohammad Reza	Molecular Detection
713	DEVELOPING MLVA TECHNIQUE AS A COMPROMISED APPROACH TOWARD MOLECULAR CHARACTERIZATION OF PASTEURELLA MULTOCIDA	Ghaderi Rainak	Molecular Detection
714	HIGH FREQUENCY OF BIOFILM RELATED GENES AND PREDOMINANCE OF AGR TYPE III AMONG STAPHYLOCOCCUS AUREUS ISOLATED FROM BOVINE WITH SUBCLINICAL MASTITIS IN YASUJ, IRAN	Khoramrooz Seyed Sajjad	Molecular Detection
715	DETECTION OF ACINETOBACTER BAUMANNII ISOLATES BY ELASA	Rasoulinejad Samaneh	Molecular Detection
716	MOLECULAR SURVEY OF THE FREQUENCY OF PVL, SEA AND SEB GENES IN STAPHYLOCOCCUS AUREUS ISOLATED FROM SKIN INFECTIONS IN RAZI HOSPITAL OF TEHRAN.	Abolghasemi Katayoon	Molecular Detection

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717	DETECTION OF HUMAN PAPILLOMAVIRUS IN CERVICAL SAMPLES AND ITS ASSOCIATION WITH CERVICAL CANCER	Shariat Panahi Seid Shervin	Molecular Detection
718	INVESTIGATION OF THE ASSOCIATION BETWEEN CHLAMYDIA TRACHOMATIS INFECTION AND CERVICAL CANCER	Shariat Panahi Seid Shervin	Molecular Detection
719	SURVEYING THE GENE CASSETTES OF CLASS 1 INTEGRON AMONG MULTI-DRUG RESISTANT ESCHERICHIA COLI ISOLATES FROM URINARY TRACT INFECTIONS COLLECTED IN ISFAHAN	Shariat Panahi Seid Shervin	Molecular Detection
720	ISOLATION AND DETERMINATION OF ANTIBIOTIC RESISTANCE PATTERNS IN ENTROCOCCUS FAECALIS ISOLATED FROM MEAT	Tajbakhsh Elahe	Molecular Detection
721	HUMAN MALIGNANCY ASSOCIATED WITH Y CHROMOSOME: GENOTYPES AND HAPLOTYPES ASSOCIATED WITH SUSCEPTIBILITY TO COLORECTAL CANCER PATIENTS	Almarzoqi Ali	Molecular Detection
722	UNDERSTANDING MOLECULAR IDENTIFICATION AND POLYPHASIC TAXONOMIC APPROACHES FOR GENETIC RELATEDNESS AND PHYLOGENETIC RELATIONSHIPS OF MICROORGANISMS	Jahani Alireza	Molecular Detection
723	RAPID DETECTION OF HIV-1 INFECTION BY LOOP-MEDIATED ISOTHERMAL AMPLIFICATION(LAMP)	Saadati Hamid	Molecular Detection
724	SEROPREVALENCE OF HEPATITIS A IN HEMODIALYSIS PATIENT CANDIDATE FOR KIDNEY TRANSPLANT YOUNGER THAN FORTY YEARS	Arabsaghari Ensieh	Molecular Detection
725	THE SCREENING PARAGONIMUS SPP.ON FRESHWATER CRAYFISH FROM ARAS DAM RESERVIOR BY MOLECULAR METHOD PCR	Fazeli Soheila	Molecular Detection
726	IDENTIFICATION OF MYCOPLASMA HOMINIS, MYCOPLASMA GENITALIUM AND UREAPLASMA UREALYTICUM IN PATIENTS WITH URINARY TRACT INFECTION BY MULTIPLEX PCR	Piri Hassan	Molecular Detection
727	MOLECULAR TYPING OF STREPTOCOCCUS PYOGENES ISOLATES FROM IRANIAN CHILDREN BY RAPD-PCR METHOD	Rahimi moghaddam Akram	Molecular Epidemiology
728	DETERMINATION OF INTESTINAL ESCHERICHIA COLI PATHOTYPES FREQUENCY IN TEHRAN PROVINCE BY PCR	Zarei Mohammad Hossein	Molecular Epidemiology

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729	GENETIC DIVERSITY OF HELICOBACTER PYLORI STRAINS ISOLATED FROM PATIENTS WITH GASTRODUODENAL DISEASES USING MULTILOCUS SEQUENCE TYPING IN KERMANSHAH	Souri Nasrin	Molecular Epidemiology
730	DETECTION OF BOVINE SALMONELLA CARRIERS AS A POTENTIAL THREAT FOR HUMAN NON-TYPHOIDAL SALMONELLOSIS IN SANANDAJ CITY	Ahmadi Elham	Molecular Epidemiology
731	PREVALENCE OF VARIOUS HEPATITIS C (HCV) GENOTYPES AMONG CHRONIC HCV PATIENTS IN A PRIVATE LABORATORY, TEHRAN, IRAN	Nemati vahedi Sara	Molecular Epidemiology
732	HIGH FREQUENCY OF SCCMEC TYPE III AND SPA TYPE T037 AND T631 AMONG MULTI DRUG RESISTANT STAPHYLOCOCCUS AUREUS ISOLATED FROM BURN PATIENTS IN SOUTHWEST OF IRAN	Khoramrooz Seyed Sajjad	Molecular Epidemiology
733	RELATIONSHIP BETWEEN TOXIN ENCODING GENES AND ANTIBIOTIC RESISTANCE PROPERTIES IN UROPATHOGENIC ESCHERICHIA COLI ISOLATED FROM IRAN	Mirzaee Mohsen	Molecular Epidemiology
734	THE FREQUENCY OF PLASMID MEDIATED QUINOLONE RESISTANCE (PMQR) DETERMINANTS IN URINARY ISOLATES OF EXTENDED-SPECTRUM B-LACTAMASE-PRODUCING ESCHERICHIA COLI	Akya Alisha	Molecular Epidemiology
735	PCR-SEROTYPING OF LISTERIA MONOCYTOGENES ISOLATED FROM CLINICAL, FOOD AND CATTLE SAMPLES	Lotfollahi Lida	Molecular Epidemiology
736	GENETIC ANALYSIS OF STAPHYLOCOCCUS AUREUS STRAINS ISOLATED FROM PATIENTS ADMITTED TOM EMAM REZA HOSPITAL IN BOJNORD	Azimian Amir	Molecular Epidemiology
737	THE FIRST REPORT OF ISOLATION OF PVL/ACME POSITIVE COMMUNITY ACQUIRED-METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS (USA300) IN IRAN	Azimian Amir	Molecular Epidemiology
738	THE NECESSITY OF OBSERVING HEALTH CARE IN AVOIDING THE PATIENT'S INFECTION	Samiee Behnaz	Molecular Epidemiology

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739	CLONING AND IDENTIFICATION OF SINGLE NUCLEOTIDE POLYMORPHISMS(SNP) OF PORA GENE FROM NEISSERIA MENINGITIDIS CLINICAL SPECIMENS	Vosough Mehrad	Molecular Epidemiology
740	PREVALENCE OF VIRULENCE ASSOCIATED GENES IN BRUCELLA SPECIES ISOLATED FROM HUMAN AND ANIMAL SOURCES IN IRAN	Hashemifar Iman	Molecular Epidemiology
741	MOLECULAR ANALYSIS OF PSEUDOMONAS AERUGINOSA STRAINS ISOLATED FROM BURN PATIENTS BY REPETITIVE EXTRAGENIC PALINDROMIC-PCR (REP-PCR) IN AHVAZ TALEGHANI HOSPITAL	Abbasi Mansooreh	Molecular Epidemiology
742	DETECTION OF CIRCULATING HUMAN NOROVIRUS IN CHILDREN LESS THAN 5 YEARS WITH ACUTE GASTROENTERITIS BY GENOGROUP SPECIFIC REAL TIME PCR	Nejati Behrooz	Molecular Epidemiology
743	MICROBIOLOGY OF PRE-DIURESIS IN ANOPHELES STEPHENSI, THE ASIAN MALARIA MOSQUITO	Rahimi Maryam	Molecular Epidemiology
744	INVESTIGATION OF PNEUMOCOCCAL COCOLONIZATION IN NASOPHARYNX OF CHILDREN UNDER 6 YEARS BY MULTIPLEX PCR	Asgarian Sanaz	Molecular Epidemiology
745	DISTRIBUTION OF STAPHYLOCOCCAL CASSETTE CHROMOSOME MEC (SCCMEC) TYPES I, II, III AND IV IN STAPHYLOCOCCUS EPIDERMIDIS AMONG PATIENTS REFERRED TO EDUCATIONAL HOSPITALS ESFAHAN, IRAN.	Halaji Mehrdad	Molecular Epidemiology
746	PREVALENCE OF DIFFERENT ESCHERICHIA COLI PATHOTYPES IN DIARRHEAL PATIENTS FROM ZANJAN AND FARS PROVINCES, IRAN	Yadani milajerdi Mehrnaz	Molecular Epidemiology
747	CONSIDERATION OF SEPTICEMIA IN NEONATAL IN NICU SECTION OF SINA HOSPITAL.	Roghani Seyyed askar	Molecular Epidemiology
748	DIAGNOSTIC METHODS OF HELICOBACTER PYLORI IN GASTRIC BIOPSY	Badi Narges	Molecular Epidemiology
749	ISOLATION OF STREPTOBACILLUS MONILIFORMIS FROM LABORATORY RAT (RATTUS NORVEGICUS)	Dehdashti Sanaz	Molecular Epidemiology

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750	DETERMINATION OF FIM H GENE AND MANNOSE SENSITIVE HAEMAGGLUTINATION ABILITY AMONG ESCHERICHIA COLI ISOLATES IN EXTRA-INTESTINAL IN RAFSANJAN CITY	Dehdashti Sanaz	Molecular Epidemiology
751	PREVALENCE OF ESCHERICHIA COLI PATHOTYPES IN KURDISTAN PROVINCE 1391-1392	Panahandeh Latifeh	Molecular Epidemiology
752	PATHOGENIC BACTERIA ON CELL PHONES TOUCH AND KEYBOARD: A SYSTEMATIC REVIEW	Akhgar Hossein	Molecular Epidemiology
753	ANTIBIOTIC RESISTANCE OF 12 PSEUDOMONAS SPP. ISOLATED FROM CLINICAL SPECIMENS OF KERMAN HOSPITALS	Rajaei Sohrab	Molecular Epidemiology
754	SYNTHESIS AND ANTIBACTERIAL PROPERTIES OF SELENIUM NANOPARTICLES AGAINST STAPHYLOCOCCUS AUREUS	Mehrbakhsh bandari Maryam alsadat	Nanotechnology and Nanomicrobiology
755	PROCEDURE OPTIMIZATION FOR GREEN SYNTHESIS OF SILVER NANOPARTICLES BY AQUEOUS EXTRACT OF BUNIUM PERSICUM (BOISS) USING AS ANTIMICROBIAL AGENT.	Jafari Parisa	Nanotechnology and Nanomicrobiology
756	IRON OXIDE NANOPARTICLES (FE3O4) ENHANCED ANTIBACTERIAL ACTIVITY OF GENTAMICIN AGAINST STAPHYLOCOCCUS AUREUS	Hosseini khomeirani Somayeh	Nanotechnology and Nanomicrobiology
757	PERFORMANCE EVALUATION OF ANTIMICROBIAL OF METAL OXIDE NANOPARTICLES AGAINST ESCHERICHIA COLI	Hosseini khomeirani Somayeh	Nanotechnology and Nanomicrobiology
758	PROCEDURE OPTIMIZATION FOR GREEN SYNTHESIS OF SILVER NANOPARTICLES BY AQUEOUS EXTRACT OF MENTHA LANGIFOLIA L. USING AS ANTIMICROBIAL AGENT.	Aghajani kalaki Zahra	Nanotechnology and Nanomicrobiology
759	ANTI BACTERIAL EFFECT OF QUANTUM DOTS NANOPARTICLE	Sadeghkhan Faride	Nanotechnology and Nanomicrobiology
760	STUDY OF THE EFFECT OF SILVER NANOPARTICLES ON BIOFILMS FORMATION BY URINARY ESCHERICHIA	Ahmadi Ailin	Nanotechnology and Nanomicrobiology
761	IN VITRO INHIBITORY EFFECT OF CHROMIUM NANOPARTICLES ON AMPC BETA-LACTAMASE PRODUCING KLEBSIELLA STRAINS	Rahimi Lyla	Nanotechnology and Nanomicrobiology

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762	SYNTHESIS AND CHARACTERIZATION OF CHITOSAN COATED IRON OXIDE NANOPARTICLES FOR BIOMEDICAL APPLICATION	Oliaei Ashkan	Nanotechnology and Nanomicrobiology
763	ANTIBACTERIAL EFFECT OF EUGENOL AND SILVER NANOPARTICLES AND THEIR INTERACTION WITH FOOD COMPONENTS	Heydarian Dehkordi Negin	Nanotechnology and Nanomicrobiology
764	EVALUATION OF IRON OXIDE NANOPARTICLE ON THE PROTOCOLECES OF ECHINOCOCCUS GRANULOSUS IN IN VITRO CONDITION	Ghasemi Nejad Almani Pooya	Nanotechnology and Nanomicrobiology
765	NANOTECHNOLOGY APPROACHES FOR DEVELOPMENT OF NOVEL NATURAL ANTIBACTERIAL PRODUCTS; PROS AND CONS	Rafati Hasan	Nanotechnology and Nanomicrobiology
766	PREPARATION AND STUDY OF ANTIBACTERIAL PROPERTIES OF VANCOMYCIN-LOADED POSITIVELY AND NEGATIVELY CHARGED MESOPOROUS SILICA NANOPARTICLES AGAINST STAPHYLOCOCCUS AUREUS	Nematzadeh Elham	Nanotechnology and Nanomicrobiology
767	THE EVALUATION OF NANOGOLD FOR UTILIZATION IN SALMONELLA SENSING	Maleksabet Narges	Nanotechnology and Nanomicrobiology
768	THE EFFECT OF PH IN CONTROL OF NANOGOLD SYNTHESIS	Maleksabet Narges	Nanotechnology and Nanomicrobiology
769	CHEMICAL FUNCTIONALIZATION OF SILICA PARTICLES FOR PURIFICATION OF PROTEINS FUSED GLUTATHIONE S-TRANSFERASE	Rezaeinezhad Nasim	Nanotechnology and Nanomicrobiology
770	SYNTHESIS OF SILVER-COPPER NANOALLOYS BY THE BIOLOGICAL METHOD AND INVESTIGATION OF ITS ANTIBACTERIAL EFFECTS ON SOME OF THE PATHOGENIC GRAM-POSITIVE AND GRAM NEGATIVE BACTERIA	Mohammadi Sheyda	Nanotechnology and Nanomicrobiology
771	LOW CYTOTOXICITY EFFECT OF DENDROSOMAL CURCUMIN ON MACROPHAGE ISOLATED FROM BALB/C MICE : IN VITRO STUDY	Razavinia Abazar	Nanotechnology and Nanomicrobiology
772	THE SYNTHESIS OF SILVER NANOPARTICLES AND EVALUATION OF THEIR IN VITRO ANTIBACTERIAL ACTIVITIES WITH GENTAMICIN AGAINST MRSE	Esmaeillou Mahsa	Nanotechnology and Nanomicrobiology
773	ISOLATION OF AGROBACTERIUM TUMEFACIENS STRAINS FROM CROWN GALL DISEASE ON GRAPE AND TOXICITY EFFECTS OF TYPICAL NANOMATERIALS ON ITS.	Ahsani irvani Maryam	Nanotechnology and Nanomicrobiology

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774	BIOLOGICAL SYNTHESIS OF SILVER NANO PARTICLES BY USING PSEUDOMONAS AERUGINOSA	Ahsani irvani Maryam	Nanotechnology and Nanomicrobiology
775	BIOSYNTHESIS OF ZNO NANOPARTICLES USING THE AZOTOBACTER	Ahsani irvani Maryam	Nanotechnology and Nanomicrobiology
776	BIOSYNTHESIS OF ANISOTROPIC CUO NANOPARTICLES USING THE BACILLUS CEREUS	Ahsani irvani Maryam	Nanotechnology and Nanomicrobiology
777	RAPID SYNTHESIS OF IRON NANOPARTICLES USING BACILLUS MEGATERIUM AND ITS CHARACTERIZATION AS AN ANTIBACTERIAL AGENT	Ahsani irvani Maryam	Nanotechnology and Nanomicrobiology
778	THE EFFECT OF TOBRAMYCIN WITH INCORPORATION BISMUTH-ETHANEDITHIOL LOADED ON NIOSOMES ON BIOFILM PRODUCED BY PSEUDOMONAS AERUGINOSA.	Mahdiun Faeze	Nanotechnology and Nanomicrobiology
779	CONJUGATION OF LYSOSTAPHIN ON THE SURFACE OF DENDRIMER AS AN ANTIBACTERIAL ENZYME	Rasouli Rahimeh	Nanotechnology and Nanomicrobiology
780	ISOLATION AND MOLECULAR IDENTIFICATION OF GOLD NANOPARTICLE-PRODUCING MICROORGANISMS	Jafari Mandana	Nanotechnology and Nanomicrobiology
781	FIRST REPORT ON BIOSYNTHESIS OF SILVER NANOPARTICLES USING ACHROMOBACTER SPANIUS	Najaf pour Reza	Nanotechnology and Nanomicrobiology
782	COMPARATIVE STUDY BASED ON MICRO-DILUTION AND PLATE COUNT METHOD FOR SYNERGISM ANTIBACTERIAL EFFECT OF MOF-5 NANOPARTICLES AND BROCCOLI EXTRACT AGAINST PSEUDOMONAS AERUGINOSA	Pezeshkpour Vahid	Nanotechnology and Nanomicrobiology
783	STUDY OF MONOCLONAL ANTIBODY DEDICATED PRODUCTION TECHNIQUES AGAINST ANTIGENS OF LEISHMANIA INFANTUM AMASTIGOTE	Nourizadeh Ezzat	Nanotechnology and Nanomicrobiology
784	APPLICATION OF NEW STRATEGIES FOR DIAGNOSIS OF THE CAUSATIVE AGENT OF KALA-AZAR	Nourizadeh Ezzat	Nanotechnology and Nanomicrobiology
785	COMPARATIVE EVALUATION OF THE EFFECTS OF IRON-OXIDE NANOPARTICLE COMPARED WITH FLUCONAZOLE ON C. KRUSEI ISOLATES	Salari Samira	Nanotechnology and Nanomicrobiology
786	EVALUATION OF ANTIFUNGAL EFFECT OF IRON OXIDE NANOPARTICLE AGAINST CANDIDA ALBICANS ISOLATES	Salari Samira	Nanotechnology and Nanomicrobiology

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787	ANTIFUNGAL EFFICACY OF IRON-OXIDE NANOPARTICLE ON CANDIDA GLABRATA ISOLATES	Salari Samira	Nanotechnology and Nanomicrobiology
788	EFFECT OF IRON-OXIDE NANOPARTICLE ON GROWTH OF CANDIDA TROPICALIS ISOLATES COMPARED WITH FLUCONAZOLE	Salari Samira	Nanotechnology and Nanomicrobiology
789	ANTICANDIDAL ACTIVITY OF FLUCONAZOLE CONJUGATED GOLD NANOPARTICLES AGAINST FLUCONAZOLE RESISTANT STRAINS OF CANDIDA ALBICANS	JAVADI ALI	Nanotechnology and Nanomicrobiology
790	ONE STEP PHYTOSYNTHESIS OF SILVER NANOPARTICLES USING REDUCING AGENT OBTAINED FROM NATURAL SOURCES FLOWERS EXTRACT OF CALENDULA OFFICINALIS AND ITS ANTIBACTERIAL ACTIVITY	Safari Fatemeh	Nanotechnology and Nanomicrobiology
791	GREEN SYNTHESIS, CHARACTERIZATION AND ANTIBACTERIAL ACTIVITY OF SILVER NANOPARTICLES BY USING MENTHA PULEGIUM LEAVES AQUEOUS EXTRACT	Safari Fatemeh	Nanotechnology and Nanomicrobiology
792	EVALUATION OF ANTIBACTERIAL ACTIVITY OF SILVER NANOPARTICLES PRODUCED BY MELIA AZEDARACH	Ojani Shahab	Nanotechnology and Nanomicrobiology
793	THE ANTIBACTERIAL EFFICACY OF SILVER NANOPARTICLES DERIVED FROM INULA ROYLEANA LEAVES	Ojani Shahab	Nanotechnology and Nanomicrobiology
794	ANTIMICROBIAL EFFECTS OF SILVER NANOPARTICLES	Ebrahimi Zahra	Nanotechnology and Nanomicrobiology
795	THE STUDY OF ANTIFUNGAL AND ANTI ADHESIVE PROPERTIES NIO THINFILMS POLYMER-MATRIX NANOCOMPOSITE	Doudi Monir	Nanotechnology and Nanomicrobiology
796	CONTROLLED SYNTHESIS OF ZNO NANOSTRUCTURE AND THEIR MORPHOLOGY-DEPENDENT ANTIFUNGAL ACTIVITIES	Doudi Monir	Nanotechnology and Nanomicrobiology
797	STUDY OF ANTIBACTERIAL CHARACTERISTICS OF SILVER NANOPARTICLES ON STAPHYLOCOCCUS AUREUS	Zayerzadeh Ehsan	Nanotechnology and Nanomicrobiology
798	FIRST REPORT ON BIOSYNTHESIS OF SILVER NANOPARTICLES USING ACHROMOBACTER SPANIUS	Yazdansetad Sajjad	Nanotechnology and Nanomicrobiology
799	PREPARATION OF PLGA NANOPARTICLES FOR ORAL VACCINE DELIVERY OF A. BAUMANNII BIOFILM ASSOCIATED PROTEIN (BAP)	Darzi eslam Elham	Nanotechnology and Nanomicrobiology

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800	BACILLUS SPECIES SCREENING FOR SILVER NANOPARTICLE SYNTHESIS	Rezaei somee Leila	Nanotechnology and Nanomicrobiology
801	ANTIBACTERIAL PROPERTIES OF GRAPHENE BASED MATERIALS	Yazdian Fatemeh	Nanotechnology and Nanomicrobiology
802	PROTEIN VACCINATION WITH HPV16 E7/PEP-1 NANOPARTICLES INDUCES STRONG PROTECTIVE IMMUNITY	Mardani Golnaz	Nanotechnology and Nanomicrobiology
803	BIOSORPTION OF LEAD BY SPORES OF BACILLUS ATROPHAEUS	Hosseini Abari Afrouzossadat	Nanotechnology and Nanomicrobiology
804	ENGINEERING OF BACILLUS SUBTILIS SPORES TO DISPLAY OF PHENOLOXIDASE ON SPORE SURFACE	Hosseini Abari Afrouzossadat	Nanotechnology and Nanomicrobiology
805	THE ANTIBACTERIAL EFFECT OF DIFFERENT SIZES OF SILVER NANOPARTICLES ON STAPHYLOCOCCUS AUREUS ISOLATES AND THEIR PLASMID PATTERN	Jahandideh Nasrin	Nanotechnology and Nanomicrobiology
806	ANTIBACTERIAL AND ANTIBIOFILM CHARACTERISTICS OF SILVER NANOPARTICLES LOADED AGAR HYDROGEL AGAINST STAPHYLOCOCCUS AUREUS	Bouryabaf Leila sadat	Nanotechnology and Nanomicrobiology
807	ANTIBACTERIAL EFFECTS OF SILVER NANOPARTICLES ON PSEUDOMONAS AERUGINOSA	Charkhian Hamed	Nanotechnology and Nanomicrobiology
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808	VEGFR2-HIGG SPECIFIC DIABODY GENE CONSTRUCTION AND EXPRESSION IN E.COLI EXPRESSION SYSTEM	Bayat Fatemeh	Nanotechnology and Nanomicrobiology
809	BIOSYNTHESIS OF ZNO NANOPARTICLES USING LUMINESCENT VIBRIOS	Barani Maryam	Nanotechnology and Nanomicrobiology
810	INVESTIGATION OF THE ANTIMICROBIAL EFFECT OF SILVER DOPED ZINC OXIDE NANOPARTICLES	Hosseini Dolat Abadi Farzaneh	Nanotechnology and Nanomicrobiology
811	HOSPITAL-ACQUIRED URINARY TRACT INFECTION , MICROBIAL CAUSATIVE AGENTS AND ANTIBIOTIC RESISTANCE PATTERN IN SOUTHERN IRAN: A PROSPECTIVE STUDY	Dehghan Farzaneh	Nosocomial Infections
812	TRENDS OF ANTIBIOTIC RESISTANCE IN METHICILLIN-RESISTANT STAPHYLOCOCCI ISOLATED FROM SHIRAZ TEACHING HOSPITALS, IRAN	Khashei Reza	Nosocomial Infections
813	STUDY OF NOSOCOMIAL INFECTIONS IN PEDIATRIC INTENSIVE CARE UNITS IN THE TEHRAN	Attarpour Yazdi Mohammad Mehdi	Nosocomial Infections

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814	DISTRIBUTION OF NAN1 VIRULENCE GENE AMONG NOSOCOMIAL ISOLATES OF PSEUDOMONAS AERUGINOSA	Mardaneh Jalal	Nosocomial Infections
815	ROLE OF ATTACHMENT FACTORS IN BIOFILM PRODUCER UROPATHOGENIC ESCHERICHIA COLI	MOORI BAKHTIARI NAGHMEH	Nosocomial Infections
816	EVALUATION OF BACTERIAL CONTAMINATION AND ANTIBIOGRAM IN CELL PHONES OF CLINICAL STAFF PERSONNEL : MATERNITY, INTENSIVE CARE AND NEONATAL WARDS ON IMAM SAJJAD AND SHAHID BEHESHTI HOSPITALS IN YASUJ CITY .	Naghmach Mohsen	Nosocomial Infections
817	THE PATTERN OF RESISTANCE IN BACTERIA THAT RESPONSIBLE FOR NOSOCOMIAL INFECTIONS IN KHATAM-AL-ANBIA HOSPITALS OF SHUSHTAR CITY.	PAYDAR ALI	Nosocomial Infections
818	THE ROLE OF CELL PHONES OF MEDICAL STUDENTS IN SPREAD OF NOSOCOMIAL BACTERIAL INFECTIONS IN AMIRALMOMENIN HOSPITAL IN SEPTEMBER 2015	Darvishi Mohammad	Nosocomial Infections
819	AN OLD DRUG FOR A NEW BUG: CLASS 1 INTEGRONS AMONG MULTIDRUG-RESISTANT ACINETOBACTER BAUMANNII	Ghasabi Farzaneh	Nosocomial Infections
820	STAPHYLOCOCCUS AUREUS AND ANTIMICROBIAL RESISTANCE ISOLATED FROM ICU PATIENTS, ENVIRONMENT AND PERSONNELS IN A TEACHING HOSPITAL IN TEHRAN, IRAN.	Hejr Hossein	Nosocomial Infections
821	PREVALENCE OF HOSPITAL-ACQUIRED INFECTIONS AND ANTIBIOTIC RESISTANCE OF THE CAUSATIVE ORGANISMS IN PATIENTS ADMITTED TO SINA HOSPITAL	Jamshidi Yasaman	Nosocomial Infections
822	FREQUENCY OF PANTON-VALENTINE LEUKOCIDIN GENE AMONG HOSPITAL ASSOCIATED METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS ISOLATES IN URMIA UNIVERSITY HOSPITALS	Sharifi Yaeghob	Nosocomial Infections
823	PREVALENCE OF MULTIDRUG RESISTANT ENTEROCOCCUS FAECIUM ISOLATED FROM PATIENTS AND HOSPITALS ENVIRONMENT IN LORESTAN PROVINCE	Goudarzi Mansour	Nosocomial Infections

Row	Title	Submission Author	Session
824	DETERMINATION OF ANTIMICROBIAL RESISTANCE PROFILE IN RELATION TO PHYLOGENETIC GROUPS AMONG UROPATHOGENIC ESCHERICHIA COLI ISOLATES AT A UNIVERSITY HOSPITAL IN URMIA, IRAN	Habibi khiavi Nazanin	Nosocomial Infections
825	TRENDS OF ANTIBIOTIC RESISTANCE IN ENTEROCOCCUS FAECALIS ISOLATES OBTAINED FROM CLINICAL SPECIMENS FROM SHIRAZ, IRAN	Hasanpour Somaye	Nosocomial Infections
826	PREVALENCE OF NASAL CARRIER STAPHYLOCOCCUS AUREUS AND THEIR ANTIBIOTIC RESISTANCE PATTERNS AMONG HEALTH CARE WORKING IN BOJNURD IMAM REZA HOSPITAL	Besharati Reza	Nosocomial Infections
827	BIOINFORMATICS STUDY OF LETHAL FACTOR PROTEIN IN BACILLUS ANTHRACIS	Rezamasouleh Farzaneh	Other related topics
828	BIOINFORMATICS STUDY OF PAL ENZYME INVOLVED IN 6-GINGEROL BIOSYNTHESIS WHICH REDUCES PSEUDOMONAS AERUGINOSA BIOFILM FORMATION	Rezamasouleh Farzaneh	Other related topics
829	AUTOMATED TELLER MACHINE (ATM) AS A POTENTIAL SOURCE OF BACTERIAL CONTAMINATION	Tarbiyat farsad Fatemeh	Other related topics
830	LEGAL ISSUES BIOTERRORISM	Jamooli Tina	Other related topics
831	ANTIBIOTIC RESISTANCE OF GRAM-NEGATIVE BACTERIA ISOLATED FROM URINARY TRACT INFECTIONS IN PREGNANT WOMEN	Amiri danduski Somaye	Other related topics
832	EXPLORING THE POSSIBILITY OF ATTACHING GOLD NANOPARTICLES BY OXYSPORUM FUSARIUM TO BETA-LACTAM ANTIBIOTICS PRODUCED AND REVIEW EXERTED BY ITS TOXICITY IN CULTURED FIBROBLAST CELL LINES	Ahmadi Farzane	Other related topics
833	DIFFERENTIATION OF MYCOBACTERIUM BOVIS STRAINS ISOLATED FROM TB INFECTED CATTLE IN WEST AZERBAIJAN PROVINCE OF IRAN BY RFLP TYPING	Rezaee Shima	Other related topics
834	A COMPARATIVE STUDY OF THE PRODUCTION OF A-AMYLASE ENZYME IN STRAINS OF ASPERGILLUS ORYZAE ON WASTE STARCH AND MOLECULAR IDENTIFICATION OF TOP ENZYME-PRODUCING STRAINS	Radmehr Mohadese	Other related topics

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835	PRODUCTION OF FUNGAL PECTINASE ENZYME BY ASPERGILLUS NIGER SPECIES BY WASTE PLANTS JUICER AND MOLECULAR IDENTIFICATION OF THEM	NEMATI NOSHIN	Other related topics
836	TREATMENT OF XANTHOMONAS CITRI SUBSP. CITRI BY NITROUS ACID AND SELECTION OF A POTENT MUTANT WITH CAPABILITY TO PRODUCE MORE XANTHAN GUM	Cheraghalikhani Safoora	Other related topics
837	A SEARCH FOR TRACES OF AFRICAN 1 CLONAL COMPLEX OF MYCOBACTERIUM BOVIS ON THE IRANIAN SOIL	Kazemnia Sara	Other related topics
838	BIOINFORMATICS STUDY OF PA20 IN BACILLUS ANTHRACIS	Haddad Raheem	Other related topics
839	ONE-STEP AND NON-CHROMATOGRAPHIC PURIFICATION OF V ANTIGEN USING ELASTIN-LIKE PROTEIN	Molae Maryam	Other related topics
840	INFLUENCE OF THE ESCHERICHIA COLI'S HOST ON THE SOLUBILITY OF RECOMBINANT PROTEINS	Farshdari Farzaneh	Other related topics
841	MICROBIAL DIVERSITY ASSESSMENT OF THE OIL LAGOONS OF KHARK ISLAND USING CULTURE DEPENDENT AND CULTURE INDEPENDENT APPROACHES	Ahmadi Elham	Other related topics
842	EFFECT OF ESSENTIAL OIL OF ANETHUM GRAVEOLENS ON INTESTINAL E. COLI ISOLATES IN BROILER CHICKENS	DEHGHAN HAMED	Other related topics
843	AN EPIDEMIOLOGICAL SURVEY ON THE PREVALENCE OF ANTHRAX IN HAMEDAN PROVINCE	Ghytasranjbar Elaheh	Other related topics
844	COMPARISON BETWEEN BACTERIA ON TOUCH-SCREEN AND KEYPAD MOBILE PHONES	Yazdanpanah MohammadHosein	Other related topics
845	ISOLATION AND IDENTIFICATION OF BACTERIA ON MOBILE PHONES IN FASA	Yazdanpanah MohammadHosein	Other related topics
846	BACTERIA IN ANTI-TUMOR THERAPY AS A NOVEL ANTICANCER EXPERIMENTAL STRATEGY	Houman sadr Faezeh	Other related topics
847	OPTIMIZATION OF LOVASTATIN PRODUCTION USING ASPERGILLUS TERREUS IN BUBBLE COLUMN BIOREACTOR	Ansari Shahin	Other related topics

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848	KINETIC PARAMETERS FOR EXTRACELLULAR POLYSACCHARIDE PRODUCTION BY CRYPTHECODINIUM COHNII MICROALGAE IN BUBBLE COLUMN BIOREACTOR	Hosseinkhani Niloofar	Other related topics
849	EVALUATION OF THE EFFECT OF ORTHO-KIN MOUTHWASH ON DENTAL PLAQUE AROUND DIFFERENT ELASTOMERIC LIGATURES IN ORTHODONTIC PATIENTS	Samie Surur	Other related topics
850	POTENTIAL OF EARTHWORMS (EISENIA FETIDA) TO BIOLOGICAL REMEDIATION OF THE GAS OIL CONTAMINATED SOIL	Jafari Farjam Nazila	Other related topics
851	OPTIMIZATION OF PYRENE BIODEGRADATION BY ACHROMOBACTER SP. ISOLATED FROM OIL -CONTAMINATED SOILS	Daliri Ensieh	Other related topics
852	INTRODUCTION AND FUNCTIONAL PRESENTATION OF TEHRAN REGIONAL REFERENCE LABORATORY OF TUBERCULOSIS	Khoshkhoo Afsaneh	Other related topics
853	ISOLATION AND IDENTIFICATION OF BDELLOVIBRIO SP. FROM ENVIRONMENTAL SAMPLES	Valizadeh Hajar	Other related topics
854	NASAL CARRIAGE OF UNCOMMON COAGULASE-NEGATIVE STAPHYLOCOCCI IN NURSES AND PHYSICIANS OF TEHRAN UNIVERSITY HOSPITALS	Salimi Elaheh	Other related topics
855	PREVALENCE OF EXTENDED-SPECTRUM β -LACTAMASE-PRODUCING ESCHERICHIA COLI IN AGRICULTURAL FIELDS OF GORGAN DISTRICT	Hoseini Arezoo	Other related topics
856	EXPRESSION AND PURIFICATION OF SOLUBLE RECOMBINANT HUMAN PARATHYROID HORMONE (RHP1-34) BY TRX TAG IN TWO STRAINS OF ESCHERICHIA COLI	Yari Sanaz	Other related topics
857	EVALUATION OF DIAGNOSTIC AND PREDICTIVE VALUES OF HELICOBACTER PYLORI TOOL ANTIGEN TEST FOR HP INFECTION IN IRANIAN DYSPEPTIC PATIENTS	Safarnezhad Tameshkel Fahimeh	Other related topics
858	SENSITIVE HIGH-RESOLUTION MELTING (HRM) ANALYSIS FOR SCREENING OF KRAS AND BRAF MUTATIONS, IN IRANIAN HUMAN METASTATIC COLORECTAL CANCER (MCRC)	Hadi Karbalaie Niya Mohammad	Other related topics

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859	CHARACTERIZATION OF UROPATHOGENS AND THEIR ANTIBIOTIC SUSCEPTIBILITY PATTERNS DERIVED FROM PATIENTS SUFFERING FROM BOTH DIARRHEA AND URINARY TRACT INFECTION IN IRAN	Saleh Moein	Other related topics
860	AUDIT OF URINARY TRACE INFECTIONS 1394 IN SHAHID KAMYAB HOSPITAL – MASHHAD-KHORASAN RAZAVI	Samiee Behnaz	Other related topics
861	CULTURE OF MICROALGAL STRAINS ISOLATED FROM PERSIAN GULF OF IRAN IN DIFFERENT SALINE MEDIA	Seyed jafari olia Mahroo sadat	Other related topics
862	CHEMICAL AND BIOLOGICAL BENZENE REMEDIATION FROM GROUNDWATER BY CALCIUM PEROXIDE NANOPARTICLES	Mosmeri Hamid	Other related topics
863	A COLUMN STUDY OF BENZENE CONTAMINATED GROUNDWATER BIOREMEDIATION	Mosmeri Hamid	Other related topics
864	ASSESSMENT OF COLIFORM CONTAMINATION TRADITIONAL BUTTER IN KERMANSHAH PROVINCE	Namaky Behjat	Other related topics
865	SURVEY OF ATOPOBIUM VAGINA IN VAGINAL SAMPLES OF SYMPTOMATIC NON-PREGNANT WOMEN BY PCR	Amirmozafari Nour	Other related topics
866	SEROLOGICAL AND MOLECULAR DIAGNOSIS OF TOXOPLASMOSIS IN PATIENTS WITH AIDS/HIV IN ARAK CITY, MARKAZY PROVINCE	Eslamirad Zahra	Other related topics
867	CHARACTERIZATION OF BLATEM GENE IN KLEBSIELLA SPP. ISOLATED FROM URINARY TRACT INFECTIONS (UTIS)	Kargar jahromi Zahra	Other related topics
868	PHENOTYPIC AND GENOTYPIC DETECTION OF ESBLs IN KLEBSIELLA SPP. ISOLATES	Kargar jahromi Zahra	Other related topics
869	EVALUATION OF ANTIBACTERIAL ACTIVITY OF MULTI-WALLED CARBON NANOTUBES AGAINST SOME BACTERIAL STRAINS	Zayerzadeh Ehsan	Other related topics
870	EVALUATION OF MICE HUMORAL IMMUNE RESPONSES AFTER INTRANASAL ADMINISTRATION OF MYCOBACTERIUM TUBERCULOSIS RECOMBINANT FUSION PROTEINS	Namvarpour Mozhdeh	Other related topics
871	NON-INFECTIOUS DISEASES RELATED TO THE HUMAN MICROBIOME	Mokhtarian Roya	Other related topics
872	ISOLATION LACCASE PRODUCER-YEAST FROM FROM BARK	Sheikhi Fatemeh	Other related topics

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873	UREASE INHIBITORY ACTIVITY OF AERIAL PARTS OF VERONICA CYMBALARIA BODARAD.	Sharifi Rad Javad	Other related topics
874	EVALUATION OF E7-HMGB1 PROTEIN EXPRESSION IN MAMMALIAN CELLS USING DIFFERENT METHODS	Talebi Somayeh	Other related topics
875	BIOFILM FORMATION IN METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS CLINICAL ISOLATES IN ILAM HOSPITALS, IRAN	Bimanand Lida	Other related topics
876	EVALUATION OF TABRIZ STUDENTS KNOWLEDGE AND ATTITUDES TOWARDS AIDS	Eslamkhah Mirsajjad	Other related topics
877	DETECTION OF BLA NDM -1, BLA VIM AND BLA IMP GENES IN PSEUDOMONAS AERUGINOSA AT TEHRAN HOSPITALS BY PCR AND GENE SEQUENCING	Erfani Yousef	Other related topics
878	ISOLATION OF HEAVY METAL RESISTANT PSEUDOMONAS SPP. AND THEIR PLANT GROWTH PROMOTING ACTIVITIES	Javadi Shirin	Other related topics
879	IN VITRO SCREENING OF PHOSPHATE AND ZINC SOLUBILIZING STRAINS OF PSEUDOMONAS SPP. FROM RHIZOSPHERIC SOILS OF A FIELD IN KERMAN, IRAN.	Javadi Shirin	Other related topics
880	STUDY OF PMMA AS ADJUVANT FOR PRODUCTION OF ANTI DIPHTHERIA SERUM ALONG WITH ALUMINUM PHOSPHATE	Abbasi Ebrahim	Other related topics
881	EVALUATION OF NATURALLY ISOLATED BACTERIOPHAGE EFFECT, MGY2, AGAINST B-LACTAM RESISTANT ESCHERICHIA COLI O157	Yousefi Robab	Other related topics
882	REDUCTIVE BIOTRANSFORMATION OF TETRACHLOROETHENE DURING AEROBIC DEGRADATION: EXPERIMENTAL EVIDENCE AND KINETICS	Badali Neda	Other related topics
883	ANTIMICROBIAL EFFECTS OF SILVER NANOPARTICLES FUNCTIONALIZED WITH IMPENEM ON ACINETOBACTER BAUMANNII	Zendegani ELHAM	Other related topics
884	STADY ON EXPRESSION OF THE FULL LENGTH HCV-E2 GENE IN YEAST PICHIA PASTORIS	Solat Rahele	Other related topics
885	HANDS SKIN MICROBIOTA COMPOSITION AND BEHAVIORAL CHARACTERISTICS	Ataie kachoe Mohammad reza	Other related topics

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886	ISOLATION OF ACTINOMYCETES PRODUCING ANTIMICROBIAL SUBSTANCES AGAINST BENEFICIAL BACTERIA AND PATHOGENS IN PLANTS	ESHAGHI EBRAHIM	Other related topics
887	DETECTION OF SOME VIRULENCE FACTORS OF ESCHERICHIA COLI ISOLATED FROM URINARY TRACT INFECTION ISOLATED FROM HOSPITALIZED PATIENTS IN QAZVIN AND KARAJ HOSPITALS	Mahdikhani Mahsa	Other related topics
888	رفتار شستشوی دست در بیمارستان تک تخصصی زنان ام البنین (س) مشهد	Seddighi Sakine	Other related topics
889	ANTIBIOTIC RESISTANT PATTERNS OF ACINETOBACTER SPP. STRAINS ISOLATED FROM PATIENTS WITH PULMONARY INFECTIONS IN TWO HOSPITALS OF KERMAN, IRAN.	Nikbakht Rezvan	Other related topics
890	RISK OF INFECTION FROM E. COLI 0157:H7 THROUGH INFORMALLY MARKETING RAW MILK IN URMIA CITY	Hajilouyan Elham	Other related topics
891	PHYSICO-CHEMICAL ANALYSIS OF PATHOGENIC AND NON-PATHOGENIC E. COLI OUTER MEMBRANE VESICLES (OMVS)	Mohammadzadeh Roghayeh	Other related topics
892	THE PREVALENCE OF PIL A AND ALGinate VIRULENCE GENES IN PSEUDOMONAS AERUGINOSA URINARY TRACT AND TRACHEAL ISOLATES	Valadbeigi Hassan	Other related topics
893	THE CORRELATION OF BETWEEN MAZEF, RELBE AND HIGBA TOXIN-ANTITOXIN SYSTEM AND BIOFILM FORMATION	Valadbeigi Hassan	Other related topics
894	بررسی استرپتوکوکوس های گروه B و الگوی مقاومت فنوتیپی القا شده به کلیندامایسین سویه های جدا شده در زنان باردار مراجعه کننده به بیمارستان صارم در سالهای ۹۳ تا ۹۴	Nomanpour Bizhan	Perinatal Microbiology and Infertility
895	ISOLATION AND IDENTIFICATION OF LACTIC ACID BACTERIA OF SOME IRANIAN TRADITIONAL SOURDOUGH	Shalbaf Saeed	Probiotics
896	ANTI-INFLAMMATORY MECHANISM OF TWO SPORE PROBIOTICS IN LPS-STIMULATED HT-29 CELL LINE	Azimirad Masoumeh	Probiotics
897	SCREENING OF COCCI ISOLATES FROM IRANIAN LOCAL DAIRY PRODUCTS FOR EXTRACELLULAR EXOPOLYSACCHARIDE PRODUCTION	Ameli Sevda	Probiotics

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898	EVALUATION OF PROBIOTIC LACTOBACILLUS SPP IN WHITE FISH (RUTILUS FRISI KUTUM)	Faeed Monireh	Probiotics
899	ISOLATION , IDENTIFICATION AND OPTIMIZATION OF LIPASE PRODUCTION USING A NOVEL LACTOBACILLUS FERMENTUM BY RESPONSE SURFACE METHODOLOGY (RSM)	Fathi gelekolaee Foruzan	Probiotics
900	EVALUATION OF PROBIOTIC POTENTIAL OF METHYLOTROPHIC YEASTS ISOLATED FROM PLANT MATERIALS	Geranpayeh Vaghei Marzieh	Probiotics
901	THE EFFECT OF ADDING ALLIUM AMPELOPRASUM L. SUBSP. IRANICUM ON SENSORY CHARACTERISTICS AND SURVIVABILITY OF LACTOBACILLUS ACIDOPHILUS IN IRANIAN WHITE CHEESE	Mehdizadeh Tooraj	Probiotics
902	EFFECT OF LACTOBACILLUS DELBRUECKII ON OXIDATIVE STRESS IN DIABETIC MICE	Dolatyari eslami Reza	Probiotics
903	EFFECT OF LACTOBACILLUS DELBRUECKII ON GAS6 IN DIABETIC MICE	Dolatyari eslami Reza	Probiotics
904	IN VIVO STUDY OF ANTIBACTERIAL EFFECTS OF LACTOBACILLUS CASEI PTCC 1608 ON PSEUDOMONAS AERUGINOSA PAO1	Hosseinzadeh Sajad	Probiotics
905	IN VITRO STUDY OF ANTIBACTERIAL EFFECTS OF LACTOBACILLUS CASEI PTCC 1608 ON PSEUDOMONAS AERUGINOSA PAO1	Hosseinzadeh Sajad	Probiotics
906	EFFECT OF ORAL ADMINISTRATION OF LACTOBACILLUS ACIDOPHILUS AND BIFIDOBACTERIUM BIFIDUM CAN INDUCE IMMUNE RESPONSE IN BALB/C MICE BEARING TRANSPLANTED BREAST TUMOR.	Keypoor Marjan	Probiotics
907	ANALYSIS OF BAX AND BCL2 GEN EXPRESSION BY REAL TIME PCR IN COLON CANCER CELL LINE TREATED WITH LACTOBACILLUS RHAMNOSUS AS A PROBIOTIC EXTRACT	Oliaei Hedieh	Probiotics
908	AN IN-SILICO SCREENING ON THERMAL STABILITY OF A SERIES OF BACTERIA DIOXYGENASE FOR PROBIOTIC DEVELOPMENT	Shahreki mojahed Safoora	Probiotics

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روز دوم ساعت ۱۸:۰۵-۱۶:۰۵ شماره پوستر ۹۰۹-۱۰۰۹			
909	بهینه سازی شرایط رشد باکتری باسیلوس سابتیلیس با کد شناسایی JQ61819، پروبیوتیک بومی ایران در مقیاس ارلن آزمایشگاهی	Abdoli Senejani Mahbubeh	Probiotics
910	LACTOBACILLUS ACIDOPHILUS EFFECT ON THE ESCHERICHIA COLI AND SHIGELLA SONNEI BACTERIA	Jafari Behboud	Probiotics
911	EFFECT OF LACTOBACILLUS CASEI STRAIN TD3 ON EXPRESSION OF 3-HYDROXY-3-METHYLGUTARYL GENE IN HYPERCHOLESTEROLEMIC RATS	Dehkohne Abolfazl	Probiotics
912	THE EFFECT OF LACTOBACILLUS CASEI , STRAIN TD3, ON WOUND HEALING IN MALE WISTAR RATS ON DAYS 3,7,14 AND 21	Dehkohne Abolfazl	Probiotics
913	ISOLATION AND EXAMINED THE ANTIMICROBIAL EFFECT OF THE INDUSTRIALCAND LOCAL PROBIOTICS ON SEVERAL SPECIES OF ANTIBIOTIC RESISTANT PATHOGENIC BACTERIA	Ahmadnejad Elnaz	Probiotics
914	THE EFFECT OF PREBIOTICS ON THE ANTIMICROBIAL ACTIVITY OF LACTOBACILLUS FERMENTUM ATCC 9338 AND ISOLATE OF THIS STARAIN.	Rezaie Elahe	Probiotics
915	THE EFFECT OF PREBIOTICS ON THE LYPOLYTIC ENZYMES ACTIVITY OF LACTOBACILLUS FERMENTUM ATCC9338 AND ISOLATE OF THIS STARAIN.	Rezaie Elahe	Probiotics
916	ISOLATION AND MOLECULAR IDENTIFICATION OF BIFIDOBACTERIUM FROM INFANT FECES OF HAFEZ HOSPITAL IN SHIRAZ	Bahmani Sepideh	Probiotics
917	ANTBACTERIAEFFECT OF SUPERNATANT LACTOBACILLUS ACIDOPHILUS ON SALMONELLA TYPHI	Porfazlali Nima	Probiotics
918	EVALUATION ANTIMICROBIAL EFFECTS SUPERNATANT OF L. ACIDOPHILUS AND ANTIBIOTIC ON SALMONELLA TYPHIATCC14028 WITH AGAR WELL DIFFUSION METHOD	Porfazlali Nima	Probiotics
919	MOLECULAR IDENTIFICATION OF STREPTOCOCCUS THERMOPHILUS ISOLATED FROM CHEESES SAMPLES IN FARS AND KERMANSHAH PROVINCE	Mirzadeh Negar	Probiotics
920	ISOLATION AND MOLECULAR IDENTIFICATION OF LACTIC ACID BACTERIA FROM TRADITIONAL AND PASTEURIZED YOGURT AND CHEESE	Shafaeian Roya	Probiotics

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921	EXTRACTION, BIOCHEMICAL AND MOLECULAR DETECTION OF YOGHURT PROBIOTIC SPECIES AND OPTIMIZATION OF MAXIMUM GROWTH CONDITIONS	Ghaffarian Zahra	Probiotics
922	OPTIMIZATION OF GROWTH CONDITIONS AND LACTIC ACID PRODUCTION OF LACTOBACILLUS DELBRUECKII SPP. BULGARICUS ISOLATED FROM YOGURT USING TAGUCHI METHOD	Ghaffarian Zahra	Probiotics
923	SCREENING OF LACTOBACILLI ISOLATES FROM IRANIAN LOCAL DAIRY PRODUCTS FOR CONNECTED EXOPOLYSACCHARIDE PRODUCTION	Mortezaeifar Amir	Probiotics
924	SCREENING OF LACTOBACILLI ISOLATES FROM IRANIAN LOCAL DAIRY PRODUCTS FOR EXTRACELLULAR EXOPOLYSACCHARIDE PRODUCTION	Mortezaeifar Amir	Probiotics
925	COMPARATIVE SURVIVAL STUDY OF ENCAPSULATED BIFIDOBACTERIUM BIFIDUM IN THE PRESENCE OF BETA-CAROTENE	POURSEYFOLLAH AZAM	Probiotics
926	DETERMINATION OF HEMOLYTIC PROPERTIES OF ISOLATED LACTOBACILLI FROM TRADITIONAL DAIRY PRODUCTS FOR SELECTION OF PROBIOTIC STRAINS	Javidmehr Mahrokh	Probiotics
927	SELECTION LACTOBACILLI ISOLATED FROM TRADITIONAL DAIRY PRODUCTS FOR RESISTANCE TO BILE OXALATE	Javidmehr Mahrokh	Probiotics
928	THE INTERACTION BETWEEN THE BRAIN AND THE GUT MICROFLORA AND THEIR ROLE IN BEHAVIORAL CHANGES	Mousavi Seyed omidreza	Probiotics
929	FREQUENCY OF GROUP B STREPTOCOCCUS AND TRICHOMONAS VAGINALIS GENITAL INFECTIONS IN PREGNANT WOMEN AND WOMEN WITH SPONTANEOUS ABORTION BY THE PCR METHOD	Ahmadi Amjad	Sexually Transmitted Disease
930	THE INFORMATION SOURCE OF STUDENTS OF ZABOL UNIVERSITIES ABOUT HIV/AIDS	Salari Saeed	Sexually Transmitted Disease
931	LATENT TUBERCULOSIS INFECTION IN HEALTH CARE WORKERS) HCWS(IN IRAN- REVIEW ARTICLE	Mansury Davood	Tuberculosis and Mycobacteria
932	EXTRACTION AND BIOLOGICAL EVALUATION OF MYCOBACTERIUM KANSASII MEMBRANE VESICLES	Hoseini Tavassol Zahra	Tuberculosis and Mycobacteria

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933	EVALUATION OF THE RFLP TB/STR ASSAY FOR RAPID DETECTION OF STREPTOMYCIN RESISTANCE IN MYCOBACTERIUM TUBERCULOSIS	Karimi Sediqe	Tuberculosis and Mycobacteria
934	SCREENING FOR GENETIC PATTERNS OF THE RPSL AND RRS GENES IN CLINICAL ISOLATES OF MYCOBACTERIUM TUBERCULOSIS IN ISFAHAN, IRAN	Karimi Sediqe	Tuberculosis and Mycobacteria
935	A SEARCH FOR TRACES OF MOST FREQUENT CLONAL COMPLEXES OF MYCOBACTERIUM BOVIS IN IRAN	TADAYON KEYVAN	Tuberculosis and Mycobacteria
936	ANTITUBERCULAR ACTIVITY AND CYTOTOXICITY EVALUATION OF NOVEL 4-SUBSTITUTED IMIDAZOLYL-2,6-DIMETHYL-N3,N5-BISARYL-1,4-DIHYDROPYRIDINE-3,5-DICARBOXAMIDES	Ghazvini Kiarash	Tuberculosis and Mycobacteria
937	PARATUBERCULOSIS IN THE ISLAMIC REPUBLIC OF IRAN	Hassani Masoud	Tuberculosis and Mycobacteria
938	COMPARISON OF DNA EXTRACTION METHODS FOR DETECTION OF NON-TUBERCULOSIS MYCOBACTERIA BY REAL-TIME PCR	Mohammadi Samira	Tuberculosis and Mycobacteria
939	IMPROVEMENT OF HEAT STABILITY OF MYCOBACTERIUM BOVIS IN LYOPHILIZED BCG VACCINE	Jahanbakhsh sefidi Fatemeh	Tuberculosis and Mycobacteria
940	DEVELOPMENT OF A CULTURE-COLORIMETRIC METHOD FOR RAPID DETERMINATION OF CFU OF MYCOBACTERIUM BOVIS B.C.G	Jahanbakhsh sefidi Fatemeh	Tuberculosis and Mycobacteria
941	MOLECULAR ANALYSIS OF ETHAMBUTOL RESISTANT M. TUBERCULOSIS STRAINS IN IRAN	SHAHBAZI NARGES	Tuberculosis and Mycobacteria
942	AN INVESTIGATION OF EPIDEMIOLOGICAL STATUS OF TUBERCULAR (TB) PATIENTS IN ARDABIL PROVINCE, IRAN, IN 2015	Modarres sadrani Seyyede negar	Tuberculosis and Mycobacteria
943	MOLECULAR IDENTIFICATION OF MYCOBACTERIUM TUBERCULOSIS COMPLEX BY RD-TYPING TECHNIQUE	Mirzaki Seyede zeinab	Tuberculosis and Mycobacteria
944	ISOLATION, MOLECULAR IDENTIFICATION AND DNA FINGERPRINTING OF MYCOBACTERIUM FROM FISH CULTURE FARMSE OFFER IN KARAJ CITY	Mobasher amini Atefeh	Tuberculosis and Mycobacteria
945	ISOLATION AND MOLECULAR IDENTIFICATION OF MYCOBACTERIUM TUBERCULOSIS COMPLEX FROM MICE INFECTED WITH MYCOBACTERIUM REGIONAL LIVESTOCK BUIN ZAHRA	Alizadeh Khatereh	Tuberculosis and Mycobacteria

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946	MOLECULAR IDENTIFICATION OF MYCOBACTERIUM TUBERCULOSIS COMPLEX BY RD-TYPING AND PCR-RFLP METHOD	Torabi Noosh afarin	Tuberculosis and Mycobacteria
947	CONSTRUCTION OF A RECOMBINANT BCG OVER-EXPRESSING RESUSCITATION-PROMOTING FACTOR E	Ashayeri-panah Mitra	Tuberculosis and Mycobacteria
948	BIOINFORMATIC CHARACTERIZATION, CLONING AND EXPRESSION OF MYCOBACTERIUM TUBERCULOSIS RPFE PROTEIN IN E. COLI	Ashayeri-panah Mitra	Tuberculosis and Mycobacteria
949	BIOINFORMATIC CHARACTERIZATION, CLONING AND EXPRESSION OF MYCOBACTERIUM TUBERCULOSIS RV1733C PROTEIN IN E. COLI	Ashayeri-panah Mitra	Tuberculosis and Mycobacteria
950	CONSTRUCTION OF A RECOMBINANT BCG OVER-EXPRESSING LATENCY-ASSOCIATED ANTIGEN RV1733C	Ashayeri-panah Mitra	Tuberculosis and Mycobacteria
951	DETERMINATION OF POLYMICROBIAL INFECTIONS AND HETERORESISTANCE IN MYCOBACTERIUM TUBERCULOSIS	Kargarpour Kamakoli Mansour	Tuberculosis and Mycobacteria
952	EVALUATION THE OCCURRENCE AND THE DRUG-RESISTANCE OF PULMONARY TUBERCULOSIS IN THE SISTAN REGION DURING 1389-1394 (2010-2016)	Shirazinia Reza	Tuberculosis and Mycobacteria
953	ISOLATION & IDENTIFICATION OF MYCOBACTERIUM TUBERCULOSIS COMPLEX BACTERIA FROM TUBERCULIN POSITIVE CATTLE AND RODENTS FROM INFECTED CATTLE FARMS IN SEMNAN PROVINCE	Rafiee Barzoki Mohammad	Tuberculosis and Mycobacteria
954	BIAS IN DETECTION OF MYCOBACTERIUM TUBERCULOSIS POLYCLONAL INFECTION	Farmanfarmaei Ghazaleh	Tuberculosis and Mycobacteria
955	GENETIC LINEAGES OF MYCOBACTERIUM TUBERCULOSIS ISOLATES IN ISFAHAN, IRAN	Riyahi zaniani Fatemeh	Tuberculosis and Mycobacteria
956	INVESTIGATION AND COMPARING OF EXTRAPULMONARY MYCOBACTERIUM TUBERCULOSIS CASES (TB) BY TYPE OF SAMPLE IN 2012 AND 2013	Taziki Masoomah	Tuberculosis and Mycobacteria
957	EVALUATION OF MULTIPLE DRUG-RESISTANT OF MYCOBACTERIUM TUBERCULOSIS (MDR) IN THE GOLESTAN, MAZANDARAN AND SEMNAN PROVINCE	Taziki Masoomah	Tuberculosis and Mycobacteria

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958	THE DETECTION OF UNIQUE STRAIN OF TUBERCULOSIS DISCOVERED IN QOM PROVINCE AND ADJACENT PROVINCES	Nimrooz Sina	Tuberculosis and Mycobacteria
959	COMPARISON OF DR AND PGRS PROBES IN RFLP TECHNIQUE TO DIFFERENTIATION OF MYCOBACTERIUM BOVIS STRAINS IN QOM PROVINCE	Nimrooz Sina	Tuberculosis and Mycobacteria
960	EVALUATION THE MAST CELLS RECRUITMENT IN LONGITUDINAL ISCHIATIC NERVE POST INJECTION OF FORMAL SALINE 5% IN RAT'S PLANTAR DERMIS	Bakhtiary Zahra	Vaccine
961	CLONING EXPRESSION AND CHARACTERIZATION OF A RECOMBINANT TRUNCATED CAPSID PROTEIN OF HEV IN ROSETTA EXPRESSION STRAIN	Divbandi Marzieh	Vaccine
962	PRODUCTION AND PURIFICATION OF PENICILLIN BINDING PROTEIN2A (PBP2A) OF METHICILIN-RESISITANT STAPHYLOCOCCUS AUREUS: IMMUNOGENICITY STUDY	Mortazavi Seyedehshadi	Vaccine
963	THE PREVALENCE OF SEXUAL RISK BEHAVIOR AND PROGNOSIS OF HIV INFECTION IN ADOLESCENTS AND YOUNG ADULTS IN LARESTAN CITY	Sekhavati Eghbal	Vaccine
964	PREVALENCE OF PEDICULOSIS IN STUDENTS OF LARESTAN CITY IN 2015	Sekhavati Eghbal	Vaccine
965	COMPARATIVE ASSESSMENT OF WHOLE CELL PERTUSSIS VACCINE POTENCY WITH SEROLOGICAL AND INTRACEREBRAL MOUSE PROTECTION METHODS	Mohammadbagher Davoud	Vaccine
966	COMPARATIVE EVALUATION OF IMMUNE RESPONSES TO LIPOPOLYSACCHARIDE AND DETOXIFIED LIPOPOLYSACCHARIDE OF LEGIONELLA PNEUMOPHILA ALONE AND IN COMBINATION WITH BOVINE SERUM ALBOMIN IN BALB/C MICE.	Papian Shaghayegh	Vaccine
967	THE EPSTEIN-BARR VIRUS (EBV) AS A TRIGGER FACTOR FOR SYSTEMIC LUPUS ERYTHEMATOSUS	Zadeh nasir Shokoufeh	Vaccine
968	EVALUATION OF AN INCREASE IN PROTEIN SYNTHESIS IN THE PARASITE PLASMODIUM VIVAX DUFFY BINDING FORM AS A MARKER PROTEIN HEMATOMA STAGE MALARIA VACCINE ARASBARAN, IRAN.	Tarzi Saeed	Vaccine

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969	IN SILICO MODELING AND CHARACTERIZATION OF CHIMERIC VACCINE USING COMPUTATIONAL TOOLS AND SERVERS	Arabi Asciabari Hadi	Vaccine
970	MAPPING OF IMMUNOGENIC DISCONTINUOUS EPITOPES ON HUMAN IGG FC REGION BY COMPUTATIONAL IMMUNOLOGY	Hajighasemi Fatemeh	Vaccine
971	THE STUDY OF PROTECTIVE EFFECT OF HEPATITIS B VACCINE IN 12 TO 24 MONTHS OLD VACCINATED CHILDREN REFERED TO TABRIZ CHILDREN HOSPITAL	Teymouri Bilesuar Asemeh	Vaccine
972	MICROBIAL VACCINES	Esmatparast Milad	Vaccine
973	COMPARATIVE CHEMO-PHYSICAL OUTER MEMBRANE VESICLES (OMVS) ANALYSIS OF PSEUDOMONAS AERUGINOSA SENSITIVE , RESISTANT AND STANDARD STRAINS	Satarian Fereshteh	Vaccine
974	THE RECOMBINANT ANTIGENS USED AS EXPERIMENTAL VACCINES AGAINST OLD WORLD CUTANEOUS LEISHMANIASIS : A SYSTEMATIC REVIEW	Ghasemi Nejad Almani Pooya	Vaccine
975	PRODUCTION OF AUTOLYSIN PROTEIN OF METHICILIN-RESISTANT STAPHYLOCOCCUS AUREUS AND EVALUATION OF PROTECTIVE ACTIVITY IN BALB/C MICE BY PASSIVE VACCINATION	Kalali Yasamin	Vaccine
976	STABILITY STUDY OF IBIBA FULL DOSE BRUCELLOSIS VACCINE AFTER RECONSTITUTE	Dostdari Sajad	Vaccine
977	DEVELOPMENT OF ANTI-BOVINE IGGIMMUNOGLOBULIN Y (IGYS) IN QUAIL	Attari roodi Yoones	Vaccine
978	POSSIBLE RELATIONSHIP BETWEEN CYTOMEGALOVIRUS INFECTION AND NEUROMYELITIS OPTICA AND MULTIPLE SCLEROSIS	Jazini Mahboobe	Vaccine
979	OPTIMIZATION OF VERO / MICROCARRIER CELL CULTURE FOR PRODUCTION OF HIGH TITER VIRUS VACCINE SEED	MOHAMMADI ASHRAF	Vaccine
980	COMPARATIVE SENSITIVITY ANALYSIS BETWEEN TWO METHODS FOR SPECIES DIFFERENTIATION AND INTERSPECIES CROSS CONTAMINATION IN ANIMAL CELL CULTURE	MOHAMMADI ASHRAF	Vaccine

Row	Title	Submission Author	Session
981	MDRA GENE AS A CANDIDATE FOR DEVELOPING VACCINE AGAINST UTI	Tokhmechi Hamideh	Vaccine
982	COMPARISON OF THREE NEW VARIETIES OF NEOSPOREA CANINUM TO INDUCE IMMUNE RESPONSE IN MOUSE	Sabouri shirazi Maryam	Vaccine
983	CLONING, EXPRESSION, PURIFICATION AND IMMUNIZATION OF HMW1, HMW2 AND HIA ADHESIN PROTEINS AS A VACCINE CANDIDATES OF NONTYPEABLE HAEMOPHILUS INFLUENZAE(NTHI)	Abbaszadeh Goudarzi Kazem	Vaccine
984	INVESTIGATION OF L1 GENE EXPRESSION FROM TYPE33 OF HUMAN PAPILLOMA VIRUS IN ESCHERICHIA COLI	Rassi Hossein	Vaccine
985	EFFECT OF DIFFERENT CONCENTRATION OF FECL3 ON SOME PATHOGENIC BACTERIA FOR PREPARATION OF IRON-INACTIVATED AGENTS	Homayoon Maryam	Vaccine
986	ORAL ADMINISTRATION OF DISPLAYED ACINETOBACTER BAUMANNII BIOFILM-ASSOCIATED PROTEIN INDUCES A PROTECTIVE IMMUNE RESPONSE IN MICE	Zadeh Hosseingholi Elaheh	Vaccine
987	DESIGNING AND IN SILICO STUDIES OF FUSION PROTEIN FLIC.MRPH AGAINST URINARY TRACT INFECTIONS CAUSED BY PROTEUS MIRABILIS	Shirzad dreshir Ali mohamad	Vaccine
988	RECOMBINANT HMW1 CORE BINDING DOMAIN AS A VACCINE CANDIDATE FOR NONTYPEABLE HAEMPHILUS INFLUENZAE	Meidaninikjeh Sepideh	Vaccine
989	PRODUCTION OF IGY ANTI MOUSE IGG ANTIBODY IN QUAIL	Veisi Kaveh	Vaccine
990	MIR-20A AND MIR-17 AND THEIR POTENTIAL TARGETS IN JURKAT CELLS	Mapar Maryam	Vaccine
991	EXTRACTION AND BIOLOGICAL EVALUATION OF MYCOBACTERIUM AVIUM COMPLEX SUBSP. AVIUM MEMBRANE VESICLES	Kamran sarkandi Mohammad	Vaccine
992	TESTING OMPS+RCAGA COMBINATION AS A NEW IMMUNIZATION CANDIDATE FOR SPLENIC, GASTRIC CLEARANCE OF BRUCELLA ABORTUS 544 AND HELICOBACTER PYLORI SS1 STRAIN INFECTIONS IN BALB/C MICE	Hossein Abadi Amir	Vaccine

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993	EFFECT OF TEMPERATURE AND CONCENTRATION OF BETA-PROPIOLACTONE ON INACTIVATION OF CELL DERIVED RABIES VIRUS	Eftekhari Zohre	Vaccine
994	CLONING AND EXPRESSION NOVEL TRUNCATED RECOMBINANT FUSION PROTEIN AGAINST URINARY TRACT INFECTIONS CAUSED BY ESCHERICHIA COLI (UPEC) AND PROTEUS MIRABILIS	Bameri Zakaria	Vaccine
995	مشکلات عفونی در نوزادان نارس بیمارستان تک تخصصی زنان حضرت ام البنین(س) مشهد	Seddighi Sakine	Vaccine
996	RECOGNITION OF ANTIGENIC REGION IN FHAB AND FHAC PROTEINS ON ACINETOBACTER BAUMANNII	Ezati mehrabani Farnoush	Vaccine
997	CLEANING VALIDATION OF MMR VACCINE PRODUCTION DESK TO ASSESS THE EFFICIENCY OF DECONTAMINATION OF MEASLES, MUMPS AND RUBELLA VIRUSES DURING CAMPAIGN	Talebshoostari Maryam	Vaccine
998	EVALUATING THE PROTECTIVE EFFECTS OF POLYVALENT ANTIGEN OF PSEUDOMONAS AERUGINOSA IN ANIMAL MODEL AS A POTENTIAL VACCINE	Rezaei benem Sanam	Vaccine
999	DESIGNING A CHIMERIC CONSTRUCT AS A SUITABLE IMMUNOGEN CANDIDATE AGAINST VIBRIO CHOLERAEE	Vakili Atina	Vaccine
1000	IN SILICO DESIGN OF A MULTI-EPITOPE DNA VACCINE AGAINST BRUCELLA SPP	Vakili Atina	Vaccine
1001	OMP34KDA AS A VACCINE CANDIDATE AGAINST ACINETOBACTER BAUMANNII	Naghipoureramy Aleme	Vaccine
1002	INACTIVATION OF ECOLI O157:H7 BY FORMALIN AND HEAT	Arshadi Nasim	Vaccine
1003	MOLECULAR DYNAMICS SIMULATIONS IMMUNOGENIC EPITOPS OF SURFACE ANTIGEN 1 (SAG1) FROM TOXOPLASMA GONDII AND HUMAN LEUKOCYTE ANTIGEN (HLA) FOR THE DESIGN OF EFFECTIVE VACCINE	Soltani Soudabeh	Vaccine
1004	COMPARISON INTERACTIONS BETWEEN IMMUNOGENIC EPITOPE OF TOXOPLASMA GONDII AND MHC CLEFT IN HUMAN AND SHEEP BY MOLECULAR DYNAMICS SIMULATIONS	Soltani Soudabeh	Vaccine

Row	Title	Submission Author	Session
1005	COMPARISON INTERACTIONS BETWEEN IMMUNOGENIC EPITOPES OF TOXOPLASMA GONDII AND MHC CLEFT IN HUMAN AND SHEEP USING MOLECULAR DYNAMICS SIMULATIONS	Soltani Soudabeh	Vaccine
1006	IMMUNOLOGICAL EVALUATION OF SALMONELLA PARATYPHI C OLIGOPOLYSACCHARIDE DIPHTHERIA TOXOID CONJUGATE IN MICE.	Behmagham Neda	Vaccine
1007	IMMUNOGENICITY OF VACJ, AN OUTER MEMBRANE LIPOPROTEIN OF ACINETOBACTER BAUMANNII	Masoumkhani Saideh	Vaccine
1008	EVALUATION OF PERTUSSIS TOXIN PRODUCTION IN B2 AND TH1S MEDIA	Moradtalab Hamid	Vaccine
1009	IMMUNIZATION WITH HPV16E7D VACCINE MODIFIED CYTOKINES PATTERN IN TUMOR MICROENVIRONMENT	Mahin samadi Pariya	Vaccine
روز سوم ساعت ۹:۱۵-۸:۰۰ شماره پوستر ۱۱۱-۱۰۱			
1010	EVALUATION OF OMP2A, OMP2B COMBINATION AS A NEW VACCINE CANDIDATE AGAINST BRUCELLOSIS	Meskini Maryam	Vaccine
1011	INVESTIGATING EFFECTS OF CARBON AND NITROGEN SOURCES ON THE CAPSULE PRODUCTION BY STREPTOCOCCUS PNEUMONIAE SEROTYPE 19F	Tarahomjoo Shirin	Vaccine
1012	IDENTIFYING CONFORMATIONAL B-CELL EPITOPES OF DIPHTHERIA TOXIN AT DIFFERENT PHs AND TEMPERATURES USING MOLECULAR DYNAMICS SIMULATIONS	Tarahomjoo Shirin	Vaccine
1013	ANALYSIS OF IMMUNOGENIC B-CELL EPITOPE REGIONS IN PLASMID STABILIZATION PROEIN OF STREPTOCOCCUS PNEUMONIAE SEROVAR 19F	Tarahomjoo Shirin	Vaccine
1014	IDENTIFICATION OF PROTECTIVE B-CELL EPITOPE REGIONS IN PILUS T-SURFACE ANTIGEN SPT-1059 OF STREPTOCOCCUS PNEUMONIAE SEROTYPE 19F	Tarahomjoo Shirin	Vaccine
1015	HUMAN IMMUNE RESPONSES AND VACCINE CANDIDATES AGAINST BRUCELLOSIS	Heidary Mohsen	Vaccine
1016	MOLECULAR CHARACTERIZATION OF RAZI PM 0002/1982, AN AVIAN VACCINE STRAIN OF PASTEURELLA MULTOCIDA, BY MULTI LOCUS SEQUENCE TYPING (MLST)	TADAYON KEYVAN	Vaccine

Row	Title	Submission Author	Session
1017	RESOLUTION POWER OF TWO TANDEM REPEAT LOCI IN DIFFERENTIATION BETWEEN THE RAZI BP0134 & RAZI 0509 VACCINE STRAINS OF BORDETELLA PERTUSSIS	TADAYON KEYVAN	Vaccine
1018	ANTIMICROBIAL SUSCEPTIBILITY OF CLOSTRIDIUM ISOLATES FROM OSTRICHES	Ezzatkah Majid	Vaccine
1019	PPD MODIFIED IMMUNE RESPONSES VERSUS KILLED LEISHMANIA VACCINE	BALKANIAN FARZANEH	Vaccine
1020	SIGNIFICANTLY HIGHER THAN THE OTHER MICE GROUPS. THE AAAAAA AAAAAA AAAAAA	Asadi Karam Mohammad Reza	Vaccine
1021	EXPRESSION, PURIFICATION AND PRODUCTION OF A RECOMBINANT PROTEIN VACCINE AGAINST S. AUREUS BIOFILM-RELATED INFECTIONS	Haghkhah Masoud	Vaccine
1022	PROTEIN LIPL32 IS A CANDIDATE SUBUNIT VACCINE AGAINST LEPTOSPIROSIS	Hashemi Tabar Gholamreza	Vaccine
1023	IDENTIFICATION AND ANTIBIOTIC RESISTANCE OF COAGULASE-NEGATIVE STAPHYLOCOCCI ISOLATED FROM NASAL CAVITY OF HEALTHY ANIMALS IN IRAN	Hosseinazadeh Somayyeh	Veterinary Microbiology
1024	PRESENCE OF PENICILLIN G RESISTANCE OF STAPHYLOCOCCUS AUREUS ISOLATED FROM MASTITIS IN CATTLE AND SHEEP	Hosseinazadeh Somayyeh	Veterinary Microbiology
1025	TURKEY ENTERITIS PREVENTION USING GARLIC AND SHALLOT POWDER	Nabinejad Abdolreza	Veterinary Microbiology
1026	THE FIRST SURVEY OF ANTIBODY TO BLUETONGUE VIRUS (BTV) IN SMALL RUMINANTS FLOCKS IN SISTAN & BALUCHESTAN PROVINCE, IRAN	Alimolaei Mojtaba	Veterinary Microbiology
1027	EVALUATION OF ANTIMICROBIAL PROPERTIES OF HEMISCORPIOUS LEPTURUS SCORPION VENOM AGAINST E.COLI	Zayerzadeh Ehsan	Veterinary Microbiology
1028	A SERO-EPIDEMIOLOGICAL STUDY OF BOVINE LEPTOSPIROSIS IN EAST REGION OF GUILAN PROVINCE	Shafighi Seyedeh Tooba	Veterinary Microbiology
1029	HIGH SEROPREVALENCE OF BLUETONGUE VIRUS ANTIBODIES IN GOAT FLOCKS IN NORTH KERMAN, IRAN	Ezzatkah Majid	Veterinary Microbiology
1030	FIRST DETECTION OF BOVINE ROTAVIRUS GROUP C CIRCULATING IN CALF POPULATION OF DAIRY FARMS OF IRAN	Nazaktabar Ahmad	Veterinary Microbiology

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1031	FIRST DETECTION OF BOVINE TOROVIRUS CAUSING DIARRHEA IN NEW BORN CALVES, IN IRAN	Nazaktabar Ahmad	Veterinary Microbiology
1032	MOLECULAR EPIDEMIOLOGY OF BOVINE CORONAVIRUS IN SAMPLES OF DIARRHEIC CALVES COLLECTED FROM 14 PROVINCES OF IRAN	Nazaktabar Ahmad	Veterinary Microbiology
1033	PASTEURELLA MULTOCIDA ST 325, A NEWLY REPORTED MULTI LOCUS SEQUENCE TYPE (MLST) CLASSIFIED WITHIN THE ST122 CLONAL COMPLEX	TADAYON KEYVAN	Veterinary Microbiology
1034	EPIDEMIOLOGICAL STUDY OF ABORTION CAUSED BY MYCOPLASMA AGALACTIAE IN BALUCHI SHEEP IN THE NORTHERN OF SISTAN AND BALUCHESTAN PROVINCE USING MOLECULAR METHOD (PCR).	Hossein abadi Ebrahim	Veterinary Microbiology
1035	EPIDEMIOLOGICAL STUDY OF ABORTION CAUSED BY CHLAMYDOPHILA ABAORTUS IN BALUCHI SHEEP IN THE NORTHERN OF SISTAN AND BALUCHESTAN PROVINCE USING MOLECULAR METHOD (PCR).	Hossein abadi Ebrahim	Veterinary Microbiology
1036	EPIDEMIOLOGICAL STUDY OF ABORTION CAUSED BY CAMPYLOBACTER FETUS IN BALUCHI SHEEP IN THE NORTHERN OF SISTAN AND BALUCHESTAN PROVINCE USING MOLECULAR METHOD (PCR).	Hossein abadi Ebrahim	Veterinary Microbiology
1037	PARATUBERCULOSIS IN IRAN, HAS THE TIME ARRIVED FOR A NATIONAL CONTROL PLAN?	TADAYON KEYVAN	Veterinary Microbiology
1038	INTERACTION OF HETEROPHILS WITH DIFFERENT PHYLOTYPES OF ESCHERICHIA COLI ISOLATED FROM CHICKEN COLIBACILLOSIS	Ahmadi Somayeh	Veterinary Microbiology
1039	LPS-PCR TYPING OF OVINE PASTEURELLA MULTOCIDA ISOLATES FROM IRAN BASED ON(L1 TO L8)OUTER CORE BIOSYNTHESIS LOCI	Merhaghgoe jalali Sedeh fahimeh	Veterinary Microbiology
1040	ANTIBIOTIC PROPHYLAXIS IN RABBIT OVARIOHYSTERECTOMY SURGERY	Mohammadiar Leila	Veterinary Microbiology
1041	DETERMINATION AND COMPARISON OF ANTIMICROBIAL SENSITIVITY OF ESCHERICHIA COLI ISOLATED FROM HEALTHY OSTRICHES IN COMPARISON WITH ISOLATES FROM INFECTED POULTRY WITH COLIBACILLOSIS	Hosseini Afsane	Veterinary Microbiology

Row	Title	Submission Author	Session
1042	A REVIEW OF THE EPIDEMIOLOGY OF MALARIA AND IMMUNOINFORMATIC STUDY OF SG1, SG2 AND SG3 PROTEINS OF SALIVARY GLAND IN ANOPHELES GAMBIAE	Khalili Sara	Veterinary Microbiology
1043	SEROLOGICAL DETECTION OF ANTI NEWCASTLE DISEASE VIRUS ANTIBODIES IN FREE RANGE CHICKEN OF FARS PROVINCE OF IRAN	Dehghani Yasamin	Veterinary Microbiology
1044	STUDY ON THE CONTAMINATION OF RAW MILK WITH E.COLI O157: H7 IN KHOUZESTAN PROVINCE	Zarnegar Iman	Veterinary Microbiology
1045	STUDY OF CLINICAL OBSERVATIONS OF EXPERIMENTAL INFECTION WITH AEROMONAS HYDROPHILA IN YELLOWFIN SEABREAM ACANTHOPAGRUS LATUS	Shirali Solmaz	Veterinary Microbiology
1046	INVESTIGATION OF THE IMMUNOGENICITY OF TRIVALENT INACTIVATED VACCINE AGAINST COLIBACILLOSIS IN POULTRY	Noori Hojatolah	Veterinary Microbiology
1047	EVALUATION THE PATTERN OF ANTIBIOTIC SENSITIVITY AND RESISTANCE OF ESCHERICHIA COLI AND SALMONELLA ISOLATED FROM AVICULTURE IN THE TABRIZ CITIES	Bageri Yasin	Veterinary Microbiology
1048	PHYLOGENETIC ANALYSIS OF COXIELLA BURNETII ISOLATES FROM DAIRY FARMS IN TEHRAN	Ahmadizadeh Changiz	Veterinary Microbiology
1049	STUDY OF THE PRESENCE OF BORDETELLA AVIUM AND ORNITHOBACTERIUM RHINOTRACHEAE IN NATIVE FLOCKS OF TURKEYS AND DETERMINATION DRUG SENSITIVITY IN ISOLATED SAMPLE	Mohammadi aghbash Elnaz	Veterinary Microbiology
1050	DETERMINATION OF ANTIBIOTICAL RESISTANCE PATTERN IN SALMONELLA ENTERITIDIS STRAINS ISOLATED FROM POULTRY SAMPLES AND THEIR DETECTION OF VIRULENCE GENES	Salami khaneshan Elaheh	Veterinary Microbiology
1051	PREVALENCE OF STAPHYLOCOCCUS AUREUS AND COAGULASE-NEGATIVE STAPHYLOCOCCI IN BOVINE MASTITIS IN TABRIZ	Rezaei ansaroudi Naeimeh	Veterinary Microbiology
1052	PREVALENCE OF METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS AND COAGULASE-NEGATIVE STAPHYLOCOCCI IN BOVINE CLINICAL MASTITIS IN TABRIZ	Rezaei ansaroudi Naeimeh	Veterinary Microbiology

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1053	PREVALENCE OF ESCHERICHIA COLI AND ANTIBIOTIC SUSCEPTIBILITY PATTERN OF ISOLATES IN BOVINE CLINICAL MASTITIS IN TABRIZ	Vahabian Samira	Veterinary Microbiology
1054	MOLECULAR CHARACTERIZATION OF COMPLETE CODING SEQUENCE OF PHOSPHOPROTEIN GENE NEW IRANIAN VIRULENT NDV DISEASE	Roustaei Samira	Veterinary Microbiology
1055	PODOVIRIDAE BACTERIOPHAGES ISOLATION AND MICROSCOPIC CHARACTERIZATION FROM URMIA LAKE, IRAN	Mohammadpoor Arjmand Arash	Viruses
1056	SCREENING OF MAJOR BLOOD-BORNE VIRUSES IN HEMODIALYSIS PATIENTS IN ZANJAN, IRAN	Samadi Elham	Viruses
1057	A SURVEY OF THE FREQUENCY OF CYTOMEGALOVIRUS-ASSOCIATED DIARRHEA IN HIV/AIDS PATIENTS USING NON-INVASIVE METHOD	Sarvari Jamal	Viruses
1058	EVALUATION SEROPREVALENCE HEPATITIS B AND C VIRUS IN SAHNEH CITY OF KERMANSHAH PROVINCE OF IRAN DURING MARCH 2010-MARCH 2016	Pooyanmehr Mehrdad	Viruses
1059	EVALUATION OF RISK FACTORS AND CLINICAL COURSE IN PATIENTS WITH HIV INFECTIONS AT TABRIZ CITY DURATION 2013-15	Bageri Yasin	Viruses
1060	FREQUENT UL27 MUTATIONS IN HIV INFECTED CLINICAL SAMPLES MAY SUGGEST ITS ROLE IN VIRUS INFECTION	Mirarab Azam	Viruses
1061	A FATAL CRIMEAN-CONGO HEMORRHAGIC FEVER FOLLOWING INFECTION WITH AN AP92 LIKE STRAIN OF CRIMEAN-CONGO HEMORRHAGIC FEVER VIRUS	Jamshidi Yasaman	Viruses
1062	INFECTIVITY OF HUMAN T -CELL VIRUS TYPE 1	Jamali Behzad	Viruses
1063	THE ROLE OF HUMAN PAPILLOMAVIRUS IN CANCER	Jamali Behzad	Viruses
1064	ASSOCIATION OF EPSTEIN-BARR VIRUS WITH TUMOR SIZE OF PATIENTS WITH ESOPHAGEAL SQUAMOUS CELL CARCINOMA	Moradi Ali	Viruses
1065	MECHANISM OF INFECTIOUS BRONCHITIS VIRUS IMMUNOPATHOGENESIS	Masoudi Shahin	Viruses

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1066	HIGH-LEVEL EXPRESSION AND ONE-STEP PURIFICATION OF RECOMBINANT ANTIGEN CONTAINING HTLV-I/-II LINEAR EPITOPES	Faramarzi Roxana	Viruses
1067	DEVELOPMENT AND EVALUATION A NOVEL REAL TIME PCR TEST BASED ON SYBR GREEN CHEMISTRY FOR QUANTIFICATION OF HEPATITIS B VIRUS DNA	Kamill Alaa	Viruses
1068	FREQUENCY OF HCV GENOTYPES 1A AND 1B IN HCV POSITIVE PATIENTS REFERRED TO CLINICAL LABORATORIES IN RASHT	Hooshmand rad Mahnaz	Viruses
1069	EXPRESSION AND SOLUBILITY DETERMINATION OF HEPATITIS B CORE ANTIGEN IN E.COLI	Hashemi khah Malihe sadat	Viruses
1070	CONSTRUCTING, MOLECULAR MODELLING AND EVALUATING A NOVEL CHIMERIC ANTIGEN CONTAINING GP46 AND P19 LINEAR EPITOPES FOR HTLV-I INFECTION SCREENING	Hashemi khah Malihe sadat	Viruses
1071	DO COMMON MITOCHONDRIAL DNA POLYMORPHISM ASSOCIATION WITH HUMAN T-CELL LEUKEMIA VIRUS TYPE I	Zolfaghari Toktam	Viruses
1072	PREVALENCE OF HERPES VIRAL ENCEPHALITIS IN CHILDREN WITH ASEPTIC MENINGOENCEPHALITIS IN IMAM REZA HOSPITAL IN THE FALL OF 1394, NORTH Khorasan, BOJNORD	Safamanesh Saghar	Viruses
1073	EXPRESSION AND PURIFICATION OF IMMUNO-DOMINANT PEPTIDE DERIVED FROM GP46-II FOR DETECTION OF HTLV-II SPECIFIC ANTIBODIES	Miyanabadi Maryam	Viruses
1074	INVESTIGATION OF ASSOCIATION OF A SINGLE NUCLEOTIDE POLYMORPHISM (RS1179251) IN INTERLEUKIN 22 GENE WITH CHRONIC HEPATITIS B	Asadi PANIZA	Viruses
1075	EVALUATION OF SERUM LEVELS OF IL-12 IN PATIENTS IN VARIOUS CLINICAL PHASES OF HEPATITIS B VIRUS INFECTION	Asadi PANIZA	Viruses
1076	ASSOCIATION OF INTERLEUKIN-21 GENE POLYMORPHISM (RS2055979) WITH SUSCEPTIBILITY TO CHRONIC HEPATITIS B VIRUS INFECTION	Asadi PANIZA	Viruses

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1077	RNA DETECTION OF RABIES VIRUS IN THE BRAINS OF SUSPECTED RABID ANIMALS USING RT-LAMP METHOD COMPARE TO REAL TIME RT-PCR TEST AS A QUANTITATIVE MOLECULAR TECHNIQUE AND DFA AS A SEROLOGIC METHOD	Naji Elahe	Viruses
1078	INVESTIGATION OF PAPILLOMA VIRUS GENOTYPES IN PATIENT'S ORAL LESIONS WITH HEAD AND NECK CANCER IN THE YEAR 1393 IN IRAN	Pouide Elham	Viruses
1079	POTENTIAL ANTIGENICITY OF THE G1-EPI TOPE BEFV ISOLATED IN IRAN	YAZDANI Fereshteh	Viruses
1080	MOLECULAR DIAGNOSIS OF HUMAN PAPILLOMAVIRUS (HPV) GENOTYPES IN TEHRAN CITY	Soltanahmadi Bahareh	Viruses
1081	CLONING AND EXPRESSION OF VP1 GENE OF FOOT AND MOUTH DISEASE VIRUSE AND FLIC GENE OF SALMONELLA IN E.COLI	Qadir Mehrnoosh	Viruses
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Oral

The 17th International and Iranian Congress of

Anaerobic Bacteria

O1 - 1039: DETECTION OF TOXIGENIC CLOSTRIDIUM DIFFICILE IN COLITIS PATIENTS STOOL BY REAL TIME PCR

Sepideh Khodaparast¹, Ashraf Mohabati Mobarez², Mohammad Vasei³, Mahmood Naderi⁴,
Fatemeh Savaheli Moghaddam⁵

1. Tarbiat Modares University , Faculty of Medical Sciences, Department of Bacteriology
2. Tarbiat Modares University , Faculty of Medical Sciences, Department of Bacteriology
3. Pathology Laboratory, Shariati Hospital, Tehran University of Medical Sciences, Tehran, Iran.
4. Liver and Pancreatobiliary Diseases Research Center, Digestive Disease Research Institute, Tehran University of Medical Sciences, Tehran, Iran.
5. Tarbiat Modares University, Faculty of Medical Sciences, Department of Bacteriology

Background and Aim: Clostridium difficile is a Gram-positive anaerobic bacillus, with the ability to produce spores and is the etiologic agent of nosocomial pathogens with widespread gastrointestinal diseases as self-limiting diarrhea to fatal colitis caused by antibiotics therapy. Clostridium. difficile can colonize the large intestine by adhesion of the bacteria to grow and produce toxin type A and toxin type B (TcdA,Tcd B), which leads to the formation of different symptoms of the disease such as pseudomembrane colitis; particularly in the elderly is one of the most important factors be considered hospital acquired infections. That's why rapid diagnosis of bacteria in patient samples is especially important.

Methods: In a cohort study at an academic medical center, samples of colitis patients with a history of antibiotic treatment collected. Stool samples cultured on the CCFA media following alcohol shock. Several methods assessed including: culture PCR, stool PCR (cdd-3, tcdA&tcdB), cell-culture toxin assay, Real-time PCR (tcdA&tcdB) cultured isolated and stool specimens. Real-time PCR performed with tcdA&tcdB gene-specific SYBR® Green primers and using Lightcycler® Systems(Roche Diagnostics).

Results: A total of 11 stool samples were positive by Real-time PCR. Sensitivity of all methods were 100%, but specificity of culture, culture PCR and culture and stool real-time PCR were 81%, 100% and 100% respectively.

Conclusion: Therefore, real-time PCR stool sample has greater value percent with higher specificity. Due to slow growing of C. difficile, rapid diagnosis from clinical samples provide effective help for the medical staff.

Keywords: Clostridium difficile, Colitis, Toxin, Culture, Real-time PCR

Applied (industrial and agricultural) Microbiology

O2 - 161: CLONING OF MUTANT ESCHERICHIA COLI PHYTASE (R92K) BY SITE DIRECTED MUTAGENESIS

Zeinab alsadat Ahmadi¹, Bijan Bambai², Ali Asghar Karkhane³

1. Department of Industrial and Environmental Biotechnology, National Institute of Genetics Engineering and Biotechnology, Tehran, Iran.
2. Department of Industrial and Environmental Biotechnology, National Institute of Genetics Engineering and Biotechnology, Tehran, Iran.
3. Department of Industrial and Environmental Biotechnology, National Institute of Genetics Engineering and Biotechnology, Tehran, Iran.

Background and Aim: Phytases (myo-inositol hexakisphosphate phosphohydrolase) are a class of phosphatase catalyzing the stepwise hydrolysis of phytate to less phosphorylated myo-inositol derivatives and inorganic phosphate, phytate is the primary form of phosphate storage in plants. Phytases are used as an animal feed additive to improve phosphate bioavailability. Among microbial phytase, *E. coli* phytase has gain commercial application in broiler feed formulation due to high specific activity, acidic pH optimum, and pepsin resistance. This study focused on cloning and expression of mutant *E. coli* phytase using site-directed mutagenesis.

Methods: For this purpose, selection of desired mutation was first conducted through bioinformatic studies, Arginine 92 was replaced to Lysine (R92K) in AppA2 encoding sequence using overlap extension PCR (SOE-PCR). The native and mutant AppA2 genes were cloned and expressed in *E. coli* Bl21(DE3) host. Subsequently, both phytases were purified.

Results: Here, we mutated the N-terminal of conserved active site sequence motif RHGX₂RP in AppA2. Both Arginine 92 substitution to Lysine and the native phytase genes were cloned in pET-26b(+) as fusion with His6-tag and transferred to *E. coli* Bl21(DE3). Considerable amount of proteins were expressed after IPTG induction and purified using affinity chromatography.

Conclusion: It is desirable to develop phytases with higher stability and specific activity to apply in animal feed industry, to decrease the use of inorganic phosphorous in animal feeds, and lower phosphorous levels in the excreted manure. Here, production of the purified recombinant phytase, enabled us to investigate the effects of point mutation on enzyme kinetics.

Keywords: Phytate, Phytase, *E. coli* phytase AppA2, Site-directed mutagenesis.

Applied Microbiology

O3 - 102: BACTERIA SET TO GIVE THE BEAUTY SECTOR A FACELIFT

Parvaneh Saffarian^{1, -2}

1. Department of microbiology, Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran
2. Department of Bacteriology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, Iran

Background and Aim: Biotechnology holds enormous promise to improve the quality of life for mankind on a global basis. The cosmetic industry globally has provided a plethora of biologic materials. These materials have a winning combination: demonstrable performance in finished formulation and –even more importantly- safety during repeated topical application.

Methods: Antioxidants, for example, are notably used in skin creams to counter the degradation of living cells. Today, they are produced in energy-intensive processes that use potentially hazardous catalysts and form unsavoury by-products. A well-tailored natural enzyme could catalyze the same reaction more efficiently, without the environmental drawbacks. They produce no hazardous waste and do away with risks of raw material shortages. The idea is to replace them with molecules derived from nature. Natural products are being harnessed to create a new breed of health-giving biomolecules. These biomolecules could endow cosmetics with pharmaceutical properties; turning them into “cosmeceuticals”. Nature-based cosmetics could also have environmental benefits for the billions beauty products sector, as they use much less energy to produce. Clostridium botulinum produces botulinum neurotoxin (BoNT) which has been used since many years ago as an injectable therapeutic agent for the treatment of some abnormal muscle contractions.

Results: Recently, successes achieved with identifying extreme enzyme systems from hydrothermal- residing marine bacteria which may provide innovative approaches to common skin exposures (i.e. air pollution, smoking and resulting changes in skin condition).

Conclusion: The upshot of all of these is that researchers are getting the chance to work out new techniques that could replace industrial chemicals in other sectors with biomolecules.

Keywords: Botulinum neurotoxin, Cosmetic industry, Cosmeceuticals, bacteria, biologic materials

O4 - 736: ENHANEMENT OF HIV-1 PROTEIN VACCINATION USING CELL PENETRATING PEPTIDES

Somayeh Kadkhodayan¹, Mehdi Sadat², Shiva Irani ³, Fatemeh Motevalli ⁴, Elnaz Agi⁵, Azam Bolhassani ⁶

1. 1 Department of Hepatitis and AIDS, Pasteur Institute of Iran, Tehran, Iran 2 Department of Biology, School of Basic Science, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. Department of Hepatitis and AIDS, Pasteur Institute of Iran, Tehran, Iran
3. Department of Biology, School of Basic Science, Science and Research Branch, Islamic Azad University, Tehran, Iran
4. Department of Hepatitis and AIDS, Pasteur Institute of Iran, Tehran, Iran
5. Department of Hepatitis and AIDS, Pasteur Institute of Iran, Tehran, Iran
6. Department of Hepatitis and AIDS, Pasteur Institute of Iran, Tehran, Iran

Background and Aim:The HIV-1 regulatory proteins tat and nef are attractive as vaccine components since they are the HIV-1 critical proteins and AIDS disease progression . For vaccine development, different types of lipid- and polymer-based vectors such as liposomes, microparticles and nanoparticles have been used for protein delivery, but with relatively poor success. Recently, a group of short, highly basic peptides known as cell-penetrating peptides (CPPs) were used to carry polypeptides and proteins into cells.

Methods:: In current study, expression and purification of Tat-Nef protein was performed in *E. coli* and transfected by the amphipathic CPPs including Pep-1 and CADY-2 into HEK-293T cells. The size and morphology of the CPPs/ Tat-Nef complexes were evaluated by scanning electron microscopy (SEM) and SDS-PAGE. The efficiency of transfection of Tat-Nef/CPP nanoparticles was analyzed and compared with FITC-antibody protein as a control ,using western blotting

Results:SEM data confirmed the formation of discrete nanoparticles with a diameter of below 300 nm. Moreover, formation of the complexes was detected using SDS-PAGE as two individual bands indicating the non-covalent interaction. the Tat-Nef protein was expressed in prokaryotic expression system and efficiently transfected using CPP delivery systems at molar ratio of 20:1. Our results showed that the transfection efficiency of Pep-based nanoparticles was similar to CADY-based nanoparticles and comparable with TurboFect-protein complexes.

Conclusion:The in vitro efficient delivery of Tat-Nef fusion protein supports the potential of CPPs as potent carriers for HIV vaccine design and it will be considered as an advantage for therapeutic purposes in Future.

Keywords:Tat,Nef, Prokaryotic expression systems, Protein purification, Cell penetrating peptides

Clinical Microbiology

O5 - 42: ASSOCIATION OF CHLAMYDIA TRACHOMATIS INFECTION WITH PRETERM DELIVERY BY A SYSTEMATIC REVIEW AND META-ANALYSIS

Rashid Ramazanzadeh¹, Amjad Ahmadi², Koroush Sayehmiri³

1. Kurdistan Uni of MedSci
2. Cellular & Molecular Research Center and Microbiology Department, Faculty of Medicine, Kurdistan University of Medical Sciences, Sanandaj, Iran.
3. Department of Social Medicine, School of Medicine, Ilam University of Medical Sciences, Ilam, Iran. 4- Clinical Microbiology Research Center, Ilam University of Medical Sciences, Ilam, Iran.

Background and Aim: Chlamydia trachomatis (CT) is one of the most common infection transmitted through sexual intercourse. The purpose of this study was to investigate the role of CT infection and preterm delivery method by a meta-analysis.

Methods: The most available article published in literature database including PubMed, Science direct, Web of Science, Google Scholar, Biological abs, Iranmedex, and SID were investigated and 21 relevant articles, performed during 1998-2014 and then a random-effects model was used for data analysis. Heterogeneity of studies was evaluated by I² index. The relationship between year of data collection, sample size, and CT infection with preterm delivery prevalence examined by meta-regression. Data were analyzed by R software and STATA [Ver 11.2].

Results: Among the 24 studies evaluated the prevalence of CT infection with preterm delivery was estimated 0.13% (CI 95%: 0.11-0.16). The prevalence of CT infection with preterm delivery based on study method including PCR 0.06 (CI 95%: 0.04-0.09), serology 0.23 (CI 95%: 0.10-0.35) and culture 0.17 (CI 95%: 0.10-0.24) was estimated. The prevalence of CT infection with preterm delivery based on study type including case-control 0.16 (CI 95%: 0.11-0.21), and cross-sectional 0.13 (CI 95%: 0.08-0.17) was estimated. the prevalence of CT infection with preterm delivery based type Continental including Europe 0.13 (CI 95% : 0.09-0.18), Asia 0.08 (CI 95% : -0.01-0.17), USA 0.15 (CI 95% : 0.08-0.22) and Africa 0.29 (CI 95% : 0.23-0.34) was estimated .

Conclusion: In regard to the results and studies performed on different populations, this meta-analysis showed no associated between preterm birth and CT.

Keywords: Preterm delivery, Preterm labor, Chlamydia trachomatis

**O6 - 282: COMPARISON OF PROPORTIONAL DIRECT AND INDIRECT METHODS
IN ANTIBIOTIC RESISTANCE IN MYCOBACTERIUM TUBERCULOSIS
DETECTION**

Sirus Amini¹, Gholamreza Hamzehloo², Afsaneh Khoshkhoo³, Mohammad Reza Allahyar⁴

1. Tehran Regional Reference laboratory of Tuberculosis, Deputy of health, Tehran University of Medical sciences
2. Tehran Regional Reference laboratory of Tuberculosis, Deputy of health, Tehran University of Medical sciences
3. Tehran Regional Reference laboratory of Tuberculosis, Deputy of health, Tehran University of Medical sciences
4. Tehran Regional Reference laboratory of Tuberculosis, Deputy of health, Tehran University of Medical sciences

Background and Aim: Time-consuming in reporting the antibiotic determination result is the most challengeable bottleneck based on proportional method in Mycobacterium Tuberculosis diagnosis labs. To overcome this problem, we hypothesized that concentrated samples (grade from 1+ to 3+) can be applied instead of colonies from same sample.

Methods: In this study 38 positive samples (treatment control and diagnostic group) decontaminated by Petroff method and resulted concentrated samples were used as direct proportional to antibiotic resistance determination. By inoculation of precipitant to Lowenstein - Jensen Medium containing Isoniazid and rifampin antibiotic, colonies were compared with the lacking-antibiotic blank and rate of resistance calculated at the critical point 1%.

Results: Results from comparison of gold standard direct and indirect methods revealed a significant difference for isoniazid and rifampin resistance. Specificity and sensitivity were not significant between two methods. Sample reporting in direct method in diagnostic sample group was between 15 to 25 days and for treatment control group were 20 to 30 days. The expecting time needed for reporting the test reduced up to 50%.

Conclusion: Based on urgent situation, both direct and indirect method can be used in parallel in Mycobacterium tuberculosis centers.

Keywords: Tuberculosis, direct, indirect, proportional, time-saving method

**O7 - 476: ANTI-QUORUM SENSING ACTIVITY OF PISTACIA ATLANTICA
METHANOLIC EXTRACT AGAINST PSEUDOMONAS AERUGINOSA PAO1**

Hannaneh Kordbacheh¹, Samad Nejad Ebrahimi², Fereshteh Eftekhari³

1. MSc Student ,Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, Velenjak, Tehran, Iran
2. Assistance Professor, Medicinal Plant and Drugs Research Institute , Shahid Beheshti University, Velenjak, Tehran, Iran
3. PhD, Associate Professor ,Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, Velenjak, Tehran, Iran

Background and Aim: *Pseudomonas aeruginosa* is a multidrug resistant pathogen and an important cause of nosocomial infections. Quorum-sensing (QS) is a process which regulates production of many virulence factors including pigment production and biofilm formation essential for establishment of chronic infections. We evaluated the inhibitory activity of some native plant extracts on biofilm formation and pigment production by *P. aeruginosa* PAO1.

Methods: Thirty native Iranian plants were screened for anti-QS activity against *P. aeruginosa* PAO1. Methanolic extracts were prepared by maceration, dried and were then dissolved in DMSO. Inhibition of biofilm formation was evaluated by the microbroth dilution method and the inhibitory effect on pyocyanin production was measured by spectrophotometry using different concentrations of the extract. The active extracts were further fractionated by HPLC and all fractions were tested for antibiofilm activity. The active fractions were also tested for inhibition of pyocyanin production. Finally, the components of the active fractions were identified by LC-DAD-MS.

Results: *Pistacia atlantica* leaves extract had the highest anti-biofilm activity at 2 mg/ml (92% inhibition) and 1 mg/ml (79% inhibition). Pyocyanin production was inhibited 100% at 2 mg/ml and 83% at 1 mg/ml. Four active HPLC fractions had minimum biofilm inhibitory concentrations (MBIC) of 0.30 mg/ml and inhibited pyocyanin production at < 0.30 mg/ml. Initial identification of the active fraction components showed that all four belonged to the flavonoid family.

Conclusion: The anti-QS ability of *Pistacia atlantica* extract suggests its potential for treatment of chronic infections caused by *Pseudomonas aeruginosa*.

Keywords: *Pseudomonas aeruginosa*, Anti-quorum-sensing, *Pistacia atlantica*, biofilm, pyocyanin.

**O8 - 570: MOLECULAR IDENTIFICATION OF DRUG RESISTANT MUTATION OF
TETRACYCLINES IN MYCOPLASMA SPP ISOLATED FROM PATIENTS WITH
MULTIPLE SCLEROSIS (MS) IN KERMAN PROVINCE.**

Maryam Naghib¹, Babak Kheirkhah²

1. PhD student in microbiology, Islamic Azad University of Kerman, Department of microbiology, Kerman, Iran
2. Assistant Professor of Microbiology, Islamic Azad University of Kerman, Department of microbiology, Kerman, Iran

Background and Aim: Multiple paralysis or Multiple Sclerosis known by the abbreviated name, MS, is an inflammatory disease in which the myelin sheath of nerve cells and oligodendrocytes in the brain and spinal cord are injured. Among the mentioned bacteria having such effect, is Mycoplasma that has word. The purpose of this study is to investigate the resistance to tetracycline in the mycoplasma bacteria isolated from the cerebrospinal fluid and urine of the patient affected by MS.

Methods: This study performed as a continuation of the studies completed to search for Mycoplasma on 80 frozen samples that one night were enhanced on PPLO broth then for 7 weeks have been passaged to PPLO broth and PPLO agar until colonies have shaped. After extracting DNA by using the specific Mycoplasma primers.

Results: In 5 samples Mycoplasma was certainly observed. After wards, Double PCR is performed to investigate the resistance of the gene 16S rRNA (alleles rrs3, rrs4). Then sequencing and preparation of phylogenetic tree done.

Conclusion: This study showed presence of the alleles of the potential of resistance to Tetracycline in Mycoplasma Spp in urine fluid. Sequencing and phylogenetic tree showed mutation in alleles (rrs3, rrs4) have been happened. It was first detected alleles (rrs3, rrs4) in human Mycoplasma Spp.

Keywords: Mycoplasma, Multiple sclerosis, Drug resistance, Tetracycline.

Drug Resistance

O10 - 561: FIRST DETECTION OF OXA-48 PRODUCING CARBAPENEMASE ESCHERICHIA COLI IN IRAN

Hamid Solgi¹, Fereshteh Shahcheraghi², Shahram Sabeti³, Mohtaram Sadat Kashi⁴, Maryam Hosseinzadeh⁵

1. Department of Bacteriology, Microbiology Research Center, Pasteur Institute of Iran, Tehran, Iran
2. Department of Bacteriology, Microbiology Research Center, Pasteur Institute of Iran, Tehran, Iran
3. Department of Pathology, Loghman Hakim Hospital, ShahidBeheshti University of Medical Sciences, Tehran, Iran
4. Loghman Hakim Hospital, Tehran, Iran
5. Loghman Hakim Hospital, Tehran, Iran

Background and Aim: The emergence of carbapenemase-producing Enterobacteriaceae is a major concern to public health. The aim of this study was molecular detection of carbapenemase-producing *Escherichia coli* isolates collected from a university hospital in Tehran, Iran.

Methods: From March 2015 to May 2016, thirty eight *E. coli* clinical isolates with reduced susceptibility to carbapenems were collected. Antibiotic susceptibility tests were performed using the disc diffusion method. The Modified Hodge Test (MHT) was performed for the screening of carbapenemases. PCR and nucleotide sequencing were employed to screen for the presence of carbapenemase-encoding genes, including *blaKPC*, *blaVIM*, *blaIMP*, *blaNDM-1* and *blaOXA-48*. The clonal relationship among isolates was analyzed by pulsed-field gel electrophoresis (PFGE).

Results: All of the isolates were resistant or intermediately susceptible to ertapenem. Only ten of the isolates also exhibited resistance to both imipenem and meropenem. The resistance rate to cephalosporins and ciprofloxacin was high. MHT was positive in 15 (39.4%) isolates. PCR and sequencing analysis revealed that the 8 (21%) isolates harbored the *blaOXA-48* gene. We did not detect *blaKPC*, *blaNDM-1*, *blaIMP* and *blaVIM* among the isolates. Six isolates contained *blaOXA-48* carbapenemase belonged to different PFGE clone and two isolates belonged to a same clone.

Conclusion: In this study, we report the first detection of *E. coli* harboring the *blaOXA-48* gene in Iran. PFGE showed that the dissemination of *blaOXA-48* gene was not spread by a single clone. Our results show that OXA-48-producing *E. coli* have started to spread into the hospitals in Iran, and detection of these isolates in Iran is important to prevent its rapid spread.

Keywords: Carbapenemase; OXA-48; *E. coli*; PFGE

O11 - 885: EVALUATING THE EXPRESSION OF MEXAB-OPRM EFFLUX PUMP GENES IN RESISTANT CLINICAL ISOLATES OF PSEUDOMONAS AERUGINOSA USING QUANTITATIVE REAL-TIME PCR METHOD.

IMAN BAHRAMI ABDEHGAH¹, Alireza Khodavandi phd²

1. Department of Microbiology, Islamic Azad University, Yasouj, Iran
2. Department of Microbiology, Islamic Azad University, Shiraz, Iran

Background and Aim: *Pseudomonas aeruginosa* is a highly drug-resistant and opportunistic pathogen. The MexAB-OprM efflux pump contributes to the intrinsic resistance to various antimicrobial agents in *Pseudomonas aeruginosa* isolated from patients. The aim of this study was to evaluate the expression of MexAB-OprM efflux pump such as MexA, MexR and gyrA as housekeeping genes using Quantitative Real-Time PCR method in ATCC 27853 strain and resistant clinical isolates.

Methods: In this cross-sectional study, resistant clinical isolates were performed using disk diffusion and broth microdilution methods according to CLSI protocols. The expression of MexA, MexR and gyrA were analyzed in resistant clinical isolates and ATCC 27853 strain in the absence drug and presence of the drugs gentamicin, piperacillin and gentamicin/ piperacillin combination.

Results: There was relatively fixed expression level of gyrA gene as the housekeeping gene in ATCC 27853 strain and resistant clinical isolates. In the compared combined with single dose of the drugs with an intended MIC concentration, was reduced in MexA gene expression, but the MexR gene expression was increased in 27853 ATCC strain and resistant clinical isolates *Pseudomonas Aeruginosa*.

Conclusion: The analysis of molecular mechanism of the possible effects of other effective genes in creating resistance phenomenon could be evaluated using other techniques of analyzing gene expression.

Keywords: *Pseudomonas aeruginosa*, Gene expression, Quantitative Real-Time PCR

**O12 - 1030: AG/SiO₂ CO-DOPED FULLERENE AS A NOVEL NANOSYSTEM FOR
EFFICIENT PHOTODYNAMIC INACTIVATION OF PSEUDOMONAS AERUGINOSA
BIOFILM**

Esmail Darabpour¹, Nasim Kashef², Mohammad Mahdi Doroodmand³

1. Department of Microbiology, School of Biology, College of Science, University of Tehran, Tehran, Iran
2. Department of Microbiology, School of Biology, College of Science, University of Tehran, Tehran, Iran
3. Department of Chemistry, College of Sciences, Shiraz University, Shiraz, Iran

Background and Aim: Nanotechnology has made a significant contribution to Photodynamic inactivation (PDI), as one of the promising alternative treatments to combat biofilm. The effectiveness of PDI using fullerene nanoparticle (as a photosensitizer) can be improved by development of innovative multifunctional nanosystems. Here we aimed to evaluate photodynamic inactivation of *Pseudomonas aeruginosa* biofilm using a novel nano-based photosensitizer (a hybrid nanosystem composed of silver, silica and fullerene).

Methods: Ag/SiO₂ co-doped fullerene nanosystem was synthesized by chemical vapor deposition (CVD) method. 24-h-old biofilms of *P. aeruginosa* were treated with the nanosystem for 10 min and subsequently exposed to white light from a light-emitting diode (LED) at fluence of 42.2 J/cm². Appropriate controls were included. Biofilm metabolic activity was quantified by colorimetry with a tetrazolium reduction assay to measure live bacteria after the treatments. To determine the effect of PDI on *P. aeruginosa* biofilm structure, three-dimensional (3D) morphology and surface of biofilm was investigated by atomic force microscopy (AFM).

Results: Ag/SiO₂ co-doped fullerene nanosystem-mediated PDI significantly reduced the metabolic activity of biofilm of *P. aeruginosa* (~100%). In the absence of light, the nanosystem did not significantly impair biofilm metabolic activity (~3%). An analysis of the AFM topography 3D-images showed that Ag/SiO₂ co-doped fullerene nanosystem-mediate PDI induced severe morphological and surface alterations (loss of the typical cell morphology and increase in surface roughness, respectively) of biofilm.

Conclusion: In conclusion, Ag/SiO₂ co-doped fullerene nanosystem-mediated PDI offer a new modality for fast and efficient destruction of *P. aeruginosa* biofilm, suggesting its potential use in chronic wound healing.

Keywords: hybride nanosystem; Nanotechnology; fullerene; photodynamic inactivation; bacterial biofilm

**O13 - 1195: NANOLIPOSOMAL MEROPENEM ENHANCES ANTIMICROBIAL
ACTIVITY AGAINST PSEUDOMONAS AERUGINOSA ISOLATES**

Morteza Milani¹, Abolfazl Akbarzadeh², Hamed Hamishekar³, Mohammad Rahmati- Yamchi⁴

1. Infectious and Tropical Diseases Research Center, Tabriz University of Medical Sciences, Tabriz, Iran.
2. Department of Medical Nanotechnology, Faculty of Advanced Medical Science, Tabriz University of Medical Science, Tabriz, Iran
3. Drug Applied Research Center, Tabriz University of Medical Sciences, Tabriz, Iran
4. Department of Medical Biotechnology, Faculty of Advanced Medical Science, Tabriz University of Medical Science, Tabriz, Iran

Background and Aim: *Pseudomonas aeruginosa* is an opportunistic gram-negative bacillus commonly associated with wide range of diseases. In this study we aim to evaluate the antibacterial activity of liposomal meropenem against to clinical isolates of *Pseudomonas aeruginosa*. *P. aeruginosa* strains were used to determine the MIC and MBC of free and liposomal meropenem. Also the effect of free and liposomes antibiotic to compare the minimum biofilm eradication concentration and inhibition of *P. aeruginosa* motility was assessed.

Methods: Meropenem-loaded liposomal formulations were prepared according to the modified ethanol injection method. A broth micro-dilution method was used to determine the MICs of free and liposomal meropenem. Also free or liposomal meropenem at 1/8 of the MIC was added to agar plates, and motility was examined.

Results: In this study the MICs and MBC of liposomal meropenem was more effective against all clinical strains were significantly lower than those of free meropenem (6.25 µg/ml vs 100 µg/ml). Additionally liposomal formulation of drug (?1.5 µg/ml) completely eradicated biofilm in all *P. aeruginosa* isolates. While the free form of antibiotic could eradicate biofilm formation in most of isolates in ?6.25 µg/ml concentration. Moreover lower concentrations of liposomal meropenem could inhibit the bacterial motility.

Conclusion: The results obviously indicate that the liposomal formulation of drug is more effective than free form of meropenem against antibiotic resistant of *P. aeruginosa* isolates.

Keywords: Antibiotic resistance, Liposomal meropenem, *P. aeruginosa*

Food and Water Microbiology

O14 - 417: EVALUATION AND COMPARISON OF CONCENTRATION AND CULTIVATION METHODS FOR DETECTION OF CLOSTRIDIUM PERFRINGENS SPORES IN WATER SAMPLES

Masoumeh Azimirad¹, Tajeddin Elahe², Alebouyeh Masoud³, Hasani Zahra⁴, Zali Mohammad Reza⁵, Mirjalali Hamed⁶

1. Foodborne and Waterborne Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
2. Foodborne and Waterborne Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
3. Foodborne and Waterborne Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
4. Foodborne and Waterborne Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
5. Gastroenterology and Liver Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
6. Foodborne and Waterborne Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran.

Background and Aim: Since *Cryptosporidium* oocysts and *Giardia* cysts together with some enteric viruses are resistant against routine chemical and mechanical drinking water treatment, *C. perfringens* spores could be good indicators to evaluate treatment processing of drinking water resources.

Methods: Serial dilutions of extracted spores were prepared in defined amounts of sterile PBS to give final concentrations: 101, 102, 104, 106 and 107 spores/mL. Filtration of diluted samples was done using 0.2µm cellulose nitrate filter membranes. After filtration two processes were performed. 1. Concentration method: the membrane was soaked in 300 ml 0.5 mM H₂SO₄ to facilitate the elution. Then, 50 ml elution buffer was added to the membrane and eluted spores were collected in sterile tubes. After centrifuge, supernatant was discarded and DNA extraction was performed on pellet. Finally, PCR was done using specific primers. 2. Cultivation method: The filtered membranes were placed on surface of egg yolk agar mediums and all mediums were incubated in anaerobic condition. The cultures results were followed to one week

Results: Cultivation method: *C. perfringens* specific dark colonies were growth in egg yolk medium supplemented by Neomycin after 48h. Limit of detection of *C. perfringens* spores for cultivation was 102 spores/ml. Concentration method: DNA fragment about 279-bp of 16S rRNA gene was acquired for concentrations 102- 107. The sample with 10 spores/ml was positive for neither cultivation method nor concentration method.



Conclusion: Concentration method is a fast and easy method that has same results compared with traditional cultivation method.

Keywords: Drinking water, *C. perfringens*, parasitic indicators, viral indicators

Microbial Metabolite and Therapy

O16 - 245: APPLICATION OF MICROBIAL EXOSOME FOR VACCINE DESIGN

Hamideh Mahmoudzadeh Hoseini¹

1. Applied Microbiology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran

Background and Aim: All type of gram positive and gram negative bacteria release the discrepant extracellular vesicles during the different growth phase of their life. This vesicles are known as outer membrane vesicles and exosomes in gram negative bacteria and gram positive one, respectively. These vesicles contain various type of proteins, mRNAs and antigens surrounding with lipid layer with different contents. However, these vesicles act as a bottle of message spreading the infection in the host body.

Methods: The presence of general and specific antigens on the surface of them lead to emerge the new properties such as immunogenicity and self- adjuvantation. When these vesicles present to immune system, they are up taken by immune cells that trigger potent specific immune responses against infections. These vesicles could deliver the antigens both passively and actively.

Results: Nowadays, an outer membrane vesicle based vaccine was approved by international agencies. These types of vaccines have some advantages and disadvantages compared with traditional microbial vaccines.

Conclusion: They are not live or attenuated microorganisms but contain key antigens. In addition modified genetic engineered microorganism can produce an exosomes containing desired antigens along with targeted therapy. Furthermore, packaging the proteins and other small molecules in lipid layer leads to resist the exosome contents against the enzymatic degradation and other environmental factors. However, the presence of the large number of antigens on the surface of exosomes could cause anergy.

Keywords: Exosome; Microbial metabolite; Vaccine; Infection

**O17 - 261: CREATING RESISTANT STEM CELLS USING MICROBIAL
METABOLITES FOR CELL THERAPY**

Raheleh Halabian¹

1. Applied Microbiology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran

Background and Aim: Stem cells (SCs) are capable of renewing themselves through cell division and can be differentiated into tissue or organ-specific cells with special functions under certain physiologic or experimental conditions. These cells are extraordinarily promising in both veterinary and human medicine in the view point of therapeutic approaches so, stem cells based cell therapy has appeared as effective therapeutic strategy for treatment of several cancers, infectious and non-infectious diseases. Numerous studies have demonstrated the remarkable immunosuppressive and antibacterial effects of SCs both in vitro and in vivo, in animal models and in humans.

Methods: Therapeutic administration of MSCs successfully inhibited the bacterial growth and enhances survival by improved clearance of pathogenic bacteria in sepsis and pneumonic conditions.

Results: In recent years, creating resistant stem cells without manipulation is a new way for stem cell therapy. Interestingly, using microbial metabolites for creating resistant stem cells is one of new hypothesis for therapy of infectious diseases, wound healing and tissue repairing.

Conclusion: Preconditioned stem cell with microbial metabolites not only increasing survival of SCs in harmful conditions, but also could be improved clearance of the bacterial infection and finally appeared as effective therapeutic strategy for treatment of several cancers, infectious and non-infectious diseases

Keywords: Stem Cells, Microbial Metabolites, Cell Therapy, infectious diseases

**O18 - 292: IMMUNOLOGICAL EFFECT OF RECOMBINANT PROTEIN OF
HELICOBACTER PYLORI IN FUNCTIONAL OF PERITONEAL MACROPHAGES**

Neda Soleimani¹

1. Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, Tehran, Iran.

Background and Aim: Helicobacter pylori is a specific pathogen found in the human stomach. The immunomodulatory effect of the fractions of Helicobacter pylori have been investigated and observed. The neutrophil-activating protein (HP-NAP) of Helicobacter pylori is a protective antigen and a major virulence factor. The aim of this study is to assess the effect of recombinant Hp-NapA helicobacter pylori on nitric oxide (NO) production by mice peritoneal macrophages. Recombinant Hp-NapA helicobacter pylori was produced. Mice peritoneal macrophages were purified and cultured. Different concentrations of recombinant Hp-NapA were used for macrophage stimulation and evaluation of NO production. Cell survival and production of nitric oxide (NO) (that in all cases also, had received LPS stimulation) were measured.

Methods: Recombinant Hp-NapA helicobacter pylori was produced. Mice peritoneal macrophages were purified and cultured. Different concentrations of recombinant Hp-NapA were used for macrophage stimulation and evaluation of NO production. Cell survival and production of nitric oxide (NO) (that in all cases also, had received LPS stimulation) were measured.

Results: The results elucidated that the stimulate effect of recombinant Hp-NapA on NO release was significant at a dose of 30 µg/ml ($P=0.01$) compared to the control group ($P=0.003$). MTT production was observed at the same dose in macrophages.

Conclusion: According to our findings, recombinant Hp-NapA do not have a distinct cytotoxic activity, it has a positive effect on NO production by peritoneal macrophages. Therefore, it is proposed that recombinant Hp-NapA can be studied further as Immunotherapy.

Keywords: recombinant Hp-NapA, Macrophages, helicobacter pylori.

O19 - 992: THE ROLE OF STAPHYLOCOCCAL ENTEROTOXIN B IN CANCER THERAPY

Abbas Ali Imani Fooladi¹

1. Applied Microbiology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran

Background and Aim: The bacterial superantigen staphylococcal enterotoxin B (SEB) is a potent inducer of anti-tumor immunity both in vitro and in vivo. In addition it is able to use as an adjuvant along with tumoral exosomes and antigens or design tumor-targeted superantigen.

Methods: The anti-tumor effect of SEB or biological structures containing SEB in mice with inoculated breast cancer cells (4T1) and fibrosarcoma (WEHI-164) was examined by intravenous (IV) and sub-cutaneous injection and the sizes of the inoculated tumors, cytokine production, necrosis, metastasis, survival time and CD4+/CD8+ T cell infiltration were determined.

Results: In the mice administered SEB a significant reduction ($P < 0.05$) of tumor size was observed in comparison with mice in control groups. Furthermore, in the mice administered SEB showed significantly higher levels of IFN-gamma, IL-2, TNF- α and CD4+/CD8+ T cell infiltration when compared with the other groups ($P < 0.05$). A significantly higher frequency of necrosis in tumor tissues was also observed in administered SEB group ($P < 0.05$).

Conclusion: Our present findings suggest that tumor cell death is caused by increased cytotoxic T-cell activity and cytokine levels in response to injection of SEB and that SEB may be a good option for use as a novel therapy in patients with breast cancer and fibrosarcoma.

Keywords: staphylococcal enterotoxin B ; cancer; immunotherapy

Molecular Epidemiology

O20 - 258: STUDY OF MOLECULAR EPIDEMIOLOGY OF MYCOBACTERIUM TUBERCULOSIS COMPLEX ISOLATED FROM PATIENTS IN THE NORTHEAST OF IRAN IN 2014 USING MIRU-VNTR AND SPOLIGOTYPING TO ASSESS GENETIC DIVERSITY OF STRAINS

Hassan Ravansalar¹, Keyvan Tadayon², Nader Mosavari³, Mohamad Derakhshan⁴, Kiarash Ghazvini⁵

1. Immunology and Microbiology Department, Sabzevar University of Medical Sciences, Sabzevar, Iran
2. Aerobic Bacterial Researches and Vaccine Production Department, Razi Vaccine & Serum Research Institute, Karaj, Iran
3. PPD Tuberculin Department, Razi Vaccine & Serum Research Institute, Karaj, Iran
4. Antimicrobial resistance Research Center, School of medicine, Mashhad University of Medical sciences, Mashhad, Iran
5. Antimicrobial resistance Research Center, School of medicine, Mashhad University of Medical sciences, Mashhad, Iran

Background and Aim: The present study investigates epidemiological diversity among Mycobacterium tuberculosis strains circulating in the Northeast of Iran using 12-loci MIRU-VNTR and spoligotyping.

Methods: This study was performed on 140 M. tuberculosis strains selected from the sputum of new cases of pulmonary tuberculosis (TB) patients in three Khorasan provinces of Iran. 12 loci MIRU-VNTR and Spoligotyping were performed in all isolates.

Results: By MIRU-VNTR analysis, 76 distinct patterns comprising of 19 clusters and 57 unique patterns were identified. Based on the results, MIRU10, MIRU 26 and ETRF were highly discriminative. By Spoligotyping analysis, 103 isolates (73.6%) were classified into 14 clusters containing 2–56 isolates and the remaining 37 isolates (26.4%) were unique patterns. By combining two techniques, 94 distinct patterns (15 clusters) contained 61 isolates (43.6%), and 79 unique patterns were identified. The discriminatory power (HGDI) of combination of two techniques was 0.962 which was higher than that of each technique alone. With trees designed by Bionumerics software, we were able to differentiate isolates with similar genetic patterns and to group them together. Two of our great close clusters were Haarlem and CAS lineage. In this study, all strains with MDR and combined (INH + RIF) resistance were related to Beijing strains. Also, homoplasmy was observed in a number of patterns.

Conclusion: The results showed that in molecular typing of MTB, using the two methods of “Spoligotyping” and “MIRU-VNTR” simultaneously could increase the genetic patterns of MTB strains in a much effective way compared to using only one method.

Keywords: Mycobacterium tuberculosis, Genotyping, MIRU-VNTR, Spoligotyping

Tuberculosis and Mycobacteria

O21 - 221: GENOTYPING OF MYCOBACTERIUM TUBERCULOSIS STRAINS DIRECTLY ON CLINICAL SAMPLES BY 24 LOCUS MIRU-VNTR METHOD

Hamidreza Sadegh¹, Mansour Kargarpour Kamakoli², Ghazaleh Farmanfarmaei³, Morteza Masoumi⁴, Farid Abdolrahimi⁵, Abolfazl Fateh⁶, Nayereh Ebrahimzadeh⁷, Fatemeh Rahimi Jamnani⁸, Farzam Vaziri⁹, Seyed Davar Siadat¹⁰

1. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran
3. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran
4. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
5. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
6. A. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran B. Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
7. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
8. A. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran B. Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
9. A. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran B. Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
10. A. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran B. Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Tuberculosis (TB) is considered as a public health concern in the world. TB is a chronic infectious disease whose etiologic agent is *Mycobacterium tuberculosis* (Mtb). Molecular procedures are useful tool to control the disease. Prompt genotyping of Mtb can greatly help in molecular epidemiology of the disease.

Methods: One hundred and thirty-nine clinical samples from TB patients referring to department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran between the years 2011 to 2016 were selected for this study. Genotyping based on 24 loci MIRU-VNTR procedure was performed directly on clinical samples.

Results: In the 139 samples studied, one hundred and thirty samples (93.5%) had different pattern. Among loci used in MIRU-VNTR loci of 2401, 580 and 577 were amplified more successfully in the most of clinical samples. Discriminative power of 2401, 2163b and 960 loci had highest variety and differentiation.

Conclusion: Genotype based on MIRU-VNTR procedure is fast and has strong differentiation for genotyping and study of Mtb infection. Performing this procedure on clinical samples and also use of loci that showing highest variety can create a faster way to get valuable data.

Keywords: *Mycobacterium tuberculosis*, clinical sample, MIRU-VNTR

Vaccine

O22 - 196: CONSTRUCTION OF RECOMBINANT FUSION FIMCH PROTEIN AS IMMUNOGEN CANDIDATE AGAINST URINARY TRACT INFECTION

Robab Mollamehralizade¹, Mahdi Paryan (Ph.D)², Fahimeh Baghbani (Ph.D)³

1. Islamic Azad university, varamin-pishva Branch
2. Ph.D of medical biotechnology-Pasteur Institute -Tehran,Iran
3. Genetic Department,School of Biology Sciences-varamin-pishva Branch,Islamic Azad university-Varamin, Iran.

Background and Aim: Urinary tract infection is one of the most common human infections and uropathogenic *Escherichia coli* strains are the most common factors. These strains are colonized in the bladder and they cause cystitis, but they can move to kidneys and to be a pyelonephritis factor. Because of the FimH protein in UPEC strains colonization and infection creation have very important role, preparation of a vaccine with this adhesin is attractive.

Methods: In this study, FimH adhesin and their attendant protein that was named FimC was selected as an immunogenic candidate. From *Escherichia coli* strains 35218, genomic DNA was extracted and fimH and fimC genes were multiply by PCR method separately. After connecting two pieces together by PCR method, the final product was cloned in the pBluescript vector and was obtained the clone containing fimCH gene by blue-white screening. After that the indicative primers were designed and after doing PCR method, the resulting product was cloned in pET23a vector. Culture and induction of gene were performed to the culture medium by adding IPTG, by transfer that vector into origami *Escherichia coli* strains. FimCH recombinant protein expression in bacteria was approved by SDS-PAGE and Western blot methods

Results: This recombinant merged protein can be used in Immunogenicity review studies on animal cases.

Conclusion: This recombinant merged protein can be used in Immunogenicity review studies on animal cases.

Keywords: Urinary tract infection, Uropathogenic *Escherichia coli*, Recombinant vaccine, FimCH protein.

**O23 - 737: IL 27 , IL12 ,TGF-BETA, VEGF GENES ANALYSIS OF CANCER BEARING
C57BL/6 MICE AFTER VACCINATION WITH FLIC_E7D & E7D-FLIC & E7D
VACCINES .**

Behazin Aria¹, Mehdi mahdavi²

1. Department of Microbiology ,Pharmaceutical science branch,Islamic Azad university
2. Department of Immunology , pasture institute of Iran , Tehran .

Background and Aim: Cervical cancer is one of the most important disease that lead to death of woman in all over the world. The world health organization (WHO)identified it as the related caused by a virus that enable the scientists to use it for either . This virus has 3 protein zones that include of Early , late and Non coding areas , the Early phase consist of E1 to E7 , but E6 and E7 are two Early oncoproteins of HPV , which are responsible for disordering in cell cycle and tumor progression of infection .

Methods: In this study the efficiency of FLIC-E7d-HPV 16, HPV16 –E7d-FLIC &E7d vaccines were investigated in tumor bearing mice models .Tumor was induced in mice with TC1 cell line , After tumor growth , the mice were divided in to five groups were injected 20 mgr of vaccine ,Tumor samples were removed and Real time analyzed at PASTOR TEHRAN .

Results: According to investigation of IL 27 , IL12, TGF-Beta, VEGF genes and HPRT control gene by using PCR-real time .

Conclusion: That was decrease of VEGF and TGF-beta genes in FLIC-E7d-HPV 16, HPV16 – E7d-FLIC groups and that was increase IL 27 , IL12 genes in E7d group.

Keywords: HPV , E7d , IL 27 , IL12 ,TGF-Beta, VEGF.

**024 - 782: CLONING, EXPRESSION AND PURIFICATION OF RECOMBINANT
HMW1, HMW2, AND HIA AS A FUSION PROTEIN FOR VACCINE CANDIDATE OF
NONTYPEABLE HAEMOPHILUS INFLUENZAE**

Ghasem Abbaszadeh Goudarzi¹, Ghasem Abbaszadeh-Goudarzi², Mohammad Reza Khorramizadeh³, Seyed Davar Siadat⁴, Ladan Teimoori-Toolabi⁵, Saeid Bouzari⁶, Sassan Rezaie⁷, Kazem Abbaszadeh-Goudarzi⁸, Mahdi Davari⁹

1. -
2. Department of Medical Biotechnology, School of Advanced Technologies in Medicine, Tehran University of medical Sciences, Tehran, Iran
3. Department of Medical Biotechnology, School of Advanced Technologies in Medicine, Tehran University of medical Sciences, Tehran, Iran
4. Department of Tuberculosis and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
5. Department of Molecular Medicine; Biotechnology Research Center; Pasteur Institute of Iran; Tehran, Iran
6. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
7. Department of Medical Mycology & Parasitology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
8. Department of Medical Biotechnology, School of Advanced Technologies in Medicine, Tehran University of medical Sciences, Tehran, Iran
9. Department of Tuberculosis and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Nontypeable *H. influenzae* (NTHi) is an important pathogen in children causing otitis media. However, there is no vaccine against NTHi-induced diseases. HMW1, HMW2 and Hia are adhesin proteins of NTHi-strains and have potentiality to provide protection against NTHi-infections. The aim of present study was to construct recombinant HMW1-HMW2-Hia as a fusion protein and evaluate immune responses against recombinant fusion protein as vaccine candidates antigens.

Methods: Binding domain of hmw1 gene (1080 bp) was amplified by PCR from genomic DNA and cloned into PET-28a vector; this vector was already modified by the insertion of a fragment named hmw2-hia into multiple cloning sites, and then was confirmed by colony-PCR, enzymatic digestion and gene sequencing. To express recombinant fusion protein, PET-28a-hmw1-hmw2-hia vector was transformed into competent BL12(DE3). Expressed protein was purified by affinity chromatography. BALB/c mice were subcutaneously immunized by purified protein in combination with Freund's adjuvant. Serum antibody responses and functionality of antibodies were determined by ELISA and SBA, respectively.

Results: In immunized group of Balb/c mice, the serum IgG responses was significantly increased against recombinant fusion protein in comparison with control, and also the antisera have shown strongly bactericidal activity against NTHi strain.

Conclusion: The results have shown that recombinant fusion protein could induce the immune system to produce antibodies which was functional to kill NTHi-strains. Based on the observation, the antisera have the possibility to provide protection against infections caused by NTHi.

Keywords: NTHi; fusion Protein; Expression Vector; affinity chromatography

**O25 - 938: GENOMIC CHARACTERIZATION OF BORDETELLA PERTUSSIS 0134, A
VACCINE STRAIN WITH HISTORIC VALUES**

FARNAZ BOROUMAND¹, KEYVAN TADAYON², MOJTABA NOUFELI³, RAINAK
GHADERI⁴, MOHAMMAD SEKHAVATI⁵, EBRAHIM ABBASI⁶, MASOUMEH FATAH
MOGHADAM⁷, PEJVAK KHAKI⁸

1. RAZI VACCINE AND SERUM RESEARCH INSTITUTE
2. RAZI VACCINE AND SERUM RESEARCH INSTITUTE
3. RAZI VACCINE AND SERUM RESEARCH INSTITUTE
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6. RAZI VACCINE AND SERUM RESEARCH INSTITUTE
7. ISLAMIC AZAD UNIVERSITY of DAMGHAN, DAMGHAN, IRAN
8. RAZI VACCINE AND SERUM RESEARCH INSTITUTE

Background and Aim: The earliest serious attempts to protect Iranian citizens against pertussis were initiated in 1952 when a domestically-developed vaccine was licensed for public use.

Methods: In order to characterize the genomic properties of the exotic strain Razi Bp 0134 currently used in manufacturing the whole cell pertussis vaccine, an 8-locus multiple-locus variable-number tandem repeat analysis (MLVA) was selected. This system uses VNTR1, VNTR2, VNTR3, VNTR5, VNTR7, VNTR8, VNTR9 and VNTR10. Technically, the PCR primers and amplification cycles were designed to enable simultaneous amplification of all the 8 loci in a single round using any traditional thermocycler.

Results: The sequencing-supported observations displayed that there were 8.9 copies of a 15 bp unit repeat (UR), 3.3 copies of a 12 bp UR, 7.2 copies of a 5 bp UR, 12.5 copies of a 6 bp UR, 3 copies of a 9 bp UR, 2 copies of a 12 bp UR, 5 copies of a 6 bp UR, 3.8 copies of a 9 bp UR at VNTR1, VNTR2, VNTR3, VNTR5, VNTR7, VNTR8, VNTR9 and VNTR10, respectively.

Conclusion: The MLVA genotyping pattern of the BP134 strain was then compared with that of the nineteen BP strains currently available at <http://www.ncbi.nlm.nih.gov/genome/genomes/1008> from rest of the world. Considering the dynamic nature of Bordetella pertussis in human hosts we assume a systematic MLVA genotyping of clinical isolates is necessary to improve the currently poor epidemiological knowledge of pertussis in Iran.

Keywords: Pertussis, Tandem Repeat, Strain, Vaccine

**O26 - 980: GENETIC ANALYSIS OF PLASMODIUM FALCIPARUM
THROMBOSPONDIN RELATED ADHESIVE PROTEIN AS A MALARIA VACCINE
CANDIDATE ANTIGEN**

Azadeh Jafaryzadeh¹, Akram Abouie Mehrizi², Sedigheh Zakeri³, Navid Dinparast Djadid⁴

1. Guilan University, Guilan Pardis
2. Malaria and Vector Research Group, Biotechnology Research Center, Pasteur Institute of Iran, Tehran, Iran
3. Malaria and Vector Research Group, Biotechnology Research Center, Pasteur Institute of Iran, Tehran, Iran
4. Malaria and Vector Research Group, Biotechnology Research Center, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: According to World Health Organization, almost half of the world's population are at the risk of malaria. Among five human malaria species transmitted to people through the bites of Anopheles mosquito, Plasmodium falciparum is the most fatal one. Beside current available controlling tools, development of efficient vaccines is crucial to elimination and eradication the malaria. However, genetic diversity of leading vaccine candidate proteins such as Plasmodium falciparum thrombospondin related adhesive protein (PfTRAP) is a challenge in the development of malaria vaccine. Hence, it is necessary to have a detailed knowledge and the genetic diversity of pftrap gene in the clinical isolates from Iranian patients infected by P. falciparum.

Methods: In this study, the pftrap gene was amplified from 40 P. falciparum worldwide database of polymorphism of PfTRAP. Here, we explored isolates collected from Chabahar city, and twenty PCR products were sequenced. Nucleotide and amino acid sequences were aligned with the 3D7 sequence as the reference strain. Using ABCpred server, the potential B-cell epitopes were identified.

Results: 27 amino acid replacements and one tri-peptide repeat insertion were determined in Iranian PfTRAP isolates. These sequences were classified in 7 distinct haplotypes.

Conclusion: In conclusion, the results of this study showed low genetic diversity in this leading vaccine candidate antigen in clinical isolates of Iranian P. falciparum. Considering PfTRAP as a pre-erythrocytic vaccine candidate antigen, our data provides valuable information to develop a PfTRAP-based vaccine.

Keywords: Genetic diversity, Plasmodium falciparum, TRAP

Viruses

O27 - 1101: DEVELOPMENT OF A SEMI NESTED POLYMERASE CHAIN REACTION METHOD FOR DETECTION AND AMPLIFICATION OF HEPATITIS B VIRUS CORE GENE

Zahraa Mohammadali¹, Seyed Masoud Hosseini², Seyed Reza Mohebbi³, Shabnam Kazemian⁴, Behta Keshavarz Pakseresht⁵, Yasin Hatami⁶, Afsaneh Sharifian⁷, Mohammad Reza Zali⁸

1. A- Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran B- Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, Tehran, Iran
2. Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, Tehran, Iran
3. Basic and Molecular Epidemiology of Gastrointestinal Disorders Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
4. Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
5. Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
6. Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
7. Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
8. Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: Hepatitis B virus (HBV) is a DNA virus with approximately 3200 base pair genome size and a member of Hepadnaviridea family. HBV Infection can lead to a series of serious liver complications such as liver cirrhosis and hepatocellular carcinoma. Variations of the HBV core gene have been observed in different populations and it seems that these variations may be associated with the presence of active liver disease. The aim of this study was to develop a polymerase chain reaction (PCR) method for detection of viral DNA and also for amplification HBV complete core gene which is useful for core variation further studies.

Methods: Sixty HBV complete genome reference sequences from different genotypes and also 100 previously submitted core gene sequences from Iranian isolates retrieved from Genbank data base. The sequences were aligned using CLUSTALX software. Proper primers were designed for highly conserved regions around core gene using GENERUNNER V4 and Oligo7 software. Core gene amplifications of HBV isolates from 40 patients were performed based on designed primers for a semi nested PCR and direct sequencing was done on PCR products to confirm the core gene complete coverage.

Results: All amplified isolates from Iranian patients belonged to Genotype D, subgenotype D1 and several genetic variations have been detected among these Iranian core sequences.

Conclusion: The established PCR method can amplify HBV core gene successfully. It is a proper, rapid and cost effective method for Core gene amplification and further genetic variation studies.

Keywords: Hepatitis B virus, Core gene, nucleotide variations, Nested PCR

Zoonosis

O28 - 51: FULL-LENGTH CHARACTERIZATION OF S1 GENE OF THREE TYPES OF 793/B AVIAN INFECTIOUS BRONCHITIS COMMERCIAL VACCINES

Waleed Almayahi ¹, Arash Ghalyanchilangeroudi², Masoud Hahsemzadeh³, Naser Sadri⁴, Behrooz Asadi⁵, Mohamad Taha Zabihi⁶

1. Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
2. Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
3. Razi Ins ,Karaj , Iran
4. Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
5. Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
6. Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran

Background and Aim:Infectious bronchitis virus (IBV) is a major cause of economic losses in the poultry industry and can be involved in respiratory disease, nephritis, and poor egg production and quality. The control of IB has become a serious problem for the poultry industry worldwide. Due to antigenic variation of the causative agent, control of the disease is difficult. To control the disease, many vaccines are being used in different countries around the world.

Methods:In the present study, the entire S 1gene of three types of 793/B-type vaccine (4/91, IB88 and 1/96) was amplified by reverse transcriptase polymerase chain reaction. Phylogenetic study was conducted using complete S1 gene sequences as phylogenetic markers. Full length sequencing of such gene of three infectious bronchitis (793/B) vaccine strains were achieved and compared with that of IB vaccine strains presented in the gene bank.

Results:The 4/91 & IB88 have 99.32% & 99.1% homology to references in Gene Bank and 1/96 vaccine has 98.2 % to FR-94047-94.

Conclusion:According to differences between our sequences with the vaccine strains that deposited in GenBank, we have to be more attention for comparing them in phylogenetic analysis and it prefer to re-sequence of the vaccines that import to the country and don't trust to the gene bank data.

Keywords:Infectious bronchitis virus; vaccines; S1 gene sequencing; Phylogenetic analysis

O29 - 131: MOLECULAR DETECTION AND GENOTYPING OF CHLAMYDIA PSITTACI IN CAPTIVE PSITTACINES AND THEIR OWNERS FROM ISFAHAN (IRAN)

Mehdi Moradi sarmeidani¹, Payman Keihani², Hasan momtaz³

1. Faculty of veterinary medicine, Islamic Azad University, Shahrekord Branch, Shahrekord, Iran
2. Department of Small animal medicine, Shahrekord Branch, Islamic Azad University, Shahrekord, IR Iran
3. Department of Microbiology, Shahrekord Branch, Islamic Azad University, Shahrekord, IR Iran

Background and Aim: We want to determine the prevalence of *C. psittaci* in captive birds and their owners by using molecular detection method (PCR). Samples were collected during 2013 from a total of 8 different species of parrots. *C. psittaci* was detected in four species of birds (50%) and all of them were asymptomatic. Sequencing was used to confirm the PCR positive results, showing that all positive samples of *C. psittaci* belonged to genotype A, representing the first report of the presence of this genotype in Iran.

Methods: Oropharyngeal and cloacal swabs were collected from 54 captive psittacine birds and their owners that refer to veterinary clinics in Isfahan (Totally 108 samples).

Results: The detection of this bacterium in captive psittacine birds shows that there is a potential risk for owners who live or have a direct contact with them and that there is a possibility of infecting other birds and humans.

Conclusion: *Chlamydomphila psittaci* is one of the factors that cause the disease in birds, various animals and humans (specially psittacines) it has special Importance and due to be zoonotic and high morbidity in birds.

Keywords: *Chlamydomphila psittaci* , Psittacine birds , PCR , Owner

**O30 - 241: EXTRACTION AND CHARACTERIZATION OF BRUCELLA ABORTUS
STRAIN RB51 ROUGH LIPOPOLYSACCHARIDE**

Ramin Bagheri Nejad¹, Armin Kalantari², Hamidreza Jalali³, Fereshteh Yazdani⁴

1. Brucellosis Department, Razi Vaccine and serum Research Institute
2. Brucellosis Department, Razi Vaccine and serum Research Institute
3. Brucellosis Department, Razi Vaccine and serum Research Institute
4. Brucellosis Department, Razi Vaccine and serum Research Institute

Background and Aim: Brucellosis is an important zoonotic disease with considerable impacts on human and animal health. *Brucella abortus* strain RB51 vaccine is used for the control and prevention of bovine brucellosis. Due to the rough phenotype of the vaccine strain, none of the routine serological tests can detect vaccinated animals. This is of paramount significance for monitoring accuracy of vaccination campaigns. In the present study we extracted the rough lipopolysaccharide (RLPS) of *Brucella abortus* strain RB51 and analyzed it immunochemically which can be further utilized as the antigen for the development of serological tests to diagnose animals immunized with the vaccine.

Methods: RLPS was extracted from acetone-dried bacterial cells using phenol-chloroform-petroleum ether method and precipitated with cold methanol reagent. The precipitated RLPS was dialyzed and lyophilized. It was then evaluated by limulus amebocyte lysate (LAL) assay, polyacrylamide gel electrophoresis (PAGE) and agar gel immunodiffusion (AGID).

Results: As our results, the extracted RLPS caused positive reaction in LAL assay characterized as gelation and turbidity. In PAGE, a band with a molecular weight about 14 KDa was identified after specific staining using silver nitrate. Radial double AGID of the RLPS with a hyperimmune serum prepared in rabbit resulted in formation of a precipitation line.

Conclusion: Our study showed phenol-chloroform-petroleum ether method can be successfully used for the extraction of RPLS from *Brucella abortus* strain RB51 confirmed by LAL assay, PAGE and AGID.

Keywords: Brucellosis, *Brucella abortus* strain RB51, Rough Lipopolysaccharide, Limulus Amebocyte Lysate (LAL), Polyacrylamide Gel Electrophoresis (PAGE), Agar Gel Immunodiffusion (AGID)

O31 - 633: E-LEARNING IN MEDICAL MICROBIOLOGY, FROM E-BOOKS TO VIRTUAL LABS

Majid Zare Bidaki¹, Ali Rajabpour Sanati²

1. Assistant Professor, Paramedical Faculty, Birjand University of Medical Sciences
2. General practitioner, Birjand University of Medical Sciences

Background and Aim: As the Web technology develops, e-learning goes ahead and now e-learning seems to be on the top of learning methods accordingly. In medical sciences, digital technology may enhance learning much more due to the nature of The courses. This research aimed to evaluate if laboratory science technology students could learn required non-manual skills and could acquire essential competencies, such as visual and mental skills in medical bacteriology laboratory course using a virtual laboratory environment including e-contents and e-interactions.

Methods: A collection of e-learning methods was employed to create a blended learning system for supporting teaching medical microbiology laboratory courses. A virtual medical microbiology laboratory was designed inside the university learning management system combing a variety of learning e-contents including interactive text, interactive pictures, videos and simulations. In practice many different learning scenarios were applied for completion of this virtual lab.

Results: The learners significantly obtained better grades in the modules which their contents had been integrated with the medical microbiology virtual lab in comparison with the modules whose complete initiation took place in the real laboratory. Also the students showed readiness to and positive attitudes towards learning in a virtual lab environment especially in a combination by practicing in a real laboratory.

Conclusion: Virtual labs for microbiology are useful in different aspects and must be designed and developed in Iranian universities.

Keywords: E-learning, Microbiology, Virtual lab



Poster

The 17th International and Iranian Congress of

Anaerobic Bacteria

P1 - 970: ANTIMICROBIAL ACTIVITY OF DIFFERENT LACTOBACILLUS ISOLATES FROM TRADITIONAL YOGURTS RURAL AND TRIBAL AREAS OF KOHGILUYEH& BOYERAHMAD AGAINST CLINICAL ISOLATES OF CLOSTRIDIUM DIFFICILE

Shahrbanoo Asgarian¹, Ashraf Mohabbati Mobarez², Reza Naghiha³, Sepideh khodaparast⁴

1. Tarbiat Modares University , Faculty of Medical Sciences, Department of Bacteriology
2. Tarbiat Modares University , Faculty of Medical Sciences, Department of Bacteriology
3. Yasouj University, Faculty of Agriculture, Department of Animal Science
4. Tarbiat Modares University , Faculty of Medical Sciences, Department of Bacteriology

Background and Aim: Lactobacilli are the well known friendly bacteria for their probiotic activities against pathogens. The inhibitory activity of different isolates of lactobacilli obtained from traditional yoghurt was investigated against the clinical isolates of clostridium difficile.

Methods: The plate spot test was used for screening of Lactobacillus isolates against clostridium difficile.

Results: Fifty one Lactobacillus isolates from traditional yoghurt showed a strong anti-clostridia activity against the clinical isolates of clostridium difficile.

Conclusion: Some lactobacilli isolates exhibit significant inhibitory activity against the clinical isolates of Clostridium difficile.

Keywords: Lactobacillus isolates, Clostridium difficile, Antibacterial activity

Applied (industrial and agricultural) Microbiology

**P2 - 14: ISOLATION AND CHARACTERIZATION OF MESOPHILIC ALPHA-AMYLASE
FROM UFM29 BACTERIUM**

Saideh Afrisham¹, Abdolhamid Namaki Shoushtari², Arastoo Badoei Dalfard³

1. MSc student of microbiology Department of Biology faculty of Shahid Bahonar University of Kerman, Kerman, Iran Yong Researchers Society, Shahid Bahonar University of kerman, kerman, Iran
2. Associate Professor of Microbiology Department of Biology faculty of Shahid Bahonar University of Kerman, Kerman, Iran.
3. Associate Professor of Biochemistary Department of Biology faculty of Shahid Bahonar University of Kerman, Kerman, Iran.

Background and Aim: Alpha-amylases are extracellular enzyme that they catalysis hydrolysis of α (1 $\rightarrow$ 4) bonds in starch. So far, alpha-amylase application has been expanded in different industrial fields; as they can be used as additive in detergents, to remove starch from fabrics, liquefaction of starch, dextrin formation in bread baking for flavor improvement and also clinical areas; therefore, in this research, isolation of an alpha-amylase producing bacterium, named UFM29 was performed from farmlands in Shahid Bahonar University of Kerman.

Methods: To relative characterization of isolated strain, some of morphological and biochemical tests was used. Screening of intended bacterial strain was performed on starch-agar medium using 1% gram's iodine solution and subsequently in liquid medium containing 0.1 % starch. Alpha-amylase production was assayed using DNS method for 24- 72h of incubation. In the end, activity and stability of this enzyme was investigated in presence of various pH.

Results: Morphological and biochemical tests showed that the isolated strain was bacillus and gram positive, catalase and gelatinase positive, utilizing citrate and fermenting lactose or saccharose sugars. After screening in liquid medium and enzyme activity assay using DNS method, it was observed that the most enzyme production yield has been occurred after 72h of incubation. After 72h, its activity and stability of enzyme solution was investigated and it was detected that the maximum activity and stability was in pH 7.

Conclusion: With regards to the production yield in solid and liquid mediums, it was resulted that the isolate can be used in various industrial processing.

Keywords: Alpha-amylase, Farmlands, Screening, Activity, Stability

**P3 - 43: STUDY ON AZO DYES BIODEGREDEATION BY ISOLATED BACTERIA FROM
TEXTILE EFFLUENT**

Husein Pourkazem¹

1. M.A student at Microbiology, Department of biology, Faculty of science, Islamic Azad University of Rasht , Rasht, Iran.

Background and Aim: Azo dyes are released into wastewater streams without any pretreatment and pollute water and soil environments. To prevent contamination of our vulnerable resources, removal of these dye pollutants is of great importance. Traditional methods of treatment are found to be expensive and have operational problems.

Methods: For this purpose, wastewater samples were collected from dye-contaminated sites to isolate Congo red decolourizing bacteria. one strains were obtained with potential for Congo red decolourization. On primary screening, an aerobic gram positive bacillus (*Bacillus* sp.) was found to have maximum observable Congo red decolourization activity. Different parameters such as various carbon source, nitrogen source, inoculum size, temperature and pH were optimized for decolourization of Congo red by using bacterial isolates. pH, nitrogen source and inoculum size were found to be most effective in dye decolorization.

Results: Enhanced decolourization was observed in presence of xylose as a carbon source and yeast extract as a nitrogen source. The optimum of inoculum size was found to be 5%. The optimum pH obtained for decolourization of Congo red by bacteria strains was 5.0. The optimum temperature was found to be 25°C. under optimal conditions maximum decolourization percentage was about 100%.

Conclusion: High decolorization extent and facile conditions show the potential for this bacterial strain to be used in the biological treatment of dyeing effluents. The results reported here warrant further investigation to establish the usefulness of these isolates for biodegradation application such as waste water treatment.

Keywords: Textile wastewater, Congo red, *B. Subtilis*, Biodegradation, Decolorization

**P4 - 97: ISOLATION OF INDIGENOUS SIDEROPHORE-PRODUCING BACTERIA AND
DETECTION OF A VARIETY OF SIDEROPHORES**

EBRAHIM ESHAGHI¹, Rahim Nosrati ², Parviz Owlia³, Mohammad Ali Malboobi⁴

1. Department of Biology, Faculty of Science, Nourdanesh Institute of Higher Education, Esfahan, Iran
2. Department of Pharmaceutical Biotechnology, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran
3. Molecular Microbiology Research Center, Shahed University, Tehran, Iran
4. Department of Plant Biotechnology, National Institute of Genetic Engineering and Biotechnology (NIGEB), Tehran, I.R. Iran

Background and Aim: Despite the abundance of iron in nature, it is the third most limiting nutrient for plants due to its minimal solubility in most soils. While certain soil microbes produce chelating agents with high iron affinity, termed siderophores. Siderophores are low molecular weight (often <10 KD) iron binding compounds synthesized by microbes in large quantity under iron limited conditions that enhance the solubility of iron. Typically, microbial siderophores are classified as catecholates, hydroxamates, and α -carboxylates, depending on the chemical nature of their coordination sites with iron. The aim of this study was to isolate indigenous siderophore-producing bacteria and detection of a variety of siderophores.

Methods: In this study, thirty-seven soil samples collected from a diverse range of slightly alkaline soil types and were evaluated for siderophore-producing bacteria. The isolates were intensively assessed for detection of nature of siderophore. Molecular weight of the extracted siderophores in sample was determined using SDS-PAGE.

Results: From 37 soil samples, a total of 18 isolates were determined as siderophore producers. The compounds identified through this method belonged to both sixteen hydroxamate and carboxylate -types, respectively. The isolates produced siderophores with molecular weights of 8 to 12 KD.

Conclusion: Chemical analysis and SDS-PAGE of extracted siderophores can be used for the identification of hydroxamate, catecholate and carboxylates siderophores.

Keywords: Siderophore, Biofertilizer, Siderophore-producing bacteria, CAS

**P5 - 104: SCREENING AND ISOLATION OF EXTRACELLULAR PROTEASE PRODUCING
HALOPHILIC BACTERIA FROM BADAB-SOURT**

Leila Satari Faghihi¹, Salman Ahmady-Asbchin², Bagher Seyedalipour³

1. Department of Molecular and Cell Biology, Faculty of Sciences, University of Mazandaran, Babolsar, Iran
2. Department of Molecular and Cell Biology, Faculty of Sciences, University of Mazandaran, Babolsar, Iran
3. Department of Molecular and Cell Biology, Faculty of Sciences, University of Mazandaran, Babolsar, Iran

Background and Aim: One of the most important classes of hydrolytic enzymes is proteases which are widely used in biotechnological applications. Many different protease producers have been recently identified and their enzymes purified and characterized, but they are not sufficient to cope the demands of industrial processes. Due to the many harsh conditions in biotechnological processes such as high temperatures, acidic or alkaline pH, high salinity and etc., it would be of great importance to recognize novel enzymes with optimum activities at extreme values of temperature, pH, and different concentration of salt.

Methods: Samples were collected from water, soil, and sediments of two springs in Badab-sourt, Mazandaran. First different colonies have been isolated on MH media and optimal growth conditions of them were investigated. Then production of extracellular protease was studied by cultivation on skimmed milk agar plates with both 5% and 10% NaCl concentration and incubated for two weeks at 37°C. Colonies with clear zone are considered to have proteolytic activity.

Results: Results indicated only five isolates can produce extracellular protease by creating clear zone around their line culture. Based on biochemical and morphological characters, three isolates (S11, S13, and S18) were selected for further study. S11 and S18 are non-motile, catalase-positive, oxidase-positive, indole-negative, aerobic, non-spore forming and Gram-positive bacillus. S13 is a non-motile, catalase-positive, oxidase-negative, indole-negative, aerobic, non-spore forming and Gram-negative Cocci, with orange pigments.

Conclusion: Recently, considerable interest has been drawn on enzymes of halophilic bacteria and their biotechnological potentials. Aim of this study was isolation of halophiles which are able to produce extracellular protease.

Keywords: Protease, Halophiles, Protease activity, Badab-sourt

P6 - 144: DECOLORIZATION OF FOUR TEXTILE AZO DYES BY NEUROSPORA SP. UTM C 5041 UNDER SALINE CONDITIONS

Setareh Moayedi Rad¹, Javad Hamed², Hamid Moghimi³

1. Department of Microbiology, Faculty of advanced sciences & technology, Pharmaceutical sciences branch, Islamic Azad University, Tehran, Iran (IAUPS)
2. Department of Microbial Biotechnology, School of biology, College of science, University of Tehran, Tehran, Iran
3. Department of Microbial Biotechnology, School of biology, College of science, University of Tehran, Tehran, Iran

Background and Aim: Wastewaters of textile processing and dye-stuff manufacture industries contain substantial amounts of salts in addition to azo dye residues. To examine salinity effects on dye removal process, a study was carried out with four azo dyes in the presence of varying concentrations of NaCl (0–100g.l⁻¹) with a previously isolated fungus, *Neurospora* sp. UTM C 5041.

Methods: The fungus *Neurospora* sp. UTM C 5041 was recently isolated from soil of Iran and preserved in University of Tehran Microorganisms Collection (UTMC). An aquatic solution medium consisting of dyes, Congo red, Acid Blue 161, Direct blue 21 and Reactive yellow ME145 at concentration of 300mg.L⁻¹ and at different salt concentrations up to 100 gNaCl.l⁻¹ were inoculated with wet fungal biomass at 170rpm, 30°C. After one hour incubation the supernatant was centrifuged (10min, 2630×g) and its absorbance was measured at 500nm.

Results: The results illustrated the ability of *Neurospora* sp. to treat azo dye-contaminated wastewater under saline conditions. The results showed that UTM C 5041 was more efficient in decolorizing the Congo red dye with dye decolorization rates of 96% in the medium containing 20g.l⁻¹ of NaCl. However, higher salinities (5–10%) could inhibit the decolorization, although there was still about 94% dye removal. The results also showed that the decolorization of other dyes by UTM C 5041 was improved as salinity increased from 2% to 10%.

Conclusion: The results of this study indicate that the *Neurospora* sp. UTM C 5041 have a potential application for bioremediation of dye-polluted saline wastewaters from textile and other dye-stuff industries.

Keywords: Decolorization, azo dyes, *Neurospora*, salinity, wastewater

**P7 - 206: OPTIMIZATION OF BACILLUS PASTEURII GROWTH CONDITION FOR
ENHANCED UREASE ACTIVITY**

Sevda Jafari¹, azita dilmaghani²

1. Drug Applied Research Center, Tabriz University of Medical Sciences, Tabriz, Iran
2. Drug Applied Research Center, Tabriz University of Medical Sciences, Tabriz, Iran

Background and Aim: Calcium carbonate is an important inorganic material and typical bio-mineral, which is widely used by several industries such as construction, medical, paint, plastic, rubber, ceramic, glass, steel, oil refining and paper. Microorganism-based approach is a new producing method for Calcium carbonate which it happens through urease activity of *Bacillus pasteurii* during the growth of the microorganism with the surrounding environmental media. The yield of urease activity plays an important role in final material production and it is affected mostly by *Bacillus pasteurii* growth conditions such as pH, temperature, cultivation medium.

Methods: Here, for optimization of growth condition, *Bacillus pasteurii*, with No. 1645 (DSMZ 33) is provided from the Persian type culture collection (PTCC). In order to optimize the growth condition to reach the maximum urease activity, the effect of three different factors of nitrogen source (Ammonium chloride, Ammonium nitrite, ammonium hydrogen phosphate), pH (8, 8.5 and 9) and temperature (25, 30, 35 °C) was investigated in three levels.

Results: The results showed that the highest urease activity is in liquid cultivation containing Ammonium chloride as a nitrogen source, pH of 8.5 and temperature of 30 °C. Moreover, the optimization of Ammonium chloride concentration demonstrated the urease activity is most preferable in 10 g/L.

Conclusion: Temperature, cultivation medium, pH play important role of urease activity in *Bacillus pasteurii* growth.

Keywords: *Bacillus*, pH, nitrogen source, urease activity

**P8 - 209: WHETHER MICROBES HAVE THE ABILITY TO CLEAN UP POLLUTED AIR
ASALUYEH?**

Mohammad Heydari¹

1. Master of Chemical Engineering, Biotechnology, Young Researchers and Elite Club membership

Background and Aim: Asaluyeh in Bushehr province was one of the remote villages where people lived in clean air. In 1998, development of oil industry in the region to begin construction of gas refineries and petrochemical complexes were, So that these remote and safe area of the country has the most polluted air. One simple method is to remove these contaminants biofiltration. In this way, by passing through a bed containing microorganisms degrading contaminants filtered out.

Methods: In this study, a number of cylindrical galvanized iron biofilter to analyze vapors of styrene, toluene and benzene from the airflow was used.

Results: In this study, the effects of air inlet flow rate, temperature, height biofilter system performance evaluated and chemical compounds in concentrations of 10-80ppm was logged. Based on the results of this study in different conditions for maximum removal efficiency of styrene, toluene and benzene, respectively, 97%, 95%, 93%, and Average flow rate of 5 liters per minute is the best.

Conclusion: The results showed that the biofilter removal efficiency can be increased by increasing the relative height and temperature changes in contaminant removal efficiency is influenced by the biofilter. In general, the biofilter is a useful method for removing contaminants studied and green and eco-friendly way and can be used in the near future to pollution Asaluyeh (capital of the country) can be used on an industrial scale.

Keywords: Asaluyeh, biofilter, polluted air

P9 - 222: ISOLATION AND IDENTIFICATION OF BACILLUS CEREUS FROM PETROLEUM PIPELINES

Arezoo Pedramfar¹, Keivan Beheshti Maal², Hossein Mirdamadian³

1. Department of Microbiology, Faculty of Biological Sciences, Falavarjan Branch, Islamic Azad University, Isfahan, Iran
2. Department of Microbiology, Faculty of Biological Sciences, Falavarjan Branch, Islamic Azad University, Isfahan, Iran
3. Department of Microbiology, Faculty of Biological Sciences, Falavarjan Branch, Islamic Azad University, Isfahan, Iran

Background and Aim: Corrosion is the main feature of the oil pipelines destruction. The main biocorrosion bacteria are sulphur reducing bacteria, iron oxidizing bacteria and manganese oxidizing bacteria. The microbial corrosion has been detected in various industries, especially in petrochemicals and oil industries. So, due to the high frequency of corrosion damages caused by bacteria in various industries, targeted investigation are challenging

Methods: The sample pipes with the corrosion were obtained from the Gandomkar petroleum pipeline station, Chaharmahal and Bakhtiari, Iran. For screening the corrosion producing bacteria the rusted pipe samples were cultured on a selective culture medium, manganese agar and incubated at 30°C for 18 hours aerobically. The purified individual colonies were subjected to macroscopic, microscopic and biochemical examinations respectively.

Results: The cultivation of corrosion based material in manganese agar after 18 hours incubation at 30°C resulted in the isolation of cream-colored colonies that had swarming. The microscopic examinations showed spore forming Gram positive bacilli. The biochemical tests such as catalase, motility, nitrate reduction and VP were positive. Based on macroscopic, microscopic and biochemical examinations the bacterial isolate was identified as *Bacillus cereus*.

Conclusion: This is the first report of isolation and identification of corrosion-producing bacteria from Gandomkar petroleum pipeline station, Chaharmahal and Bakhtiari, Iran. The isolated bacterium was identified as *Bacillus cereus* based on microscopic and biochemical examinations. This study confirmed the role of bacteria in the corrosion of oil pipelines. The biological procedures for preventing the microbial corrosion could be an asset and considered as a potential in petroleum and industrial microbiology.

Keywords: *Bacillus cereus*, Industrial Microbiology, Microbial Corrosion, Petroleum, Pipeline.

**P10 - 231: THE AMOUNT OF COLIFORM CONTAMINATION OF SURROUNDING WATERS
IN THE SOUTH BASIN OF THE CASPIAN SEA PROVINCE OF MAZANDARAN IN
DIFFERENT SEASONS (SPRING, SUMMER, AUTUMN AND WINTER)**

Majid Sadeghpour¹, Ali bahadorani², Pargol Ghavam Mostafavi³, Ali Mashinchian Moradi⁴

1. Author
2. Searcher
3. Supervisor
4. Supervisor

Background and Aim: northern cities, especially in the southern Caspian Sea province of Mazandaran, estuaries and coastal beaches in this area are continuously exposed to microbial contamination. The aim of this study was to evaluate the microbial contamination of water Area coast of the Caspian Sea Mazandaran Province respectively.

Methods: To evaluate the microbial quality of the water estuaries of rivers in Mazandaran Province 5 stations (Noshahr, light, Mahmoud Abad, Fereydunkenar, Babolsar) during the fall and winter of 1393 and spring and summer of 1394 were sampled and the number of total coliform, E. coli, total Fecal, temperature and pH were determined by standard methods.

Results: The mean number of aerobic bacteria in winter in Noshahr, with cfu / dl 362 sea water and in the fall the lowest in Babolsar with cfu / dl 4305 accounted for the highest rate of sea water. The lowest average total coliform in the winter of Noshahr, with cfu / dl 123 seawater and the highest in summer in Babolsar with cfu / dl 3209 was sea water. The lowest mean total Fecal in winter in Noshahr cfu / dl 31 seawater and the highest in summer in Babolsar cfu / dl 1560 was seawater.

Conclusion: The study showed that there is pollution in all coastal areas of the province. Especially from the West to the East will study indicates Water coast of the province of indicator bacteria, contamination and health problems for swimmers and tourists as a factor to be considered.

Keywords: Caspian Sea, the Caspian coastal waters, microbial contamination, E. coli, coliforms

**P11 - 240: ISOLATION AND IDENTIFICATION OF GOLD NANOPARTICLE EXTRA
CELLULAR PRODUCING BACILLUS FROM SOIL SAMPLE IN FARS PROVINCE**

Sepide Ebrahimi Fard¹

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Background and Aim:: Biological sources of microorganisms such as *Bacillus* are playing a major role in the reduction of metallic nanoparticles gold, as it emerges as an eco-friendly and exciting approach in nanotechnology. The purpose of this study is isolation and identification of gold nanoparticle extra cellular producing bacteria from soil sample in Fars province.

Methods:: To performing this study, 40soil sample were collected and the ability of gold nanoparticles production from each the isolates were assessed. After culturing soil samples, nutrient agar media were incubated at 37 ° C for 24h and then, bacteria were isolated based on morphology colonyand gram stain. For identification nanoparticle producing isolated bacillus, the isolates were cultured in nutrient broth and were incubated for 24 h.ThenHAuCl₄ aqueous solutionwas added. HAuCl₄ was reduced as Au⁺ ions, which confirmed the presence of nanoparticles by the color change of pale yellow to purple.

Results:: In this study, 65 gram positive and negative bacillus isolated from soil samples. 15 isolated bacteria can produce gold nanoparticle by extra cellular synthesis.The minimum and maximum peaks were observed at 540 nmat 24th hours by UV-Visible spectroscopy spectra of the gold nanoparticles. X-ray diffraction (XRD) analysis determined the polycrystalline nature ofgold nanoparticles.

Conclusion:As a result of the studies, the frequency of nanoparticle producing bacteria is 21% and it is low percent in the soil of Shiraz province.

Keywords:Bacilluses,gold nanoparticles,soil,Fars

P12 - 333: STUDING THE SALT STRESS EFFECTS ON SOME PHYSIOLOGICAL AND MORPHOLOGICAL RESPONSES OF CYANOBACTERIUM NOSTOC SP.FS77 WITH EMPHASIZE ON POTENTIALITY IN AGRICULTURAL BIOTECHNOLOGY

Zynab Badeli¹, Roghayeh Badeli², Shadman Shokravi³

1. Department of Pathobiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
2. Pharmaceutical science Branch, Islamic Azad University, Tehran, Iran
3. Department of biology, Gorgan Branch, Islamic Azad Univ, Gorgan, Iran

Background and Aim: Heterocystous cyanobacteria play a significant contribution in maintaining soil fertility. Despite the occurrence of paddy fields, wheat fields and woodland in north Iran, less attention has been paid to the role of cyanobacteria in these ecosystems. In this study cyanobacterium Nostoc sp.FS77 which are provided from Golestan province paddies under mixed conditions of limited light, limited carbon dioxide and salinity fluctuation.

Methods: After the sample soil culturation, cyanobacterium Nostoc sp.FS77 has been isolated and identified and exposed to the culture medium BG0-11 under limited light 2 uE.m-2.s-1, continuous white light and in 28°C temperature which was refrained of aeration and carbon dioxide inoculation. A wide range of sodium chloride (0-15%) has been treated. The growth is evaluated by optical density. salinity amelioration ability with EC meter, nitrogenase activity with acetylene reduction test and gas chromatography, photosynthesis activity with nmolO₂/mgw.min, ammonium liberation through phenat method. The morphological adaptation is done by means of microscope and fluorescence microscope.

Results: The growth and Ammonium liberation reach to maximum between (0-4-12%) salinity. variation of spatial formation oval-cylindrical especially in salinities up to 12% is higher. This genus appear in intermediate passage tensions 4% to 12% salinities recovering of photosynthesis and nitrogenase system. salinity amelioration ability, particularly in salinities (0-4-12%) is significant in liquid culture.

Conclusion: Finally this genus considerations in practical programs to choose effective samples as suitable initiators in agriculture biotechnology.

Keywords: Agricultural biotechnology ; Ammonium liberation ; Nitrogenase ; Nostoc sp.FS77 ; Photosynthesis ; Salinity

**P13 - 373: EVALUATION OF KINETIC OF DIFFERENTIAL FACTORS IN ARCHAEA
HALOBACTERIUM SALINARUM**

Akram Najafabadi samani¹, Amir Salehi Najafabadi², Mohammad Ali Amoozegar³

1. Islamic Azad University of Shahrekord, College of Biology, Shahrekord, Iran
2. Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran
3. Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran.

Background and Aim: Biologic process of quorum-sensing is regulatory system of gene expression associated to cell density in bacterial cells which caused behavioral diversity in the bacterial populations through extracellular secretory signals and intra-population interactions. N-acylhomoserinelacton (AHL) is the main signal of quorum-sensing among gram negative bacteria. Here we investigate the presence of differentiation factors in *Halobacterium salinarum* as a model organism in domain archaea .

Methods: Firstly to determine the presence of these molecules the production kinetic and its relation to the growth cycle has been studied via daily sampling of the fermentation broth. The maximum production rate of AHLs in the *H. salinarum* it was the second day of fermentation. Then at the specific time intervals the crude extract of the fermentation media was extracted and the results were used to study the kinetic and investigate the effect of exogen addition of the extract to the fermentation media.

Results: There was no evident of oxygen limitation during the growth cycle of *H. salinarum*; and the low rate of oxygen consumption could give the impression that this archaea is microaerophilic. In order to evaluate the best exogen addition protocol the OTR profile of the fermentation process for both strains has been studied via milibioreactor.

Conclusion: Overall results show that the addition of 5 nm concentration at the hour 10 after inoculation, 15 nm concentration at the hour 10, and 20 nm concentration at the hour 20 are the optimum time and concentrations of exogen addition of the crude extract into the *H. salinarum* growth medium.

Keywords: quorum sensing, *Halobacterium salinarum*, N-acyl homoserine lacton, OTR

**P14 - 401: INFLUENCE OF PHYSIOLOGICAL CELL STAGES ON THEBAINE
BIOTRANSFORMATION**

Nazanin Ataee¹, Jamshid Fooladi², Mohammad Hasan Namaei³, Fateme Mirzajani⁴

1. Department of Microbiology, The faculty of Biological Sciences, Alzahra University, Vanak, Tehran, Iran
2. Department of Biotechnology, The faculty of Biological Sciences, Alzahra University, Vanak, Tehran, Iran
3. Birjand Hepatitis Research Center, Birjand University of Medical Sciences, Ghafary Ave., Birjand, Iran
4. Department of Biotechnology, The Faculty of Renewable Energies & New Technologies Engineering (NET), ShahidBeheshti University, G.C., Tehran, Iran. Department of Nanobiotechnology, Protein Research Center (PRC), ShahidBeheshti University, G.C., Tehran, Iran

Background and Aim: Microbial transformation may be potentially easier and more efficient to produce morphine alkaloids as pharmacological materials with agonist and antagonist activities. Morphine alkaloids establish an important class of pharmaceuticals due to their powerful analgesic. The main goal of this study was to find the appropriate physiological condition of bacterial strain for synthesis of morphine alkaloids from thebaine.

Methods: The bacterium was selected by screening isolates obtained from nature in some parts of our previous works. The 5 L fermentor was used to produce the whole cells and during the growth cycle, samples were withdrawn every 30 min and the turbidity of culture and biomass weight were determined. Biotransformation tests were designed in buffer medium supplemented with thebaine as a precursor and using resting cells of this strain during exponential growth and stationary phases as biocatalysts. Biotransformation products were extracted with solution containing 68% (v/v) acetonitrile and the HPLC were used to monitor codeine and morphine in transformation process.

Results: It was shown that this strain transformed thebaine to codeine and morphine during early stationary phase (5 hours) after washing and converting it to resting cells but no codeine and morphine achieved in early, mid and late logarithmic phase.

Conclusion: It can be concluded from this study that the physiological condition dramatically affect the biotransformation process.

Keywords: Thebaine, Biotransformation, HPLC, Codeine, Morphine

**P15 - 450: EVALUATION SOME OF SANITIZATION METHODS FOR BACTERIA
ELIMINATION IN OCIMUM AND MENTHA GENUS**

Reyhaneh Danaeipour¹, Ali Ayesh²

1. Department of Research and development, laboratory of Quality control, Arya Mehr Giah Company, Qom, Iran.
2. Department of Research and development, laboratory of Quality control, Arya Mehr Giah Company, Qom, Iran.

Background and Aim: Fresh produce is popular worldwide. At the same time, outbreaks of food-borne illnesses associated with the consumption of fresh produce have increased. Plants are progressively known as vectors for food-borne illness and the most predominant bacteria of the aerobic gut normal flora and the major pathogen contributing to outbreaks of foodborne illness associated with fresh produce. Post-harvest washing of fresh produce, usually with chlorine, is an important method for pathogen reduction. The objectives of this study were to investigate the effective of various-sanitizing methods and to evaluate the microbiological quality in fresh edible vegetables.

Methods: Ocimum and mentha genus were prepared from farms. Different exposure times, temperature and acidity of chlorine were studied. Then, all samples were tested about total count of bacteria, count of coliform, E. coli, Enterococcus, mold and yeast.

Results: All samples studied had contamination. In microbial Ocimum analysis, all examinations sanitized by various methods were about national standards of Iran and microbial flora had sensibly decreased; E. coli was almost removed, after used sanitizers. All microorganisms were removed by chlorine sanitizers (PH: 5), in microbial Mentha genus investigation; Almost, in methods washed by chlorine (PH: 7) were Similarity obtained results.

Conclusion: Chlorine associated with different factors such as temperature and acidity affected on microbial flora. E. coli removed from chlorine-sanitized samples. There was a few studies such this investigation on raw vegetables in Iran, therefore we can't compare the results of this investigation with them.

Keywords: Ocimum, Mentha, E. coli, chlorine, microbial flora.

P16 - 466: EVALUATION OF MICROBIAL CONTAMINATION IN WATERS (DISPOSAL, DRINKING AND NATURAL) IN URMIA

Maryam Abbasi ghaznag¹, Hasan Mlekinejad², Amir Rahimirad³, Ilnaz Mozafarian⁴

1. Urmia food and drug control lab, Urmia Medical University
2. Food and Drug Department, Urmia Medical University
3. Urmia food and drug control lab, Urmia Medical University
4. Urmia food and drug control lab, Urmia Medical University

Background and Aim:For this purpose, this article evaluate quality of disposal waters used in food factories of Western Azarbaijan province of Iran. So quality of drinking and natural water samples were delivered to Urmia food and drug control lab during a 9 months period of time has been evaluated.

Methods:Samples were experimented as it is mentioned in Isiri 7023, 5869 and microbiological handbook of food and drug organization from the point of microbial contamination. Microfiltration method was used (0.45 μ). Volume of sample was 250 ml for each test. Samples were evaluated from the point of contamination to Coliforms, Escherichia, fecal Streptococci, Clostridium, Pseudomonas, Campylobacter and Yersinia.

Results:From 36 samples of disposal water, two were not in accordance with microbiological handbook of food and drug organization due to contamination with Pseudomonas. Others were in accordance with it. From 12 samples of drinking water, one was not in accordance with Isiri 7023. It includes contamination with cyanobacteria. Others were in accordance with it and microbiological handbook. From 9 samples of natural water, all were accordance with microbiological handbook.

Conclusion:From inspection of results,we can conclude the situation in case of drinking and natural waters is acceptable from the point of microbial contamination. Although in case of one drinking water sample, cyanobacteria contamination was observed that needs better sanitary operations from algae. About quality of disposal waters, it is better to use perfect sanitary operations for providing healthy and hygienic water.

Keywords:Microbial contamination, Disposal water, Drinking water, Natural water and Western Azarbaijan province.

P17 - 479: OPTIMIZATION OF COLD-ACTIVE PROTEASE PRODUCTION BY THE COLD TOLERANT BACTERIUM STENOTROPHOMONAS SP. WITH ONE FACTOR AT A TIME METHODOLOGY

Reihaneh Nikbakhti¹, Bahar Shahnava², Ahmad Asoodeh³

1. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran.
2. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran.
3. Department of Chemistry, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran.

Background and Aim: Cold active enzymes have high catalytic efficiency at low temperature because this enzyme increased flexibility of the active sites. These enzymes are used in the leather industry, waste water analysis, detergents, food etc.

Methods: The aim of this study was to optimize cold-active protease from *Stenotrophomonas* sp. by one factor at a time (OFAT) method. The best initial pH was determined by adjusting the pH of production medium at 6, 7, 9, and 11. The impact of different carbon sources (glucose, lactose, sucrose, and starch) was investigated by adding 1% (w/v) of each one to the production medium. To examine the effect of inoculation level on protease production, 0.5%, 1.5%, 2.5%, and 3.5% (v/v) of bacterial suspension containing about 1.5×10^8 cell/ml was used.

Results: The highest level of protease production occurred after 48 hours (0.312 Uml⁻¹). The highest level of protease was produced at pH 9 (0.601 Uml⁻¹), while further increase in medium pH decreased enzyme production. Adding starch to the production culture increased protease production (0.643 Uml⁻¹).

Conclusion: Cold-adapted proteases thus can be use to optimize present day industrial processes and for developing future technologies with less energy inputs and process cost by removing the cost of heat inactivation step.

Keywords: protease, optimization, *Stenotrophomonas* sp.

**P18 - 510: BIODESULFURIZATION OF DIBENZOTHIOPHENE WITH ENTROBACTER
BAB3164 ISOLATED FROM OIL CONTAMINATED SOIL IN ABADAN RIFINERY**

Shima Shantiaee¹

1. Msc.of microbiology

Background and Aim: Combustion of fuels containing sulfur, leading to the formation of pollutants such as CO₂ and creat acid rain, destruction of farmland and damage to the building facades. Since existing methods for desulfurization of fuels, such as hydrogen desulfurization, has disadvantage, for several years, the best method is to use biological methods. Desulfurization biological advantage over the hydrosulfurization of sulfur compounds such as dibenzothiophene , benzothiophene is being less expensive, less production of hydrogen and carbon dioxide and doing this at ambient temperature and normal pressure. Given that the refinery had not been used extensively suitable desulfurization of isolated bacteria in this article, the bacteria in soil bacteria isolated parts of the refinery for good desulfurization was investigated.

Methods: 3 soil samples from different areas of study refinery were collected. After specimen inoculation, growing bacteria, microbial and biochemical tests were identified. Bacteria capable of metabolizing Benzothiophene isolated, and types of able to remove sulfur dioxide, Benzothiophene, by using of growth model and test Gibbs was screened . And 16S rRNA-PCR techniques were used to confirm the strains obtained.

Results: From 3 samples 2 bacteria were isolated and between them 6 isoulated are importance due to ability of desulfurization.

Conclusion: In this bacteria indigenous in order to Entrobacter specie was categorized.

Keywords: biological desulfurization, Debenzothiophene, Entrobacter sp. BAB-3164

**P19 - 522: ISOLATION AND SCREENING OF PIGMENT PRODUCING ACTINOBACTERIA
FROM SOIL**

Mahdieh Ranjbari¹, Mehran Kianirad², Maliheh Safavi³, Ali Sheikhinezhad⁴, Mahnaz Hadizadeh⁵, Sanaz Jafari⁶

1. Iranian Research Organization for Science and Technology, Faculty of Biotechnology
2. Iranian Research Organization for Science and Technology
3. Iranian Research Organization for Science and Technology
4. Iranian Research Organization for Science and Technology
5. Iranian Research Organization for Science and Technology
6. Iranian Research Organization for Science and Technology

Background and Aim: Microorganisms have become a potential source for biopigment production due to their advantages over other biological resources in terms of availability, high growth rate, cost efficiency, yield and easy downstream processing. Pigments not only act as coloring agents in various food processing, dyes, cosmetics and pharmaceuticals but also possess antioxidant, anticancer, anti-inflammatory, anti-microbial activities.

Methods: In this study, samples were collected from soils of Semnan district, Fuman jungles, Orumieh lake and soil pot. An accurately weighed sample of sieved soil (1g) was transferred to 100 ml of saline solution and incubated on rotary shaker (150 rpm), then diluted aliquots were serially diluted and were spread over the surface of the Brain Heart Infusion (BHI) Agar. All plates were incubated at 28°C for 2 weeks. Colonies of pigment producing Actinobacteria were isolated and cultured on Yeast Extract-Malt Extract Agar (ISP Medium 2).

Results: Among twenty-five different Actinobacteria species, five strains with the ability of production of pigments such as (melanin) black, (carotenoid) yellow, red and orange were found and were kept for further studies.

Conclusion: The present study attests to the existence of a rich microbial diversity in Iran soil that needs more attention due to its important role in microbial world.

Keywords: biopigment, actinobacteria, antioxidant, anti-inflammatory, anticancer

P20 - 533: COMPARISON OF DIFFERENT METHODS IN PROTEIN A IMMOBILIZATION

Seyed Mehdi Qafari¹, Gholamreza Ahmadian², Mehdi Mohammadi³, Nasim Rezaeinezhad⁴

1. National Institute of Genetic Engineering and Biotechnology Shahrak-e Pajooresh, km 15, Tehran - Karaj Highway, Tehran, Iran
2. National Institute of Genetic Engineering and Biotechnology Shahrak-e Pajooresh, km 15, Tehran - Karaj Highway, Tehran, Iran
3. National Institute of Genetic Engineering and Biotechnology Shahrak-e Pajooresh, km 15, Tehran - Karaj Highway, Tehran, Iran
4. National Institute of Genetic Engineering and Biotechnology Shahrak-e Pajooresh, km 15, Tehran - Karaj Highway, Tehran, Iran

Background and Aim: Protein A is one of the *Staphylococcus aureus*'s virulence cell surface proteins which binds to immunoglobulin G. This protein is used for purification of immunoglobulin G and production of monoclonal antibodies. For this purpose, protein A must be first immobilized on the surface of proper beads. In the present study, different methods of protein A immobilization on the surface of three different beads have been compared.

Methods: three different approaches for immobilization of protein A were compared to each other. First, implementing polyhydroxyethylmethacrylate (PHEMA) microbeads by CNBr as the catalyst, second, immobilizing protein A on poly (EGDMA/HEMA) microbeads in borate buffer and finally, immobilizing protein A on a golden surface by protein A-gold binding domain fusion protein.

Results: The first two methods were based on chemical reactions that establish covalent bonds. Due to the chemical nature of the reactions, immobilization on the surface of beads occurs randomly in the first two methods. On the other hand, the third method is seemed to be site-specific and oriented. That's why protein A attaches to the golden surfaces with the higher immunoglobulin binding affinity and specificity.

Conclusion: According to the obtained data, the two former methods are more cost efficient but less accurate in comparison with using golden surfaces.

Keywords: Protein A, immobilization, purification

**P21 - 577: EVALUATION OF ERMSF TRANSFORMATION IN SACCHAROPOLYSPORA
ERYTHRAEA FOR ENHANCEMENT OF ERYTHROMYCIN**

Sanam Adnani Forghani¹, Hossein Rassi², Bahman Tabaray³

1. Department of Biology , Karaj Islamic Azad University
2. Department of Biology , Karaj Islamic Azad University
3. Department of Biology , Karaj Islamic Azad University

Background and Aim: Erythromycin and tylosin antibiotics are macrolide antibiotics that produce by *Saccharopolyspora erythraea* and *Streptomyces fradiae* respectively. Today, transformation method in wild strains use to produce more effective antibiotics. In this study, transformation of *ermSF* gene from *S. fradiae* in *S. erythraea* for enhancement of erythromycin.

Methods: For this purpose, production of tylosin antibiotics was investigated in *S. fradiae* and appropriate methods to determine the amount of tylosin was investigated in wild type. first, *ermSF* of tylosin biosynthetic genes amplified by gene-specific primers. The PCR product of the *ermSF* gene constructed into T vector and pTG19-ERMSF plasmid was made.

Results: The plasmid was transformed into *E. coli* strain DH5 α and recombinant colonies containing the *ermSF* gene by blue and white screening was confirmed. In the next step, protoplasts of the *S. erythraea* were prepared and DNA transformation was performed according to standard procedures.

Conclusion: In total, 300 recombinant colonies isolated in primary screening and then 10 colonies detected increased production in the fermentation medium. Finally, recombinant RHE87 with 25/2 mg per ml antibiotics production and increasing of 150-fold compared to wild type were selected.

Keywords: *ermSF* transformation , *Saccharopolyspora erythraea* , enhancement of erythromycin

**P22 - 580: INTRODUCTION OF SAROCLADIUM SP. AS A POTENT OLEAGINOUS YEAST
STRAIN FOR PRODUCTION OF BIOFUEL**

Siavash Azari¹, Mahzad Nikbakhtradi², Marjan Ostovar³, Hoda Nouri⁴, Ahmad Farhad Talebi⁵, Hamid Moghimi⁶

1. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran.
2. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran.
3. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran.
4. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran.
5. Genetic Department, Faculty of Biotechnology, Semnan University, Semnan, 35131-19111, Iran
6. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran.

Background and Aim: Rapid population growth and accumulation of pollutants in the atmosphere during the past decades has created an increasing demand for adoption of clean energies as a replacement to fossil fuels. The aim of the present study was to evaluate the ability of oleaginous yeasts as a worthy oil feedstock in biodiesels production industry.

Methods: Initially, 108 isolates were screened on OYEM5 medium. Sudan B black staining and lipid extraction with methanol-chloroform were performed to each strain. Internal Transcribed Spacer (ITS) gene was targeted for molecular identification. Optimization of growth and lipid production were carried out using Response Surface Methodology (RSM). Finally, fatty acid (FA) profiling was performed using gas chromatography (GC).

Results: Isolate ADH57 was selected as the best isolate based on staining and initial biolipid production of 1.47 g/L. Phylogenetic analysis showed 99 % similarity to genus *Sarocladium*. Optimization process showed that the highest lipid production could be obtained during the following incubation condition: fermentation time 7 days, initial pH 6, glycerol concentration 5 % v/v, and glucose concentration 1.07 % w/v. Having compared to the control, optimization procedure resulted in more than two and three fold increase in biomass and lipid yield, respectively. Analyses of the extracted lipids showed that oleic acid (C18:1) and palmitic acid (C16:0) were the dominant FAs produced by 51 and 35 %, respectively.

Conclusion: The estimated biodiesel properties of the extracted oil from the *Sarocladium* sp. ADH57 strain confirm that studied strain could produce high amounts of useful FAs which could potentially be used for biodiesel production.

Keywords: Oleaginous yeasts; *Sarocladium* sp.; Biodiesel; Fatty Acid Profiling.

P23 - 624: CLONING OF A CHROMOSOME-ENCODED CATECHOL 2, 3-DIOXYGENASE(METAPYROCATCHASE) GENE FROM ACINETOBACTER OLEIVORANS GSN15

Fatemeh Babazadeh¹, SaraGharavi², ZahraMoosavi-Nejad³

1. Biotechnology Department, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
2. Biotechnology Department, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
3. Biotechnology Department, Faculty of Biological Sciences, Alzahra University, Tehran, Iran

Background and Aim: Catechol 2, 3-dioxygenase (C23O), an extradiol-type dioxygenase cleaving the aromatic C–C bond at the meta position of dihydroxylated aromatic substrates, catalyzes the conversion of catechol to 2-hydroxymuconic semialdehyde.

Methods: A pair of PCR primers was designed based on the conserved end sequence of the known C23O-encoding genes from *Acinetobacter* sp. For metapyrocatechase gene amplification, the total genomic DNA of strain GSN15 was used as template and the PCR reaction (50 µl final volume) contained 10×PCR buffer, 5µl; 25 mM MgCl₂, 4µl; 5 mM dNTP, 2µl; 20µM primer, 1µl each; template DNA, 100 ng; Taq polymerase (5000 U/ml), 0.5µl; and sterile distilled water, 35.5µl. The cycling parameters were 7 min at 94°C followed by 30 cycles of 94°C for 1 min, 59°C for 1 min, and 72°C for 2 min, with the 72°C segment of the final cycle extended to 10 min before cooling to 4°C. The resulting PCR product and vector were digested with EcoRI and SacI. Digested PCR product was subsequently cloned into digested pET28a (+), then transformed into competent *E. coli* DH5α in order to increase the number of recombinant plasmids.

Results: The presence of the metapyrocatechase gene in the transformants was verified and the cloned gene sequenced by using dideoxy chain termination protocol.

Conclusion: The results from sequencing of the amplified gene cloned in *E. coli* (DH5α), shows 85% identity with *Acinetobacter oleivorans* sequences registered in NCBI databases.

Keywords: Catechol 2,3-dioxygenase-cloning- meta-cleavage

**P24 - 629: BIOTREATMENT OF INDUSTRIAL CATTLE POLLUTANT GASES BY
BIOFILTRATION**

Sahar Karami rubati¹

1. Islamic Azad University of Ahar

Background and Aim:Compound such as Ammonia and Hydrogen Sulfide are pollutant gases. Ammonia is colorless, but irritant and smelly, while H₂S is corrosive, extremely toxic, and also smelly. Large amounts of NH₃ and H₂S are generated and released from industrial processes, such as petrochemical refining, metallurgy, food preparation, livestock farming, leather manufacturing, waste-water treatment and treatment of fuels. The aim of this research is to achieve an efficient and cheap methods to remove NH₃ and H₂S from industrial factories.

Methods:This research was done in 2013 at Environmental lab of Iranian Ghaza Azmaa. Biofilter cylinders are 30 cm each and made of glass. Each cylinder is filled with Peat soil, Oak, Leaves soil, Activated sludge of soft drink industry, Straw, Organic fertilizer and Shell in different arrangements. After matching beds with mentioned gases, in the final stage Ammonia and Hydrogen Sulfide gases were passed separately through the cylinder with inflow and outflow. Elimination percentage of Ammonia and Hydrogen Sulfide gases which were evaluated by Spectrophotometry methods and degrading bacteria of these gases were studied by Biochemical methods

Results:Among the four cylinders, the ones that were filled with Peat soil, Leaves soil and straw recorded 100% elimination in comparison with others, and also Pseudomonas and gram-positive Bacillus were dominant bacteria of these cylinders

Conclusion:According to the results, designed filters of present study can be used as a useful model for future researches which want to investigate the elimination of Ammonia and Hydrogen Sulfide gases of industry.

Keywords:Biofilter- pollutant- Industrial cattle

**P25 - 663: THE COMPUTATIONAL EVALUATION OF ACTIVITY OF SIMULATED
BACILLUS SUBTILIS α -AMYLASE (PDB: 1UA7)**

Zahra Eslamifar¹, Reza Ghaffaripour²

1. Department of biochemistry, School of paramedicine, Dezful University of Medical Sciences, Dezful, Iran.
2. School of paramedicine, Dezful University of Medical Sciences, Dezful, Iran

Background and Aim: α -amylases are necessary for the hydrolysis of starch to oligosaccharides. Because of the high solubility of starch at high temperatures, the thermostable α -amylases have the important role in this industry. In this study, on the simulated enzyme, the topics such as energy, GyrationRadius and RamachandranPlot surveyed at 310K-400K.

Methods: The α -amylase (PDB:1UA7) simulated by MonteCarlo(OPLS) and MolecularDynamics(OPLS) and so LangevinDynamics(OPLS and MM+) by hyperchem8.0 in 310-400K. Then kinetic, potential and totalEnergy determined. GyrationRadius and RamachandranPlot studied on simulated enzyme by VMD 1.9.1 software.

Results: The stability energy by: 1-MonteCarlo(OPLS) and MolecularDynamics(OPLS), increased with the temperature increasing and didn't showed thermo stability. 2-LangevinDynamics (MM+), has showed at 360-400K. 3-LangevinDynamics(OPLS), increased at 360-380K and then decreased at 390K. The quantity of the calculated GyrationRadius for: MolecularDynamics (OPLS) and LangevinDynamics (MM+) showed the most radius at 400K and RamachandranPlot showed the catalyticSite AminoAcids are in allowed location.

Conclusion: The increasing of temperature and finally the increasing of GyrationRadius leads to displacement of AminoAcids in CatalyticSite and leads to the enzyme inactivity. RamachandranPlot shows the permissible location of AminoAcids for enzyme activity. In order to investigation of maximum GyrationRadius at 400K and in fact maintenance of enzyme activity, RamachandranPlot surveyed. This study showed the CatalyticSite AminoAcids of BacillusSubtilis α -amylase (consisting of GLU208, ASP176, ASP269) in the simulated enzyme by LangevinDynamics(MM+) at 400K are still in the allowed location and so in this temperature, simulated enzyme is still active.

Keywords: BacillusSubtilis α -amylase, GyrationRadius, ramachandranplot, enzyme activity.

**P26 - 667: EVALUATION OF SIMPLE CARBON SOURCES IN MICROBIAL FUEL CELL
USING URMIA LAKE SEDIMENT**

Shahnaz Mohammadi¹, Gholamreza Zarrini², Iraj Ahadzadeh³

1. Department of Biology, Faculty of Natural Sciences, University of Tabriz, Tabriz, Iran
2. Department of Biology, Faculty of Natural Sciences, University of Tabriz, Tabriz, Iran
3. Department of Physical Chemistry, Faculty of Chemistry, University of Tabriz, Tabriz, Iran

Background and Aim: The discontinuation of energy supply will result in energy crisis, so looking for alternative energy sources have taken scientists' attention. Microbial fuel cells (MFCs) are one of the promising and possible options. Sediment MFCs exploit the present electroactive microorganisms by which electricity production and decomposition of organic matter occur. Exogenous nutritional elements such as acetate and lactate were examined in such fuel cells based on Urmia lake sediment is the aim of this study.

Methods: Single chambered SMFCs were designed in one liter bottles which half of them were filled with Urmia lake sediment as the anodic part where electrogenic consortium are present and the other half with lake water as cathodic part. Graphite plates were used as electrodes attached to copper wires. A fixed external resistor was installed on external circuit in order to stabilize cell performance and produce power. Different carbon sources, acetate and lactate, were added into anode part due to evaluation the response of microbial consortium to the added nutritional elements.

Results: In accordance with the graphs, fuel cells which received external nutrients demonstrated higher electrochemical performances, acetate received fuel cell 1.21 ± 0.65 mW/m² and lactate added cell 4.44 ± 1.41 mW/m² in contrast to the control fuel cell 1.92 mW/m² which were indicated in the graphs. The present microbial consortium may utilize lactate efficiently due to the higher electrochemical performance.

Conclusion: According to the results, addition of external simple carbon sources increases the performance of SMFCs, meanwhile lactate depicts more increasing effect.

Keywords: microbial fuel cell- Urmia lake- electrogene

**P27 - 681: ISOLATION AND CHARACTERIZATION OF HEAVY METAL RESISTANT
ACINETOBACTER SP. AND ITS POTENTIAL FOR CU BIOSORPTION**

Maryam Ashrafi gerdeh¹, Maryam Ghane²

1. M.Sc of Microbiology, Islamic Azad University Islamshahr Branch, Tehran, Iran
2. *Assistant Professor of Microbiology, Islamic Azad University Islamshahr Branch, Tehran, Iran.

Background and Aim: Bioremediation is the most efficient and least costly method for treating heavy metal contaminated soils. The aim of this study was isolation of copper (Cu²⁺) resistant bacteria and evaluation of their biosorption capacity

Methods: Screening of resistant strains was carried out in Luria Bertani Agar plate containing 1 mM of copper. The minimum inhibitory concentration (MIC) of Cu²⁺ was investigated by agar dilution method and heavy metal removal carried out by atomic absorption spectroscopy. The selected isolate was identified in accordance with Bergey's Manual of Systematic Bacteriology. Phylogenetic analysis was performed based on 16S rRNA gene sequences

Results: In this study a gram negative, non-motile short rod-shaped and heavy metal resistant bacterial strain was isolated from industrial effluents. The optimum temperature and pH for the growth of the strain were 33°C and 7, respectively. The MIC of copper was 3 and up to 51% of copper was removed at the Cu²⁺ concentration of 1 mM. The isolate was resistant to ampicillin, cephalotin and gentamicin. Phylogenetic analysis based on 16S rRNA gene sequences indicated that the isolate belongs to the genus *Acinetobacter* with 99% similarity to *Acinetobacter junni* isolate OUT-c17; then designated as *Acinetobacter* sp. HM_AF8 (Accession Number: JN600958)

Conclusion: Based on the data obtained in this study, it can be concluded that *Acinetobacter* sp. HM_AF8 can be used for bioremediation of copper from effluents

Keywords: *Acinetobacter* sp. HM_AF8, bioremediation, 16S rRNA, copper removal

**P28 - 704: ISOLATION AND IDENTIFICATION OF CELLULOLYTIC BACTERIA FROM
SOIL AND LEAVES IN KERMAN - IRAN**

Farshid Khosravi¹, Mouj khaleghi ², Hormazd Naghavi ³

1. M.Sc of Microbiology, Department of Biology, Faculty of Science, Shahid Bahonar University of Kerman- Iran- Farshid.khosravi2320@gmail.com
2. Assistant Professor of Microbiology, Department of Biology, Faculty of Science, Shahid Bahonar University of Kerman- Iran
3. Assistant Professor of Microbiology, Department of Soil Science, Kerman Agricultural and Natural Resources Research Center, Kerman- Iran,

Background and Aim: Microbial cellulases benefit tremendously from their high potential into application in various industries including pulp, paper, textile, biofuel production, food, feed industry and agriculture. The present investigation indicates isolation and identification of thermophilic (50°C) and mesophilic (37°C) cellulolytic bacteria from the soil and leaves at Kerman.

Methods: These cellulolytic bacteria were isolated and purified using serial dilution method after that, The medium used for isolation of cellulolytic bacteria contains carboxymethylcellulose (CMC) and filter paper as the sole source of carbon. Screening of purified bacteria was performed in order to identify cellulase-producing bacteria by Congo red test.

Results: Among the cellulolytic strains, 22 mesophilic and 17 thermophilic strains have been selected for biochemical characteristics and Gram staining. These bacteria were compared with each other based on cellulase activity, the percentage of growth and extracellular protein amounts.

Conclusion: In addition, the strains with highest enzyme activity were determined by DNS method. The isolated US-5 and US-7 strains rapidly grew and produced cellulase.

Keywords: Cellulose, Cellulolytic bacteria, Thermophilic bacteria, Cellulase, Carboxymethyl cellulose.

**P29 - 718: STRAIN IMPROVEMENT AND OPTIMIZATION STUDIES FOR ENHANCED
PRODUCTION OF ERYTHROMYCIN IN SACCHAROPOLYSPORA ERYTHRAEA BY UV
MUTAGENESIS**

Narges Falahpoor¹, Hossein Rassi², Esmail Asly³

1. Department of Biology , Karaj Islamic Azad University
2. Department of Biology , Karaj Islamic Azad University
3. Department of Biology , Karaj Islamic Azad University

Background and Aim: *Saccharopolyspora erythraea* is a Gram-positive filamentous bacterium. It is one of the most widely exploited strains for the industrial-scale production of erythromycin A. Over the past 50 years, the *S. erythraea* strain improvement has been carried out mainly by UV mutagenesis.

Methods: In the present study, *S. erythraea* was mutagenized using UV lights and selection by tylosin resistance mutant to improve erythromycin yield. In other sides, to improve the yield of erythromycin in mutant, effects of various parameters such as carbon concentration were analysed.

Results: The high erythromycin producing strains were isolated by Plaque Agar and increase of 87% was observed when colonies of *S. erythraea* were exposed to UV radiation , when compared to wild type strain. For the second step of screening, a mutant strain (RHU233) with a production of 1.39 mg erythromycin per ml was isolated, which was 2 times more productive than the wild type. It was found that glycerol can be used as an alternate carbon source in erythromycin production medium.

Conclusion: These optimized conditions could be used for the commercial production of this unique antibiotic.

Keywords: Strain improvement, production of erythromycin, *Saccharopolyspora erythraea* by UV mutagenesis

**P30 - 725: ISOLATION OF AN UREOLYTIC BACTERIUM FROM HOUSEFLY FOR
IMPROVEMENT OF COMPRESSIVE STRENGTH OF MORTAR**

Mahlagha Sohrabi¹, Gholamreza Zarrini², Masood farzam³

1. Department of Biology, Faculty of Natural sciences, University of Tabriz, Tabriz, Iran
2. Department of Biology, Faculty of Natural sciences, University of Tabriz, Tabriz, Iran
3. Department of Structural Engineering Faculty of Civil Engineering, University of Tabriz, Tabriz, Iran

Background and Aim: Concrete is susceptible to micro crack formation and also it has pores. Water and other deleterious substances can ingress from this micro cracks and pores into concrete. Ureolytic bacteria can fill micro cracks and pores of concrete by production of calcium carbonate and improve its durability. This process is called Microbiologically Induced Calcite Precipitation (MICP). In present study, an ureolytic bacterium was isolated and used to improve compressive strength of concrete.

Methods: Ureolytic bacteria strain was isolated from a housefly by urea-based methods. This bacterium was cultured in TSB medium. The culture is centrifuged after 48h and its medium is removed. Then the bacterial cells with and without urea-calcium lactate solution were added to mortar paste during its preparation. Fresh mortar cubes cured in lime-water and its compressive strength was tested after 7, 14 and 28 days. The bacterial isolate was identified by 16S rRNA gene sequencing analysis.

Results: A spore-forming alkali-resistant ureolytic bacteria strain, TSI15 was isolated from a housefly. Its effect on the mortar was represented that incorporation of TSI15 with urea-calcium lactate solution in mortar matrix, is increased the compressive strength about 40% in comparison with control cubes. TSI15 was identified as *Sporosarcina newyorkensis* having 99 % similarity with *Sporosarcina newyorkensis*, strain R-31323

Conclusion: *Sporosarcina newyorkensis* strain TSI15 with urea and calcium lactate as carbon resource can improves compressive strength of cement-sand mortar and concrete and prolongs their life.

Keywords: Concrete, Compressive Strength of Mortar, ureolytic bacteria

**P31 - 738: PRODUCTION ENHANCEMENT OF EPIDERMAL GROWTH FACTOR (EGF) IN
E. COLI BATCH CULTURE**

Valiollah Babaeipour¹, Mohamad Mehdi Namvaran², Hossein Vahidi³, Firouz Ebrahimi⁴, Fatemeh Abarghoui⁵

1. Malek Ashtar University of Technology
2. Shahid Beheshti University of Medical Sciences
3. Shahid Beheshti University of Medical Sciences
4. Faculty of Basic Sciences, Imam Hossein University
5. Faculty of New Technologies, Shahid Beheshti University of Medical Sciences

Background and Aim: Epidermal Growth Factor (EGF) is a one-chain polypeptide which is produced from different tissue in human. It has a lot of applications in medicine and Pharmaceutical Science. The best way for production of this protein is recombinant DNA technology, fed-batch fermentation process and High cell density culture for E. coli. The optimal expression of EGF in E. coli can be easily achieved when the growth and induction conditions are properly controlled and harmonized.

Methods: It was found that type and amounts of different of media components in both of growth and production phases, induction conditions including induction temperature, cell density in induction time, induction duration, type and amount of inducer) have profound effects on yield and overall productivity of recombinant protein is produced. In this study production of recombinant human EGF was increased by investigation effects of type of media and temperature in induction duration E. coli BL21 (DE3) [pET28a-egf] batch culture. Hence kinetics of recombinant bacteria growth and rhEGF production investigated at three different medium LB, TB and 32Y with different temperatures such as 24, 28, 32 and 37°C.

Results: The maximum rhEGF production was obtained from TB medium at 28°C with IPTG concentration of 0.1mM. The final OD600 and dry cell weight at this condition were 12.2 and 5.61g/L respectively. The maximum amount of rhEGF production was 2.24 g/l.

Conclusion: The produced rhEGF is one of the highest amounts of recombinant proteins which have been reported up to now in shake flask batch culture.

Keywords: Escherichia coli, Epidermal Growth Factor (EGF) , over-expression, medium, induction temperature

**P32 - 749: BIOFIXATION OF CO₂ WITH ISOLATED MICROALGAE IN PHOTOTROPHIC
CONDITION**

Ali Sheykhinejad¹, Sanaz Jafari², Fatemeh Sheykhinejad³

1. Iranian Res Org for Sci & Tech, Tehran
2. IROST
3. IAU

Background and Aim: One of the major green house gases (GHGs) leading to global warming is carbon dioxide. CO₂ makes up 68% of the estimated total greenhouse gas emissions. Microalgal biofixation of carbon dioxide has recently gained renewed interest as a promising strategy for CO₂ mitigation

Methods: Isolated microalgae was batch cultivated and cultures were illuminated with besides cold fluorescent lamps and air was provided from the bottom by applying an air pump. The total mass of carbon fed into the systems was compared to biomass production.

Results: The rate of mixing required careful optimization: when too low, maximal productivity could not be obtained, and high rate of mixing resulted in cell damage and reduced output. This study examines quantitatively the effect of the rate of mixing on biomass productivity of microalgae at different type of mixing with air and carbon dioxide.

Conclusion: This study shows that with gas-sparging used for mixing and CO₂ feeding, efficient resource utilization and carbon recycling require careful design of photobioreactors and confirmed that the range of CO₂ concentration used in the experiments was cost-effective for mass culture

Keywords: Biofixation, CO₂, Microalgae, phototrophic condition

**P33 - 755: ENHANCEMENT OF TYLOSIN PRODUCTION BY TRANSFORMATION OF BLDD
GENE FROM *S. ERYTHRAEA* IN *S. FRADIEA***

Fatemeh Maleki¹, Hossein Rassi², Jalil Vand Yousefi³

1. Department of Biology , Karaj Islamic Azad University
2. Department of Biology , Karaj Islamic Azad University
3. Department of Biology , Karaj Islamic Azad University

Background and Aim: Tylosin is composed of a polyketide lactone substituted with three deoxyhexose sugars that biosynthesized by the *Streptomyces fradiae*. In order to produce tylosin efficiently presumably requires control mechanisms that balance the yields of the constituent metabolic pathways together with switches that allow for temporal regulation of antibiotic production. In other hand, BldD, a global regulatory protein concurrently regulates the synthesis of erythromycin and morphological differentiation and the inactivation of the bldD gene reduced erythromycin production 7-fold in the WT strain of *S. erythraea*. In this study, transformation of bldD gene from *S. erythraea* in *S. fradiae* for enhancement of tylosin .

Methods: bldD of erythromycin biosynthetic genes amplified by gene-specific primers. The PCR product of the bldD gene constructed into T vector and pTG19- bldD plasmid was made. In the next step, protoplasts of the *S. fradiae* were prepared and DNA transformation was performed according to standard procedures.

Results: In total, 123 recombinant colonies isolated in primary screening and then 3 colonies detected increased tylosin production in the fermentation medium.

Conclusion: Finally, recombinant RHBLDD2 with 1.51 mg per ml antibiotics production and increasing of 2-fold compared to wild type were selected.

Keywords: Enhancement of tylosin , bldD gene , *S. fradiae*

**P34 - 798: LACCASE PRODUCTION FROM SUCROSE BY RECOMBINANT YARROWIA
LIPOLYTICA**

Marzie Moradi¹, Farshad Darvishi², Catherine Madzak³, Claude Jolival⁴

1. 1Department of Microbiology, Faculty of Science, University of Maragheh, Maragheh, Iran
2. 1Department of Microbiology, Faculty of Science, University of Maragheh, Maragheh, Iran
3. UMR GMPA, AgroParisTech, INRA, Université Paris-Saclay, 78850 Thiverval-Grignon, France.
4. Sorbonne Universités, UPMC Univ Paris 06, CNRS, Laboratoire de Réactivité de Surface, Paris, France.

Background and Aim: Laccases are multi-copper enzymes that oxidized various aromatic and non-aromatic compounds and have diverse industrial applications from xenobiotic compounds degradation to biofuel production. The aim of this study was to investigate the effect of sucrose as a substrate on the laccase production by a recombinant strain of *Yarrowia lipolytica* in bioreactor

Methods: A batch culture of *Y. lipolytica* YL4 in 5 L bioreactor was carried out with 1.5 L of modified PPB medium containing 10% sucrose as a sole carbon source. The yeast cell growth was monitored by direct counting method on a haemocytometer. Laccase activity was determined spectrophotometrically by monitoring ABTS oxidation at 420 nm.

Results: The laccase activity reached to 6.7 U/mL in bioreactor with modified PPB medium after 48 h which is 33.5 fold higher than PPB medium containing 2% glucose in the previous studies.

Conclusion: Sucrose as a cost-effective and sole carbon source could be used to large scale production of laccase and other recombinant protein by *Y. lipolytica*.

Keywords: Laccase, *Yarrowia lipolytica*, *Trametes versicolor*, Sucrose, Bioreactor.

**P35 - 799: THE USE OF RECOMBINANT LACCASE OF YARROWIA LIPOLYTICA FOR
DECOLORIZATION OF ENVIRONMENTAL POLLUTANT DYES**

Marzie Moradi¹, FarshadDarvishi², Catherine Madzak³, Claude Jolival⁴

1. Department of Microbiology, Faculty of Science, University of Maragheh, Maragheh, Iran.
2. Department of Microbiology, Faculty of Science, University of Maragheh, Maragheh, Iran.
3. UMR GMPA, AgroParisTech, INRA, Université Paris-Saclay, 78850 Thiverval-Grignon, France.
4. Sorbonne Universités, UPMC Univ Paris 06, CNRS, Laboratoire de Réactivité de Surface, Paris, France.

Background and Aim: Laccases have various environmental applications, such as textile dye bleaching, pulp delignification and bioremediation of wastewater. The aim of the study was evaluate the ability of laccase from recombinant *Yarrowia lipolytica* for decolorization of some environmental pollutant dyes.

Methods: The supernatant of *Yarrowia lipolytica* YL4 culture containing laccase was used to decolorization of seven dyes Bromocresol purple, Safranin, Malachite green, Kristal violet, Bromothymol blue, Nigrosine and Phenol red. The maximum absorbance and decolorization of each dye was determined using microtiter plate reader. The effects of pH, concentration of enzyme and incubation time were investigated on decolorization.

Results: The laccase of *Y. lipolytica* YL4 was able to decolorization of dyes. The effect of incubation time was important which decolorization efficiency was reached more than 90 percent after 48 hours.

Conclusion: The laccase of *Y. lipolytica* was able to decolorization of environmental pollutant dyes that could be used to bioremediation of industrial wastewater.

Keywords: Laccase, *Yarrowia lipolytica*, Decolorization, Environmental pollutant dyes.

P36 - 804: SCREENING OF NATIVE MICROALGAE FOR LIPID PRODUCTION

Nafise Dani¹, Davood zare², Mahnaz Mazaheri Assadi³, Neda Soltani⁴, Shiva Irani⁵

1. student at Islamic Azad University Research and Science Branch ,Tehran, Iran
2. Science and Technology (IROST), Tehran, IRAN
3. Science and Technology (IROST), Tehran, IRAN
4. Iranian Academic Center for Education, Culture and Research ACECR, Tehran, IRAN
5. Islamic Azad University Research and Science Branch ,Tehran, Iran

Background and Aim: Finding alternative sources of energy has been attended by many countries as petroleum based fuels are decreasing and environmental pollution is rising, dramatically. The biological fuels, especially biodiesel production using microalgae, as a potential source of renewable energy, has recently been attracted by many investigators. At present study, screening of native microalgae to produce lipid components will be discussed

Methods: Microalgae were 16 species including 14 species collected from Waste paper factories in Kashan and isolated in Iranian Research Organisation for Science and Technology (IROST) along with 2 other species of *Chlorella* sp and *Spirulina* sp which has been received from Iranian Academic Center for Education and IROST as gift, respectively. Cells densities were estimated using cell haemocytometer and UV absorption at 690 nm up to 21 day and specific growth rate were calculated for each species. For estimation of lipid production, cells were harvested at the end of life cycle when UV absorption of samples at 690 nm reached to 2.78×10^6 Cells were centrifuged at $6000 \times g$ and dry biomass was determined. Lipid was extracted according to method of Zang 2009

Results: Among 16 microalgae, *Chlorella vulgaris* showed the highest specific growth rate (0.1?), biomass (1.1 g l⁻¹) and oil (0.114 g l⁻¹) productivity. The amount of oil in *Microcystis*, *Spirulina*, *Nostoc* , *Anabaena* and *Phormidium* was 0.086, 0.1, 0.0625, 0.0223 and 0.008 g l⁻¹ , respectively.

Conclusion: By increasing the worldwide energy consumption, utilizing of fossil fuels has also been risen. Thus, finding renewable sources of energy such as biodiesel is essential

Keywords: Microalgae, Biodiesel, Growth rate , Lipid productivity

P37 - 805: ISOLATION AND MOLECULAR IDENTIFICATION OF LEAD(PB) RESISTANT BACTERIA FROM SEWAGE OF SEVERAL INDUSTRIAL FACTORIES IN ISFAHAN PROVINCE.

Marzieh sadat Mirsafaei¹, Monir Doudi², Bagher Yakhchali³

1. MSc Student in Microbiology, NourDanesh Institute of Higher Education, Meymeh, Isfahan, Iran
2. Assistant Professor, Department of Microbiology, Falavarjan Branch, Islamic Azad University, Falavarjan, Isfahan, Iran. Corresponding: Email: Monirdoudi@yahoo.com OR Doudi@iaufala.ac.ir
3. Associate professor, National Institute of Genetic Engineering and Biotechnology, Tehran, Iran

Background and Aim: Lead is toxic heavy metal that industrial use from that caused widespread contamination in the in the environment. Because of the vast spread of the disease caused by the existence of lead in industrial wastewater, it seems that expulsion of this metal by bioremediation and transposition of this method with other ineffective chemical method, can be an important progress in developing procedure of industrial wastewater systems

Methods: In order to isolate and identify the lead resistant bacteria, sampling of sewage of several industrial factories in Isfahan province was done. The pour plate method was used to count the heterotrophic bacteria. To isolate the lead-resistant bacteria, agar dilution method and PHG II agar medium containing 0.5 mM of the lead were used. Then, the bacteria purification procedure was performed and the minimum inhibitory concentration growth of bacteria was determined for lead at concentrations 1, 2, 4, 8, 16 and 32 mM. Then amount of biosorption of lead by strains that had showed the highest resistance to lead by atomic absorption system was moduled. Molecular identification of the resistant and lead absorbent bacteria was performed by second determination of the 16S rDNA sequence

Results: In this study, 4 lead resistant isolates were identified that among of them *Bacillus subtilis* strain MDYND103 bacteria showed highest levels of resistance and absorbance to lead (MIC=3.5mM)

Conclusion: As regards that the bacteria examined in this study were able to absorb lead in vitro, therefore it seems that they are good candidates for biological removal of lead from contaminated wastewater

Keywords: Heavy metal resistant bacteria, Lead, Industrial wastewater, Molecular identification, MIC

**P38 - 820: IMPROVEMENT OF ACTINOMYCIN PRODUCTION BY TRANSFORMATION OF
DRRA, DRRB , DNRI AND AFSR GENES FROM S. PEUCETIUS IN S. ANTIBIOTICUS BY
PCR CLONING**

Hossein Rassi¹, Behnam Nazari²

1. Department of Biology , Karaj Islamic Azad University
2. National Institute for Agro-Environmental Sciences, Ibaraki, Japan

Background and Aim: Streptomyces peucetius, a microorganism that produces the anticancer drugs doxorubicin and daunorubicin and self-resistance to these antibiotics in S. peucetius is conferred by the drrAB locus that codes for two proteins, DrrA and DrrB. doxorubicin biosynthesis in S. peucetius is regulated by several genes activated transcriptional regulators dnrN, dnrO, dnrI and afsR . Biosynthesis of doxorubicin (DXR) is tightly regulated, limiting its production in Streptomyces peucetius cultures.

Methods: The several genes drrA, drrB , dnrI and afsR genes from S. peucetius from S. peucetius ATCC 27952 were amplified by PCR and cloned into the pTG-19 vector and the constructed plasmids were transformed into S. antibioticus.

Results: The results showed that drrA, drrB , dnrI and afsR genes was transformed correctly. After confirming recombinant, white colonies were selected and the desired gene was isolated. The recombinant strains produced more actinomycin than the parental strain, when dnrI and afsR genes introduced in S. antibioticus but not in introduce drrA, drrB and plasmids.

Conclusion: DnrI activator protein binds to promoter elements of biosynthetic and resistance genes to turn them on.

Keywords: actinomycin production , dnrI and afsR genes ,S. peucetius and PCR cloning

**P39 - 842: PRODUCTION OF CLAVULANIC ACID BY STREPTOMYCES CLAVULIGERUS
WITH USING NATIVE NITROGEN SOURCE RAPESEED MEAL BY MICROBIAL
FERMENTATION METHOD**

Ramin Shahrad¹, Saeed Akbarzadeh Kolahi², Fahimeh Nemati³

1. Department of Microbiology , Faculty of Advanced Sciences & Technology , pharmaceutical Sciences Branch, Islamic Azad University , Tehran - Iran (IAUPS)
2. Department of Microbiology , Faculty of Advanced Sciences & Technology , pharmaceutical Sciences Branch, Islamic Azad University , Tehran - Iran (IAUPS)
3. Department of Biotechnology , Faculty of Advanced Sciences & Technology , pharmaceutical Sciences Branch, Islamic Azad University , Tehran - Iran (IAUPS)

Background and Aim:Clavulanic acid, is one betalactamase inhibitor ,which produced by Streptomyces Clavuligerus. This product plays an important role in the production of Amoxiclav. In fermentation nitrogen substrate which is one of the main components and expensive parts of this production stage. Therefore, the use of nitrogen sources with acceptable efficiency and being native is important within the industry.

Methods:In this study, for the production of Clavulanic Acid, the strains of Streptomyces Clavuligerus PTCC 1705 is used in the Microbial fermentation method and rapeseed nitrogen source is used instead of soybean flour. Samples containing spore suspension in seeding medium is kept for two days in the seeding medium, in a shaker incubator at 200 rpm and at the constant temperature of 28 ° C and then after choosing the best sample, and inoculating the fermentation medium and replacing the nitrogen source with rapeseed meal it will remain incubated in the shaker for 9 days at 200 rpm and a constant temperature of 28 ° C. In the specified days, using the above mentioned method, the PH , PMW and morphology is measured and the amount of Clavulanic Acid produced observed with Spectrophotometry and HPLC

Results:The sample with the highest amount of Clavulanic Acid containing 25 gr/L of Rapeseed meal was produced on the eighth day.

Conclusion:Considering the price of Rapeseed meal in comparison with that of soybean flour, and having almost same results in the amount produced, it seems to be a suitable alternative as a replacement for Nitrogen source.

Keywords:Rapeseed (canola) meal, Beta-lactamase inhibitors, Clavulanic Acid, Streptomyces Clavuligerus.

P40 - 864: OPTIMIZATION OF SACCHAROMYCES CEREVISIAE FOR TOLERANCE OF FURFURAL DENSITY BY IMMOBILIZATION IN ALGINATE-CHITOSAN MICROCAPSULE.

Parmida Gerami¹, Azadeh Tofighi², Arash Asadirad³

1. Departments of Microbiology, Zanzan Branch, Islamic Azad University
2. Science and Research Branch, Islamic Azad University, Tehran, Iran
3. Zanzan Branch, Islamic Azad University, Zanzan, iran

Background and Aim: Over the last few decades, the negative impacts of fossil fuel on the environment is one of the main causes of global warming, the progressive demand for energy and the inevitable depletion of the world's energy supply creates a need for a new source of energy such as bioethanol from lignocellulosic waste by yeast. One of the main problems during the hydrolysis is produce compounds like furfural, that have negative impact on the cell viability. In this study by immobilization technic solved the problem.

Methods: In this study, *Saccharomyces cerevisiae* strain (F19) was obtained from the university of Tehran. Immobilization in alginate and chitosan was conducted by using the dropping method in calcium chloride in three size. Chemical stress was 3 g/L furfural. Ethanol quantification were determined via HPLC method, Glucose concentration was measured by enzymatic method (kit D-Glucose.parsazmoon) and the cell mass was adjusted by standard diagram and optical density.

Results: The most optimal efficiency in the production of ethanol and consumed sugar, infusing (3g/L) furfural, was related to the manner of immobilized zymogenic cell in mixed matrix of alginate and chitosan at the size of large beads which was 12.69% higher than free cell.

Conclusion: We can conclude based on our findings, that immobilization can increase the efficiency of ethanol production under chemical tension more than free cell.

Keywords: *Saccharomyces cerevisiae*, immobilization, alginate, chitosan

**P41 - 903: ISOLATION OF PROTEASE PRODUCING MODERATELY HALOPHILIC
BACTERIA FROM SALINE SOIL**

Nilufar Ghorbani¹, Maryam Ghane²

1. M.Sc of Microbiology, Islamic Azad University Islamshahr Branch, Tehran, Iran
2. Assistant Professor of Microbiology, Islamic Azad University Islamshahr Branch, Tehran, Iran.

Background and Aim: Halophiles are excellent source of enzymes that are not only salt stable, but also can withstand and carry out reactions efficiently under extreme conditions. Moderately halophilic microorganisms are able to grow in media containing a wide range of elevated NaCl concentrations (3-15% NaCl). Considerable attention has been focused on enzymes of moderately halophilic bacteria, since they have substantial biotechnological potential. The aim of this study was isolation of moderately halophilic bacteria from saline soil which are capable of producing protease.

Methods: Soil samples were collected from Saline soil in Karaj, Alborz province, Iran. Halophilic bacteria were isolated by serial dilution method in saline nutrient agar plate (containing 10% NaCl). Proteolytic activity was screened in a saline skim milk. Protease activity was assessed through in vitro colorimetric assays for general proteases. Identification of isolates was carried out by biochemical and physiological assays.

Results: In the preliminary screening, 10 isolates exhibited proteolytic activity on saline skim milk agar plates. The optimum temperature for growth of the isolates were 35-37 °C. The isolates were able to grow in media containing 3- 15 % NaCl and optimum pH for growth was 7.5- 9.5. All the isolates exhibited protease activity. Among the isolates, strain C17 exhibited highest protease activity with 0.3 unit/mL of supernatant.

Conclusion: The results of this study indicate that moderately halophilic strain C17 could display potential role in protease production.

Keywords: moderately halophilic, protease, halophilic enzymes.

**P42 - 904: ISOLATION OF AMYLASE PRODUCING HALOPHILIC BACTERIA FROM
SEDIMENTS OF SALINE RIVER IN ESHTEHARD**

Mojgan Saryazdi¹, maryam ghane²

1. 1 M.Sc of Microbiology, Islamic Azad University Islamshahr Branch, Tehran, Iran
2. 2*Assistant Professor of Microbiology, Islamic Azad University Islamshahr Branch, Tehran, Iran.

Background and Aim: Halophilic microorganisms are a potential source of enzymes which are capable of functioning under high concentration of salt, wide range of pH value and temperature at which other proteins will usually precipitate or denature. The objective of present study was isolation of moderately halophilic bacteria from sediments of Saline River which are capable of producing amylase.

Methods: Sediment samples were collected from Saline River in Eshtehard, Alborz province, Iran. Halophilic bacteria were isolated by serial dilution method in saline nutrient agar plates (containing 10% NaCl). Amylolytic activity was screened on saline nutrient agar plate with 1% starch. Amylase activity was assessed through in vitro colorimetric assays for amylase. Identification of the isolates was carried out by biochemical and physiological assays.

Results: In this study 10 bacterial strains exhibited amylase activity on saline starch nutrient agar. The optimum temperature for growth of the isolates were 35-45 °C. The isolates were able to grow in media containing 3- 15 % NaCl and optimum pH for growth was 8- 9.5. All the isolates exhibited amylase activity. Among the isolates, strain L17 exhibited highest amylase activity. Strain L17 was a gram positive rod, catalase positive, indole and VP negative. It produced acid from glucose and was able to hydrolyse casein and starch. The results from biochemical tests identified strain L17 as bacillus sp.

Conclusion: The results of this study indicate that moderately halophilic strain L17 could display potential role in amylase production.

Keywords: halophilic bacteria, amylase, halophilic enzymes.

**P43 - 914: ISOLATION OF DIFFERENT RHIZOBACTERIA FROM RHIZOSPHERIC SOILS
WITH DIFFERENT PLANT GROWTH PROMOTING TRAITS**

Fakhreh Sharifi¹, Farokh Rokhbakhsh-Zamin ², Seyed Mohamadreza Khoshroo ³

1. : Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
2. : Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
3. : Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.

Background and Aim: The rhizosphere zone has been defined as the volume of soil directly influenced by the presence of living plant roots or soil compartment influenced by the root. Plant growth promoting rhizobacteria (PGPR) are a group of bacteria that can be found in the rhizosphere, in association with roots which can enhance the growth of plant directly or indirectly.

Methods: In the present study, six rhizospheric soil samples were collected from farms of Kerman in Iran. A total of 43 rhizobacteria were isolated and in vitro screening tests were performed for different plant growth promoting traits such as phosphate and zinc oxide solubilization, nitrogen fixation, Nitrate reduction, Ammonia production.

Results: In the present work, seven bacterial isolates were positive for phosphate solubilization. Nitrogen fixation was shown by almost all the bacterial isolates. Three isolates were positive for zinc oxide solubilization. Seven isolates were positive for ammonia production and Nitrate reduction. Seven isolates were found to be Phosphatase positive. Ability to grow in pH between 4 and 9, 9% salt resistance, ability to withstand heat up to 40 ° C was shown by 13 isolates. Seven isolates were showing maximum plant growth promotion activities.

Conclusion: According to the results, these isolates with good in vitro traits may be utilized for biofertilizer formulation under local agro-climatic conditions of warm and dry areas of Iran.

Keywords: phosphate and zinc oxide solubilization, nitrogen fixation, Nitrate reduction, Ammonia production.

**P44 - 925: COMPARATIVE PROTEASE ACTIVITY OF ARCHANGIUM GEPHYRA UTM C
4007 WITH OTHER POTENT SERINE PROTEASE PRODUCERS**

Nasim Roohi zohrab¹, Fatemeh Mohamadipanah²

1. 1Department of Microbial Biotechnology, School of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran.
2. 1Department of Microbial Biotechnology, School of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran.

Background and Aim: Bacterial proteases have attracted more attentions in recent years due to the growing demand in food, pharmaceuticals, bioremediation, biotransformation, and detergent industry. Myxobacteria are gram-negative bacteria with extraordinary ability to produce novel classes of natural products. They produce several exoenzymes to lyse different biological macromolecules. In this study, we quantitatively compared the protease activity of serine protease from three representatives of Myxobacteria (*Archangium gephyra* UTM C 4007), Actinobacteria (*Nocardiopsis arvandica* UTM C 1492) and Bacillus members (*Bacillus cereus* UTM C 2390) which are current source of most commercial protease.

Methods: Qualitative assessment of protease activity was performed by evaluation of skim milk hydrolysis. The diameter of clearing zones were measured after 24h hour incubation. Protease activity was determined by monitoring the increase in absorbance at 450 nm of a reaction mixture containing 3% azocasein as the substrate.

Results: All representatives showed relatively the same protease activity in qualitative assessment with slightly higher clear zone which was observed for *Bacillus cereus* (13mm that followed by *Archangium gephyra* and *Nocardiopsis arvandica* with 11mm and 10mm respectively). In qualitative assessment, azocasein hydrolysis by *Archangium gephyra* was 0.683Unit, higher than *Nocardiopsis arvandica* with enzyme activity of 0.539Unit while *Bacillus cereus* showed azocaseinase activity of 0.932Unit.

Conclusion: This study showed that other than classic *Bacillus* strains, other resource of serine protease including Myxobacteria or Actinobacteria have rather the same potency. This study introduces *Archangium gephyra* as a non-conventional source of highly active serine protease which can be evaluated in further studies to find applications in biotechnology.

Keywords: Protease activity, *Archangium gephyra*, Actinobacteria, *Bacillus*

**P45 - 930: INFLUENCE OF PERMEABILITY OF MICROBIAL CELLS ON THEBAINE
BIOTRANSFORMATION**

Nazanin Ataee¹, Jamshid Fooladi², Mohammad Hasan Namaei³, Fateme Mirzajani⁴

1. Department of Microbiology, The faculty of Biological Science, Alzahra University, Vanak, Tehran, Iran. ataee1357@yahoo.com
2. Department of Biotechnology, The faculty of Biological Science, Alzahra University, Vanak, Tehran
3. Birjand Hepatitis Research Center, Birjand University of Medical Sciences, Ghafary Ave., Birjand, Iran
4. Department of Biotechnology, The Faculty of New Technologies Engineering (NTE), ShahidBeheshti University, G.C., Tehran, Iran. Department of Nanobiotechnology, Protein Research Center (PRC), ShahidBeheshti University, G.C., Tehran, Iran.

Background and Aim: The main goal of this work was to study the effect of antibiotics on changing the permeability for thebaine biotransformation activity of native *Bacillus*.

Methods: Kirby-Bauer method is used to determine the effects of nine antibiotics (ceftazidime, cephalothin, penicillin, ceftizoxime, cefixim, doxycycline, ampicillin, cefotaxime and cephalixin) on the growth rate of *Bacillus*. The zones around antibiotic disks were measured and one antibiotic was selected for permeability of cell wall integrity. The whole cells were produced in complex medium and at the late logarithmic phase the antibiotic was added then biomass harvested in early stationary phase. Biotransformation tests were designed in buffer medium supplemented with thebaine as a precursor. Biotransformation products were extracted with 68% (v/v) acetonitrile and monitored by HPLC method.

Results: This strain is sensitive to eight antibiotics and clear rings were more than 25 mm except penicillin which the zone of inhibition was 13mm. The biomass weight in the sample with penicillin in low dose was as the same as the sample without penicillin (control cells). But the growth rate of cells was suppressed by penicillin in high dose and the biomass weight was decreased in this sample. It was shown that the sample without penicillin was produced codeine and morphine in the biotransformation process. But no production obtained with the treated cells with penicillin. Maybe the permeable cells could not accumulate thebaine in the cells for biotransformation.

Conclusion: It can be concluded that penicillin was not only effective on biotransformation but also it caused to cease this process and no production obtained.

Keywords: Thebaine, Biotransformation, *Bacillus*, penicillin

**P46 - 961: ISOLATION AND IDENTIFICATION OF PHOSPHATE SOLUBILIZING
RHIZOBACTERIA WITH PLANT GROWTH PROMOTING ACTIVITIES**

Zohreh Parvan¹, Farokh Rokhbakhsh-Zamin ², seyed Mohamadreza khoshroo ³

1. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
2. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
3. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.

Background and Aim: Harmful effects of chemical phosphate fertilizers on human health and environment highlight the role of biofertilizers. Phosphorus is one of the most important macro nutrient required for plant growth but it has limited availability in soil. Some of the soil bacteria named as phosphate solubilizing rhizobacteria able to dissolve inorganic phosphate during their metabolic processes, directly and indirectly. The aim of this study was isolation and identification of phosphate solubilizing rhizobacteria from soil samples collected from a farm in Kerman, Iran

Methods: Bacterial strains were isolated from the saline soil of Kerman district, Kerman, after serial dilution of soil solution on nutrient agar. Isolates were identified by their colony characteristics, spore morphology and microscopic observations. The isolates were studied for phosphate solubilizing ability on Sperber medium. Clear zone Presence around the colonies was detected and the storage of selective bacterial was done by using glycerol stock solution method.

Results: From 100 isolated rhizobacteria at the first part, 40 could produce clear zone on the Sperber agar plates after one week

Conclusion: In conclusion, screening of rhizobacteria from rhizosphere of different plants helped in the selection of various phosphate-solubilizing organisms. Ammonia, catalase enzyme producers are superior strains for use as possible bio-inoculants and have the potential to increase the available phosphate in the soil, which in turn will help to minimize the P-fertilizer application, reduce environmental pollution, promote sustainable agriculture and increase yields of agricultural plants in Kerman and other regions of Iran. Field trials with selected strains from this study are now planned.

Keywords: phosphate solubilizing bacteria, rhizobacteria, Biofertilizer.

**P47 - 983: THE ISOLATION AND IDENTIFICATION OF PANTOEA COFFEIPHILA
ASSOCIATED WITH SUMMER SQUASH WATER-SOAKED SYMPTOM IN IRAN**

Parisa Emamy¹, J. Hayati², M. Mehrabi-Koushki³

1. M.Sc. Student of plant pathology
2. Associate Professor of plant pathology
3. Assistant Professor of plant pathology

Background and Aim: Summer squash (*Cucurbita pepo*) grows in warm climates including Khuzestan province. During 2014 and 2015, the summer squash water-soaked samples were collected from squash fields of Dezful.

Methods: Small slices of summer squash were cut from the boarder of healthy and infected parts and surface-sterilized. Plant slices were crushed in peptone water and inoculated on nutrient agar (NA) plates by streaking. A colony that had the dominant population in most samples caused symptoms of hypersensitive response on geranium leaf and were selected for more characterization. This isolate was gram-negative, oxidase-negative and facultative anaerobic. This isolate not be also able to rot potato tuber slices, to produce fluorescence on KING'S B medium (KB) and to hydrolyze tween 80. A colony from purified culture was inoculated to a tube containing 7 ml LB liquid medium and incubated at 28°C on a rotary shaker incubator at 200 rpm for 24 hours. Bacterial cells were harvested in centrifuge tubes and their DNA was extracted by alkaline lysis method and using lysozyme.

Results: Polymerase chain reaction was performed using universal primer pairs of 27F and 1492R which amplify 1500bp from 16srRNA region. Amplified fragments was purified and then sequenced. The sequences were edited and assembled and deposited in NCBI under GenBank accession number KX266886. The consensus 16S rDNA sequence showed a 99% of sequence identity to type strain of *Pantoea coffeiphila* Ca04 (KJ427829).

Conclusion: To our knowledge, this is the first report of *P. coffeiphila* from Iran.

Keywords: pathogen, *Pantoea coffeiphila*, summer squash, 16s rRNA.

**P48 - 988: THE ISOLATION AND IDENTIFICATION OF ENDOPHYTIC BACTERIUM,
ENTEROBACTER ASBURIAE, FROM CACTUS IN IRAN**

Parisa Emamy¹, J. Hayati², M. Mehrabi-Koushki³

1. M.Sc. Student of plant pathology
2. Associate Professor of plant pathology
3. Assistant Professor of plant pathology

Background and Aim: Endophytic bacteria are between saprophytic and phyto-pathogenic bacteria. In order to detect and identify endophytic bacteria on cactus (*Stetsonia coryn*), during 2015 and 2016, cactus samples were collected in paper bags from several greenhouse of Ahvaz Township.

Methods: To isolate bacteria, the parts of plants were surface-sterilized in sodium hypochlorite 1% for two minutes, and then washed two times by sterilized distilled water. Plant slices were placed in peptone water for 20 minutes and inoculated on nutrient agar (NA) plates. The bacterial colonies were creamy and metallic green color on NA and EMB culture media, respectively. The isolated bacteria were gram-negative, oxidase-negative, catalase-positive, facultative anaerobic and motile. The hypersensitive response was positive on *Geranium* but the isolates were not virulent. For molecular identification, the bacterial colony was inoculated into a tube containing 7 ml LB liquid medium and incubated at 28°C on a rotary shaker incubator at 200 rpm for 24 hours. Bacterial cells were harvested in centrifuge tubes and their DNA was extracted by alkaline lysis method and using lysozyme. Polymerase chain reaction was performed using universal primer pairs of 27F and 1492R for amplification of 1500bp from 16srRNA region.

Results: Amplified fragments were purified and then sequenced. One of the sequences were edited, assembled and deposited in GenBank (KX267850). The consensus 16S rDNA sequence showed a 99% of sequence identity to type strain of *Enterobacter asburiae* ATCC 35953 (CP011863).

Conclusion: To our knowledge, this is the first report of *E. asburiae* as endophyte from Iran.

Keywords: Endophytic bacteria, Cactus, *Enterobacter asburiae*

P49 - 1006: IN VITRO PLANT GROWTH PROMOTING ACTIVITIES OF PHOSPHATE AND ZINC SOLUBILIZING RHIZOBACTERIA ISOLATED FROM A FIELD IN KERMAN, IRAN.

Nooshin Jalali rigi¹, Farokh Rokhbakhsh-Zamin - Corresponding², Seyed Mohamadreza Khoshroo³

1. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
2. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
3. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.

Background and Aim: Plant growth promoting rhizobacteria (PGPR) accounts for about 2-5% of total the rhizobacteria involved in plant growth promotion and especially under stress conditions. Phosphate solubilization, biological nitrogen fixation, improvement of plant nutrients uptake are some of the regulators that profoundly influence plant growth. In this study, tracking rhizobacteria with nitrogen-fixing properties mostly was followed.

Methods: In this study, 40 isolates from some fields in Kerman were isolated for finding nitrogen fixer rhizobacteria. Phosphate and zinc solubilization tests, reduction of nitrate, cellulase production as well as type of hemolysis and DNase activities were checked.

Results: Three isolates as n29-n34-n37 had the ability to fix nitrogen and phosphate solubilization but only n34 had the ability to solubilize zinc oxide. Nitrate reduction test results were positive for all three mentioned strains. Two isolates n37-n39 were cellulase producers. Hemolysis of all three items was negative but DNase about n34-n37 was positive.

Conclusion: According to the results about n29 strain, it may be used as a new bio-fertilizer if further additional In vivo tests will be performed.

Keywords: PGPR, nitrogen fixers, Phosphate and zinc solubilizer, Hemolysis, DNase

**P50 - 1018: SCREENING SALT ADAPTED PLANT GROWTH PROMOTING
RHIZOBACTERIA FROM AGRICULTURAL FIELDS IN KERMAN, IRAN**

Vali Riazi¹, Farokh Rokhbakhsh-Zamin ², Seyed Mohamadreza Khoshroo ³

1. : Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
2. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
3. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.

Background and Aim:Phosphorus is one of the most important nutrients for plants with limited amounts in the soil. The importance of rhizospheric bacterial phosphate solubilization has been well explained recently. However, the performance of these rhizobacteria is greatly affected by various environmental stresses such as salt stress. In this study, phosphate solubilizing rhizobacteria with salt tolerance were isolated from rhizospheric soils and identified by morphological and biochemical tests.

Methods:Rhizospheric soil samples were collected from agricultural fields in Kerman. Samples were added in Thompson's broth medium. After seven days at 30oC of incubation in this medium, subculturing with serial dilution method was performed on luria agar for obtaining single cell colonies. Phosphate solubilizing bacteria were screened on the basis of their phosphate solubilization on sperber agar medium and strains with high ability were then tested against wide range of salt stresses.

Results:After several subculturing tests of soil samples on luria agar, 54 rhizobacteria were isolated. Phosphate and zinc solubilization test was performed by using sperber medium and test plates were placed in 30oC for seven days. Most of the rhizobacteria could grow on the plates containing phosphate and about half of them could solubilize the phosphate and it can be observed via halo around rhizobacterial colonies and accordingly solubilization efficiencies were calculated. Among the isolated rhizobacteria, only one isolate could solubilize zinc oxide.

Conclusion:Results suggest that selected PGPR isolated from agricultural fields were able to regenerate the saline lands and maximize agricultural benefits. Some additional In vivo tests are going now for final confirmation.

Keywords:PGPR-phosphate dissolution test-zinc dissolution test-salt resistant rhizobacteria

P51 - 1069: STUDYING THE EFFECT OF AERATION ON GROWTH AND DECOMPOSITION OF MINERAL SULFUR COMPOUNDS BY ISOB 14 A NEW BACTERIA ISOLATED

Fatemeh Nazari¹, Mohammad-Esmaeel Kafayati ², Jamshid Raheb³

1. National Institute of Genetic Engineering and Biotechnology (NIGEB)
2. Amirkabir University of Technology
3. National Institute of Genetic Engineering and Biotechnology (NIGEB)

Background and Aim:Applying of efficient and effective sulfur oxidizing bacteria, is the best way to biological remove of harmful sulfur compounds that have origins in natural and caused by different industries. Some of the main factors affecting the process of oxidation of sulfur compounds, were included type of medium, amount of inoculum and aeration, pH and temperature. In this project, was studied the effects of aeration on the growth and decomposition of inorganic sulfur compounds by ISOB 14 (Iranian Sulfur Oxidizing Bacteria) isolated bacteria.

Methods:At first was proceeded to sampling, enrichment, isolation and purification of appropriate strain and then morphological, biochemical, physiological and genetic identification of bacterium was performed. After investigations, ISOB 14, was cultured in mineral medium containing trace elements, in temperature of 30°C, pH 6.6 and 120, 150 and 180rpm aeration speed of shaker incubator for 5 days and then growth and inorganic sulfur compounds oxidation of bacteria evaluated with using of the optical density of bacteria in 400 and 600 and ion chromatography respectively.

Results:The results of this study showed that ISOB 14, was had the highest growth at 180rpm aeration speed. In this amount of aeration, this strain was oxidized thiosulfate completely as an electron donor and production of sulfate amount of 5500ppm.

Conclusion:According to the studies of this project, ISOB 14 is a chemolithoautotrophic strain with high potential for degradation and removal of mineral sulfur compounds for its utilization in industrial process.

Keywords: Sulfur oxidizing bacteria, biological remove, aeration speed, ISOB 14

P52 - 1088: THE MEDIUM PH AND TEMPERATURE OPTIMIZATION OF ISOB 14 A NEW BACTERIA ISOLATED

Fatemeh Nazari¹, Jamshid Raheb², Mohammad-Esmaeel Kafayati³

1. National Institute of Genetic Engineering and Biotechnology (NIGEB)
2. National Institute of Genetic Engineering and Biotechnology (NIGEB)
3. Amirkabir University of Technology

Background and Aim: Decomposition and removal of inorganic sulfur compounds, one of the major issues is the case study for researchers because of several environmental problems, such as acid rain, etc. In the biological methods was used of SOB (Sulfur Oxidizing Bacteria). Among the important factors affecting on growth and decomposition of inorganic sulfur compounds, can be noted to pH and temperature of the medium. The aim of this project was the optimization of these factors.

Methods: In this study, sampling, isolation and identification of bacteria capable for mineral sulfur compounds oxidation was performed from Iranian petrochemical. And then was proceeding to the medium temperature and pH optimization of isolated bacteria. ISOB 14 (Iranian Sulfur Oxidizing Bacteria) were cultured at various pH 6.6, 6.8 and 7, temperatures 26, 28 and 30°C at 150 rpm for 5 days in the shaker incubator to evaluated growth by optical density of bacteria in 400 and 600nm and degradation of sulfur compounds by ion chromatography.

Results: The results of this study showed that ISOB 14, isolated bacteria was had the highest growth at pH 6.6 and 30°C and after 24 hours was abled to degradation of thiosulfate completely and 6000ppm sulfate, is formed in the medium of bacteria.

Conclusion: According to the results and the conducted studies by other researchers was seemed that ISOB 14 is a very efficient strain in analysis of inorganic sulfur compounds. This strain has the ability to use it in the process of removal of inorganic sulfur compounds, particularly hydrogen sulfide from petrochemical industry.

Keywords: inorganic sulfur compounds, ISOB 14, degradation, optimization

**P53 - 1089: INVESTIGATION OF DIFFERENT SALINITY EFFECTS ON THE BIOMASS
PRODUCTION OF SPIRULINA PLATENSIS**

Fatemeh Yaghoobizadeh¹

1. Shahid Chamran University of Ahwaz

Background and Aim: Spirulina is a spiral microalga in size from 0.2 to 0.3mm. It has a unique ability of growing naturally in some alkaline lakes, in both tropical and subtropical parts of the world. Spirulina can be cultivated and grown in both freshwater and seawater medium. Adaptation to salinity and temperature are vital to the cultivation of Spirulina.

Methods: It is verified that various physiochemical composition of growth medium have effects on biomass production of microalgae. Therefore, in this study, salinity was selected for study of its capability on enhance the growth of *S. platensis*. For this purpose, Zarrouk's medium supplemented with various concentrations of NaCl (i.e. 0.5g/L, 1g/L, 3g/L and 8g/L). After inoculation, samples were withdrawn in predefined intervals. The growth was determined using measurement of OD550nm and dry weight determination.

Results: After 16days, the obtaining results showed that the 8g/L concentration of NaCl, was support the growth of microalgae more than other salinities.

Conclusion: Spirulina is type of filamentous blue green alga due to the capacity to produce bioactive components such as vitamins, minerals, polyunsaturated fatty acid, carotenes, and other pigments that have an antioxidant activity. Proteins (60%-70%), vitamins, essential amino acid, minerals and essential fatty acid such as palmitic acid, linolenic acid and linoleic acid are produced by Spirulina. For these reasons, it is very helpful to optimization its growth conditions by the purpose of increasing the biomass production.

Keywords: Salinity, growth, spirulina

**P54 - 1090: NITROGEN FIXATION AND PHOSPHATE SOLUBILIZATION BY A
RHIZOBACTERIUM STRAIN IAU3001 ISOLATED FROM A FIELD IN KERMAN, IRAN.**

Elnaz Molaie¹, Farokh Rokhbakhsh-Zamin², Seyed Mohamadreza Khoshroo³

1. : Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
2. : Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
3. : Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.

Background and Aim: Atmospheric nitrogen is unavailable to the plants. Some plant growth promoting rhizobacteria have the ability to fix atmospheric nitrogen and provide it to plants. Phosphorus is the second most important nutrient for plants, after nitrogen. Different bacterial species particularly some rhizospheric colonizing bacteria have the ability to liberate organic phosphates or to solubilize insoluble inorganic phosphate compounds.

Methods: 35 colonies isolated from rhizospheric soils and their abilities about nitrogen fixation and phosphate solubilization were determined. For nitrogen fixation test, bacteria washed three times with normal saline and each suspension spotted on Burk and Ashby's media. Inoculated plates incubated in 30°C for 24-48 hours and growth of bacteria was observed. In phosphate solubilization, Sperber medium was used. This medium was supplemented with $\text{Ca}_3(\text{PO}_4)_2$ as P source. Inoculated plates by spotting were incubated in 30 °C for 7 days. A clear zone around each spot was considered as the positive evidence of phosphate solubilization. The phosphate solubilization efficiency (SE) was calculated according to the following formula: $\text{SE} = [\text{Halo zone (z)}/\text{Diameter of colonies (n)}]100$.

Results: Isolated IAU3001 strain showed nitrogen fixation with a phosphate solubilization ($\text{SE}=285.71$).

Conclusion: IAU3001 strain had a good ability in nitrogen fixation as well as phosphate solubilization in comparison to the other isolated bacteria. So, it may be good choice for plant growth because nitrogen and phosphorus are two important elements for plants growth and it has good potential to be used as a bioinoculant.

Keywords:: Solubilization of Phosphate and zinc, Plant Growth Promotion, Rhizobacteria

**P55 - 1091: PLANT GROWTH PROMOTING ACTIVITY OF RHIZOBACTERIUM STRAIN
IAUK3001**

Elnaz Molaie¹, Farokh Rokhbakhsh-Zamin², Seyed Mohamadreza Khoshroo³

1. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
2. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
3. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.

Background and Aim: Atmospheric nitrogen is unavailable to the plants. Some plant growth promoting rhizobacteria have the ability to fix atmospheric nitrogen and provide it to plants. Phosphorus is the second most important nutrient for plants, after nitrogen. Different bacterial species particularly some rhizospheric colonizing bacteria have the ability to liberate organic phosphates or to solubilize insoluble inorganic phosphate compounds.

Methods: 35 colonies isolated from rhizospheric soils and their abilities about nitrogen fixation and phosphate solubilization were determined. For nitrogen fixation test, bacteria washed three times with normal saline and each suspension spotted on Burk and Ashby's media. Inoculated plates incubated in 30°C for 24-48 hours and growth of bacteria was observed. In phosphate solubilization, Sperber medium was used. This medium was supplemented with $\text{Ca}_3(\text{PO}_4)_2$ as P source. Inoculated plates by spotting were incubated in 30 °C for 7 days. A clear zone around each spot was considered as the positive evidence of phosphate solubilization. The phosphate solubilization efficiency (SE) was calculated according to the following formula: $\text{SE} = [\text{Halo zone (z)} / \text{Diameter of colonies (n)}] 100$.

Results: Isolated IAUK3001 strain showed nitrogen fixation with a phosphate solubilization ($\text{SE} = 285.71$).

Conclusion: IAUK3001 strain had a good ability in nitrogen fixation as well as phosphate solubilization in comparison to the other isolated bacteria. So, it may be good choice for plant growth because nitrogen and phosphorus are two important elements for plants growth. And it has good potential to be used as a bioinoculant.

Keywords: Solubilization of Phosphate and zinc, Plant Growth Promotion, Rhizobacteria

**P56 - 1110: ISOLATION OF RESISTANT BACTERIA TO SELENATE, COPPER, MERCURY
AND LEAD**

Fatemeh Yaghoobizadeh¹, Mohammad Roayaei Ardekani²

1. Shahid Chamran University of Ahwaz
2. Shahid Chamran University of Ahwaz

Background and Aim: The metals are introduced into the environment during mining, refining of ores, industrial processes and etc.. Unlike other pollutants, heavy metals are getting important because they can't be decomposed by in situ biological means. Therefore it is necessary to remove them from waste waters before discharge due to their harmful effects on environmental quality and human health.

Methods: To isolate the resistant bacteria serial dilutions of wastewater and sludge samples, cultured on mLBA medium supplemented with different concentrations of selenate, copper, lead and mercury, separately. Incubation was done at 30°C for 72hr. Resistance threshold was study by determination of MIC at the range 32.5-1200mM for selenate, 2-64mM for copper, 25-800ppm for mercury and 2-64mM for lead in mLB broth, MBC and disc diffusion methods.

Results: Herein we first isolated 300 bacteria using LBA medium containing different levels of heavy metals. Then using screening methods, 8 more resistant bacteria isolated that MIC for them determined in LB broth medium supplemented with: Se, 1200 and 600 mM; Pb, 16 and 8 mM; Cu, 8 mM and Hg, 400 ppm. More research, including morphological, biochemical, phylogenetical characterization to be continued.

Conclusion: Remediation technologies that are used to cleaning up this pollution are: Physical and chemical methods. But these technologies are expensive, not eco-friendly and usually depending on concentration of waste materials. Therefore in recent decades several approaches considered using microorganisms such as algal, fungal and bacterial biomass.

Keywords: Heavy metal, bacteria, resistance

**P57 - 1210: DETECTION OF PETROLEUM CONTAMINATION USING BIOLOGICAL
SYSTEM BASED ON BIOLUMINESCENCE PRODUCTION BY VIBRIO FISCHERI**

Nafiseh Sadat Naghavi¹, Mahdieh Golgoljam², Faezeh Samiepour³

1. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran,
2. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran,
3. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran,

Background and Aim: Bioluminescence is a biochemical process in which energy in a chemical reaction is released in the form of light. In present study, we used bioluminescence property of *Vibrio fischeri* isolated and identified from Persian gold as a biosensor for detection of low concentrations of petroleum in water.

Methods: Concentrations of 1, 5, 10, 15, 20, 30, 50 and 100 mg/ml white petroleum were added to Marin broth medium. After 24 h incubation in 25°C, light emission was assayed by illuminometer according to control medium which was without petroleum.

Results: The bacterium in control medium emitted light with average of 8 units per second whereas in sample media it was decreased as it was finished in the concentration of 10 mg/ml.

Conclusion: Because of high prevalent of oil recovery and translocation, contamination of water is one of important environmental problems in our country. In the present study we designed a biological system for detection of low amounts of oil contamination in water which can negatively effect on the natural ecosystems as sea water.

Keywords: Bioluminescence, *Vibrio fischeri*, petroleum contamination, Biosensor

P58 - 1222: AMMONIA PRODUCTION AND ZINC SOLUBILIZATION BY IAUK3005 STRAIN RHIZOBACTERIUM ISOLATED FROM A FIELD IN KERMAN, IRAN.

Elnaz Molaie¹, Farokh Rokhbakhsh-Zamin², Seyed Mohamadreza Khoshroo³

1. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
2. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
3. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.

Background and Aim: Nitrogen is an essential element for all plants. Plant growth promoting rhizobacteria (PGPR) have the ability to fix atmospheric nitrogen into ammonia and make it available for plants. The role of Zinc in the nutrition, physiology and especially its importance for activity of many enzymes is widely studied. This insoluble zinc can be reverted back to available soluble form by PGPR.

Methods: Thirty five colonies were isolated from rhizospheric soil and their abilities about ammonia production and Zinc solubilization were determined. Production of ammonia was checked. First, isolates were grown in peptone water at 30°C for 4 days. Then, 1ml of Nessler's reagent was added to each tube. Finally, development of faint yellow color indicated small amounts of ammonia and deep yellow to brownish color showed maximum amount of ammonia production. About zinc solubilization, all isolates were streaked on an agar medium containing zinc oxide and incubated for 6 days at 28°C. Plates were observed for clearing zones around the bacterial colony. The Zinc solubilization efficiency SE = [Halo zone (z)/Diameter of colonies (n)]100.

Results: Isolated IAUK3005 strain showed maximum ammonia production with a Zinc solubilization (SE=187.5). This strain had a good ability in ammonia production as well as Zinc solubilization in comparison the other isolated bacteria.

Conclusion: According to the results, this strain may be a good choice for plant growth. It has good potential to be used as a bioinoculant in the future.

Keywords: PGPR, IAUK3005 strain, Zinc solubilization

**P59 - 1260: THE EFFECT OF PLANT GROWTH PROMOTING RHIZOBACTERIA ON
SEEDLING STAGE OF SUN FLOWER**

Fatemeh Saadatnasri¹, Farokh Rokhbakhsh-Zamin ², Nadia Kazemi-Pour³

1. Affiliation: Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
2. Affiliation: Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
3. Affiliation: Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.

Background and Aim: The dramatic increasing of human population and chemical fertilizer effects on human health has made many attempts to develop biofertilizers. Used rhizobacteria in biofertilizers have several plant growth promoting activities.

Methods: Sampling was performed from rhizospheric soils of different agricultural fields in Kerman. Different bacterial strains were isolated from rhizospheric samples. These isolate were screened in vitro for their plant growth-promoting activities such as solubilization of inorganic phosphate, ammonia (NH₃), catalase. Their resistance to environmental stress was evaluated, too.

Results: 30 rhizobacteria were isolated and they were labeled by the strain numbers as IAUK2301-2330. According to the results of in vitro PGPR tests, 3 strains selected as 2304, 2307 and 2313. All of selected strains were resistant to the different temperatures between 25-42°C, salt concentrations between 5-7 and PH=4-8. Their phosphate solubilization efficiency was recorded as 333.33, 350 and 250 respectively. Pot experiment by these strains was performed and positive meaningful plant growth promoting activities were observed on shoot height, root length and dry weight of sun flower

Conclusion: According to the In vitro as well as in vivo results, three selected rhizobacterial strains may have a good potential for field experiments before usage as the new biofertilizers.

Keywords: Keywords: Phosphate solubilization, Pot experiment, PGPR

**P60 - 1261: EFFECTS OF PHOSPHATE AND ZINC SOLUBILIZING RHIZOBACTERIA ON
TEPARY BEAN**

Fakhereh Sharifi¹, Farokh Rokhbakhsh-Zamin², Seyed Mohamadreza Khoshroo³

1. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
2. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
3. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.

Background and Aim: Phosphate and zinc are essential nutrients required for plants growth. Soils are generally low in Phosphate and zinc readily available for plant growth. Some rhizobacteria are known to be involved in the solubilization of insoluble P and zinc oxide. Applying these bacteria to field soils as the biofertilizer may enhance the growth of plants by solubilizing the insoluble phosphate and zinc.

Methods: 43 bacteria were isolated from the rhizosphere of one agricultural field in Kerman district, and a collection of 13 bacteria were screened for phosphate and zinc oxide solubilization in vitro. Other tests such as nitrogen fixation, Nitrate reduction and ammonia production were performed, too.

Results: In this study, two isolates (IAUTCC2304) and (IAUTCC2307) solubilized both phosphate and zinc oxide. They showed the highest phosphate solubilization as 255.6 mm and 267 mm, respectively. Halo diameter and solubilization zinc oxide efficiency of (IAUTCC2304) and (IAUTCC2307) were 725 mm and 580 mm, respectively. These isolates also were positive for nitrogen fixation, ammonia production and Nitrate reduction. They grew in temperature at 40°C, pH ranging from 4.0 to 9.0 and they were tolerant to NaCl concentration between 4 and 9%. Pot experiment with teparybean was done and the effect of these two isolates was evaluated. Root height, shoot length and dry weight had significant positive changes according to the ANOVA analysis.

Conclusion: According to the results, these isolates have a good potential of teparybean growth promotion especially in the condition of phosphate limitation as well as other adverse factors.

Keywords: phosphate and zinc oxide solubilization, nitrogen fixation, tepary bean, rhizobacteria

Applied Microbiology

P61 - 121: ACTINOMYCETES IN ANTIBIOTICA RESEARCH AT THE HELMHOLTZ CENTRE FOR INFECTION RESEARCH

Joachim Wink¹

1. Helmholtz Centre for Infection Research

Background and Aim: The microbial strain collection of the HZI has its focus on Myxobacteria and other uncommon microorganisms, especially rare Actinobacteria. Our actinobacterial strain collection comprises approximately 3000 strains. About 1000 of these are new isolates from diverse regions and different genera especially of the so called rare groups. Most of these strains have been isolated by the use of uncommon methods or together with partner institutes from many different countries all over the world.

Methods: In the course of an antimicrobial discovery program we prepared crude extracts in standardized procedures and these undergo a routine biological and chemical screening. In addition we are working on the induction of so called “silent genes” within interesting strains to exploit the genetic potential of these organisms. In a so called “oldie approach” we study antibiotics from the early time of antibiotic research which were dropped at this time when they did not fit to the portfolio. Also our group is responsible for the “Compendium of Actinobacteria”, an electronic handbook for biology and secondary metabolites of this bacterial class.

Results: 1. Actinobacteria Novel isolates as source for new antibiotics Development of new isolation methods Establishing of long time cooperations 2. Induction of „silent“ genes 3. Extract Screening „The standard process“ Establishing incubation systems in microtiter format for Actinobacteria 4. „Oldie“ approach 5. Compendium of Actinobacteria

Conclusion: Examples of the actual work in the strain collection are presented in the talk

Keywords: Actinobacteria; Taxonomy; Secondary Metabolites; Antibiotics

P62 - 122: BACTERIAL DEGRADATION OF WASTEWATER CONTAINING CYANIDE AND ITS EVALUATION USING BIOLUMINESCENCE

Ali Asadi¹, Mohseni, M², Chaichi, M.³

1. Department of Molecular and Cell Biology, University of Mazandaran, Babolsar, Iran
2. Department of Molecular and Cell Biology, University of Mazandaran, Babolsar, Iran
3. Department of Analytical Chemistry, University of Mazandaran, Babolsar, Iran

Background and Aim: انسان یک ترکیب سمی و خطرناک برای تمام موجودات زنده است که در مقیاس وسیعی توسط سیانید برای حذف سیانید در فاضلاب های صنعتی است. نیاز به تولید شده و باعث آلودگی محیط زیست می گردد. تجزیه زیستی بهترین روش توسعه روش های بسیار برآورد خطرات ناشی از انتشار مواد آلی و معدنی مضر در محیط زیست منجر به ابزارهای موثر برای تغییرات شدت نورتابی تحت تاثیر مواد سمی است. تجزیه میکروبی سیانید حساس به مواد سمی شده است. اساس سمیت سنجی بر پایه است. پنج جدایه با توانایی تجزیه سیانید به آلوده و سنجش سمیت آن با استفاده از باکتری نورافشان از اهداف پژوهش حاضر در پساب سیانید در محیط حداقل از رسوبات مناطق آلوده جداسازی شد. غنی سازی باکتری های تجزیه کننده عنوان تنها منبع کربن و نیترژن انجام شد. تجزیه سیانید و تولید آمونیاک در محیط کشت با استفاده از روش حاوی ۶/۷ میلی مولار پتاسیم سیانید و در شرایط قلیایی سیانید و افزایش غلظت آمونیاک و نیز رشد باکتری پیکریک اسید و معرف نسلر سنجیده شد. نتایج یک رابطه مستقیم بین کاهش غلظت به علاوه باکتری نورافشان. نشان داد که سیانید در مدت ۷۲ ساعت در ۳۳ درجه سانتی گراد کاملاً تجزیه شد را نشان داد. همچنین نتایج نورتابی باکتری به شدت کاهش یافت قادر به تشخیص غلظت های بسیار پایین سیانید بود و

Methods: حل شده به محیط کشت حداقل غنی سازی باکتری های تجزیه کننده پساب های سیانیدی یک میلی لیتر نمونه خاک برای تنظیم شد 2/9 در NaOH محیط کشت به وسیله pH. سیانید افزوده شد

Results: باکتری

Conclusion: باکتری

Keywords:: سیانید، تجزیه زیستی، سنجش زیستی، بیولوژیست

**P63 - 157: COMPARISON OF PRODUCTION OF HYALURONIC ACID FROM
STREPTOCOCCUS SALIVARIUS SUBSP. THERMOPHILUS AND ISOLATED
STREPTOCOCCUS THERMOPHILUS SAMPLES FROM YOGHURT AND OPTIMIZATION
OF THE GROWTH CONDITIONS**

Diba Tabatabaei¹

1. graduate master of microbiology

Background and Aim: Hyaluronic acid (HA), also known by Hyaluronan. Streptococcus equi . Zoepidemicus is the primary strain for producing HA; However, being pathogenic for humans has led to the restriction of the use of this strain. The necessity for using it, lead to investigate non-pathogenic strains to produce. The most non-pathogenic strain is Streptococcus thermophilus. In this study ,the microbial production of HA and the optimization of culture conditions were investigated

Methods: Streptococcus salvarius sub. thermophilus was prepared from the Bank of Scientific and Industrial Research of Iran (PTCC1738) . To separate Streptococcus thermophilus strains from yogurts, three types of yogurts were used. They were cultured by Pour-plate method on STA medium. To identify the isolated strains, biochemical tests and polymerase chain reaction, were used. Bacterial strains isolated from yoghurts were identified as Streptococcus thermophilus MN-BM-A02, Streptococcus thermophilus JIM8231, Streptococcus thermophilus MN-ZLW- 002 . To separate the capsule strains, each strain was cultured on STB medium, then they were centrifuged. In order to purify the samples, ethanol and charcoal were used. To optimize production, different factors were studied.

Results: Results showed that ,carbon, nitrogen, temperature, pH and types of medium were effective on microbial production of HA.

Conclusion: glucose and fructose, yeast extract, Tryptone, Temperature 50 ° C, pH 6.2, STA-rich medium to increase growth and HA production in each 4-strain was effective.

Keywords: Hyaluronic acid, Streptococcus thermophilus, Optimization of culture, PCR

P64 - 164: PURIFICATION AND EVALUATION OF POLYSACCHARIDE INTERCELLULAR ADHESION (PIA) ANTIGEN FROM STAPHYLOCOCCUS EPIDERMIDIS.

Bahman Mirzaei¹, Seyed Davar Siadat², Seyed fazlollah Moosavi³, Ryhane Babaei⁴, Farzam Vaziri⁵,
Mohammad Shahrooei⁶

1. Department of Microbiology, Microbial research center, Pasteur Institute of Iran, Tehran. Microbiology Research Center (MRC) Pasteur Institute of Iran.
2. Department of Mycobacteriology and pulmonary research center, Pasteur Institute of Iran, Tehran. Microbiology Research Center (MRC) Pasteur Institute of Iran.
3. 2Department of Microbiology, Microbial research center, Pasteur Institute of Iran, Tehran. Microbiology Research Center (MRC) Pasteur Institute of Iran.
4. Department of Microbiology, Microbial research center, Pasteur Institute of Iran, Tehran. Microbiology Research Center (MRC) Pasteur Institute of Iran.
5. Department of Mycobacteriology and pulmonary research center, Pasteur Institute of Iran, Tehran. Microbiology Research Center (MRC) Pasteur Institute of Iran.
6. Laboratory of Medical Microbiology, Department of Medical Diagnostic Sciences, KU Leuven, U.Z. Gasthuisberg, Herestraat 49 CDG 8th floor, B-3000 Leuven, Belgium.

Background and Aim: The polysaccharide intercellular adhesion (PIA), confers major functional effects in biofilm formation, which bear important in pathogenicity of the *Staphylococcus epidermidis*.

Methods: Following the identification of biofilm forming strains by biochemical and molecular methods, isogenic strain was prepared and in vitro biofilm formation assay was performed consequently. By parallel analysis of both PIA positive and PIA negative strains using size exclusion chromatography by Fast Protein Liquid Chromatography (FPLC) method, respective PIA were purified. Recovered polysaccharide intercellular adhesion (PIA) was examined by colorimetric and hemagglutination assay. Finally, recovered PIA was analyzed by using Fourier Transform Infrared spectroscopy (FTIR) and Proton Nuclear Magnetic Resonance spectroscopy (H1- NMR) methods.

Results:. By the parallel purification process and comparison of the obtained graphs from the fast protein liquid chromatography (FPLC) detector, fractions near the void volume were determined as polysaccharide intercellular adhesion. The colorimetric and hemagglutination assays were applied and the content of carbohydrates (Hexose= 620 µg/ml, Hexosamine= 5700 µg/ml and Ketoses= 170 µg/ml) and hemagglutination titer (1: 128). In recovered polysaccharide were determined.

Conclusion: This study shows, polysaccharide intercellular adhesion (PIA) has a significant role in occurrence of the biofilm formation in *Staphylococcus epidermidis* strains. The recovered polysaccharide and its molecular weight analyzed within the near void volume of the utilized column.

Keywords: Polysaccharide Intracellular Adhesion; FPLC; *Staphylococcus epidermidis*; Biofilm formation.

**P65 - 184: STRUCTURAL MINIATURIZATION OF THE EXOTOXIN A OF THE
PSEUDOMONAS FOR IMMUNOTOXINS DEVELOPMENT**

Seyyed ali Hoseinian¹, Aliakbar Haddad-Mashadrizheh², Mohammadreza Saberi³

1. Department of Biology, Science and Research branch, Islamic Azad University, Khorasan Razavi, Neyshabur, Iran
2. Cell and molecular biotechnology research group, institute of biotechnology, and Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
3. Department of Pharmaceutical Chemistry, Faculty of Pharmacy, University of Medical Sciences, Mashhad, Iran

Background and Aim: Exotoxin A of the Pseudomonas (PEA) is a potentially cytotoxic factor for immunotoxins (ITs) designing, via targeting tumor specific antigens as well as inhibition of the protein synthesis. Nonetheless, the molecular size of the factor is a challenge for the penetration of the factor to the solid tumor. So, PEA miniaturization based on the application of the capacity of the enzymatic active domain (domain III) is an approach to overcome this problem. Bearing in mind, the structural stability as well as functional capacity of the domain III was considered in this study compared to the PEA.

Methods: In this regard, 3D structure of the PEA with the ID number: 1IKQ was retrieved from PDB. Discovery Studio 3.0 was used for the domain III separation of the PEA. GROMACS 5.07, containing gromos9643a1 force field were used for simulation in 37°C (310°K), 100ps of the time for NVT and NPT steps and 2000ps for MD step.

Results: The results of this analysis revealed that the RMSD values of the domain III are much less in the most steps compared to the PEA (specifically 5 steps with the RMSD difference = 1). However, the RMSF showed equal values (except for 8 amino acids with the RMSD difference > 1). Moreover, the alignments of the secondary structure of the domain III represented 26 refolding including 10 beta → coil, 2 alpha → coil, 3 turn → coil, 7 coil → beta, 3 coil → alpha and 1 coil → turn.

Conclusion: Overall, the result of the study showed the structural stability of the domain III without any changes in active site. So, it seems that the use of the domain III may lead to maintaining its functionality in the composition of the immunotoxins.

Keywords: Pseudomonas exotoxin A, Domain III, Stability, GROMACS 5.07

**P66 - 185: ISOLATION OF HALOPHILIC BACTERIA PRODUCING ANTIFUNGAL AGENTS
FROM SEMNAN PROVINCES (IRAN)**

Babak Elyasifar¹, Sevda Jafari², Azita Dilmaghani³

1. PhD student, Pharmaceutical Biotechnology, Faculty of Pharmacy, Tabriz University of Medical Sciences, Tabriz, Iran
2. PhD student, Pharmaceutical Biotechnology, Faculty of Pharmacy, Tabriz University of Medical Sciences, Tabriz, Iran
3. Assistant Professor of Pharmaceutical Biotechnology, Faculty of Pharmacy, Tabriz University of Medical Sciences, Tabriz, Iran

Background and Aim: Nowadays, resistance of human fungal pathogens to existent antifungal agents is the most important concern in antimicrobial therapy. Halophilic bacteria are able to become as a novel source of medicinal products such as antimicrobial compounds and antitumor materials. Halophilic bacteria are mostly found in natural environments containing high concentration of NaCl. In Iran, the soils of Semnan deserts also have this potential to be a rich source of halophilic bacteria.

Methods: In this research, eight halophilic bacteria were isolated from the soil of Semnan province. The classes of halophilic bacteria were identified then they were evaluated for production of antimicrobial agent by disk diffusion method. After that, the isolated bacteria were identified by concerning the 16S rRNA sequencing technique.

Results: The results of experiments demonstrated that the isolated bacteria belong to the genus *Halobacillus* and they are mostly moderately halophilic bacteria. Among the isolated bacteria, one of them showed extent antifungal behavior against human pathogeneses of *Candida Albicans*, which is an opportunistic fungus and resistant to existing antifungal agents.

Conclusion: Therefore, developing new antifungal compounds to combat the emerging resistant forms of pathogens are required.

Keywords: Antifungal, halophilic bacteria, antimicrobial therapy

**P67 - 251: MICROCIN TYPING AND EVALUATION OF PROBIOTIC POTENTIAL OF
DIARRHEAGENIC E. COLI**

Sheida Etehad Asnaf¹, DR, Mohamad kargar²

1. Azad University of JAHROM
2. Azad University of JAHROM

Background and Aim: Microcins are miscellaneous group of bacteriocins which are produced by some of *E. coli* species to suppress the growth of other strains of *E. coli*. The capacity of producing microcins increases the virulence capacity of these bacteria. This study aimed to detection, characterization and determining the frequency of microcins coding genes (H47, B17, J25, V, C7 and L) and their inhibitory efficiency on *E. coli* O157:H7.

Methods: In this study, 200 samples of Diarrheagenic *E. coli* were isolated from patients. The biochemical tests were used to verify the presence of *E. coli* in samples. The presence and frequency of microcins in isolated *E. coli* were analyzed using PCR method with 6 pair of microcins specific primers. Moreover, the inhibitory effect of microcins was analyzed using MIC test on Diarrheagenic *E. coli* O157:H7.

Results: Among 200 sample of *E. coli* isolated in this study, the presence of microcins was verified in 108 samples. The most frequent microcins were H47 and microcin V, respectively. The presence of these microcins is related to pathogenicity and virulence of *E. coli* species.

Conclusion: The inhibitory test of microcins on *E. coli* O157:H7 shows that microcin V is the most powerful microcins among the others. Microcins H47 and C7 had low inhibitory effect. The other microcins had not inhibitory effect on *E. coli* O157:H7 and there were no synergic effect between microcins in inhibitory capacity.

Keywords: Diarrheagenic *E. coli*, Microcins, Probiotic

**P68 - 273: CULTURE OPTIMIZATION OF ANTIFUNGAL METABOLITE PRODUCTION IN
THE BACTERIUM BACILLUS LICHENIFORMIS**

Athar Beigi Saki¹, Mehdi Razzaghi-Abyaneh^{*2}

1. 1Department of Biotechnology, Faculty of Advanced Sciences & Technology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran - Iran (IAUPS)
2. 2Department of Mycology, Pasteur Institute of Iran, Thran 13164, Iran

Background and Aim: The bacterium *Bacillus licheniformis*, as an extremophile, is mostly found in soil. It is a good source of antifungal metabolites, so highly used in studying of antifungal drugs processes. It was tested for its antifungal activity against four fungi, *Aspergillus flavus*, *A. fumigatus*, *A. niger* and *Candida albicans*.

Methods:: *Bacillus licheniformis* was cultured in three different liquid media, including Tryptic Soy broth (TSB), Brain-heart infusion (BHI) and Glucose-Yeast extract (GY) at 25°C, 30°C and 35°C, for 24, 48, 72, 96 and 120 hours. Bacterial cell free culture filtrate (BCCF) was tested for antifungal activity by co-culture, disk diffusion and micro bioassay techniques.

Results: The BCCF showed strong antifungal activity against all tested fungi. The best growth media with high amount of antifungal metabolites was TSB, and the optimum temperature and incubation time were 30 °C and 72 hours, accordingly.

Conclusion: Our results indicated that *B. licheniformis* is a potential candidate to produce effective antifungal metabolites against medically important yeasts and moulds depending on time, temperature and culture media compositions.

Keywords: Extremophiles, *Aspergillus fumigatus*, *Aspergillus flavus*, *Aspergillus niger*, *Candida albicans*, Antifungal activity

**P69 - 294: EVALUATION OF THE ISFAHAN COMPOST SAMPLES AFTER PROCESSING IN
TERMS OF COLIFORMS**

Elham Fathi¹, Keivan Beheshti-Maal², Hossein Mirdamadian³

1. Department of Microbiology, Faculty of Biological Sciences, Falavarjan Branch, Islamic Azad University, Isfahan, Iran
2. Department of Microbiology, Faculty of Biological Sciences, Falavarjan Branch, Islamic Azad University, Isfahan, Iran
3. Department of Microbiology, Faculty of Biological Sciences, Falavarjan Branch, Islamic Azad University, Isfahan, Iran

Background and Aim: Composting is an aerobic and natural process in which microorganisms decompose organic material into simple materials. Municipal Waste containing organic materials may include different types of pathogens that are infectious for human, animals and plants. Consequently the contaminated compost could cause health risks during storage, collection, transportation, processing and operation as a fertilizer.

Methods: The EMB culture media were used for primary screening of probable coliforms in the compost. For identification of isolates on EMB, Gram staining and biochemical tests (TSI, IMViC, Urease and SIM) were fulfilled. The MPN test of compost was carried out using lactose broth media in 3 sets of 5 tubes. Then the media were incubated at 35°C overnight and the MPN was measured.

Results: After the cultivation of compost samples on EMB, the small purple colonies with metallic green luster were appeared. The microscopic examinations showed Gram-negative bacilli and coccobacilli bacteria. The biochemical tests confirmed that isolate was related to *Escherichia coli*. The MPN of compost samples in first week of processing was >1600. The MPN of compost samples in the second, third and fourth weeks of processing were 1600, 160 and 17, respectively.

Conclusion: In this research, we isolated and identified the *E. coli* from compost samples of the Isfahan compost processing factory. It showed that the pathogenic bacteria could be present in compost if the composting process was not completed and consequently is resulted in the distribution of pathogenic bacteria through parks and farms.

Keywords: Coliforms, Compost, *Escherichia coli*, MPN, Pathogenic Bacteria

**P70 - 295: ENHANCEMENT OF DEGRADATION ORGANOPHOSPHORUS PESTICIDES BY
INTRASPECIFIC PROTOPLAST FUSION OF NATIVE CITROBACTER BACTERIA
MUTANT STRAINS.**

Mohammad Sadegh Beikverdi¹, Ali Mohammad Latifi², Ardeshtir Hesampour³, Morteza Mirzaei⁴

1. Young Researchers and Elite club, Central Tehran Branch, Islamic Azad University, Tehran, Iran
2. Applied Biotechnology Research Center, Baqiyatallah University of Medical Science, Tehran, Iran.
3. Department of Biology, Faculty of Basic Sciences, Islamic Azad University central Tehran Branch, Tehran, Iran
4. Applied Biotechnology Research Center, Baqiyatallah University of Medical Science, Tehran, Iran.

Background and Aim: Trace amounts of pesticides containing organophosphorus compounds (OPs) have been detected in surface and ground waters, and have caused increasing public and scientific concerns. Ops are acetylcholine esterase inhibitors and have been reported as the third cause of poisoning and the main cause of mortality due to poisoning. Whereas most used chemical and physical methods to decontaminate OPs have many defects and problems, so a safe technology for biodegradation is required. Many microorganisms have been found potent to break down Ops, however, their performance in biodegrading OPs needs to be increased. Considerable successes in studying molecular mechanisms of bacterial mutagenesis induced by various factors have been achieved. Mutant strains were obtained from the acclimatized species by genome shuffling using protoplast fusion.

Methods: Native citrobacter mutated with UV and EthBr was obtained from Applied Biotechnology Center of Baghiyatallah University. Protoplast fusion was done according to Weiss et al and Dai and Copley method: 500cc fresh cells were harvested, washed with Tris HCl 10mM, and resuspended in Tris 0.1M (containing 20% sucrose, lysozyme 40µg/ml, EDTA 0.1 M). Protoplasts were added to regeneration media, the mixture was then centrifuged, resuspended in regeneration media and incubated for 10h at 100rpm at 37 oC. Finally, the sample was inoculated on MSM-agar medium with different concentrations of Diazinon

Results: The mutant cells achieved by protoplast fusion could grow at the maximum concentration of Diazinon (11 g/l).

Conclusion: Consequently, protoplast fusion showed an enhanced function of enzyme compared to native strains and also strains with unknown genome.

Keywords: protoplast fusion, Organophosphorus, Pesticides, Native Citrobacter

**P71 - 296: RELATION BETWEEN ALKANE HYDROXYLASE GENE AND DEGRADATION
OF CRUDE OIL BY SOME MARINE BACTERIA**

Ziba Mehdipour¹, hosseinali Sasan², Mehdi Hassanshahian³

1. Department of Biology, Faculty of Science, Shahid Bahonar University of Kerman- Iran
2. Department of Biology, Faculty of Science, Shahid Bahonar University of Kerman- Iran
3. Department of Biology, Faculty of Science, Shahid Bahonar University of Kerman- Iran

Background and Aim: Today hydrocarbon pollution is the most important environmental problem. Biological methods can play an important role in removing these contaminants to the environment. This study was aimed to isolate aliphatic compounds degrading bacteria and identify the best degrading strain.

Methods: Sampling of waste oil depot took in the city of Kerman, Tehran and hydrocarbon-contaminated soils. Alkane degrading bacteria were isolated by using enrichment Bushnel-Hass medium containing hexadecane (as source carbon). In order to identify superior strains, a part of 16SrDNA gene was amplified by PCR and then sequenced. Also, the presence of alkane's hydroxylase gene in these strains was confirmed by using specific primers.

Results:: A total of fifteen alkane degrading bacteria were isolated which 8 strains were selected as superior strains. These strains belonged to the genus of *Rhodococcus jostii*, *Stenotrophomonas maltophilia* strain M2, *Achromobacter piechaudii*, *Tsukamurella atyrosinosolvens*, *Pseudomonas fluorescens*, *Rhodococcus erythropolis*, *Stenotrophomonas maltophilia* strain Q1, *Pseudomonas aeruginosa*. In this study, the highest growth rate of strains was in concentrations 2.5 percent of hexadecane and the lowest was found in 7 percent. Also, all of the strains have alkane hydroxylase.

Conclusion: Our results indicated that there is a high diversity of degradative bacteria in Iran ecosystem and their ability to degrade petroleum wastewater. So, with a proper management of these bacteria can be used to minimize pollution caused by waste oil industries.

Keywords: Biodegradation, Alkane hydrolase, PCR.

**P72 - 319: CONSTRUCTION OF EXPRESSION PLASMID BASED ON THE ARABINOSE
PROMOTER CAREERING THE IPAB GENE IN THE E.COLI**

Fateme Nasrollahi boroujeni¹, Ali Asqar Deldar²

1. Department of Biotechnology, Malek-Ashtar University of Technology, Tehran , Iran.
2. Department of Biotechnology, Malek-Ashtar University of Technology, Tehran , Iran.

Background and Aim: The virulence plasmid of the Gram negative pathogen *Shigella* generates many virulence factors within the *ipa-mxi-spa* region. *Shigella* spread via fecal-oral and person-to-person transmission which causes human bloody diarrhea. In Asia alone, it is estimated that there are 125 million infections and 14,000 deaths due to shigellosis annually. *IpaB* is an essential virulence factor for the control of T3SS secretion, phagosome escape, and macrophage apoptosis which *IpaB* is essential for *Shigella* infection and pathogenicity.

Methods: Expression plasmid based on the *araBAD* promoter is designed for tight control of background expression and l-arabinose dependent graded expression of the target protein. The genes encoding the *ipaB* and GFP were cloned in *Escherichia coli*. We constructed plasmid expressing a green fluorescent protein from the *araBAD* promoter to quantify expressed gene products during the bacterial cells growth at intermediate induction levels.

Results: We successfully created promoter-reporter plasmids for studying the promoter activity of virulence gene of *Shigella*. The RBS of the virulence factor was used in preparation of this plasmid. We demonstrated that the promoter of *ipaB*-GFP gene was activated when *E.coli* was grown in a LB-broth medium, as evidenced by the expression of GFP in these cells.

Conclusion: we generated *ipaB* and an ampicillin-resistant coding version of *pBAD* with GFP reporter under the control of arabinose-dependent promoters to provide *IpaB* expressing plasmid.

Keywords: *IpaB* protein, *araBAD* promoter, *Escherichia coli*, *Shigella*,

**P73 - 349: EVALUATION OF EXTREMOZYMES IN COLD TOLERANT BACTERIAL
ISOLATES FROM OSHTORANKUH MOUNTAINS**

Elham Lashani¹, Bahar Shahnava², Ali Makhdoumi³

1. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran.
2. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran.
3. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran.

Background and Aim: Recently, potential applications for the cold adapted microorganisms and microbial products including cold-active enzymes have been highlighted. Cold-activated hydrolytic enzymes have numerous potential applications in the detergent, food, textile and animal feed industry, but relatively little is known about the diversity of cold-activated bacteria producing these enzymes.

Methods: In this study, we isolated psychrophilic and psychrotolerant bacteria from Oshtorankuh situated in the Zagros Mountains, located in Lorestan Province, and evaluated production of their extracellular hydrolytic enzymes. Strains were isolated from soil samples on different media including TSA, ANB, ANB-SE, Soil extract agar, R2A and ISP II and incubated in 4 and 20° C. In order to detect the production of extracellular enzymes, different enzymatic media were performed.

Results: A total 430 bacterial strains were isolated that 99.5 % were identified as psychrotolerant or psychrophilic. The Gram-negative strains were more than Gram-positives. To determine of functional diversity, we evaluated production of hydrolytic enzymes including amylase, protease, gelatinase, lipase, urease, keratinase, cellulase, DNase and pectinase. %2.2 producing eight enzymes and %21.5 producing four enzymes showed the high and low rate of enzyme production, respectively. The highest enzyme production was associated to protease (%79.5), gelatinase (%71), lipase (%52.2) and keratinase (%51). Biodegradability of cellulose, pectin and urea was shown in 40, 30, and 34.7 percentages of strains, respectively.

Conclusion: Identification and characterization of these strains able to degrade biopolymers open up the new horizons in biotechnology.

Keywords: Cold tolerant bacteria, extracellular enzymes, Oshtorankuh

**P74 - 352: PRODUCTION OF BIOPLASTIC FROM RHIZOBIUM LEGUMINOSARUM
ISOLATED FROM CLOVER**

Momeneh Ghanaat¹, Mohammad Reza Kuchaki², Abdoljalil Eiri³, Rezvan Alvandi⁴, Fateme Zabolli⁵

1. Department of Microbiology, Islamic Azad University, Tonekabon Branch, Tonekabon, Iran
2. Department of Microbiology, Islamic Azad University, Tonekabon Branch, Tonekabon, Iran
3. Department of biology, Ayatollah Amoli Branch, Islamic Azad University, Amol, Iran
4. Department of Computer, Islamic Azad University, Toyserkan Branch, Toyserkan, Iran
5. Department of biology, Ayatollah Amoli Branch, Islamic Azad University, Amol, Iran

Background and Aim: Bacterial strains are able to produce biopolymers that are used as new resources for different industries. Among biopolymers that are used in industries, poly-beta-hydroxy butyrate (PHB) is more significant and practical. In this study we evaluated production of bioplastic from *Rhizobium leguminosarum* isolated from clover

Methods: Sampling was conducted from 6 different regions. After culturing and purifying the bacteria, the differential biochemical tests were used to identify them and *Rhizobium* colonies isolated from each of 6 regions were investigated. Medium YEM (Yeast Extract Monnitrol) was used to isolate the bacteria, then the PHB production was investigated by using different carbon sources (glucose, maltose, galactose and starch). DCW and DCB were measured.

Results: Results showed that from the 6 isolated colonies, 4 colonies (R1, R4, R6, R2) have the highest production of PHB that produced more than 10 mg/l PHB, and among these isolates only R1 is produced 32.4 mg/l PHB. After adding different carbon sources, production in the presence of starch was the highest and in the presence of glucose was the lowest. R1 in the presence of starch and maltose showed a high production, while the cell biomass (DCB) for this sample in the presence of glucose was the highest.

Conclusion: Based on similar studies in Iran and other countries, and based on studies of industrial strains producing PHB, bacteria isolated in this study, are one of the most important producers of PHB and can be used in many different industries.

Keywords: *Rhizobium leguminosarum*, clover, poly beta hydroxybutyrate

**P75 - 365: INCREASED BIOLOGICAL REMOVAL OF PETROLEUM HYDROCARBONS BY
YEAST MIX-CULTURES OF SAROCLADIUM SP. AND CRYPTOCOCCUS SP.**

Aliyeh Kamyabi¹, Hoda Nouri², Hamid Moghimi³

1. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran.
2. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran.
3. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran. Corresponding author: hmoghimi@ut.ac.ir

Background and Aim: The present study was conducted to evaluate the co-culture ability of two yeast isolates *Sarocladium* sp. and *Cryptococcus* sp. comparing to their individual cultures in surfactant production and oil degradation.

Methods: A comparison of individual culture and co-culture for oil degradation (by Total Petroleum Hydrocarbon (TPH) assay and HPLC method), biosurfactant production (by Do Nouy method), emulsification activity (by Spectroscopy method) and cell surface hydrophobicity (MATH assay) were done in Minimal Salt Medium (MSM) with 1% crude oil.

Results: The results showed that individual cultures of each strain was capable of producing surfactant and degraded oil and pyrene, but the synergistic effect was observed when the co-culture strategy was applied. Results showed that oil removal and biomass production were about 28 and 35% higher in co-culture than individual cultures. Comparison between produced biosurfactant and chemical surfactants showed that individual cultures could reduce the surface tension same as SDS and about 10% better than Tween80. Results indicated that the co-culture could reduce the surface tension 10 and 20% more than SDS and Tween80, respectively. Both individual cultures of *Sarocladium* sp. and *Cryptococcus* sp. showed good Emulsification Activity (EA) (0.329 and 0.412 respectively), but 33 and 67% increasing in EA was measured in co-culture, respectively. Finally, 40% increasing for pyrene degradation was measured in co-culture of *Sarocladium* sp. and *Cryptococcus* sp.

Conclusion: According to our results, the co-culture system exhibited better performance and this study will promote the understanding of the synergistic effect of yeast co-culture oil degradation.

Keywords: Co-culture, *Sarocladium* sp., *Cryptococcus* sp., Biosurfactant, Oil biodegradation, Pyrene.

**P76 - 369: MYCOSORPTION OF DIFFERENT AZO DYES BY SAROCLADIUM SP. FOR
BIODECOLORIZATION OF TEXTILE EFFLUENTS**

Hoda Nouri¹, Aliyeh Kamyabi², Hamid Moghimi³

1. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran.
2. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran.
3. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran. Corresponding author: hmoghimi@ut.ac.ir

Background and Aim: Azo dyes are recalcitrant xenobiotic compounds which usually cannot be removed by traditional treatment. In the present study Remazol black bio-decolorization was investigated by halotolerant yeast *Sarocladium* sp.

Methods: In this study, within 17 isolated yeast strains, the best strain with biosorption ability was selected and identified subsequently. Afterwards, the variance between wet and dry biomass in their biosorption ability was studied. Furthermore, decolorization rate in different concentrations of azo dye and salt was performed. Finally, the selected strain ability in biosorption was studied in different types and a mixture of mono-, di- and tri- azo dyes.

Results: ADH17 isolate with 97% mycosorption of Remazol black (100 mg L⁻¹) was the best. Molecular identification showed 100% similarity to *Sarocladium* sp. Results illustrated that dry biomass could absorb the dye four times more than the wet. The mycosorption ability of the strain in different concentration of salt have no detectable changes in biosorption rate. The assessments with other dyes showed that this strain could absorb a broad range of azo dyes including mono-, di- and tri- azo and acidic, basic and reactive dyes as well. The maximum biosorption was 97.43% as for Reactive red17 and the minimum was 87.96% as for Reactive yellow17. Further evaluation indicated that this strain had a significant uptake in dyes mixture.

Conclusion: The obtained results indicate that *Sarocladium* sp. has a high ability for azo dye biosorption and is a suitable strain for treating of textile wastewater.

Keywords: Azo dyes, Biosorption, *Sarocladium* sp., Remazol black.

**P77 - 391: GENETIC DIVERSITY OF RHIZOSPHERE BACTERIA ASSOCIATED WITH
DIFFERENT CHICKPEA CULTIVARS**

Nadia Azizpour¹, Kiomars Rouhrazi²

1. Department of Agriculture, Malekan branch, Islamic Azad University, Malekan, Iran
2. Department of Agriculture, Malekan branch, Islamic Azad University, Malekan, Iran

Background and Aim: The rhizosphere is the soil zone strongly affected by plant roots and is a “hot spot” for microbial colonization and activity. Except for some pathogens, many rhizosphere microorganisms can improve the growth and health of plants by various mechanisms, such as nitrogen fixation or production of plant hormones.

Methods: Soil samples were collected from fields in the suburb of Saghez and Baneh, Iran. To obtain rhizosphere samples, the plants were uprooted from pots and the root-attached soil particles were eliminated. A loop-full of the soil suspension was streaked on NA medium and incubated at 28°C. When applicable, two colonies of each morphological type were selected for further testing. The DNA of strains was isolated by alkaline lysis method. For assess the genetic diversity of strains, Repetitive sequence-based PCR was performed using the BOX primer, and the ERIC primers.

Results: Totally 50 strains were isolated from 5 sites located mainly in northwestern Iran. The phenotypic features were compared by cluster analysis. Chickpea isolates were differentiated into fine clusters at 77 % similarity level. Cophenetic correlation coefficient for the dendrogram obtained from the combined data set of all primers was 0.936. Using the BOX primers, the percentage of polymorphic loci was 72.31% whereas with ERIC primers it was 54.2%. The phylogenetic analysis based on 16S rRNA gene sequences showed that representative isolates were closely related to *Pseudomonas putida*, *M. ciceri* and *p. flueroscens*.

Conclusion: The results demonstrated the existence of a considerable genetic diversity among bacteria isolated from chickpea in West Azarbayjan province of Iran.

Keywords: Box-PCR-ERIC-PCR, chickpea, 16S rRNA, Genetic diversity

**P78 - 392: PAENIBACILLUS POLYMYXA A RHIZOSPHER BACTERIA OF CHICKPEA AS
ANTAGONIST AGAINST ASCOCHYTA RABIEI**

Nadia Azizpour¹, Kiomars Rouhrazi²

1. Department of Agriculture, Malekan branch, Islamic Azad University, Malekan, Iran
2. Department of Agriculture, Malekan branch, Islamic Azad University, Malekan, Iran

Background and Aim: The control of the soil-borne pathogens is difficult because of their ecological behavior, their extremely broad host range and the high survival rate of resistant forms, under different environmental conditions. In recent years, several bacterial and fungal antagonists against plant pathogenic fungi have been described.

Methods: For isolation of bacteria, serial dilutions of the resulting root wash were plated on nutrient agar . Antagonistic activity of the rhizosphere bacterial isolates against *Ascochyta rabiei* was tested in vitro using plate chloroform method. Phenotypic tests for identification of strains were performed. PCR amplification for 16S rDNA was performed using primers 27F and 1541R. The 16S rDNA sequences were edited by using the Chromas program. Multiple sequence alignment of concatenated sequence data of 16S rRNA was performed with the Clustal W program.

Results: In Gram's staining, the morphology of the isolated bacteria (A1), small rod shaped and Gram positive bacilli. The A1 was positive for catalase, MR and indole test and acid production from mannitol, rhamnose, lactose, maltose, sucrose, glucose and dextrose. The isolate reacted negatively in tests for V-P and urease. Based on phenotypic properties and 16S rRNA gene sequencing, the A1 strain was identified as *Paenibacillus polymyxa*

Conclusion: This study describes our approach for identification and testing rhizosphere isolates from chickpea for antagonistic effects on the growth of *A. rabiei*. From eight isolates, one showed strong antagonistic activity against the pathogen with clear inhibition zone. Based on biochemical and genetic properties, the most efficient isolate was identified as *P. polymyxa*

Keywords: *Ascochyta rabiei* , 16S rDNA , *Paenibacillus polymyxa*, phenotypic properties

P79 - 415: ISOLATION AND CHARACTERIZATION OF HALOTOLERANT PURPLE NON SULFUR BACTERIA, FROM KARAJ SOILS

Mehrdad Jalilvand¹, Vida Tafakori², Mohammad Ali Amoozegar³

1. Extremophile Laboratory, Department of Microbiology, School of Biology, College of Science, University of Tehran, 14155-6455 Qods, Tehran, Iran
2. Department of Cellular and Molecular Science, School of Biological Science, Kharazmi University, Tehran, Iran.
3. Extremophile Laboratory, Department of Microbiology, School of Biology, College of Science, University of Tehran, 14155-6455 Qods, Tehran, Iran

Background and Aim: Purple non-sulfur bacteria (PNSB) constitute a non-taxonomic group of gram-negative anoxyphototrophic bacteria. This group of microorganisms grows in diverse environments and produces different natural components such as carotenoid pigments.

Methods: In this research the initial isolation of the bacteria was carried out using modified synthetic Pfennig medium under anaerobic conditions with a liquid paraffin layer on the surface of the agar and fluorescent light (2.5 klx) at $30 \pm 2^\circ\text{C}$ from Karaj soils. The colonies with the reddish pigments were isolated and characterized using colony appearance, gram staining, cell morphology, motility test, and 16S rRNA gene sequencing analysis. For 16S rRNA gene sequencing analysis after DNA extraction, PCR reaction was performed with prokaryotic universal primers.

Results: Bacterial identification performed and according to the obtained results the isolated halotolerant bacterium has identified as *Rhodobacter* spp.

Conclusion: The results showed that the use of liquid paraffin layer is a simple and useful method for isolation of Purple non-sulfur bacteria. The isolated halotolerant bacterium can produce pigments as the natural dyes in the future studies.

Keywords: Halotolerant, Purple non sulfur bacteria, anoxyphototroph, pigment.

**P80 - 416: OPTIMIZATION OF PURIFICATION DIPHTHERIA TOXOID USING DIFFERENT
RESEN**

Meisam Akrami¹, Mojtaba Noofeli², Ali Nazari Shirvan³, Mitra Sadat Tabatabaei⁴

1. Department of Biology, Faculty of Science, Islamic Azad University Central Tehran Branch, Iran
2. Department of human bacterial vaccines, Razi Vaccine and Serum Research Institute, Karaj, Iran
3. Department of Proteomics and Biochemistry, Razi Vaccine and Serum Research Institute, Karaj, Iran
4. Department of Biology, Faculty of Science, Islamic Azad University Central Tehran Branch, Iran

Background and Aim: Diphtheria toxin (DT) is produced by *Corynebacterium diphtheria*. This toxin is a protein including 535 amino acid with MW=60 kDa. DT toxin is a potent exotoxin that causes diphtheria as an acute and fatal bacterial disease in human. This toxin catalyzes the transfer of NAD⁺ to a diphthamide residue in eEF-2. Formalin Inactivated of this toxin as a toxoid are being used as a vaccine. Purification of the toxoid by the chromatography methods has a pivotal role in industry.

Methods: The bacteria was grown for 16 hours at 37°C in fermentor. The supernatant was inactivated by formalin and then toxoid precipitated by adding 25% ammonium sulfate. Precipitated toxoid was purified by size exclusion column chromatography (Sephadex G-75 & Sephacryl S100). Collected fractions were analyzed for their amount of protein by spectrophotometer at 280 nm. Different peaks with high LF were applied on SDS-Page to estimate their purity.

Results: Results revealed toxoid peak was the first one in both column. Although Sephacryl-S100 showed the best separation than the Sephadex. In SDS-PAGE, toxoid has a single band with 60kD molecular weight for both resins while in G75 there were few impurities. These impurities of extra bands around 30kD was also seen in other columns such as G25 and G50.

Conclusion: Specifically DT- toxoid is purified by a variety of size exclusion chromatography resins. Sephacryl S100 and G75 showed a good separation of the molecule from the other ingredients. This could be an efficient platform to purify DT-toxoid.

Keywords: Diphtheria, Toxoid, Chromatography, Vaccine

P81 - 424: EXTRACELLULAR SYNTHESIS OF SILVER NANOPARTICLES USING SULFATE REDUCING BACTERIUM ISOLATED FROM SEDIMENTS OF THE CASPIAN SEA

Seyedeh maryam Ekrami¹, Mojtaba Mohseni², Omelia Nazari³

1. Department of Molecular and Cell Biology, University of Mazandaran, Babolsar, Iran
2. Department of Molecular and Cell Biology, University of Mazandaran, Babolsar, Iran
3. Department of Organic Chemistry, University of Mazandaran, Babolsar, Iran

Background and Aim: Nanoparticles are synthesized using different chemical and physical methods. The biological approaches to the synthesis of nanoparticles are better than chemical and physical procedures because of low energy and time expenditure. This method requires neither toxic solvents nor any dangerous material for the environment. Various microorganisms have the ability to synthesize nanoparticles but the usage of metal reducing bacteria is very noticeable. In this research, biosynthesis of silver nanoparticles has been explored by *Shewanella* sp., a sulfate reducing bacterium.

Methods: Samples from sediments of the Caspian Sea were collected and a sulfate reducing bacterium was isolated. The isolate was evaluated based on its ability to synthesis silver nanoparticles. The sulfate reducing isolate was inoculated in LB medium and incubated at 28 °C for 24 hours. The culture supernatant was examined for its ability to produce silver nanoparticles. About one mL of the supernatant was added to 100 mL of silver nitrate solution at a concentration of 50 mM then incubated at 28 °C for 24 hours.

Results: The appearance of brown color in solution indicated the formation of silver nanoparticles. The UV-Vis spectrum exhibited an absorption band at around 420nm, suggesting the formation of silver nanoparticles. SEM studies showed that the silver nanoparticles were fairly uniform in size with a spherical shape and an average diameter of 44 nm.

Conclusion: The results of this study showed that the sulfate reducing isolate has the ability to produce silver nanoparticles.

Keywords: silver nanoparticles, *Shewanella*, sulfate reducing bacterium

**P82 - 425: BIODEGRADATION OF 2,4-DICHLOROPHENOXY ACETIC ACID USING
BACTERIA ISOLATED FROM SOIL**

Khadije Khojamli¹, Mojtaba Mohseni², Mohamad Javad Chaichi³

1. Department of Molecular and Cell Biology, University of Mazandaran, Babolsar, Iran
2. Department of Molecular and Cell Biology, University of Mazandaran, Babolsar, Iran
3. Department of Analytical Chemistry, University of Mazandaran, Babolsar, Iran

Background and Aim: The herbicide 2,4-dichlorophenoxy acetic acid (2,4-D) is extensively applied in agricultural fields worldwide and it can contaminate groundwater by direct washing or irrigation. Influx of this pollutant to water supplies can cause pernicious effects on human health and the environment. Many methods are proposed for treatment of this kind of pollution; however, the safest and cheapest method is the use of microorganisms for degradation of the 2,4-D. The aims of this study are the isolation and characterization of 2,4-D degrading bacteria from agricultural soil.

Methods: The collected soil samples were transferred into a mineral medium containing 2,4-D as a sole carbon and energy source. The flasks were incubated on an orbital shaker at 28 °C and 150 rpm for 5 days. The 2,4-D degrading bacteria were isolated after four times of subculturing into the fresh medium containing 2,4-D. Degradation of 2,4-D was determined by measuring the concentration of chlorine in the growth culture using chloride electrode.

Results: The results demonstrated that the isolated bacteria had a potential to degrade 2,4-D as a sole carbon and energy source. In addition, more than 95% of 2,4-D were degraded after 72 hours.

Conclusion: The results of this study revealed that these isolates are the appropriate candidates for the degradation of 2,4-D and they can be used for cleaning up the contaminated areas.

Keywords: 2,4-dichlorophenoxy acetic acid, biodegradation, bacteria, soil

P83 - 427: ISOLATION OF EXOELECTROGENIC SHEWANELLA SP. FROM NATURAL ENVIRONMENTS FOR THE GENERATION OF ELECTRICITY IN MICROBIAL FUEL CELLS

Seyedeh maryam Ekrami¹, Mojtaba Mohseni², Omelia Nazari³

1. Department of Molecular and Cell Biology, University of Mazandaran, Babolsar, Iran
2. Department of Molecular and Cell Biology, University of Mazandaran, Babolsar, Iran
3. Department of Organic Chemistry, University of Mazandaran, Babolsar, Iran

Background and Aim: In recent years, due to the energy crisis caused by population growth, industrialization, fossil fuel limitation and environmental pollution, microbial fuel cells are considered as a clean and renewable source of energy. A microbial fuel cell is a bioreactor that converts chemical energy of organic compounds to electrical energy through catalytic reactions of microorganisms under anaerobic conditions. Isolation of the sulfate reducing *Shewanella* and investigation of its ability to produce electricity were the aims of this study.

Methods: After collecting the samples from sediments of the Caspian Sea, a sulfate reducing bacterium was isolated, and then its ability to produce electricity was evaluated using microbial fuel cells. The sulfate reducing isolate was inoculated in LB medium and incubated at 30 °C for 24 hours. Afterwards, the culture was transferred into the anode chamber containing the LB medium. Neutral red was used as an intermediate electron transport and electrodes were made of graphite.

Results: Results showed that the isolate was able to produce electricity with a maximum open circuit voltage of 701 mV. In addition, a maximum power density and a maximum current density were evaluated as 140.817 mW m⁻² and 395 mA m⁻², respectively.

Conclusion: The results of this study demonstrated that the *Shewanella* sp. isolated from the sediments had the ability to produce electricity in microbial fuel cells.

Keywords: microbial fuel cells, *Shewanella*, sulfate reducing bacterium

**P84 - 446: TETRACOSANE DEGRADATION BY NATIVE STRAINS ISOLATED FROM OIL
CONTAMINATED SOILS**

Elham Kanoori¹, Mohammad Roayaei Ardakani², Hossein Motamedi³, Arash Mouradzadegan⁴

1. Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Iran
2. Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Iran
3. Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Iran
4. Department of Chemistry, Faculty of Science, Shahid Chamran University of Ahvaz, Iran

Background and Aim: Oil contamination in Iran due to high extraction and refinery of oil compounds, is one of the most important pollutants for environment. Bioremediation is one of the principal strategies for remediation, where the pollutants can be degraded by microorganisms their enzymes. The aim of this study is isolation of tetracosane-degrading bacteria from oil-contaminated soils of Gachsaran and evaluation of their degradation potential in order to be used for bioremediation.

Methods: In order to isolate oil-degrading bacteria, samples were collected from oil-polluted soils from two sites of Gachsaran zone. Enrichment, isolation and purification of oil-degrading bacteria were performed in basal salt mineral medium containing tetracosane. The more active isolate was selected based on Gas chromatography analysis and then identified using biochemical tests.

Results: As a result of this research, a suitable tetracosane degrader was identified that was able to degrade 40% of tetracosane in culture medium during 14 days of incubation. This isolate was identified as gram positive cocci.

Conclusion: Screening of polluted area can lead to isolation of suitable and potent degrader strains that can be used for bioremediation purposes. The strain that was introduced in this study was selected from an area with long time pollution history and must further studies be accomplished to optimize its biodegradation ability.

Keywords: Tetracosane, Bioremediation, Oil contamination.

**P85 - 448: INTRODUCING AN ATRAZINE DEGRADING BACTERIUM ISOLATED FROM
SOIL OF SUGARCANE FIELD**

Roya Rajaei¹, Hossein Motamedi², Hossein Najafzadeh Varzi³

1. Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Iran
2. Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Iran
3. Department of Basic Science, Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz, Iran

Background and Aim:-chloro-4-ethylamino-6-isopropyl amino- 1,3,5- triazine) is one of the s-triazine herbicides, that is mostly used in all of the agricultural fields such as corn and sugarcane around the world. Atrazine is the hazardous for the environment especially for human health and can be carcinogenic for human and animals. So its elimination from the environment is important. Among the methods used for removing atrazine from the environment, biodegradation is the best method. The aim of this study was finding atrazine degrading bacteria from soil of sugarcane field.

Methods:Soil samples were collected from the two sugarcane fields. After initial enrichment, atrazine degrading bacteria were isolated and purified through culturing in mineral salt medium containing 100mg/l atrazine as the sole source of carbon and nitrogen. The residues atrazine in the medium and the rate of biodegradation was analyzed by HPLC. The isolates were identified based on phenotypic methods such as staining, biochemical tests and enzymatic tests.

Results:As a result of this study a potent atrazine degrader was identified as a gram negative bacilli. This species was able to approximately degrade 69 percent of atrazine during 72 h of incubation

Conclusion:With regard to the environmental side effects of atrazine, it seems that using atrazine degrading bacteria such as found in this research can be useful for soil decontamination and bioremediation.

Keywords:Atrazine, Biodegradation, Bioremediation

P86 - 456: DEGRADATION OF 2,4,6-TRINITROTOLUENE BY TWO NATIVE ISOLATED BACTERIA

Mehdi Ali begloui¹, Ensieh Salehghamari², Amir Salehi-Najafabadi³, Mohammad Ali Amoozegar⁴

1. Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran.
2. Department of Cellular and Molecular Science, School of Biological Science, Kharazmi University, Karaj, Iran.
3. Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran.
4. Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran.

Background and Aim: Some chemical compounds such as 2,4,6-trinitrotoluene resist degradation because of their stable and tight structures, and remain in the environment, presenting significant risks of toxicity and mutagenicity on both human health and natural ecosystems.

Methods: The nitrite ion concentration in aqueous solution was determined by a colorimetric method through the formation of a reddish purple azo dye produced by coupling diazotized sulfanilic acid with N-(1-naphthyl)-ethylenediamine dihydrochloride. Before HPLC analyses all samples were centrifuged (11,000 g, 8 min) and filtrated (membrane pore size: 0.4 µm). HPLC analyses were performed on an Eurospher 1 RP C18 column (300×0.4 mm) with methanol-water (45 : 55) as the mobile phase, with a flow rate of 1.2 mL/min.

Results: Among 75 isolated bacteria from TNT contaminated soil, two strains were more potent for TNT degradation in aerobic condition. These strains showed good growth with disappearance of TNT and concomitantly release of nitrite over the period of incubation time. The identified amino and nitro derivatives produced by these two strains from TNT degradation were 2-nitrotoluene (2-NT), 4-nitrotoluene (4-NT), 2-amino-4,6-dinitrotoluene (2-ADNT) and 4-amino-2,6-dinitrotoluene (4-ADNT). Nitrite liberation was consistently found coincided with TNT disappearance from the medium. Degradation of TNT was accompanied by stoichiometric release of 0.68 mol nitrite/mol TNT.

Conclusion: The disappearance of TNT was completely within 5 days by the two isolates. This is encouraging, and may indicate their potential in bioremediation of TNT contaminated soils.

Keywords: 2,4,6-trinitrotoluene, biodegradation, nitrite liberation

**P87 - 461: PROPOSAL OF NEW METHODS FOR LONG-TERM PRESERVATION OF SALT-
LOVING MICROORGANISMS IN IBRC**

Sharareh Harirchi¹, Shokufeh Rafieyan², Mohaddaseh Ramezani³, Seyed Abolhassan Shahzadeh Fazeli⁴

1. Microorganisms Bank, Iranian Biological Resource Centre (IBRC), ACECR, Tehran, Iran
2. Microorganisms Bank, Iranian Biological Resource Centre (IBRC), ACECR, Tehran, Iran
3. Microorganisms Bank, Iranian Biological Resource Centre (IBRC), ACECR, Tehran, Iran
4. 1 Microorganisms Bank, Iranian Biological Resource Centre (IBRC), ACECR, Tehran, Iran 2 Department of Molecular and Cellular Biology, Faculty of Basic Sciences and Advanced Technologies in Biology, University of Science and Culture, Tehran, Iran

Background and Aim: Halophiles -salt-loving- are organisms that thrive in high salt concentrations. While most halophiles are classified into the archaea domain, there are also bacterial halophiles and some eukaryota, such as the alga or fungus. Halophiles are categorized as slight, moderate, or extreme, by the extent of their halotolerance. Slight halophiles prefer 0.3 to 0.8 M (1.7 to 4.8%), moderate halophiles 0.8 to 3.4 M (4.7 to 20%), and extreme halophiles 3.4 to 5.1 M (20 to 30%) salt content. Halophiles require sodium chloride (salt) for growth, in contrast to halotolerant organisms, which do not require salt but can grow under saline conditions.

Methods: For long-term preservation of halophilic microorganisms in Iranian Biological Resource Center (IBRC) a modified liquid drying (L-drying) and freeze-drying methods were applied for various types of halophilic bacteria and archaea. Lyo-protectants included 25% skim milk, a simple disaccharide (sucrose) and suitable media for each genus. In L-drying method applied to extremely halophilic microorganisms, skim milk was dried and then microbial suspension added.

Results: All Samples freeze-dried by freeze-dryer model ALPHA 2-4 LSC, Christ Ltd, Germany. Freeze-dried genera included Halophilic bacteria (*Bacillus*, *Vibrio*, *Pseudomonas*, *Chromohalobacter*, *Halobacillus* and *Halomonas*) and archaea (*Halopenitus*, *Halovarius*, *Halovenus*, *Marinobacter* and *Salinibacter*) survived after freeze-drying process and periodical QC results confirmed the success of modified methods for freeze-drying of halophilic bacteria and archaea deposited in IBRC.

Conclusion: On the basis of this study we are able to propose these modified methods for freeze-drying of halophilic microorganism especially extremely halophiles.

Keywords: Halophiles, Preservation, Freeze-dried, L-drying

**P88 - 469: INVESTIGATION BIOREMOVAL ORGANIC SULFUR OF COAL BY
PERCOLATION LEACHING AND BACTERIA ISOLATED**

Mohammadreza Kouchaki¹, Abdoljalil Eiri ², Rezvan Alvandi³

1. Islamic Azad Uni , Tonekabon
2. Department of biology, Ayatollah Amoli Branch, Islamic Azad University, Amol, Iran
3. Department of Computer, Islamic Azad University, Toyserkan Branch, Toyserkan, Iran

Background and Aim: A major disadvantage associated with use of coal as a fuel is emission of SO₂ into the environment during direct combustion. Aim this study investigation bioremoval organic sulfur of coal by percolation leaching and bacteria isolated

Methods: The removal of organic sulfur by MR-2 bacteria has isolated from Hashoni coal mine in Kerman in the bioleaching column has been tested. Column contained one of the fractions ranging from 0.5-12mm. The process included two stages: stabilization of pH and bioremoval for 40 days. The rate of removal of organic sulfur in this column through production of 2-HBP in bioleaching solution as a final material by Gibb's reagent has been. The bacteria cell number in the solution and pH was determined by direct counting and pH meter.

Results: The result show that the rate of removal of organic sulfur at the first days has increased and the increasability rate of 2-HBP in bioleaching solution that is toxicity for bacteria cause had decreased removal the rate of organic sulfur of coal by bacteria.

Conclusion:: The MR-2 bacteria can removal 21% from organic sulfur and 32% from total sulfur in a period of 40 days, for a particle size of 0.5-12m

Keywords: Bioremoval; coal; percolation

**P89 - 484: DSBA SIGNAL PEPTIDE DIRECTS RECOMBINANT HUMAN GROWTH
HORMONE TO PERIPLASMIC SPACE OF E. COLI**

Masoomeh Mirzaiee¹, Ali asghar Deldar², Ali Bahrami³

1. Molecular Genetics department, Research Centre for Biosciences and Biotechnology, Malek -Ashtar University of Technology, Tehran, Iran
2. Molecular Genetics department, Research Centre for Biosciences and Biotechnology, Malek -Ashtar University of Technology, Tehran, Iran
3. Molecular Genetics department, Research Centre for Biosciences and Biotechnology, Malek -Ashtar University of Technology, Tehran, Iran

Background and Aim: growth hormone is a single globular protein consisting of 191 amino acids with a molecular weight of about 22KDa. Secretion of the protein to periplasmic space of E.coli required a signal peptide. According to previous reports signal peptide of DsbA protein that we used here is a good candidate to do that.

Methods: synthetic recombinant human growth hormone (rhgh) coding DNA preceded by DsbA signal coding regions cloned into pET21a. The resulting plasmid transformed into E.coli BL21 and after induction with IPTG expression evaluated by SDS-PAGE that followed by blotting.

Results: SDS-PAGE and thereafter western blotting revealed that rhgh expressed and was detectable in both cytoplasm and periplasmic space.

Conclusion: In the bacterial cytoplasm rhgh produced as a 192 aa polypeptides in the inclusion body form. This polypeptides have a formyl methionine at N-terminus .It seems that fMet of the recombinant hormone might stimulate immunological responses .A solution of this potentially problem is the use of signal sequences to direct this hormone into periplasmic space, and DsbA might be a suitable candidate.

Keywords: Growth hormone, signal peptides, E. coli, DsbA, expression, cloning.

**P90 - 486: AUTO INDUCTION; A SIMPLE PROTOCOL FOR EXPRESSION OF
RECOMBINANT PROTEIN IN E. COLI.**

Masoomeh Mirzaiee¹, Ali asghar Deldar², Nargess Nasrollahi³

1. Molecular Genetics department, Research Centre for Biosciences and Biotechnology, Malek -Ashtar University of Technology, Tehran, Iran
2. Molecular Genetics department, Research Centre for Biosciences and Biotechnology, Malek -Ashtar University of Technology, Tehran, Iran
3. Molecular Genetics department, Research Centre for Biosciences and Biotechnology, Malek -Ashtar University of Technology, Tehran, Iran

Background and Aim: Human growth hormone (hGH) has the strongest influence role in stimulation growth, cell reproduction, and cell regeneration in humans. It is synthesized and reserved by somatotroph cells of the anterior pituitary gland (hGH). This protein can be used to treat hGH deficiency, Prader-Willi syndrome and Turner syndrome.

Methods: To achieve high levels of soluble form of recombinant human growth hormone (hGH) we performed cloning and expression of a synthetic hGH gene in BL21 and Rosetta gami strains of E. coli. A 573 base synthetic hgh gene fragment was amplified by PCR and cloned into expression vector pET21a in XhoI and NdeI restriction enzymes sites. The medium consist of minerals such as copper, iron, magnesium and other substances such as 0.2% lactose and 0.05% glucose were used. The culture incubated at 37 c with 250 rpm. This expression system, and metabolic balancing of media, allowed development of reliable non-inducing and auto-inducing media in which bacteria grow to high densities.

Results: Our results indicate auto-inducing media, bacterial strains, temperature and induction time affect the production of hGH. Auto-induction allows efficient screening of many clones in parallel for expression and solubility. SDS-PAGE results displayed a 22 kDa protein band that confirmed by western blotting technique.

Conclusion: Here in we used an inducible expression technique led to development of a simple and straight forward protocol for the auto-induced expression of recombinant protein in E.coli.

Keywords: Growth hormone, Auto induction, E. coli, expression.

**P91 - 489: THE EFFECT OF DIFFERENT CARBON AND NITROGEN SOURCES ON
ANTIBACTERIAL PRODUCTION BY STREPTOMYCES SP.ACS 116 ISOLATED FROM
OMAN SEA**

Razieh Zargari Orozaki¹, Bahar Shahnava², Abolghasem Danesh³, Mahsa Sadeghzadeh⁴

1. Ferdowsi University of Mashhad-Faculty of sciences-Department of Biology
2. Ferdowsi University of Mashhad-Faculty of sciences-Department of Biology
3. Mashhad university of medical sciences-Faculty of pharmacy
4. Ferdowsi University of Mashhad-Faculty of sciences-Department of Biology

Background and Aim: Antibiotic resistance has long been an issue for human populations. Streptomyces is a genus of filamentous bacteria with a great genomic potential for secondary metabolites production and is one of the main sources for antibiotics. Marine Streptomyces are emerging as a new source for novel bioactive products with distinctive chemical and biological characteristics. The aim of this study was to test different carbon and nitrogen sources with different concentrations to find the optimum condition for antibacterial production of Streptomyces sp.ACS116 isolated from Oman Sea.

Methods: 4 carbon sources including Glucose, Dextrose, Starch and Glycerol and 5 nitrogen sources including Pepton, Trypton, Malt extract, Yeast extract and Soy extract were tested by one factor at the time method and after 7 days of fermentation, the extracts were tested on standard pathogen staphylococcus aureus PTCC 1431 by agar well diffusion method and the inhibition zones were measured. After optimizing the source, different concentrations of the best nitrogen and carbon sources were tested by the same method to find the optimum concentration.

Results: The results showed that Dextrin with 2% W/V for carbon source and Pepton with 1.8 % W/V were the optimum condition for antimicrobial production by this strain.

Conclusion: The optimum condition increased the antimicrobial production (inhibition zone) by 2 folds. This proves the importance of carbon and nitrogen source on antibiotic production by Streptomyces.

Keywords: Streptomyces, Anti-Bacterial Agents, microorganism fermentation extract [Supplementary Concept]

**P92 - 492: THE INFLUENCE OF MINERALS ON ANTIBACTERIAL SECONDARY
METABOLITE PRODUCTION BY STREPTOMYCES SP.ACS 116 ISOLATED FROM OMAN
SEA**

Razieh Zargari Orozaki¹, Abolghasem Danesh², Bahar Shahnava³, Mahsa Sadeghzadeh⁴

1. Ferdowsi University of Mashhad-Faculty of sciences-Department of Biology
2. Mashhad university of medical sciences-Faculty of pharmacy
3. Ferdowsi University of Mashhad-Faculty of sciences-Department of Biology
4. Ferdowsi University of Mashhad-Faculty of sciences-Department of Biology

Background and Aim: Streptomyces is a genus of filamentous bacteria that is well known for its great ability to produce a vast range of antibiotics and bioactive products. Given the fact that antibiotic resistance has become a serious medical issue in the world, it is of paramount importance to explore for novel antimicrobial resources. Studies showed that minerals including NaCl, K₂HPO₄ and MgSO₄ have positive effect on antimicrobial production by Streptomyces. The aim of this study is to test the influence of these minerals on antibacterial production of Streptomyces sp.ACS116.

Methods: Different concentrations of these minerals ranging from 0.01 to 0.1 % W/V for K₂HPO₄ and MgSO₄ and 0.5 to 2.5 % W/V for NaCl were added to the medium and after 7 days of incubation, inhibition zones were measured by agar well diffusion method on Staphylococcus aureus PTCC 1431.

Results: The results showed that K₂HPO₄ with 0.025 % W/V concentration has a substantial positive impact on antibacterial production of this strain, increasing the production by 2.5 fold compared to negative control. The optimum concentration for NaCl was 1.5 %W/V which increased the production and MgSO₄ had no significant influence on the production.

Conclusion: minerals have significant impact on antimicrobial production by Streptomyces.

Keywords: Streptomyces, Anti-Bacterial Agents, microorganism fermentation extract [Supplementary Concept]

**P93 - 493: COMPARISON OF PROTEIN PROFILES OF ISOLATES STRAINS OF
BURKHOLDERIAMALLEI IN IRAN'S AND MALEIN PRODUCING STRAINS OF RAZI
INSTITUTE**

Mahdi Babaie¹, Nader Mosavari², Shojaat Dastipour³

1. Young Researchers and Elites Club, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. Razi Vaccine and Serum Research Institute, Karaj, Iran.
3. Razi Vaccine and Serum Research Institute, Karaj, Iran.

Background and Aim: *Burkholderiamallei* and *Burkholderiapseudomallei*, are causing glanders disease. At present there is no available vaccine or effective treatment for glanders. Surface proteins play crucial roles in the host-pathogen interaction and have been exploited as vaccine candidates and diagnostic targets. In the present study, proteins isolated from *B. mallei* and *B. pseudomallei* culture supernatant were separated using gel electrophoresis.

Methods: The molecular weights of the *B. mallei* and *B. pseudomallei* proteins estimated by using sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE).

Results: Proteins from different strains of *B. mallei* and *B. pseudomallei* cells were separated by SDS-Page. Approximately twenty distinct protein lines could be detected after Coomassie blue staining. Most of the proteins had molecular masses about 35-66 kDa.

Conclusion: Surface located proteins have important roles in the pathogenesis of diseases caused by many microorganisms. These proteins identified 35 proteins, while screening with human sera identified 12 immunogenic proteins. Nine of these proteins were identified by both methods indicating that they may be both surface located and immunogenic. These proteins will be evaluated further as vaccine candidates and diagnostic targets.

Keywords: *Burkholderiamallei*, *Burkholderiapseudomallei*, glanders, gel electrophoresis.

**P94 - 494: ANTI-MRSA METABOLITES PRODUCED BY CO-CULTURED ACTINOMYCETES
ISOLATED FROM HOZ-SULTAN SALT LAKE, QOM**

Fatemeh Taheri¹, Marzieh Hosseini ², Ensieh Salehghamari ³

1. Department of Cellular and Molecular Science, School of Biological Science, Kharazmi University, Karaj, Iran
2. 1. Department of Cellular and Molecular Science, School of Biological Science, Kharazmi University, Karaj, Iran
3. 1. Department of Cellular and Molecular Science, School of Biological Science, Kharazmi University, Karaj, Iran. Email: esaleh@khu.ac.ir, ensiehsalehghamari@gmail.com

Background and Aim:Infections caused by multidrug-resistant bacteria specifically Methicillin resistant *Staphylococcus aureus* (MRSA) continue to be a worldwide problem. Also actinomycetes, have long been a remarkable source of useful therapeutics. Here a binary interspecies interaction assay used to mine for new secondary metabolites.

Methods:In this research, 40 isolated actinomycetes from Hoz-Sultan Salt Lake were isolated with different treatments including dry heat, wet heat, phenol and SDS in media cultures: Glycerol casein agar, Soil extract agar, ZSSE, IM2, IM1, ISP2 and Starch casein containing 0, 5 and 10% of NaCl. Among them 8 strains were not halophil or halotolerant. They were evaluated for antimicrobial activity against *S. aureus* ATCC 25923 (MRSA). Actinomycetes were cultured on Glycerol casein medium in a binary array and incubated at 29°C for 5 d. Antagonism was detected by formation of an inhibition zone by overlaying the entire interaction plate with a layer of agar containing MRSA.

Results:Binary interspecies interaction assays were determined some induction and inhibition of anti-MRSA metabolite production. 2 isolates including act6 (actinomycete) and act7 were induced anti-MRSA metabolite production of strains act4 and act2 respectively and 1 isolate including act7 inhibited act1.

Conclusion:Genome sequencing revealed secondary metabolite gene clusters and the growing appreciation that the exchange of small molecules mediates inter- and intraspecies communication suggest that bacterial interaction assays should be reassessed as a potential conduit for the discovery of new small molecules.

Keywords:Binary array, Induction, Interactinomycete interaction, Isolation media, MRSA, Secondary metabolite

**P95 - 523: TEMPERATURE EFFECT ON α -LUFFIN EXPRESSION AND SOLUBILITY RATE
IN ESCHERIACHIA COLI BACTERIA AS A HOST**

Shaghayegh Namvar¹, Fatemeh Davami², Hoda Jahandar³, Leila Nematollahi⁴, Farzaneh Barkhordari⁵

1. Department of Biotechnology; Pharmaceutical Sciences Branch; Islamic Azad University; Tehran – Iran (IAUPS)
2. Biotechnology Research Center; Pasteur Institute of Iran
3. Department of Biotechnology , Faculty of Advanced Sciences & Technology , Pharmaceutical Sciences Branch, Islamic Azad University ,Tehran – Iran (IAUPS)
4. Biotechnology Research Center; Pasteur Institute of Iran
5. Biotechnology Research Center; Pasteur Institute of Iran

Background and Aim: Escherichia coli a gram negative, rod shaped bacterium is one of the most popular hosts for protein expression in biotechnology laboratories. In spite of its simplicity, expressed proteins are mostly in insoluble form, called inclusion bodies. Several strategies can overcome this problem. Changing the growth medium and co-expression of chaperones are some of these approaches. Reducing the temperature is another strategy to improve the soluble production of recombinant proteins in E. coli. Lower temperatures decrease the protein aggregation. α -Luffin, a type I ribosome-inactivating protein (RIPs), belongs to a group of enzymes attacking eukaryotic ribosomes having inhibitory effects on protein synthesis. RIPs have biomedical properties, such as antitumor and antiviral activity. The influence of different temperatures on α -luffin, a plant RIP, expression and solubility in EnBase cultivation medium investigated at different times after induction.

Methods: α -Luffin gene was synthesized based on sequence data. The recombinant vector was transformed into E. coli and transformants were selected with Kanamycin. Recombinant cells were grown in EnBase medium. Protein expression was induced by addition of Rhamnose. Expression and solubility investigated at 25°C, 30°C, 37°C and different induction time. (4, 6, 8, 12, 24 hours). Protein expression is evaluated by SDS-PAGE and western blot analysis.

Results: According to the results; at 25°C and 24 hours after induction, the maximum expression of α -luffin was observed in EnBase medium. However, recombinant protein induced at 30°C, showed optimum solubility rate.

Conclusion: Our results revealed that reducing induction temperatures has led to enhanced expression and solubility of recombinant α -luffin, in Enbase cultivation system.

Keywords: Escherichia coli , α -luffin , Temperature

**P96 - 527: ISOLATION & SCREENING OF ORGANIC SOLVENT- TOLERANT BACTERIA
SOIL OF ZANJAN CONTAMINATED BY OIL**

Parimah Rostami¹

1. Islamic Azad University Of Zanjan

Background and Aim: Due to the uncontrolled increase in environmental pollution with organic solvents, it's necessary to plan some processes for environmental cleanup, specially by using native bacteria. This study aims to isolate and identify bacteria which are compatible with organic solvents and also optimizing the condition of organic solvents' decomposition by bacteria.

Methods: Therefore, contaminated soil with petroleum and petroleum compounds were sampled. To isolate the bacteria, they were cultured on hand made media. The tolerance of bacteria in different volume of organic solvents which includes acetonitrile and gasoline were measured at different pH and temperatures within 6 days on other hand made media by spectrophotometric method. Further, the respiratory activities of sample of contaminated soil with organic solvents were measured.

Results: Base on the results, *Bacillus* genus was the selected bacteria. The best concentration for both of organic solvents for optimum bacterial growth and bioremediation was 2.5 cc and the optimum pH was 6.2. The optimum temperature and time for bacterial growth and bioremediation of organic solvents for acetonitrile and gasoline was 28°C and respectively were days of five, six.

Conclusion: According to power of isolated *Bacillus* genus in bioremediation of various of solvents, this bacteria is appropriate. However, to obtain better results, optimization of temperature, pH and concentration is required.

Keywords: Bioremediation, Organic solvents, Petroleum hydrocarbons, *Bacillus*, Biometer flask

**P97 - 529: ISOLATION & SCREENING OF - TOLERANT BACTERIA SOIL CONTAMINATED
BY OIL**

Parimah Rostami¹

1. Islamic Azad University Of Zanjan

Background and Aim: Due to the uncontrolled increase in environmental pollution with organic solvents, it's necessary to plan some processes for environmental cleanup, specially by using native bacteria. This study aims to isolate and identify bacteria which are compatible with organic solvents and also optimizing the condition of organic solvents' decomposition by bacteria.

Methods: Therefore, contaminated soil with petroleum and petroleum compounds were sampled. To isolate the bacteria, they were cultured on hand made media. The tolerance of bacteria in different volume of organic solvents which includes toluene and diesel were measured at different pH and temperatures within 6 days on other hand made media by spectrophotometric method. Further, the respiratory activities of sample of contaminated soil with organic solvents were measured.

Results: Base on the results, Bacillus genus was the selected bacteria. The best concentration for both of organic solvents for optimum bacterial growth and bioremediation was 2.5 cc and the optimum pH was 6.2. The optimum temperature and time for bacterial growth and bioremediation of organic solvents for toluene and diesel was 35°C and respectively were days of four and six.

Conclusion: According to power of isolated Bacillus genus in bioremediation of various of solvents, this bacteria is appropriate. However, to obtain better results, optimization of temperature, pH and concentration is required.

Keywords: Bioremediation, Organic solvents, Petroleum hydrocarbons, Bacillus, Biometer flask

P98 - 555: ISOLATION AND IDENTIFICATION OF LIPASE PRODUCING BACTERIA FROM OILY WASTEWATER

NEDA DIBANEZHAD¹, Roya moravej²

1. Department of Biology, Sanandaj Branch, Islamic Azad university, Sanandaj, Iran.
2. Department of Biology, Sanandaj Branch, Islamic Azad university, Sanandaj, Iran.

Background and Aim: pollution due to oil sewage is one of the most critical types of pollution leading to destructive environmental and economic consequences. Biodegradation of oil sewage is a useful method concentrated on during past years. Isolation of microorganisms which can produce lipase enzyme may be used for different purposes along with enzyme producing for bio treatment of sewage. Thus, the present study aims to isolation and identification of lipase producing bacteria from oily wastewater.

Methods: for this purpose, samples were taken from oil sewage exiting from factories manufacturing herbal oils and dairies. Bacteria with white halo around them were isolated as bacteria producing lipase enzyme. Then this isolates were identified by morphological and biochemical methods. Enzyme activity was measured by qualitative and spectrophotometry method. level of lipase enzyme production was examined by spectrophotometry that showed the amount of enzyme which releases 1 μ g paranitrophenol per milliliter per minute.

Results: Thus it became clear that 4 types of the isolates had the highest level of enzyme production. Among that, the maximum and minimum halo diameter on Tributyrin agar was related to R2(9mm) with the highest level of lipase production and R4(3.6mm) with the lowest amount of that, respectively. Then the isolates were detected for molecular identify by 16SrRNA and sequencing.

Conclusion: According to lipase enzyme required in industry at the country and the activity of lipase produce bacteria introduced in this study, it seems that the use of native strains could be effective to achieve production of the enzyme lipase in the country.

Keywords: isolation, bacterial lipase activity, 16SrRNA, sequencing

**P99 - 562: STUDY OF BIOFILM FORMATION OF RHODOCOCCLUS SP. USING
MICROPLATE METHOD**

Elham Adhami¹, Dr Soheil Aghaei², Dr Mohammad-Reza Zolfaghari³

1. Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran.
2. Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran.
3. Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran.

Background and Aim: Rhodococci according to possess large genome, their active metabolism is highly regarded for bioremediation and biodegradation of pollutants, surfactant production and industrial syntheses (Bell, Philp, Aw, & Christofi, 1998). A hallmark trait of biofilms is increased resistance to antimicrobial agents compared to the resistance of free-swimming organisms (Teitzel & Parsek, 2003). Therefore in this investigation, biofilm formation by Rhodococcus isolates was studied. The purpose of this research was biofilm formation of Rhodococcus isolates using microplate method.

Methods: Bacterial strain used in this investigation was isolated by Aghaei et al (2014) from agricultural and manganese mine soils in Qom, Iran. Biofilm formation was performed at 30° C and 37 ° C in TSB (tryptic soy broth) and BHI (brain heart infusion) broth, at 24, 48, 72 and 96 hours in 96-well microplate (Katiyar, Vishwakarma, & Kaistha, 2012).

Results: The best conditions for biofilm formation of Rhodococcus isolates was determined at 30°C in BHI broth, at 96 hours.

Conclusion: It seems microplate method for biofilm formation in comparison with other methods is more convenient and cheaper.

Keywords: Rhodococcus sp., Biofilm formation, microplate method

**P100 - 567: THE EFFECT OF HEAVY METALS IN THE PRODUCTION OF PIGMENTS IN
RHODOCOCCLUS RHODOCHROUS**

mahdieh sadat Haddad¹, Doctor soheil Aghaee², Doctor mohsen Zargar³

1. Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran.
2. Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran.
3. Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran.

Background and Aim: Microbial pigments are one of the important source for the search of antimicrobial agents and molecules with importance in the field of biotechnology that can be used natural colorant as well as antimicrobial agents in place of antibiotic (Rashid, Fakruddin et al. 2014). One of pigment-producing bacteria is *Rhodococcus* (Borisova 2011). study pigment production and the effect of different concentration of kinds of the toxic metals such as ferric chlorid, zinc chlorid, cobalt nitrate and copper nitrate in the production of pigments (carotenoid) in native strains *Rhodococcus* isolated from soils around mine manganese city of Qom.

Methods: Study of pigment production in different of culture media such as TSA, BHI AGAR, LB AGAR, BENNET AGAR, ISP5 and different temperatures of 25 °C, 30 °C and 35 °C and concentrations of toxic metals including 12/5 ppm, 25 ppm and 37 ppm (Buzzini, Martini et al. 2005) in native strains *Rhodococcus*.

Results: The statistical analysis showed that the optimal pigment production in this bacterial strains is at temperature 30°C, culture medium TSA, FECL3 37 ppm.

Conclusion: According to the result of this research and because of non-pathogenic strains of the native *Rhodococcus* and due to microbial pigments have many advantages over artificial and inorganic colors (Kirti, Amita et al. 2014), its use is recommended in pigment production in various industries.

Keywords: *Rhodococcus*- Pigment- Heavy metals

**P101 - 611: INVESTIGATION ON NAPHTHALENE BIODEGRADATION ABILITY IN A
BACILLUS SP. CONSORTIUM**

Mahshid Mousavi¹, Abbas Akhavan sepahi², Taher Nejadsattari³

1. M.Sc. Student, Department of Microbiology, Tehran Science and Research Branch, Islamic Azad University, Tehran. Iran
2. Associate professor of Microbiology, Department of Microbiology, North Tehran branch, Islamic Azad University, Tehran, Iran
3. Associate professor of Biology, Department of Biology, Tehran Science and Research Branch, Islamic Azad University, Tehran, Iran

Background and Aim: Polycyclic aromatic hydrocarbons (PAHs) are ubiquitous contaminants in the environment with potential mutagenicity and carcinogenicity. PAH bioremediation is considered as an effective and environmentally cleanup technology. *Bacillus* spp. is one of the bacteria which degrade these contaminants. In this study we isolated *Bacillus* sp. in soil samples with potential of naphthalene degradation and compared *Bacillus* spp. consortium and pure cultures biodegradation rate.

Methods: Ten soil samples were collected from Tehran and around Tehran and *Bacillus* strains were isolated and identified by biochemical and molecular methods. After that, the amount of biosurfactant production was measured by Tensiometer and emulsification test was conducted on it. Then, the naphthalene degradation ability was studied by the consortium. Eventually, GC analysis was conducted on the consortium for naphthalene biodegradation investigation. Optimized growth conditions were also determined.

Results: The isolates contained *Bacillus cereus*, *Paenibacillus lactis*, *Bacillus fusiformis* and *Bacillus subtilis*. All of the isolates had surface tension amount less than 40(mN/m) and growth in blood agar medium. It shows that all of them can produce biosurfactant, effectively. The surface tension amount for consortium was lower than pure cultures. In addition, the consortium showed the ability to tolerate 1000 ppm naphthalene concentration in medium and the maximum growth amount was in pH=6, 200 ppm naphthalene concentration, 150 rpm of shaker speed and yeast extract as an additional nitrogen source.

Conclusion: The obtained results revealed that consortium of four isolates had more ability in naphthalene degradation as shown in other studies.

Keywords: Naphthalene, *Bacillus* sp., Consortium, Bioremediation

**P102 - 647: ISOTHERMS AND KINETICS STUDIES FOR BIOSORPTION OF CADMIUM
FROM AQUEOUS SOLUTION BY COCHLIOBOLUS AUSTRALIENSIS UTMC 5042**

Fatemeh sadat Khajeh mohammadilar¹, Javad Hamed², Hamid Moghimi³

1. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran.
2. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran. Microbial Technology and Products Research Center, University of Tehran, Tehran, Iran.
3. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran.

Background and Aim: Cadmium is an extremely toxic metal commonly found in industrial wastewater. Biosorption is an efficient method for removal of heavy metals. The aim of current study was evaluate kinetic and isotherm equations of *Cochliobolus australiensis* UTMC 5042 for Cd biosorption.

Methods: For isotherm analysis, adsorption at different Cd concentrations (50, 100, 200, 400 and 800 mg/L) was evaluated after 4 hour. Experimental data were analyzed by model equations Langmuir and Freundlich isotherms. To investigate the adsorption kinetics, the isolates experiments were performed at concentrations of 200 mg/L and samples were withdrawn at different interval times (2, 5, 10, 20, 30, 60, 120 and 240 min). The biosorption kinetic data were tested with pseudo first-order and pseudo second-order rate equations. Finally the samples were analyzed by inductively coupled plasma (ICP).

Results: The experimental data indicate that adsorption kinetics follow pseudo second-order rate equation ($R^2 = 0.997$) and chemisorption is the rate limiting step for the removal of cadmium under the studied experimental conditions. The linear regression coefficient (R^2) for Langmuir and Freundlich model is 0.953 and 0.978, respectively. The KF value and the monolayer saturation capacity (q_{max}) were found to be 1.324 g/L and 27.027 mg/g, respectively. Our results indicated the cadmium adsorption capacity of *C. australiensis* UTMC 5042 was significant as a new high capacity biological Cd sorption agent.

Conclusion: It was found that the biomass obtained from *C. australiensis* UTMC 5042 was a good biosorbent for cadmium removal from wastewater.

Keywords: *Cochliobolus australiensis* UTMC 5042, Langmuir, Freundlich, pseudo second-order kinetic

**P103 - 648: EFFECT OF PRETREATMENT ON THE BIOSORPTION OF CADMIUM BY
COCHLIOBOLUS AUSTRALIENSIS UTM 5042**

Fatemeh sadat Khajeh mohammadilar¹, Javad Hamed², Hamid Moghimi³

1. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran.
2. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran. Microbial Technology and Products Research Center, University of Tehran, Tehran, Iran.
3. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran.

Background and Aim: Heavy metals such as cadmium are the main toxic pollutants in industrial wastewaters. Here we introduced a biological agent for Cd biosorption.

Methods: In the previous studies had shown that *C. australiensis* UTM 5042 is a suitable strain for biosorption of Cd. 0.2 g of dried biomass were treated by NaOH (0.5 N), acetic acid (10%), Dimethyl Sulfoxide (DMSO) (10%), methanol (50%), acetic anhydride (10%), $\text{Ca}(\text{NO}_3)_2$ (0.2 M), formaldehyde (10%), acetone (50% v/v) and autoclave. Samples were centrifuged at 4000 rpm and supernatant was evaluated using inductively coupled plasma (ICP).

Results: The results showed that biomass pretreatment by NaOH, $\text{Ca}(\text{NO}_3)_2$ and DMSO increased 83% to 99%, 95% and 94% of cadmium biosorption, respectively. However, biomass treatment by acetic acid, formaldehyde and acetic anhydride decreased 23%, 30% and 35% biosorption efficiency respectively. Also it was shown that autoclave, acetone and methanol pretreatments caused no change in the biosorption capacity of *C. australiensis* UTM 5042. Our results showed alkaline treatment by NaOH (0.5 N) was the best pretreatment for increasing of Cd biosorption.

Conclusion: Current study demonstrated that alkali treatment could release polymers such as polysaccharides that have a high affinity towards Cd biosorption. In opposite, acid treatment of *C. australiensis* UTM 5042 has significantly decreased the biosorption. The reduction of Cd adsorption capacity by formaldehyde and acetic anhydride suggest the involvement of amino and hydroxyl groups are the main functional groups on biosorption process.

Keywords: Heavy metal, biosorption, pretreatment, *Cochliobolus australiensis* UTM 5042

**P104 - 666: EVALUATION OF THE ANTIMICROBIAL ACTIVITY OF PROBIOTIC
BACTERIA ESCHERICHIA COLI ISOLATED FROM DIFFERENT NATURAL SOURCES
HEMORRHAGIC E.COLI O157H7**

Karami Sahar¹, mohammad roayaei², Fateme azizi³

1. MSc in Microbiology, faculty of biology, Shahid Chamran University of Ahvaz
2. Professor of microbiology, faculty of biology, Shahid Chamran University of Ahvaz
3. MSc in Microbiology, faculty of biology, Shahid Chamran University of Ahvaz

Background and Aim: Probiotics are living organisms that play a role in the prevention and treatment of many diseases. Diarrheal diseases in all age groups in all geographic regions of the world happens, EHEC strain O157: H7 Escherichia coli intestinal pathogens are one of the most important and one of the main causes of diarrhea in developing countries are Therefore, treatment is necessary.

Methods: In this study, five species of probiotic bacteria was isolated and identified various natural sources and then antimicrobial effect of these species in two ways disc (agar (Disk diffusion and the wells (Well diffusion agar) (using a bacteria culture supernatant) the two strains of pathogenic E. coli by measuring the diameter of growth in the two methods were compared.

Results: A total of 13 isolates were isolated and molecular identification were randomly selected 5 isolates, 5 isolates significant antimicrobial effect in either way on the strain O157: H7 EHEC strains showed inhibitory effect did not show it.

Conclusion: As a result of this study, significant antimicrobial effect of the probiotic bacteria strain O157: H7 is the most important enteric pathogens were found. The increasing use of probiotics as a natural and modern methods to reduce and prevent various diseases is recommended.

Keywords: Probiotics , intestinal pathogens, Escherichia coli, EHEC

**P105 - 673: AN IN SILICO COMPARATIVE INVESTIGATION OF THE ANTIMICROBIAL
ACTIVITY OF THE AMYLOIDOGENIC MUTANTS AND WILD TYPE OF HUMAN
LYSOZYME**

Seyyed ali Hoseinian¹, Vahid Mirzabaiati², Seyedeh Samira Hosseinzadeh³

1. Department of Biology, Science and Research branch, Islamic Azad University, Khorasan Razavi, Neyshabur, Iran
2. Department of Biology, Science and Research branch, Islamic Azad University, Khorasan Razavi, Neyshabur, Iran
3. Department of biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran

Background and Aim: The human lysozyme (hLYS) kills bacteria by hydrolyzing the peptidoglycan layer of the cell wall of certain bacterial species; hence its application as a natural antimicrobial agent has been suggested. Many attempts to broaden the antimicrobial spectrum of lysozyme have been made in the past decade or so. We have focused on the antimicrobial activity of the two natural amyloidogenic mutants (I56T, D67H) of hLYS compared to its wild type (WT).

Methods: In this regard, the 3D structures of the WT, I56T, and D67H with the ID numbers: 1LZ1, 1LOZ, 1LYY; respectively; and 9LYZ (The bacterial cell wall trisaccharide NAM-NAG-NAM bonded to the lysozyme) for the ligand separation; were retrieved from PDB. Discovery Studio3.0 was used for the water and ligand molecules separation of the structures. GROMACS5.07, containing gromos9643a1force field was used for the simulations in 10000ps (10ns) for MD step. The docking and the affinity evaluation were accomplished by AutoDockTools1.5.6.

Results: The simulations results revealed that the native conformations of all three structures have been maintained. Also, the docking results analyses with three repeats for each sample were demonstrating the affinity values: -7.5, -7.3, and -7.3kcal/mol for WT; -6.2, -5.9, -5.9kcal/mol for D67H; -8.0, -8.0, -7.7kcal/mol for I56T.

Conclusion: Overall, the results of the study showed the higher affinity to the ligand for I56T, and the lower affinity for D67H, in compared with WT. So, it seems that the I56T mutant has increased the antimicrobial activity, and it may be considered as a beneficial mutation to improving lysozyme activity.

Keywords: Lysozyme, Antimicrobial activity, Amyloidogenic mutants, AutoDockTools1.5.6

**P106 - 699: INTRODUCING NEW METHODS FOR SELECTIVE ISOLATION OF
STREPTOMYCES AND NON-STREPTOMYCES ACTINOBACTERIA FROM MARINE
SAMPLES**

Faezeh Almasi¹, Fatemeh Mohammadipanah², Javad Hamed³

1. Department of Microbial Biotechnology, School of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, 14155-6455, Tehran, Iran University of Tehran Microorganisms Collection (UTMC), Microbial Technology and Products (MTP) Research Center, University of Tehran, Tehran, Iran
2. Department of Microbial Biotechnology, School of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, 14155-6455, Tehran, Iran University of Tehran Microorganisms Collection (UTMC), Microbial Technology and Products (MTP) Research Center, University of Tehran, Tehran, Iran
3. Department of Microbial Biotechnology, School of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, 14155-6455, Tehran, Iran University of Tehran Microorganisms Collection (UTMC), Microbial Technology and Products (MTP) Research Center, University of Tehran, Tehran, Iran

Background and Aim: Among the three major habitats, the marine provides the largest inhabitable space for microorganisms. However, the distribution of actinobacteria as an outstanding resource of potent biocompounds in the sea is largely unexplored. As estimates suggest less than 1% of total bacterial species can be recovered using standard methods of cultivation. Moreover, probable reliance on other bacteria for essential nutrients and growth inhibition by fast growing ones may be the probable reasons for low culturability of marine actinobacteria. Therefore, designing cultivation methods considering such important interactions seems an important issue.

Methods: In the present study 20 marine sediment samples were cultured using two novel practical methods for isolation of actinobacteria. One of these methods employs Combination of Diffusion and microbial Tap Chamber (DT chamber) which is a mix of media and diluted environmental sample sandwiched between common papers. The principle of second method was the soil substrate membrane system (SSMS) that colony formation occurs on common papers in immediate contact with the slurry of soil substrate incubated for 3 months.

Results: Among tested papers more colonies were isolated using fruit wrapping kraft coated paper, Light weight coated paper and waxed paper with 28%, 25% and 20% of obtained isolates, respectively. Another finding was that the majority of the isolates (63.9%) obtained by modified SSMS had LL DAP while about 70% of isolates recovered by DT chamber were non-Streptomyces (*Promicromonospora*, *Oerskovia*, *Nocadioides* and *Nocardia*)

Conclusion: DT chambers and SSMS may be more select approach for isolation of Streptomyces and non-Streptomyces actinobacteria, respectively.

Keywords: marine actinobacteria, DT chamber, soil substrate membrane system (SSMS)

**P107 - 711: ISOLATION AND CLONING OF ASPERGILLUS NIGER GLUCOSE OXIDASE IN
YARROWIA LIPOLYTICA EXPRESSION MONOCOPY VECTOR**

Fatemeh Khadivi derakhshan¹, Farshad Darvishi ², Catherine Madzak ³

1. Department of Microbiology, Faculty of Science, karaj Branch, Islamic Azad University, karaj, Iran.
2. Department of Microbiology, Faculty of Science, University of Maragheh, Maragheh, Iran.
3. UMR GMPA, AgroParisTech, INRA, Université Paris-Saclay, 78850 Thiverval-Grignon, France.

Background and Aim:Glucose oxidase (GOX) also known as notatin (EC 1.1.3.4) is an oxido-reductase that catalyses the oxidation of glucose to hydrogen peroxide and D-glucono- δ -lactone. Glucose oxidase is an important enzyme which is currently used in chemical, clinical and pharmaceutical, food and beverage industries. The aim of this study was isolation and cloning of *Aspergillus niger* glucose oxidase in *Yarrowia lipolytica* expression monocopy vector and transform into *Escherichia coli*.

Methods:The *A. niger* ATCC 9202 genomic DNA was isolated by Moller method, then the GOX gene of *A. niger* amplified by PCR using specific primers containing SfiI and KpnI restriction site. The plasmid pINA1296 and GOX gene fragment were digested by the restriction enzymes, and then ligation was done using T4 DNA ligase. The shuttle vector pINA1296 containing GOX gene was transformed into *E. coli* competent cells. Positive colonies detected by Colony-PCR.

Results:Successful integration of the GOX gene fragment in the *Yarrowia lipolytica* expression shuttle vector pINA1296 was confirmed by colony-PCR. Electrophoresis results show that 1.8 kb band of GOX gene in the positive transformants of *E. coli* and extracted recombinant vectors.

Conclusion:The new recombinant vector containing GOX gene could be used to expression *A. niger* glucose oxidase in yeast *Y. lipolytica*, and it is possible to easy and large-scale production of glucose oxidase in the yeast.

Keywords:Glucose oxidase, *Aspergillus niger*, *Yarrowia lipolytica*, *Escherichia coli*, Transformation.

P108 - 739: PURIFICATION OF DIPHTHERIA TOXIN BY SEPHACRYL SIZE EXCLUSION CHROMATOGRAPHY

Meisam Akrami¹, Mojtaba Noofeli², Ali Nazari Shirvan³, Mitra Sadat Tabatabaei⁴

1. Department of Biology, Faculty of Science, Islamic Azad University Central Tehran Branch, Iran
2. Department of human bacterial vaccines, Razi Vaccine and Serum Research Institute, Karaj, Iran
3. Department of Proteomics and Biochemistry, Razi Vaccine and Serum Research Institute, Karaj, Iran
4. Department of Biology, Faculty of Science, Islamic Azad University Central Tehran Branch, Iran

Background and Aim: Diphtheria toxin is produced by *Corynebacterium diphtheria*. Diphtheria toxin is 60kDa composed of two peptide chains, fragment A and B, linked by a disulfide bond. DT toxin is a potent exotoxin that causes diphtheria as an acute and fatal bacterial disease in human.

Methods: The bacteria was grown for 72 h at 37°C in fermentor. The supernatant of 12% ammonium sulfate was precipitated by adding extra 14% ammonium sulfate and separated by centrifuge at 10000 rpm for 30 min. Precipitated toxin was purified by size exclusion column chromatography Sephacryl-S100. Collected fractions were analyzed for their amount of toxin by spectrophotometer at 280 nm. Different peaks with high LF were applied on SDS-Page to estimate their purity. This column was checked for its capacity with different volume of sample and also a varied range of flow rate.

Results: Results revealed first peak included toxin in all range of parameters. In all conditions SDS-PAGE toxin showed a single band with 60kD under non reducing situation two single band with 60kD and 30kD under reducing situation. With increasing the loading sample, the separation was seen at 12% of bed volume with a high LF activity and pure fraction.

Conclusion: In this study we focused on optimizing of DT toxin by Sephacryl S100 that revealed a good behavior in separation. This column can be replaced to conventional methods for purifying of DT toxin in large scale production in industry for vaccine development.

Keywords: Purification, Diphtheria, Toxin, Chromatography

**P109 - 740: DESIGN, CLONING AND EXPRESSION OF A CYSTEINE CONTAINING
MUTANT OF STREPTOKINASE**

Mahsa Rezaei¹, Fahimeh Baghbani Arani², Reza Arabi Mianroodi³

1. Department of Microbiology, Faculty of Biological Sciences, Varamin-Pishva Branch, Islamic Azad University, Varamin
2. Department of Genetics & Biotechnology, Faculty of Biological Sciences, Varamin-Pishva Branch, Islamic Azad University, Varamin
3. Research and development department, Research and production complex, Pasteur Institute of Iran, Karaj

Background and Aim: Streptokinase is a potent plasminogen activator with widespread clinical use as a thrombolytic agent. However, its use is not risk free, because of its immunogenicity, hemorrhagic complications and relatively short half- life in circulation. Specific PEGylation of cysteine residue is a useful technique for reducing most of these complications. The aim of the present study was designing and production of a cysteine containing mutant streptokinase, to be used for specific PEGylation.

Methods: Glutamic acid 263, which is a surface amino acid in the structure of streptokinase protein, was selected for replacement with cysteine amino acid by site directed mutagenesis. The Glu263 codon was changed to cysteine codon in streptokinase gene, by SOEing PCR technique. Then, the intact and mutated streptokinase genes were inserted into expression vector pET-26(+). The constructs were transformed in *Escherichia coli* Rosetta (DE3) strain and the proteins were expressed by IPTG induction. The proteins were confirmed by SDS-PAGE and western blot analysis, purified by Ni-NTA agarose affinity chromatography under denaturing condition with urea and Sephadex G-25 column was applied to remove urea for refolding of the proteins.

Results: The results of this project showed that by using aforesaid vector and host, cysteine containing mutant gene is expressed well.

Conclusion: This study indicated that the cysteine analogue 263 can be represented as an appropriate candidate for specific PEGylation in future studies.

Keywords: Streptokinase, PEGylation, Cysteine analogue

**P110 - 768: SCREENING AND ISOLATION OF ASPARAGINASE PRODUCING BACTERIA
FROM CONTAMINATE SOIL OF SLAUGHTER HOUSE WASTE.**

Nasrin Gholami¹

1. shahid beheshti university

Background and Aim: L-asparaginase is a potential anti-carcinogenic enzyme.

Methods: Three different soil samples of contaminated soil of slaughter house waste were screened for potential producers of L-asparaginase using modified nutrient broth agar containing L-asparagine and phenol red indicator with pH 7. The strain isolated from slaughter house soil sample showed the maximum activity. The selected strain was characterized by biochemical tests as per the bergey's manual of determinative bacteriology and was found to be staphylococcus species.

Results: We isolated 4 bacterial strain with asparaginase activity from soil of slaughter house waste and one bacterium with high asparaginase activity was selected for our studies. The maximum enzyme activity showed by 24 hrs culture at 37 o C.

Conclusion: From this work, it was clearly shows that slaughter house soil samples can provide a rich source of L-asparaginase producing bacteria when compared to other soil sediments and construction area soil sediments show very low L-asparaginase producing bacteria. In contrast, almost all potent isolates showed nearest enzyme activity.

Keywords:: L-asparaginase, enzyme activity, bacteria.

**P111 - 769: DETECTION AND ISOLATION OF L-ASPARAGINASE AND LIPASE
PRODUCING BACTERIA FROM SOIL**

Nasrin Gholami¹

1. shahid beheshti university

Background and Aim:L-asparaginase is a candidate enzyme for anti-neoplastic agent against acute lymphoblastic leukemia and also extensively use in the food industry for prevention of acrylamide formation. L-asparaginase is widely distributed among microorganisms

Methods:In this study, cocci isolated from contaminate soil of slaughter house waste and screened for L-asparaginase activity. Production of L-asparaginase was carried out by using M9 and M9 broth medium. lipase production assayed on medium containing Rhodamine. L-asparaginase activity assay by nesslerization. then assay of protein done by lowry method

Results:According to morphological and biochemical properties, this bacterium is the new species of cocci genus. this bacteria sent for 16S rDNA sequencing.

Conclusion:Activity of L-asparaginase in this bacterium could apply for lymphoblastic leukemia treatment. In addition to isolated asparaginase from this bacterium has no glutaminase activity that has made the enzyme suitable candidate for treatment purpose.

Keywords:L-asparaginase enzyme, M9 broth medium, Rhodamine, lymphoblastic leukemia, L-asparagine, cocci

P112 - 780: THE EFFECT OF BURN GEL NAMED “ BURNOGEL” AGAINST BIOFILM OF P. AERUGINOSA ISOLATED FROM BURN PATIENTS

Morvarid Shafiei¹, Dr. Morvarid Shafiei², Dr. Farhad Shafiei³

1. -
2. Department of Bacteriology, Pasteur Institute of Iran
3. Department of Dental Biomaterials, School of Dentistry Tehran University of Medical sciences

Background and Aim: Burn injury as one of the most common and devastating forms of trauma, is a major public health problem worldwide. *Pseudomonas aeruginosa* as an important life-threatening nosocomial pathogen plays an important role in serious infections in burn patients. In this study, the effect of Burnogel, a gel which is composed of three herbal extracts, against 130 isolates of *P. aeruginosa* from burn patients was studied.

Methods: Burnogel - a compound consisting of three plant extracts- was prepared. A total of 130 isolates of *P. aeruginosa* from different burn patients and *P. aeruginosa* PAO1 were investigated. Antimicrobial susceptibility of Burnogel was performed according to the standard CLSI guideline. The anti-biofilm effects were assessed using microtiter plate method.

Results: It was observed that Burnogel presented high antibacterial activity against *P. aeruginosa* planktonic cells. Burnogel was efficient to disperse 3-day- old biofilm structures.

Conclusion: Finally, it can be suggested that Burnogel can be applied as antimicrobial and anti-biofilm agent against *P. aeruginosa* in burn patients.

Keywords: Burnogel, Biofilm, *P. aeruginosa*

**P113 - 816: A STUDY OF PECTINASE ENZYME GENE IN HALOPHILIC BACTERIA FROM
SALT LAKE IRAN**

Zohre Nasrollahzade¹, Eniseh Saleh-Ghamari², Mohammad Tahmaseb³, Mohammad Ali Amoozegar⁴

1. Msc Student of Genetics, Faculty of Biological Sciences, Kharazmi University, Tehran, Iran
2. Assistant Professor of Microbiology, Faculty of Biological Sciences, Kharazmi University, Tehran, Iran
3. Assistant Professor of Genetics, Faculty of Biological Sciences, Kharazmi University, Tehran, Iran
4. Associated Professor of Microbiology, Tehran University, Tehran, Iran

Background and Aim: Pectinase or pectinolytic enzymes are enzymatic complex including pectin methyl esterase, pectin lyase and polygalacturonase which degrade pectin in intermediate plant cell wall. Finding the microorganisms with ability of synthesis of these enzyme in extreme environmental condition such as temperature, pH or salt concentration could have beneficial application in industry. In this project we screened these microorganisms from natural extreme condition and studied the genes responsible of coding pectinase enzymes.

Methods: Isolated microorganisms from Urmia, Inche boron and Gomeishan Ponds were cultured on a medium containing pectin precursor and positively selected regarding appearance halo by KI/I indicator. In order to screen the pectinase gene, the genomes were amplified using appropriate primers. The products then cloned and sequenced.

Results: Seventeen isolated samples were positively identified among 130 ones which came from Gomeishan with 10 samples, Inche Boron with 6 samples and Urima ponds with 1 sample.

Conclusion: After sequencing the PCR products from 17 positive samples of halophile bacteria, the phylogenic tree was established for introducing the evolutionary relationship between pectin lyase gene in different strains. In conclusion, the sequence of pectinase gene showed significant homology between studied stains.

Keywords: Pectinase Enzyme ,halophilic bacteria ,Molecular Screening

**P114 - 817: PHYSIOLOGICAL CHARACTERIZATION OF CHLORELLA AND
SELENASTRUM SP. AS PROTEIN AND LIPID SOURCE IN VARIOUS CULTURES**

Ladan Baftechi¹, Neda Soltani², Zeinab Behzadian³

1. Dep. Petroleum Microbiology, Research Institute of Applied Science of ACECR, Shahid Beheshti Univ., Tehran
2. Dep. Petroleum Microbiology, Research Institute of Applied Science of ACECR, Shahid Beheshti Univ., Tehran
3. Dep. Petroleum Microbiology, Research Institute of Applied Science of ACECR, Shahid Beheshti Univ., Tehran

Background and Aim: Microalgae are ubiquitous microorganisms and have the ability to grow wherever they have access to sunlight and simple nutrients. Their rate of growth and also synthesis of various metabolites are affected by the availability of addition of certain specific compounds and appropriate aeration. So study the effect of different cultures on the physiology of two applied microalgae (Chlorella and Selenastrum) as lipid and protein source have done.

Methods: Chlorella and Selenastrum sp. provided from culture collection of ACECR. They have cultured in two different medium N8 and BG11 for about a month. Their growth rate were measured by spectrometry method in 750 nm. Chlorophyll contents by Marker 1972 and total proteins by Bradford 1976 were measured at the logarithmic phase of growth. Total lipids by Bligh and Dyer 1995 and EPS (Exocellular Polymeric Substances) by Dubois 1956 measured during the stationary phase of growth.

Results: Results showed that both of the specimens have more growth rate in BG11 but the the rate of Chlorella ($\mu=0.098 \text{ d}^{-1}$) was higher than Selenastrum sp. ($.084 \text{ d}^{-1}$). Chlorella sp. had more chlorophyll in N8. Comparison of proteins showed no significant differences but Selenastrum sp. had more lipids while Chlorella sp. had more EPS in BG11 medium.

Conclusion: According to the results it can be concluded that BG11 is a suitable culture for the growth of these specimens. But N8 is more suitable for their biochemical activities except secretion of EPS that has increased in BG11 by Chlorella sp. .

Keywords:: Chlorella, EPS, lipids, mediums, proteins, Selenastrum.

**P115 - 821: EVOLUTIONARY ENGINEERING OF NATIVE CITROBACTER STRAIN TO
IMPROVE THE PERFORMANCE ON ORGANOPHOSPHORUS PESTICIDES
DEGRADATION BY GENOME SHUFFLING**

Mohammad Sadegh Beikverdi¹, Ali Mohammad Latifi², Ardeshtir Hesampour³, Morteza Mirzaei⁴

1. Department of Biology, Faculty of Basic Sciences, Islamic Azad University central Tehran Branch, Tehran, Iran
2. Applied Biotechnology Research Center, Baqiyatallah University of Medical Science, Tehran, Iran.
3. Department of Biology, Faculty of Basic Sciences, Islamic Azad University central Tehran Branch, Tehran, Iran
4. Applied Biotechnology Research Center, Baqiyatallah University of Medical Science, Tehran, Iran.

Background and Aim: Organophosphorus pesticides are common chemicals to protect crops and livestock. Ops are acetylcholine esterase inhibitors and have been reported as the third cause of poisoning and the main cause of mortality due to poisoning. Whereas most used chemical and physical methods to decontaminate OPs have many defects, so a safe technology for biodegradation is required. microorganisms have been found potent to break down Ops. successes in studying molecular mechanisms of bacterial mutagenesis induced by factors have been achieved. Mutant strains were obtained from the acclimatized species by Genome Shuffling using protoplast fusion

Methods: Native citrobacter was first mutated using UV (for 3, 10 and 15 min) and EthBr (50, 100, 150 and 200 µg/ml), based on Weiss et al method. Protoplast fusion was then done according to Dai and Copley method: 500cc of the fresh mutated cells were harvested, washed with Tris HCl 10mM, and resuspended in Tris 0.1M (containing 20% sucrose, lysozyme 40µg/ml, EDTA 0.1 M). Protoplasts were added to regeneration media, the mixture was then centrifuged, resuspended in regeneration media and incubated for 10h at 100rpm at 37 °C. The sample was inoculated on MSM-agar medium with different concentrations of Diazinon.

Results: The maximum concentration in which UV-mutated cells could grow was 5g/L (for 3 min) and for EthBr-mutated cells were 8g/L (200µg/ml EthBr), in result, the protoplast fusion mutated cells could grow at a higher concentration of 11 g/L Diazinon

Conclusion: Consequently, Genome Shuffling showed an enhanced function of enzyme compared to native strains and also strains with unknown genome.

Keywords: Native Citrobacter, Organophosphorus Pesticides , Evolutionary Engineering

**P116 - 835: OPTIMIZATION OF CARBON AND NITROGEN SOURCES AND THEIR
CONCENTRATION FOR ANTIMICROBIAL METABOLITES PRODUCTION BY
STREPTOMYCES ACS135**

Mahsa Sadeghzadeh¹, bahar shahnavaz², abolghasem danesh³, razieh zargari orozaki⁴

1. 1Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
2. 1Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
3. Biotechnology research center, Mashhad University of Medical Sciences, Mashhad, Iran
4. 1Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran

Background and Aim: The discovery of marine Streptomyces with antimicrobial activity caused marine Streptomyces considered as an important source to find new secondary metabolites. Recently discovery new compound from terrestrial Streptomyces had decreased. The goal was optimization carbon and nitrogen sources and their concentration to increase antimicrobial metabolites by Streptomyces ACS 135 isolated from Oman Sea. We hope the bioactive compound will be novel

Methods: Agar well diffusion assay use to identify the optimize carbon and nitrogen sources and their concentration. In optimization of carbon and nitrogen sources use different materials. The carbon sources include glucose, starch, dextrin, glycerol and nitrogen sources contain soy pepton, tripton, yeast, malt, pepton and ammonium sulfate. We tried different concentration for each sources

Results: According to the test, the suitable carbon sources is dextrin with concentration of 2% and the optimize nitrogen sources is tripton with concentration of 1.6%. We repeated every test in 3 times

Conclusion: The result show after optimization diameter of inhibition zone doubled in compare of before it. Finally it demonstrated increasing production of bioactive metabolites by Streptomyces ACS135

Keywords: optimization, inhibition zone, bioactive metabolites, strptomyces ACS 135

P117 - 845: THE EFFECT OF MINERAL PARAMETERS ON PRODUCTION OF BIOACTIVE COMPOUNDS BY STREPTOMYCES ACS 135

Mahsa Sadeghzadeh¹, abolghasem danesh², bahar shahnavaz³, razieh zargari orozaki⁴

1. 1Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
2. Biotechnology research center, Mashhad University of Medical Sciences, Mashhad, Iran
3. 1Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
4. 1Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran

Background and Aim: Recently, researchers noticed to production of novel antibiotics by marine Streptomyces. Nowadays many novel antibiotic discover from marine Streptomyces. Because of antibiotic resistance, discovery of novel antibiotic was accentuated. The goal is study effect of mineral parameters on production of bioactive compound by Streptomyces ACS 135 isolated of Oman Sea.

Methods: To achieve this goal, fermentation of the strain last for seven day and after centrifuging media and isolating supernatant, we used agar well diffusion test. We tried five different concentration to check the influence of each parameter.

Results: The production of antimicrobial compounds was high when the strain was cultured in media with sodium chloride at the concentration of 1%, Dipotassium phosphate at the concentration of 0.1%. Magnesium sulfate had no influence on production of antimicrobial compounds

Conclusion: We concluded diameter of inhibition zone enhanced after optimization and it showed minerals concentration had considerable effect on production of bioactive metabolite by Streptomyces ACS 135.

Keywords: Mineral parameters, optimization, antimicrobial compound, fermentation, Streptomyces ACS 135

**P118 - 852: ISOLATION AND IDENTIFICATION OF PHB PRODUCING BACTERIA FROM
WASTE OF FACTORY**

Nazila Gholam Veisi¹, Roya Moravej², Sirvan Mohammadi Azar³

1. Department of Biology, Sanandaj Branch, Islamic Azad university, sanandaj, Iran
2. Department of Biology, Sanandaj Branch, Islamic Azad university, sanandaj, Iran
3. Department of Chemistry, Sanandaj Branch, Islamic Azad university, sanandaj, Iran

Background and Aim: Today, applying plastic materials in various parts of life including industry, medicine and agriculture take a great place. But, the main drawback in applying these polymers is their resistance against biodegradation and accumulation in environment and create environmental pollution. One way to solve this problem is to produce and apply degradable plastics. A group of biodegradable polymers is known as polyhydroxyalkanoates (PHAs). Polyhydroxy butyrate (PHB) is one of the most important compounds of PHA that a group of bacteria which can produce it as one of storage sources of Carbon and energy is through intracellular. The research aim is to isolate and identify the producer bacteria of PHB of waste water, soil and sludge of factory.

Methods: This work is to isolate PHB-producing bacteria from waste of Istak factory. Samples collected from waste and soils in Sanandaj, bacterial isolates were screened for PHB production using Sudan Black B staining, five isolates exhibited strong PHB production. Then, these strains were characterized by morphological, biochemical tests and 16s rRNA sequencing. The recovered polymers were confirmed by GC-MS method.

Results: Through gas chromatography isolations were detected as PHB producer bacteria by means of sequencing 16s rRNA, in which among them the highest rate of production is related to *Pseudomonas* sp.

Conclusion: Aiming to simple food requirements, bacteria producing PHB biopolymer, applying factory waste, not only produce biodegradable plastics, but also reduce environmental pollution.

Keywords: Biodegradable Polymer; Waste; polyhydroxyalkanoates; Sudan Black B; GC-MS; *Pseudomonas* sp.

**P119 - 854: ISOLATION AND IDENTIFICATION OF OIL- PRODUCING NOSTOC AS A
POTENTIAL FOR BIODIESEL PRODUCTION**

Susan Solati¹

1. MSc. Student of Microbiology, Biology Dep., Faculty of Sciences, Islamic Azad University.,Falavarjan, Iran

Background and Aim:In today's world the widespread use of fossil fuel such as petroleum, coal and natural gas, cause several environmental sequences which triggers the research for finding alternative fuels. Additionally, diminishing petroleum reserves is the biggest motivation behind the increasing number of researches. a number of studies have shown that biodiesel fuel are defined as fatty acid methyl esters derived from various renewable lipid resources . because of their renewable characteristic biodiesel fuels are notable alternatives to solve the worldwide energy problem. The microorganism such as bacteria, yeasts, molds and algae can accumulate lipids at more than 20% of their biomass are defined as oleaginous species.

Methods:different municipal wastewater lagoon samples screened for isolation of cyanobacterial strains. the cyanobacteria cells were culture in 250 ml Erlenmeyer flasks containing 100 ml BG-11 medium. illuminated by cool white fluorescent lamps ,pH 8, 25 ° C and rotating at 120 rpm for 25 days. lipid was extracted with chloroform – methanol solution. cyanobacteria sp with the highest lipid activity was identified according to microscopic and macroscopic characters and 16SrRNA sequences.

Results:in this research, the maximum lipid content could be achieved in the BG-11 medium containing 1g/l NaNO₃ , at pH 8 after 20 days. The maximum lipid contents was measured as 30% for Nostoc.

Conclusion:according to the results, cyanobacteria can be a source of production for biodiesel. even though there are not any reports on the lipid accumulation properties of the cyanobacteria cells for biodiesel production, high lipid accumulation properties was found for the Nostoc.

Keywords:Biodiesel; Cyanobacteria; Municipal wastewater; Nostoc

**P120 - 860: TRIM69 AS A SUITABLE CANDIDATE FOR IMMUNOTOXINS DESIGNING
WITH WIDE RANGE TARGETS AS WELL AS OVARIAN CANCER**

Razieh Sabagh¹, Aliakbar Haddad-Mashadrizesh², Samaneh Dolataabadi³

1. Department of biology, Science and Research branch, Islamic Azad University, Khorasan Razavi, Neyshabur, Iran
2. Cell and molecular biotechnology research group, institute of biotechnology, and Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
3. Department of biology, Science and Research branch, Islamic Azad University, Khorasan Razavi, Neyshabur, Iran

Background and Aim: Cancers, as a major source of the mortality in the world, are causing by the various environmental and internal factors. So, there are various commercial or in developing approaches for diagnosis, prevention and treatment of these diseases in the global health network. In this regard, immunotoxin development is a promising and new method for targeting malignancies cells.

Methods: In this regard, comparative analysis on the in-silico expression of the cell surface specific antigens of the ovarian cancer led to reveal the high and specific expression of the MAGE4 for this type of cancer.

Results: Moreover, our survey for detection the corresponding ligands of the MAGE4, white string programs, led to reveal the PSMD10, TRIM69, UQCRB, CTAG1B, EID3, NSMCE4A, NSMCE1, UBC, MSX1 and MSX2 as specific ligands with suitable binding affinity to the antigen.

Conclusion: Nonetheless, ligands validation based on the length, affinity to the antigen, post-translation modification as well as topology of the ligands with corresponding molecule to the cells showed that the TRIM69 is an ideal candidate for immunotoxin development with ability to targeting MAGE4.

Keywords: Cancer, immunotoxin, antigen, ligand

**P121 - 871: MAGNETIC PROPERTIES OF MAGNETOSPIRILLUM GRYPHISWALDENSE IN
MAGNETIC FIELD**

Shima Jeddi¹, Farinaz Roshani², leila Hatami Giklou³, Seyed Fazlollah Mousavi⁴

1. Alzahra University of Tehran, Department of Physics
2. Alzahra University of Tehran, Department of Physics
3. Pasteur Institute of Iran, Department of Microbiology
4. Pasteur Institute of Iran, Department of Microbiology

Background and Aim: Magnetotactic bacteria is a group of anaerobic or microaerobic gram negative prokaryotes that align and swim along magnetic field lines due to paramagnetic intracellular structure called magnetosome in size of 30 to 120 nm. To have a proper orientation they must be placed on a straight line consecutively, so their magnetic moments can added together. Compared to artificial magnetic nanoparticle, magnetosomes have more applications because they have controlled morphology, high stability and high paramagnetic property. Some of their important applications are nucleic separation and isolation, immobilization of enzymes, drug, antibody and protein delivery, MRI contrast agent and hyperthermia in biogenic, heavy metal separator in industry. Considering that in most of these applications the magnetic behaviors of cells are important, hence the collective guidance and movement of these cells in various environmental conditions must be studied. In this study we investigate the effect of concentrations of iron in culture medium on magnetic behavior of a group of magnetotactic bacteria called *Magnetospirillum gryphiswaldense*.

Methods: First the bacteria were cultured in suggested medium culture of DSMZ with different concentrations of iron and oxygen. Then the magnetic properties of them investigated by placing the cultured suspensions in the external magnetic field and analyzing by some applications and theory methods.

Results: The results are in progress.

Conclusion: considering that the results are In progress it is expected we can achieve applied magnetic properties of these cells and the nanoparticles of them.

Keywords: Magnetotactic Bacteria, *Magnetospirillum gryphiswaldense*, Magnetosomes, Magnetic Field

**P122 - 888: DIPHTHERIA TOXOID PRECIPITATION BY AMMONIUM SULPHATE IN TWO
CONDITIONS DRY AND LIQUID FORMS**

Meisam Akrami¹, Mojtaba Noofeli², Ali Nazari Shirvan³, Mitra Sadat Tabatabaei⁴

1. Department of Biology, Faculty of Science, Islamic Azad University Central Tehran Branch, Iran
2. Department of human bacterial vaccines, Razi Vaccine and Serum Research Institute, Karaj, Iran
3. Department of Proteomics and Biochemistry, Razi Vaccine and Serum Research Institute, Karaj, Iran
4. Department of Biology, Faculty of Science, Islamic Azad University Central Tehran Branch, Iran

Background and Aim: Diphtheria toxin is an extracellular protein of *Corynebacterium diphtheria* that inhibits protein synthesis and kills susceptible cells. The gene that encodes DT (tox) is present in some corynephages, DT is only produced by *C. diphtheria* isolates that harbor tox⁺ phages. This toxin is a protein including 535 amino acid with MW=60 kDa. DT toxin is a potent exotoxin that causes diphtheria as an acute and fatal bacterial disease in human.

Methods: The bacteria was grown for 72 h at 37°C in fermentor. The supernatant of 12% ammonium sulfate was precipitated by adding extra 14% ammonium sulfate and separated by centrifuge at 10000 rpm for 30 min. The diphtheria toxoid precipitation saturated solution 4.3 M and salt dry ammonium sulfate with different percentages were used. Results of this methods was studied with SDS PAGE and (Lateral flow test) LF TEST.

Results: Results revealed the ammonium sulfate solution 4.3 M compared with dry salt has better result . All conditions SDS-PAGE toxin showed a band with 60kD in two forms but precipitation by solution 4.3 M revealed a good behavior in separation and this method have low impurity band compared with dry salt and has better LF.

Conclusion: In this study we focused on optimizing of DT toxin precipitation by ammonium sulphate in two conditions dry and liquid forms ,the ammonium sulfate solution 4.3 M revealed a good behavior in separation. Precipitation by supersaturated solution 4.3 M replaced to conventional methods for purifying of DT toxin in large scale production in industry for vaccine development.

Keywords: Diphtheria, Precipitation, Toxoid, Ammonium sulphate

P123 - 926: CLONING AND EXPRESSION OF THE RECOMBINANT EPEX IN PICHIA PASTORIS

Mozhdeh Zamani¹, Najmeh Zarei², Atieh Hashemi³, Masoumeh Rajabibazl⁴

1. Department of Biotechnology, Faculty of Advanced Sciences & Technology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran – Iran (IAUPS)
2. Biotechnology department, Pasteur Institute of Iran, Tehran, Iran
3. Department of Pharmaceutical Biotechnology, School of Pharmacy, Shahid Beheshti University of Medical Sciences, Tehran, Iran
4. Department of Clinical Biochemistry, Faculty of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: Epithelial cell adhesion molecule (EpCAM) is a membrane glycoprotein that is overexpressed on the majority of tumor cells of epithelial origin and thereby can be used as a target of immunodetection and immunotherapy of cancer. During the last two decades, the yeast *Pichia pastoris* (*P. pastoris*) has become a popular host for the production of recombinant proteins because it combines the advantages of both mammalian and prokaryotic expression systems. In this study, we used the *Pichia* expression system to express EpCAM extracellular domain (EpEX).

Methods: Here, the codon optimized EpEX gene was cloned into the pPICZαB and transformed in GS115 strain via electroporation. To detect the recombinant protein expression, the culture supernatants of the transformants were analyzed by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and western blotting. The expression levels of EpEX were evaluated by scanning the intensity of the bands.

Results: Successfully cloned EpEX gene into the pPICZαB vector was confirmed by restriction analysis and sequencing. The transformants with genome containing inserted pPICZαB- EpEX were confirmed via PCR amplification of genomic DNA using AOX1 primers. The protein bands around 50 kDa were clearly detected in the SDS gel. Cell free supernatants were further analyzed by western blotting using mouse anti-6XHis tag antibody. The results displayed bands at the appropriate size.

Conclusion: The presented data show the ability of *P. Pastoris* in the expression of recombinant EpEX which may be used in development of cancer immunodetection and immunotherapy.

Keywords: Cloning, Expression, *Pichia pastoris*, EpCAM, EpEX

**P124 - 933: AN INVESTIGATION ON THE STABILITY OF THE CATALYTIC DOMAIN OF
DIPHThERIA TOXIN IN SEPARATED SITUATION**

Mohammad Fatehi abdol abadi¹, Aliakbar Haddad-Mashadrizesh², Jafar Saeidi³

1. Department of Biology, Science and Research branch, Islamic Azad University, Khorasan Razavi, Neyshabur, Iran
2. Cell and Molecular Biotechnology Research Group, Institute of Biotechnology, Ferdowsi University of Mashhad, Mashhad, Iran and Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
3. Department of Biology, Science and Research branch, Islamic Azad University, Khorasan Razavi, Neyshabur, Iran

Background and Aim: Diphtheria toxin, as a critical therapeutic factor in immunotoxins development, is consisting of two parts A and B. The A fragment is containing the active site of this toxin, which are considered in this study for the evaluation the stability of it in separated situation.

Methods: At the first step, 3D structure of the toxin with the ID: 1XTD was retrieved from PDB. Discovery Studio3.0 Client was used for removing the water molecules, ligands and catalytic domain from the intact toxin. Simulation of catalytic domain compared to intact diphtheria toxin, were performed using GROMACS5.07, gromos96 43a1 force field. It was performed in 310°K for NVT, NPT, MD; and 2ns of time for MD step. RMSD and RMSF plots were drawn by excel. Moreover, the alignment structures of the catalytic domain and intact toxin were shown by Pymol software.

Results: The result of RMSF plot indicate that the about 11% of the amino acids of the catalytic domain is more than of them in the native structure. On the other hand, this plot showed that the differences in the RMSF values for about 15 amino acids is greater than 0.1. More analysis demonstrate that the RMSF values of five amino acid from six of them, which are situated in the active site of the catalytic domain, are less than of them in the intact toxin.

Conclusion: In general, the results of this investigation indicate that the stability of the catalytic domain as well as active site, in separated form, is more than of them in intact toxin.

Keywords: DiphtheriaToxin, Therapeutic factor, Catalytic domain, Active site, GROMACS-5.0.7

**P125 - 987: A STUDY ON THE EFFECT OF CALCIUM PEROXIDE NANOPARTICLES AND
FE (II) IONS ON MICROBIAL POPULATION OF GROUNDWATER IN MODIFIED FENTON
REACTION**

Fatemeh Gholami¹, Mohammad Ali Amoozegar², Mahmoud Shavandi³, Seyed Mohammad Mehdi
Dastgheib⁴

1. Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran
2. Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran
3. Ecology and Environmental Pollution Control Research Group, Environment and Biotechnology Research Division, Research Institute of Petroleum Industry (RIPI), Tehran, Iran
4. Microbiology and Biotechnology Group, Environment and Biotechnology Research Division, Research Institute of Petroleum Industry (RIPI), Tehran, Iran

Background and Aim: Polycyclic aromatic hydrocarbons (PAHs) are amongst the most widespread contaminations in groundwater. Among various techniques for remediation PAHs from groundwater, application of calcium peroxide (CaO₂) is regarding as one of the most accepting techniques. In present investigation, CaO₂ nanoparticles were synthesized and the effect of nanoparticles on the microbial population of the groundwater were studied in batch experiments in the presence and absence of Fe²⁺ ions

Methods: Batch experiments were conducted in 100 ml vials which contained groundwater and 200 mg/l of CaO₂. To study the effect of nanoparticles on the microorganisms in chemical oxidation process (modified Fenton reaction), 200 mg/l of FeSO₄ was added to the vials. The effect of nanoparticles on dissolved oxygen (DO), pH and microbial population of the groundwater were investigated within 43 days

Results: Dissolved oxygen of the groundwater in presence of CaO₂ increased from 5 (blank) to 8.02 mg/l. Addition of Fe²⁺ ions to the groundwater and CaO₂ resulted in 7.8 mg/l for DO level. Furthermore, in presence of Fe²⁺ ions, pH of the groundwater was controlled and kept below 8.34 within 43 days. Whereas, without application of FeSO₄, pH raised to 9.1 for the sample with CaO₂. Microbial population was completely controlled by nanoparticles after 2 days, while presence of Fe²⁺ ions increased microbial count to 2.9 log cfu/ml within 43 days by neutralization of the environment

Conclusion: Addition of Fe (II) ions to the groundwater in presence of CaO₂ nanoparticles neutralize the pH and can be helpful for improving the pollution remediation from groundwater

Keywords: groundwater, peroxide calcium, fenton reaction

**P126 - 991: BIOREMEDIATION OF NAPHTHALENE CONTAMINATED GROUNDWATER
BY MAGNESIUM PEROXIDE (MGO₂) NANOPARTICLE**

Fatemeh Gholami¹, Mohammad Ali Amoozegar², Mahmoud Shavandi³, Seyed Mohammad Mehdi Dastgheib⁴

1. Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran
2. Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran
3. Ecology and Environmental Pollution Control Research Group, Environment and Biotechnology Research Division, Research Institute of Petroleum Industry (RIPI), Tehran, Iran
4. Microbiology and Biotechnology Group, Environment and Biotechnology Research Division, Research Institute of Petroleum Industry (RIPI), Tehran, Iran

Background and Aim: As ubiquitous pollutants of groundwater, polycyclic aromatic hydrocarbons are major concerns in developed and developing countries. Due to their nonpolar nature and high stability, these components tend to accumulate in the environment. Bioremediation is a cost-effective and environmentally friendly technique which can be applied for PAHs contaminated groundwater. In the present study, magnesium peroxide (MgO₂) nanoparticles (as a solid oxygen releasing compound) used to bioremediate naphthalene from groundwater

Methods: Batch experiments were conducted in 100ml headspace vials to study the naphthalene bioremediation from groundwater by MgO₂ nanoparticles. Each vial contained 300 mg/l nanoparticles and 20 mg/l naphthalene in the groundwater. To study the effect of microorganisms on the remediation efficiency, a sample was prepared by addition of autoclaved groundwater. The effect of nanoparticles on dissolved oxygen (DO), pH, microbial population and naphthalene concentration in groundwater were investigated within 22 days. Standard plate count (SPC) method was applied to study the microbial population on R2A agar. Naphthalene concentration was measured by HPLC

Results: Results showed 100% naphthalene bioremediation for MgO₂ nanoparticles after 15 days. Whereas, the sample which contained sterile groundwater removed pollutant completely from groundwater within 22 days. MgO₂ was able to raise the DO of the groundwater to 9.8 and 12.48 mg/l for biotic and abiotic samples, respectively. Furthermore, application of MgO₂ in groundwater resulted in increasing the microbial population from 3 to 6.38 log cfu/ml at the end of the experiment

Conclusion: Naphthalene remediated efficiently from groundwater in presence of synthesized nanoparticles by increasing in DO and preparation of oxidative condition.

Keywords: Bioremediation, polycyclic aromatic hydrocarbons, groundwater

**P127 - 1008: EXPRESSION OF EPCAM EXTRACELLULAR DOMAIN AS A CANDIDATE
VACCINE IN COLORECTAL CANCER IN E.COLI**

Farideh Rasouli kery bozorg¹, Atieh Hashemi², Malihe keramati³, Masoumeh Rajabibazl⁴

1. Department of Biotechnology, Faculty of Advanced Sciences & Technology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran - Iran (IAUPS)
2. Department of Pharmaceutical Biotechnology, School of Pharmacy, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. Assistant Professor, Pilot of nanobiotechnology Department, Pasteur institute of IRAN, Tehran, Iran
4. Department of Clinical Biochemistry, Faculty of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: Cancer vaccination has become an important focus of oncology in recent years. Active immunization with tumor-associated antigens such as immunogenic epitopes of epithelial cell adhesion molecule (EpCAM) is thought to potentially overcome the reoccurrence of metastasis. EpCAM extracellular domain (EpEX) epitopes are of immunogenic epitopes expressed by the EpCAM antigen. Due to fast growth rate, cheap fermentation media and clear genetics, we tested E. coli as a preferred host for the expression of the EpEX as a potential colorectal cancer vaccine.

Methods: A codon optimized gene expressing EpEX vector was synthetically prepared and cloned in Pet32a(+) vector under the control of an IPTG inducible T7 promoter. The EpEX /Pet32a(+) construct was simultaneously transformed and expressed in the Rossetta (DE3) E. coli strain. Transformants were grown 3h in Ty2x media at 30°C and when the culture OD600 reached 0/7-0/9, protein expression was induced by addition of IPTG to a final concentration of 0/25 mM.

Results: Constructed plasmid was approved by sequencing reaction and restriction enzyme analysis. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and western blot analysis using mouse anti-6XHis tag antibody showed an estimated 50 kDa-size protein band corresponding to the recombinant EpEX.

Conclusion: These findings imply the ability of E.coli in the expression of recombinant extracellular domain of EpCAM which may be used as a potential candidate vaccine in colorectal cancer.

Keywords: EpCAM extracellular domain, E.coli, expression,

**P128 - 1021: THE COMPARATIVE INVESTIGATION OF THE ANTIMICROBIAL EFFECTS
OF THE HEN EGG LYSOZYME ENZYME IN WILD AND MUTANT STRAINS**

Vahid Mirzabayati¹, Seyyed Ali Hosseini², Mohammad Fatehi Abdolabadi³

1. Department of Biology, Science and Research Branch, Islamic Azad University, Neyshabur, Khorasan Razavi, Iran.
2. Department of Biology, Science and Research Branch, Islamic Azad University, Neyshabur, Khorasan Razavi, Iran.
3. Department of Biology, Science and Research Branch, Islamic Azad University, Neyshabur, Khorasan Razavi, Iran.

Background and Aim: The Lysozyme is an enzyme (129 amino acid residues) that catalyzes the hydrolysis of the P-1,6 glycosidic linkage of The peptidoglycan in the bacterial cell wall. The study of mutations that substrate binding of sub sites D-F in D48A and the activity against (GlcNAc)₅ were decreased.

Methods: The egg-White lysozyme with Pdbid: 9LYZ received from the PDB site. The next step is choosing some of the mutant lysozyme, then performs the early Dockings were performed by AutoDockTools1.5.6, thus the mutant lysozyme with Pdbid : 3WVY the higher binding affinity was selected. Then, the simulations were performed by GROMACS5.0.7 with gromos96 43a1 force field; and 10ns of time for MD step. In the next step, there was docking on PDB files by AutoDockVina Software. Finally, the alignment and analysis of protein modes was done by Pymol.

Results: For each simulated lysozyme we Performed 3 Dockings. Results for main lysozyme: -7.8, 7.7, and -7.8 kcal/mol. and result for mutant lysozyme: -6.3, - 6.7, -6.5 kcal/mol.

Conclusion: As an overall conclusion, this study shows us that the ligand binding affinity to main receptor (9LYZ) is higher Than the mutant receptor (3WVY). Also studying results proves that main lysozyme has the much higher antimicrobial effects than the mutant lysozyme.

Keywords: Lysozyme, Antimicrobial activity, GROMACS 5.0.7, AutoDockTools1.5.6

**P129 - 1063: BIOINFORMATICS STUDIES, CLONING AND EXPRESSION OF FUSION
PROTEIN MRPA.FLIC OF PROTEUS MIRABILIS AS A NEW TARGET AGAINST URINARY
TRACT INFECTION**

Shabnam Bahadori¹, Mohammad Reza Asadi Karam², Mehri Habibi³

1. North Tehran Branch, Islamic Azad University, Tehran, Iran
2. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
3. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran; m_habibi1362@yahoo.com

Background and Aim: *Proteus mirabilis* is a common cause of nosocomial urinary tract infection (UTI) in humans. It is frequently associated with complicated UTI, which occurs in patients with functional and/or structural abnormalities in the urinary tract. MR/P pili by having the adhesin MrpH are among the most important virulence factors of *P. mirabilis*. In addition to the role of flagellin (FliC) as structural component of flagella in bacterial pathogenesis, it is able to activate immune responses via Toll-like receptor 5 (TLR5). Thus, flagellin could be considered as potent adjuvant in designing new vaccines. In this study, with in silico studies, different forms of fusion protein MrpA with FliC were assessed and expressed in *E. coli*.

Methods: Different forms of FliC and MrpA fusion protein were modeled using the I-Tasser server. The validity of structures was investigated using RAMPAGE and ProSA web. Modeled structures were docked to TLR-5 using Hex docking server. Depending on the energy value and pose of interaction, the best fusion form was selected and subjected to cloning into pET28a vector and expressed in BL21 (DE3) host.

Results: Fusion protein consisting of MrpA.FliC showed the best interaction affinity to the receptor (TLR5). Cloning of this fusion was confirmed by DNA sequencing and its expression was observed on SDS-PAGE and confirmed by western blotting.

Conclusion: According to our in silico results, MrpA.FliC fusion protein showed the best interaction tendency to the receptor. This fusion protein was successfully cloned and expressed in *E. coli*. The ability of this fusion protein in activating immune responses is under study.

Keywords: Urinary Tract Infection, *Proteus Mirabilis*, In silico studies, Flagellin, MR/P pili, Fusion protein

**P130 - 1147: ISOLATION AND IDENTIFICATION BACTERIA RHIZOBIUM OF ROOT
NODULE PLANTS.**

EBRAHIM ESHAGHI¹, Hossein Mirzayi ², Mehrad Vosough³, Rahim Nosrati ⁴

1. Department of Biology, Faculty of Science, Nourdanesh Institute of Higher Education, Esfahan, Iran
2. Department of Microbiology, Islamic Azad University of Qom, Qom, Iran
3. Department of Biology, Faculty of Science, Nourdanesh Institute of Higher Education, Esfahan, Iran
4. Department of Pharmaceutical Biotechnology, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran

Background and Aim: Bacteria of family Rhizobiaceae are symbiotic and effectively convert atmospheric nitrogen which is utilized by the host. Rhizobiaceae family contains six genera namely Rhizobium, Sinorhizobium, Mesorhizobium, Allorhizobium, Azorhizobium and Bradyrhizobium. These rhizobia are characterized into two groups on the basis of growth rate. First group is fast grower rhizobia and second is slow grower rhizobia.

Methods: 32 Collection of plant: Root nodules were collected from young and healthy seedling of Pea plant. The detached root nodules were washed in tap water to remove the adhering soil particles from nodule surface. Nodules were dipped in 0.1% mercuric chloride (HgCl₂) solution for 30 sec and later washed successively ten times with sterilized distilled water to remove the traces of toxic HgCl₂. Surface sterilized nodules were transferred in test tube containing 5 mL sterilized distilled water. These nodules were crushed with the help of sterilized glass rod to obtain a milky suspension of bacterioids. These were streaked on YEMA containing Congo red. The plates were sealed by parafilm to avoid contamination and incubated at 28±1°C for 24-48 h. Bradyrhizobium or Rhizobium colonies were remained white, translucent, elevated and mucilaginous, after 24-72 h, whereas contaminations turned red. The colonies were picked up and transferred to YEMA slant for further characterization.

Results: 30 Rhizobiaceae bacteria were isolated from 32 samples collected. Gram staining was negative in all bacteria tests were positive.

Conclusion: Rhizobacteria effectively colonize plant root and increase plant growth by production of various plant growth hormones, N₂ fixation and biological control activity.

Keywords: Root nodules, Rhizobiaceae, N₂ fixation, YEMA

P131 - 1162: GENERATION OF ELECTRICITY USING MICROBIAL FUEL CELL

Elnaz Afshari¹

1. Young Researchers & Elite Club, Pharmaceutical Sciences Branch, Islamic Azad University (IAUPS), Tehran, Iran

Background and Aim: Microbial fuel cell (MFC) is a bio-electrochemical system that uses the natural metabolisms of microbes to produce electrical power. Recently the need of clean forms, renewable of energy and wastewater treatment have triggered wide research interest in developing the MFC technology.

Methods: MFC technology consists of two chambers that are separated by a semi-permeable membrane. In one compartment (under anaerobic anoxic conditions) an anode and in another room (aerobic anoxic conditions) a cathode were located. The cathode has been connected with anode. This process is based on oxidative reactions, where a compound is oxidized by microbes and electron transfer to cathode finally.

Results: Electricity-generating bacteria in anaerobic anode chamber of MFC produce protons and electrons through anaerobic respiration of substrates. The produced electrons are transferred to anode surface and then from external circuit travel to cathode, where they reduce oxygen to water. The transfer of electrons from the anode to the cathode and the potential difference between the electron acceptor and respiratory system, led to the generation of an electrical current.

Conclusion: By applying bacteria as anodic catalyst, MFC can directly convert biomass energy into electrical energy, provided a new way for biomass utilization and bioremediation. Also it can be used to provide energy of efficient small electrical devices in remote locations (eg scientific control devices in the fields of the deep sea) and the simultaneous production of electricity used in wastewater treatment.

Keywords: Electricity-generating bacteria, MFC, Bioremediation, Wastewater Treatment.

**P132 - 1171: DESIGN OF FR3 SYNTHETIC PEPTIDE AND EVALUATION OF ITS
ANTIBACTERIAL AND CYTOTOXIC EFFECTS.**

Seyed Mohammad Mahdi Ghahari¹, Mahdi Fasihi Ramandi²

1. Department of Immunology, Mazandaran University of medical science, Tehran, Iran
2. Department of Biotechnology, Baghiatallah university of medical science, Tehran, Iran

Background and Aim: With increasing antimicrobial resistance to common antibiotics, development of alternative therapeutic strategies are necessary. In the recent years, novel peptide antibiotics with activity wide range against of bacteria were introduced. In this study, antibacterial activity of FR3 peptide (NRWCFAGRR) against twelve pathogenic bacterial was evaluated

Methods: To investigation the antimicrobial activity, minimal inhibitory concentration, minimal bactericidal concentration, bacterial killing assay and nitrite oxide production were utilized with different concentrations (1.6- 200 µg/ml). Cytotoxic effect of peptide was evaluated by MTT assay. Cell viability of Hella cell line was investigated by MTT assay and nitrite oxide production measured by Griess method

Results: Result of MIC of FR3 peptide was 200- more than 400 µg/ml. also MBC result 200- more than 400 µg/ml. Result of hemolysis assay was 1.2 percent at 1mg/ml concentration. Nitrite oxide production of macrophage cell line j774 was 18.012 at 6.3 µg/ml concentration in 24h

Conclusion: As a result FR3 peptide has strong cytotoxicity on Hella cell line and show MIC range at the high concentration of this peptide. However, nitrite oxide production which was evaluated at the first time indicated that this peptide could stimulate adaptive and innate immunity. Therefore, FR3 peptide with stimulation immune system responses could be a good adoption for future studies.

Keywords: antimicrobial peptide. Cationic peptide. Minimal inhibitory concentration. Minimal bactericidal concentration. Nitrite oxide

**P133 - 1189: OPTIMIZATION OF INDUCER CONCENTRATION FOR RECOMBINANT
ACTIVIN A EXPRESSION**

Nahid Biroonro¹, Nahid biroonro1², Zahra hajihassan²³

1. 1: MSc student of University of Tehran, Faculty of new sciences and technologies, University of Tehran, Tehran, Iran
2. :2: Assistant professor of University of Tehran, Faculty of new sciences and technologies, University of Tehran, Tehran, Iran Corresponding author: hajihasan@ut.ac.ir

Background and Aim:Activin A, a member of the transforming growth factor β superfamily, plays important roles in numerous physiological processes such as cell differentiation and remodeling, regeneration and repair of tissues from various organs. Due to the vast clinical applications and low production from natural resources, recombinant production of it is necessary. So in this project, recombinant Activin A was expressed in DE3 strain of E. coli using pET21a vector. To achieve the highest levels of production, the effect of lactose and IPTG concentrations as inducers on expression of recombinant Activin A was studied by RSM method.

Methods:The corresponding vector was transformed to DE3 strain and the Activin A was expressed by induction of the promoter using different concentrations of lactose and IPTG. After 4 hours, total proteins were extracted using 8M urea and the protein concentration was measured by Bradford method.

Results:Our results showed that the highest concentration of the protein was achieved by 25 μ m and 2.25 μ m of lactose and IPTG respectively.

Conclusion:Using RSM, the best approach for optimization of biological processes could help us to obtain the best concentration of inducers for Activin A expression very fast and without more trial and errors.

Keywords:Optimization,RSM,IPTG,Lactose,

**P134 - 1203: OPTIMIZATION OF ENVIRONMENTAL CONDITION FOR BIO-PLASTIC (PHB)
PRODUCTION BY ALCALIGENES EUTROPHA PTCC1615**

Mahasti Rasoli¹, Ezat Asgarani², Mohammad reza soudi³

1. Alzahra University
2. Alzahra University
3. Alzahra University

Background and Aim: PHB is the polyester that forms of reproducible sources by many organisms under conditions of nutrient limitation (no balance of nutrient).

Methods: In this study inoculation of bacterial suspension with 0.5(v/v) in 500 ml Erlenmeyer flasks containing 100 ml of production medium was done for producing of PHB and then bacterial culture was evaluated in variable temperature and pH and agitation speed for optimization for 48 h in the shaker.

Results: Result showed that bacteria have maximum amount PHB production in temperature 35°C and 180 rpm and pH 7. Batch cultivation further performed in flask under optimized condition gave maximum cell biomass of 2.364 g/l with a PHB content of 0.9880 g/l. Also evaluated growth kinetic of bacteria (production of PHB in variable times) was shown that PHB production started after 15 h and after 48 h obtained maximum cell biomass to 1.86 g/l with a PHB content of 0.9645 g/l.

Conclusion: Some studies have shown that some bacteria, especially Gram-negative ones produce PHB up to 70% of dry cell weight under additional carbon source and nutrient limitation condition (N, P etc.) In this study content of PHB produced by *Alcaligenes eutropha* was 41.7957 % of D.C.W in the optimization condition.

Keywords: poly- β -hydroxybutyrate, PHB, *Alcaligenes eutropha*, Optimization of environmental condition

P135 - 1225: OVEREXPRESSION OPTIMIZATION OF AN ANTI-EPCAM EXTRACELLULAR DOMAIN SINGLE CHAIN VARIABLE FRAGMENT IN ESCHERICHIA COLI

Reyhaneh Najafi Soulari¹, Atieh Hashemi², Malihe keramati³, Masoumeh Rajabibazl⁴

1. Department of Biotechnology, Faculty of Advanced Sciences & Technology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran - Iran (IAUPS)
2. Department of Pharmaceutical Biotechnology, School of Pharmacy, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. Assistant Professor, Pilot of nanobiotechnology Department, Pasteur institute of IRAN, Tehran, Iran
4. Department of Clinical Biochemistry, Faculty of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: Epithelial cell adhesion molecule (EpCAM) is a well-established target antigen that is overexpressed on the cell surface of various human carcinomas. In normal epithelia, EpCAM expression is limited to the basolateral membrane. Due to this difference, it has been extensively studied in antibody-mediated imaging and immunotherapy of human carcinomas. Recently recombinant monoclonal antibody mediated immunotherapy has been developed in cancer therapy. The single chain variable fragment (ScFv) is a valuable alternative to an intact antibody. here, we report the optimization of anti-EpCAM-ScFv expression in an E. coli host of BL21 (DE3) based on tuning of three cultivation variables, including inducer concentration, temperature and post-induction time.

Methods: For optimization of anti-EpCAM-ScFv expression, cultivations were performed under different IPTG concentrations (0.25, 0.50, 1, 2) and temperatures (25, 30, 37°C). At the final expression time, cell density of each sample (OD₆₀₀) was measured. The cells were harvested by centrifugation at 10000 rpm for 5 min and the pellets were resuspended in a lysis buffer. Proteins were then separated by SDS-PAGE. The expression level of proteins was determined by densitometry analysis of polyacrylamide gels using TL120 software.

Results: Our results show that the inducer concentration (0.50 mM) and seven-hour post-induction incubation at 30 °C were sufficient to produce high level of ScFv.

Conclusion: Optimization of conditions during recombinant protein production for improved yield is a major goal for protein scientists. To this end, here, we reported an effective strategy for high level expression of the ScFv molecule against extracellular domain of EpCAM.

Keywords: EpCAM, ScFv, Optimization, Overexpression

P136 - 1226: PRODUCTION OF FIBROLYTIC ENZYMES BY A LOCAL YEAST STRAIN OF CONICHAETA SP.

Fateme Barati¹, Fatemeh Barati², Mohammad Reza Soudi³, Shaghayegh Nasr⁴, Azade Azadmard⁵

1. -
2. Alzahra University
3. Alzahra University
4. Iranian Biological Resource Center
5. Alzahra University

Background and Aim:Members of Conichaeta species are a number of polymorphic wood-related phytopathogenic yeast species. Capability of invading plant cell wall makes the species a suitable subject for the study of fibrolytic enzymes

Methods:In this study a local strain of Conichaeata sp. was used and starch-free wheat bran was prepared and qualified using Iodine solution. Fiber digestion was examined by flask culture method under mesophilic and aerobic conditions within 6 days. Ability of the strain for lignin hydrolysis via laccase production and degradation of cellulose and hemicellulose were tested in agar plates.

Results:The results showed that the native yeast strain is able to grow on fibers. Result of the test for releasing reductive simple sugars was positive. The experiments confirmed the production of cellulase and xylanase but no lignin hydrolyzing enzyme was produced on the basis of crystal violet decolorization and guaiacol degradation tests.

Conclusion:The yeast strain possesses the capability of fiber digestion and it can be a candidate for further studies on production of hydrolytic enzyme and functional feed.

Keywords: Conichaeata sp., Cellulase, Xylanase, wheat bran, yeast

**P137 - 1232: SECRETORY POLYSACCHARIDE DEGRADING ENZYMES IN CERTAIN
LOCAL YEAST SPECIES**

Azadeh Azadmard¹, Mohammad Reza Soudi², Shaghayegh Nasr³, Fatemeh Barati⁴

1. Alzahra University
2. Alzahra University
3. Iranian Biological Resource Center
4. Alzahra University

Background and Aim: A number of commercial polysaccharide degrading enzymes are produced by fungi. In contrast to filamentous fungi, production of carbohydrase enzymes is a rare trait among yeasts.

Methods: In this research, a number of appropriate yeast species were, isolated from different area of country, obtained from IBRC. Capability of enzyme production and secretion against a number of plant, algal and microbial polysaccharides including cellulose, carboxy methyl cellulose, xanthan, xylan, alginate, pectin and starch was investigated under mesophilic conditions within 5 days. Iodine, congo red and ruthenium red were used as reagents to show the halo zones of degradation in agar plates.

Results: Seven strains out of 12 could produce from 1 to 6 of the hydrolytic enzymes. Production of amylase, alginase, CMCase, pectinase, xylanase and xanthanase were observed. The most potent enzyme activities were observed in case of amylase and xanthanase and the weakest activity revealed in case of alginase on the basis of semi-quantitative tests.

Conclusion: Yeasts are generally recognized as safe organisms for food and feed applications. Thus, further investigation of such polysaccharide degrading enzymes is recommended.

Keywords:: carbohydrase, yeast, cellulose, carboxy methyl cellulose, xanthan, xylan, alginate, pectin, starch

**P138 - 1233: ANTAGONISTIC ACTIVITIES OF TRICHODERMA SPP. ON SCLEROTINIA
SCLEROTIORUM ROT OF SUNFLOWER**

Seyed Majid Safari¹, Kiomars Rouhrazi²

1. Department of Agriculture, Malekan branch, Islamic Azad University, Malekan, Iran
2. Department of Agriculture, Malekan branch, Islamic Azad University, Malekan, Iran

Background and Aim: *Trichoderma* spp. has been widely used in biological control studies against several commercial phytopathogens. However, little attention has been paid to their ability to control *Sclerotinia sclerotiorum*. This genus is rapidly growing colonies bearing tufted, repeatedly branched conidiophores with lageniform phialides and green conidia born

Methods: Twenty isolates of *Trichoderma* species were isolated from different rhizospheric soil samples collected from different places located in West Azarbayjan. Isolates were recovered from soil by a serial dilution method. The precolonized plate method was used to assay mycoparasitic abilities of all *Trichoderma* isolates towards *S. sclerotiorum* isolates. The reduction in growth and inhibition zone in the dual culture test was used as the criteria to evaluate the in vitro antagonistic property of *Trichoderma* spp

Results: Out of *Trichoderma* spp. Isolates. two species were found i.e. *Trichoderma harzianum* and *Trichoderma virens* in rhizosphere of sunflower. *T. harzianum* and *T. virens* were consistently found to be the effect inhibitor reduction in radial growth of all pathogens of *S. sclerotiorum* with an highest inhibition rate (80 %) with H1 and less inhibition rate (60%) with V2. The result of dual culture show that *Trichoderma harzianum* is a highly significant antagonistic agent ($P \leq 0.05$) inhibited the mycelial growth of *S. sclerotiorum*. Volatile metabolites generally had lower effects on the mycelial growth of *Sclerotinia* than the non-volatile ones

Conclusion: *Trichoderma* species are among important antagonists of pathogenic fungi. In this study antagonistic activities including competition and colonization against *S. sclerotiorum* with an inhibition rate of 86%.

Keywords: antagonistic activity. *Sclerotinia sclerotiorum*. *Trichoderma* spp.

**P139 - 1234: CLONING AND EXPRESSION OF RECOMBINANT GENE OF
ORGANOPHOSPHORUS HYDROLASE ENZYME**

Rasool Rahimizadeh¹, Ali Mohammad Latifi ², Mohammad Hosein sanati ³, Morteza Mirzaei ⁴,
Mohammad sadegh beykverdi ⁵

1. 1. Division of cellular and molecular biology, Department of biology, Nourdanesh University of Meymeh, Meymeh, Isfahan, Iran
2. 2. Applied Biotechnology Research Center, Baqiyatallah University of Medical Science, Tehran, Iran. Electronic address: amlatifi290@gmail.com
3. 1. Division of cellular and molecular biology, Department of biology, Nourdanesh University of Meymeh, Meymeh, Isfahan, Iran
4. 2. Applied Biotechnology Research Center, Baqiyatallah University of Medical Science, Tehran, Iran.
5. 2. Applied Biotechnology Research Center, Baqiyatallah University of Medical Science, Tehran, Iran.

Background and Aim: Organophosphorus hydrolase (OPH) is a bacterial enzyme that has been shown to degrade a wide range of neurotoxic organophosphate nerve agents. However, the effectiveness of degradation varies dramatically, ranging from highly efficient with paraoxon to relatively slow with methyl parathion.

Methods: Recombinant gene of Organophosphorus hydrolase enzyme were obtained from applied biotechnology center of Baqiyatallah university. Genes has been digested by Restriction enzymes. pET 28a vector was digested by the same restriction enzymes either. Genes was inserted in the vector and ligated by DNA T4 ligase by incubation an overnight in 13°C. Cloning was performed into E.Coli BL21 by thermal shock. Cloned bacteria was cultured on LB Agar medium with 20ug/ml kanamycin antibiotic for an overnight in 37°C. Grown colonies was sub cultured on LB Broth medium with 40ug/ml kanamycin antibiotic for an overnight in 37°C. IPTG was added to mediums with 0.5 mM final concentration and 20 uL of those was transformed on MSM agar medium containing 50, 100 and 200ug/mL Diazinon and incubate 3 days in 37°C. Native OPH enzyme was used as Control. survived cell were selected and cultivated on LB broth medium. Native OPH enzyme was used as Control.

Results: It was found the cloned bacteria could grows on 200 ug/mL Diazinon.

Conclusion: OPH enzyme gene has a good expression in E.Coli.

Keywords: Cloning and Expression, Organophosphorus Hydrolase, OPH enzyme

**P140 - 1237: DNA SHUFFLING OF A FAMILY OF ORGANOPHOSPHORUS HYDROLASE
ENZYME**

Rasool Rahimizadeh¹, Ali Mohammad Latifi², Mohammad Hosein sanati³, Morteza Mirzaei⁴, Mohammad sadegh beykverdi⁵

1. 1. Division of cellular and molecular biology, Department of biology, Nourdanesh University of Meymeh, Meymeh, Isfahan, Iran
2. 2. Applied Biotechnology Research Center, Baqiyatallah University of Medical Science, Tehran, Iran. Electronic address: amlatifi290@gmail.com
3. 1. Division of cellular and molecular biology, Department of biology, Nourdanesh University of Meymeh, Meymeh, Isfahan, Iran
4. 2. Applied Biotechnology Research Center, Baqiyatallah University of Medical Science, Tehran, Iran.
5. 2. Applied Biotechnology Research Center, Baqiyatallah University of Medical Science, Tehran, Iran.

Background and Aim: DNA shuffling is a powerful process for directed evolution, which generates diversity by recombination, combining useful mutations from individual genes. Organophosphorus hydrolase (OPH) is a bacterial enzyme that has been shown to degrade a wide range of neurotoxic organophosphate nerve agents. However, the effectiveness of degradation varies dramatically, ranging from highly efficient with paraoxon to relatively slow with methyl parathion. Sequential cycles of DNA shuffling and screening were used to fine-tune and enhance the activity of OPH towards poorly degraded substrates.

Methods: Genes of a family of Organophosphorus hydrolase enzymes were obtained from applied biotechnology center of Baqiyatallah university. After amplifying PCR (95°C, 10 min, (30*(94°C, 45s, 60°C, 45s, 72°C, 1min), 10min 72°C) genes were cleaved by DNase I. Then digestion was proved by Gel electrophoresis. Fragments of DNA were assembled to desired size by PCR with no primers and products was ran on 1% agarose gel electrophoresis.

Results: After DNA Digestion by DNase I, DNA smear on 2% Agarose gel was seen. Finally after performing electrophoresis test, the sharp band of desired size of DNA has been observed.

Conclusion: Consequently, this study showed that DNA Shuffling method can be used for gene manipulation.

Keywords: DNA Shuffling, Organophosphorus hydrolase, Enzyme manipulation,

**P141 - 1238: MOLECULAR CLONING OF HYALURONAN SYNTHASE AND ITS
EXPRESSION IN E. COLI BL21 (DE3)**

Parsa Parsian¹, Maliheh Keramati², Reza Ahangari Cohan³, Haleh Bakhshandeh⁴

1. Islamic Azad university - North Tehran Branch, Pasteur Institute of Iran
2. Pasteur Institute of Iran
3. Pasteur Institute of Iran
4. Pasteur Institute of Iran

Background and Aim: Hyaluronic acid (HA) is a high molecular weight polymer comprised of d-glucuronic acid and d-N-acetylglucosamine subunits. The hydrophilic biopolymer is abundant in tissues of humans and animals and due to high viscosity, non-immunogenicity and biocompatible properties, widely used in tissue engineering and medicine. This study aimed to clone and express the Hyaluronan synthase gene, an enzyme responsible for HA synthesis, in E.coli BL21 (DE3) strain, using pET system.

Methods: Hyaluronan synthase gene was amplified using specific primers (5'-GGAATTCATATGAGAACATTAAAAACCTCATAACTG-3' and 5'-CCCGCTCGAGTAATAATTTTTTACGTGTTCC-3') on *Streptococcus equi* subsp. *zooepidemicus* genomic DNA and subsequently cloned into pET21a+ plasmid using XhoI and NdeI restriction enzymes. The accuracy of the construct was confirmed by restriction map analysis and sequencing. The gene was expressed in E. coli BL21 (DE3) cells after induction by 1 mM of isopropyl beta-D thiogalactopyranoside (IPTG) and analyzed by 12% SDS-PAGE and coomassie blue staining.

Results: Electrophoresis of digested recombinant pET21a+ plasmid, showed a 1256 bp band of Hyaluronan synthase gene. SDS-PAGE analysis showed a 48.85 KDa band of protein product induced after induction with 1 mM IPTG.

Conclusion: In the present study, Hyaluronan synthase gene was successfully amplified from *Streptococcus equi* subsp. *zooepidemicus* genomic DNA, cloned and expressed using pET21a+ expression vector in E.coli BL21 (DE3) strain. This enzyme can be further used for assessment of HA synthase activity.

Keywords: Molecular Cloning, Expression, Hyaluronan synthase, E.coli BL21 (DE3) strain

**P142 - 1245: OVERPRODUCTION OF RECOMBINANT HUMAN GROWTH HORMONE IN
BATCH CULTURE IN E.COLI USING PLACKET- BURMAN STATISTICAL METHODS**

Valiollah Babaeipour¹, Reyhane Keshavarz², Ali Bahrami³

1. Department of Bioscience and Biotechnology, Malek Ashtar University of Technology
2. Department of Bioscience and Biotechnology, Malek Ashtar University of Technology
3. Department of Bioscience and Biotechnology, Malek Ashtar University of Technology

Background and Aim: Human growth hormone or somatotropin is a polypeptide chain consisting of 191 amino acids with a molecular weight of 22 kDa and contains two disulfide bonds that are secreted by the pituitary gland in the brain. Human growth hormone include the whole range of biological activity, and thus have wide therapeutic applications. Recombinant DNA technology, to produce a safe and abundant rhGH in different recombinant systems without the risk of transmission of human pathogens is possible.

Methods: To optimize production of Recombinant Human Growth Hormone, effect of 8 parameters (concentration of the carbon source, induction time and the growth temperature, carbon source, the concentration of magnesium sulfate, the yeast extract peptone, the inductor and buffering capacity) on the growth and production of recombinant proteins in bacteria complex culture medium using statistical methods platelets - Bremen 1 were evaluated.

Results: The results showed 1) induction temperature in 37 °C, carbon source such glucose and proportion 1:1 of yeast extract to peptone than the highest effect on protein production. 2) Magnesium sulphate increases the amount of protein expression and reduce the amount of biomass used. 3) under optimal conditions and factors, the amount of 0.66 g/l of recombinant protein in 4 hour after induction

Conclusion: The obtained results is the one of the highest values ever reported for production of recombinant proteins in batch culture.

Keywords: Human Growth Hormone, E.coli Rosetta-gami, Optimization Production, Recombinant Protein Production

Clinical Microbiology

P143 - 6: PREVALENCE OF BACTERIAL VAGINOSIS AND SENSITIVITIES TO DIFFERENT ANTIBIOTICS IN FERTILE/INFERTILE WOMEN REFERRING TO ARDABIL HEALTH CENTERS

Elnaz Baezzat¹, behboud jafari², roghayeh dargahi³

1. Department of Microbiology, Ahar Branch, Islamic Azad University, Ahar, Iran
2. Department of Microbiology, Ahar Branch, Islamic Azad University, Ahar, Iran
3. Department of Midwifery, University of medical sciences, Ardabil, Iran

Background and Aim: Bacterial vaginosis (BV) is associated with changes in normal vaginal microflora through which risk of pelvic inflammatory diseases and vaginal infections increase in women with BV. This study aims at determining the frequency of BV and antibiotic sensitivity in fertile and infertile women referring to Ardabil health centers.

Methods: This was a descriptive-analytical study conducted on 130 patients admitted to health centers in order to determine the prevalence of BV and antibiotic sensitivity and antibiogram test was performed in this regard. Besides, BV diagnostic tests were carried out based on demonstrating three of the four Amsel's criteria.

Results: preterm delivery and abortion have a significant relationship with BV ($P < 0.05$). The prevalence of BV was significantly associated with IUD contraceptive ($P < 0.05$). It was found that there is a significant reduction in the number of lactobacilli and an increase in BV ($P < 0.05$). Moreover, having sensitivity to different antibiotics has been correlated with the bacterial vaginosis.

Conclusion: There was a statistically significant difference in the prevalence of BV among fertile and infertile people. The prevalence of BV in fertile and in infertile women was 38% and 59% respectively. The bacterium was sensitive to clindamycin antibiotics and resistant to metronidazole in the conducted antibiogram. Moreover, 66.6% of the fertile women enrolled in the study were using IUD contraceptive.

Keywords: Bacterial Vaginosis (BV); Resistance to Antibiotics; Pregnancy; Ardabil

**P144 - 7: ANTIMICROBIAL RESISTANCE PATTERN OF PATHOGENIC BACTERIA
ISOLATED FROM CLINICAL SAMPLES (ROUHANI AND YAHYANEJAD HOSPITALS)**

Farahnaz Sadighian¹, Zahra Naderian², Shahandeh Zahra³, Eslamdost Zohreh⁴, Ghasemtabar Hamed⁵

1. Department of Laboratory Medicine(School of Medicine), Paramedical Faculty, Babol University of Medical Sciences, Iran.
2. Department of Laboratory Medicine(School of Medicine), Paramedical Faculty, Babol University of Medical Sciences, Iran.
3. Department of Laboratory Medicine(School of Medicine), Paramedical Faculty, Babol University of Medical Sciences, Iran.
4. Yahyanejad hospital, Babol University of Medical Sciences, Iran.
5. Rouhani hospital, Babol University of Medical Sciences, Iran.

Background and Aim:The Occurrences of healthcare-associated infections are more than 2 million in a year, which can lead to human and financial losses. One of the best strategies for preventing the spread of bacterial infections is diagnosis of bacterial agents and resistant to antibiotics. Aim of this study is antibiotic resistance pattern of pathogenic bacteria isolated from clinical specimens at two hospitals.

Methods:In this retrospective study, from 1/1/1393 to 30/6/1393, the bacteria were isolated from clinical specimens of patients who referred to Rouhani and Yahyanejad hospitals (Babol, north of Iran) were examined. The suitable differential mediums were used for diagnosis. AST was also performed by disk diffusion method to determine antibiotic sensitivity by CLSI 2011 protocol. Data were analyzed by using of the SPSS21 software.

Results:From 1264 clinical samples, 1072 bacteria were diagnosed. The most frequency of isolated bacteria was E.coli(39.1%). Acintobacterea isolated from sputum were 100% resistant to Ciprofloxacin, Gentamycin and Ceftazidim. Also, Pseudomonas aeroginosa isolated from sputum had high resistance against antibiotics. The most prevalence of bacteria was observed in Intensive-Care-Unit patient samples at Rouhani hospital (14.7%) and Emergency patient samples at Yahyanejad hospital (40.5%).

Conclusion:With regard to the high rates of antibiotic resistance bacteria in hospitals, and isolated bacteria from Intensive-Care-Unit patients who have higher risk of infection, it is recommended infection prevention and control strategies are designed to prevent the spread of bacterial infections especially multi-drug resistant bacteria.

Keywords:antibiotic resistance, clinical specimens, Acintobacterea, Pseudomonas

**P145 - 8: THE SERO-EPIDEMIOLOGY OF INFECTIOUS MONONUCLEOSIS IN
NEYSHABUR DURING 2010-2014**

Mohammad Salehi¹, Abdolmajid Ghasemian², Seyyed Khalil Shokouhi Mostafavi³

1. 1-Medical Diagnostic Laboratory of Neyshabour, Center of Medical, Pathological and Genetic Diagnostic Services, Iranian Academic Center for Education, Culture and Research (ACECR), Mashhad Branch, Mashhad, Iran
2. Department of Microbiology, Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran
3. Department of Microbiology, Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran

Background and Aim:EBV is a human herpesvirus that infects more than 90% of the world's population. Although, benign and asymptomatic for most cases, the infection can cause many nonmalignant and malignant disorders of lymphoid and epithelial origins. The objective of this study was detection of IM prevalence in Neyshabur, Northeast Iran from 2010-2014.

Methods:This cross-sectional descriptive epidemiological survey was performed in Neyshabur between 2010 and 2014 to reveal the prevalence of infectious mononucleosis. A total of 114 patients were studied. Briefly, patients with positive test for specific IgG and IgM were determined as positive cases.

Results:The overall prevalence of IM was 14%. The mean age $\pm$ SD for infectious mono test is 18.96 ± 15.79 . the age groups of 0-10 and 21-30 years old, were the most positive cases in this period. In addition, 31-40 and upper 50 years were not positive cases. Male patients were significantly more positive and likewise, it was observed that the spring and summer seasons had significantly higher positive cases of IM. Among the five years of this study, it was a decreasing status from 2010 (23.1%) to 2014 (9.1%), although a slight fluctuation was occurred.

Conclusion:The prevalence of IM was low in Neyshabur city. Moreover, children and male patients had relatively higher prevalence of the disease. Furthermore, it was observed a higher rate of IM in the spring and summer seasons.

Keywords:Epstein-Barr virus, infectious mononucleosis, Neyshabur city, Iran

**P146 - 12: THE RELATIONSHIP OF HELICOBACTER PYLORI INFECTION AND SERUM
LEVEL OF FERRITIN, TIBC, TRANSFERRIN AND IL-17 IN INFECTED AND HEALTHY
CHILDREN**

Mohammad Salehi¹, Abdolmajid Ghasemian², Mehdi Bozorgi Mazandarani³

1. Medical Diagnostic Laboratory of Neyshabour, Center of Medical, Pathological and Genetic Diagnostic Services, Iranian Academic Center for Education, Culture and Research (ACECR), Mashhad Branch, Mashhad, Iran
2. Department of Microbiology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, Iran
3. Department of Microbiology, Islamic Azad University, Karaj, Iran

Background and Aim: *Helicobacter pylori* is related to iron deficiency anemia (IDA) and inflammatory responses causing ulcer and carcinoma of gastric and duodenum. Moreover, it causes the deficiency of factors associated with iron adsorption and transfer.

Methods: Methods: In the present study, the role of the bacterium in the anemia and several related factors including TIBC, ferritin and transferrin and also the amount of IL-17 expression was compared between two groups of children aging 3-14 years old. For the assessment of *H. pylori*, Euroimmune (Germany) kit was used for the ELIZA test according to the instructions of manufacturer. Furthermore, for the measurement of IL-17 level, ELISA test (IBL commercial specific kit, Germany) was used. The population of children included 100 members including 50 infected and 50 healthy controls.

Results: Results: in the infected children, the serum level of iron, ferritin and transterin was significantly lower, but the TIBC was different. Furthermore, the srum level of IL-17 was significantly higher in the infected group.

Conclusion: *H.pylori* could play a role in anemia and induction of inflammatory responses, with a significant increase in the IL-17 level among the infected children.

Keywords: *H.pylori*, anemia, inflammation, IL-17

**P147 - 13: ISOLATION AND IDENTIFICATION OF MOLECULAR CHLAMYDIA
TRACHOMATIS FROM GENITAL TRACT OF FERTILE WOMEN REFERRING TO
AFZALIPOUR INFERTILITY HOSPITAL IN KERMAN**

Samaneh Rafati¹, Babak Kheirkhah²

1. Department Of Microbiology, Kerman Science and Research Branch, Islamic Azad University, Kerman, Iran. Department Of Microbiology, Kerman Branch, Islamic Azad University, Kerman, Iran.
2. Department Of Microbiology, Kerman Science and Research Branch, Islamic Azad University, Kerman, Iran. Department Of Microbiology, Kerman Branch, Islamic Azad University, Kerman, Iran.

Background and Aim: Chlamydia is one of the most common pathogens which transmitted via genital path. Chlamydia Trachomatis affects both sexes, but in the sexual active women is more effective than men. The aim of this study was identification of molecular Chlamydia Trachomatis from genital tract of fertile woman.

Methods: In this descriptive- sectional research, 53 vaginal swab specimens of healthy and fertile women examine with polymerase chain reaction (PCR) method. The PCR products were purified and nucleotide sequencing was performed. Nucleotide sequences were compared with MEGA software and samples were analyzed and plotted based phylogenetic tree by Neighbor-Joining Tree method.

Results: 4 specimens (7.55%) were infected with Chlamydia Trachomatis species. Four isolates in this study are based on nucleotide acid sequence at two different series. In the two first series, isolate of Chlamydia Trachomatis placed in one branch and in the second series, three isolates in one branch has been studied.

Conclusion: The results showed that there is no different between isolated strains in fertile and infertile couples. Studies showed that orf8 gene is a general and pathogenic gene of Chlamydia Trachomatis. The Chlamydia Trachomatis strains in Kerman are similar to other strains in Iran and other regions of the world and it is not native strain.

Keywords: Chlamydia Trachomatis, fertile Women, Phylogenetic Tree, Molecular Identification, Orf8

**P148 - 18: PREVALENCE OF HELICOBACTER PYLORI INFECTION IN NEYSHABUR, IRAN
DURING 2010-2014**

Mohammad Salehi¹, Nafiseh Taati², Seyyed Khalil Shokuhi Mostafavi³

1. Medical Diagnostic Laboratory of Neyshabour, Center of Medical, Pathological and Genetic Diagnostic Services, Iranian Academic Center for Education, Culture and Research (ACECR), Mashhad Branch, Mashhad, Iran
2. Department of Microbiology, Faculty of Medical Sciences, Alborz University, Karaj, Iran
3. Department of Microbiology, Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran

Background and Aim: *H. pylori* prevalence has continuously decreased during recent years in Iran. The aim of this study was determination of *H. pylori* prevalence in Neyshabur city Northeast Iran during 2010-2015.

Methods: A total of 11596 participants (3681 males and 7915 females) were included. The *H. pylori* Kit (Pishtaz teb) with a Stat Fax 3200 (USA) ELISA reader that had a sensitivity of 95% and specificity of 98% were used. Any titer above 12 units was considered positive for IgG, IgA and IgM (Negative <8, Equivocal 8-12, Positive >12).

Results: The overall IgA, IgG and IgM positive sera samples among participants were 442 (3.81%), 4500 (38.8%) and 628 (2.31%) respectively. The IgA sero-positivity was significantly higher among ages of upper 51. There was no significant difference between male and female patients regarding IgA and IgG sero-positive samples, but for IgM females had a significant higher rate. Furthermore, there was no significant alteration in IgA, IgG and IgM sero-positivity during 2010-2014.

Conclusion: The prevalence of *H. pylori* in Neyshabur city is high in the healthy population. Furthermore, the *H. pylori* prevalence was not seen to change from 2010 to 2014 in the city. Effective approaches to improve sanitary purposes, and educational and socioeconomic status should be implemented to minimize and control *H. pylori* infection.

Keywords: *H. pylori*, sero-prevalence, Neyshabur city, ELISA

**P149 - 32: DETECTION OF KLEBSIELLA PNEUMONIAE PRODUCING CARBAPENEMASE
BY MODIFIED HODGE TEST FROM CLINICAL SAMPLES OF TOHID HOSPITAL IN
SANANDAJ**

PEGAH SHAKIB¹, Amjad Ahmadi², Morovvat Taheri Kalani³, Rashid Ramezan Zadeh⁴, Samaneh Rouhi⁵

1. Student Research Committee, Kurdistan University of Medical Sciences, Sanandaj, Iran, Cellular & Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran, Microbiology Department, Kurdistan University of Medical Sciences, Sanandaj, Iran.
2. MSc, Department of Microbiology, Kurdistan University of Medical Sciences, Sanandaj, Iran
3. School of Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran
4. Cellular & Molecular Research Center and Microbiology Department, Kurdistan University of Medical Sciences, Sanandaj, Iran
5. Student Research Committee, Kurdistan University of Medical Sciences, Sanandaj, Iran, Cellular & Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran, Microbiology Department, Kurdistan University of Medical Sciences, Sanandaj, Iran.

Background and Aim: Introduction: *Klebsiella pneumoniae* is Gram-negative bacilli and positive lactose of Enterobacteriaceae family. *Klebsiella pneumoniae* is considered one of the causes of nosocomial infections that recently resistance to carbapenem antibiotics (e.g imipenem, meropenem). Carbapenemase enzymes (KPC) are mainly cause factors of carbapenem resistance. The aim of this study was detection of *klebsiella pneumoniae* producing carbapenemase by Modified Hodge Test from clinical samples of tohid hospital in Sanandaj.

Methods: Materials and methods: In this cross-sectional study during a 6 month period from October to March 2016, 26 *Klebsiella pneumoniae* were collected from clinical samples (blood, urine, sputum, or wound swab) of tohid hospital in Sanandaj. The biochemical tests were identified. The antibiotic susceptibility testing was performed by disk diffusion. Then, Modified Hodge Test (MHT) was employed for isolation of KPC -producing *K.pneumoniae* according to CLSI by the disc diffusion method and using ertapenem disk (10µ) (Roscoe, Danmark) and *Escherichia coli* ATCC 25922 on Mueller-Hinton agar (Merck, UK). *K.pneumoniae* ATTC 13883 was used as a positive control.

Results: From 26 strains of *klebsiella pneumoniae* isolates , 5 strains were carbapenemase enzyme production and testing Hodge leaf clover inhibition zone around the isolates were observed.

Conclusion: The results of this study compared to other studies suggest that *Klebsiella pneumoniae* isolated from Sanandaj relatively low resistance to carbapenemes.

Keywords: detection, *klebsiella pneumoniae* , carbapenemase producing , Modified Hodge Test(MHT)

P150 - 36: ASSOCIATION OF HELICOBACTER PYLORI INFECTION WITH THE ABO AND RH BLOOD GROUPS IN IN MILITARY STUDENTS AND SOLDIERS

Adel Naimi¹, Saeed Solali², Shahrokh Iravani³, Tohid Jafari koshki⁴

1. MSc Student in Hematology and blood transfusion medicine, Student research committee, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran
2. Assistant Professor, Hematology and Transfusion Medicine Part, Department of Immunology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran
3. Associate professor, AJA Cancer Research Center (ACRC), Aja University of Medical Sciences, Tehran, Iran
4. PhD Candidate in medical statistics, Department of Biostatistics, School of Medical Sciences, Tarbiat Modares University, Tehran, Iran

Background and Aim: *Helicobacter pylori* (H.Pylori) is one of the most common bacterial infections worldwide. It causes chronic gastritis associated with peptic ulcer and with the development of gastric cancer. Epidemiological studies performed prior demonstrated that individuals who were blood group O were more likely to develop peptic ulcers. Our aim of this study was to investigate relation between the prevalence of H.Pylori infection in military students, soldiers and ABO, Rh blood group in Tehran.

Methods: The study group was composed of 417 individuals aged 18-27 years who were military students of AJAUMS (Aja University of Medical Sciences), University of Afsari Imam Ali and soldiers. All individuals completed questionnaires including personal health and hygiene information. ABO, Rh blood group phenotypes were determined by a standard hemagglutination test. The serum samples were analyzed for anti-H.pylori IgG by ELISA method. Collected data of study analyzed using SPSS-16 software with Chi-square test.

Results: Overallly 182 (43.6%) of 417 subjects were seropositive and 235 (56.3%) of subjects were seronegative. Prevalence of infection in AJAUMS students was less than compared to other groups and it was statistically significant. also prevalence of infection in group of persons with more than five family members was significantly higher than group with family members less than 5 persons. Frequency of O, A, B and AB blood groups were 37.6%, 33.1%, 20.9% and 8.4%.

Conclusion: We didn't find any association between ABO, Rh blood group with H.pylori infection.

Keywords: *Helicobacter Pylori*, ABO blood group, Rh blood group, seropositive, military students

**P151 - 39: PHENOTIPIC AND GENOTIPIC SCREENING OF VIRULENCE FACTORS OF
ENTEROCOCCUS FAECIUM AND ENTEROCOCCUS FAECALIS ISOLATED FROM
ZANJAN HOSPITALS**

Vahid Lohrasbi¹, Habib Zeighami², Fakhri Haghi³

1. Master of Science Medical Microbiology ,Department of Microbiology and Virology, Zanzan University of Medical Sciences, Zanzan, Iran
2. Assistant Professor of Bacteriology ,Department of Microbiology and Virology, Zanzan University of Medical Sciences, Zanzan, Iran
3. Assistant Professor of Bacteriology ,Department of Microbiology and Virology, Zanzan University of Medical Sciences, Zanzan, Iran

Background and Aim:Enterococcus species are opportunistic pathogens that are part of the normal gut microbiota of both humans and animals, and can survive in a diverse range of harsh conditions. Enterococci also produce many virulence factors, including Pathogenicity island (PAI), cytolysin (cylA), enterococcal surface protein (esp) and gelatinase (gelE). The aim of the present study was to estimate the potential virulence factors in enterococci and to ascertain their prevalence in from Zanzan Hospitals in 2015.

Methods:After isolating and identifying 100 strains of enterococci from clinical specimens ,the enterococcus isolates were identified by biochemical confirmation tests. Specific primers were designed for detection of the four potential virulence genes (PAI ,gelE, esp and cylA) by PCR assay. Parallel, phenotypic assays were performed.

Results:In this study, of 100 clinical specimens, 69 isolates (69%) were positive for E. faecalis and 10 isolates (10%) were E. faecium and 21 isolates (21%) were other species of Enterococcus. The prevalence of the PAI, gelE, cylA and Esp virulence genes amongst the 100 Enterococcus species was 39%, 19%, 26%, and 58%, respectively. Parallel, phenotypic assays were performed 35% Hemolysis, 25% Gelatinase and 74% Biofilm productions.

Conclusion:Finally, the current study revealed that, the overall rate of virulence gene carriage amongst the E. faecalis group was significantly higher than in the E. faecium group or the “other” group. PCR has a high specificity compared to other phenotypic methods.

Keywords:Enterococcus, virulence factors, PCR, Phenotypic, Genotypic

**P152 - 45: CONSTRUCTION OF A RECOMBINANT BACMID DNA CONTAINING
INFLUENZA A VIRUS HEMAGGLUTININ GENE USING A SITE-SPECIFIC
TRANSPOSITION MECHANISM**

Mohammadreza Shafaati¹, Akhavan Elnaz², Yazdani Shagayegh³

1. Department of cellular & molecular biology IAU, Hamadan Branch, Hamadan, Iran
2. Department of Microbiology IAU, Damaghan Branch, Damaghan, Semnan, Iran
3. Department of Virology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: In recent years, Influenza viruses have caused widely spread moderate to severe infections in all around the world and there is no Influenza vaccine that can protect people only with one dose injection till now. Therefore, producing a universal vaccine based on virus like particle (VLP) can be ideal. Objectives: In this study, the full-length of HA gene was isolated using specific primers and cloned into the baculovirus derived bacmid shuttle vector to produce recombinant HA-protein in insect cell.

Methods: In this experimental study, HA gene ORF from Influenza A Virus of H9N2 was amplified by RT-PCR to produce HA cDNA. The amplicon was cloned firstly into T/A cloning vector and then subcloned into pFastBacDual donor plasmid through SalI/HindIII sites. The recombinant HA-pFastBacDual vector was transferred to E.coli DH10Bac cells, to insert the HA gene into the bacmid DNA via a site-specific transposition process. The recombinant bacmid was then extracted from white colonies and was further analyzed by a PCR panel using HA specific and M13 universal primers.

Results: Results showed that the HA-containing recombinant bacmid has been constructed successfully using the transposition mechanism between pFastBacDual-HA and bacmid, and was verified by the mentioned PCR panel.

Conclusion: The constructed recombinant baculovirus in this work has proper characteristics to produce H9N2 influenza virus-like particles in Sf9 cells.

Keywords: Influenza A virus, hemagglutinin protein, Baculovirus

**P153 - 48: FIRST REPORT OF DIVERSITY LEVELS AMONG ESCHERICHIA COLI
ISOLATED FROM PATIENTS WITH DIFFERENT CLINICAL SYMPTOMS OF URINARY
TRACT INFECTIONS IN TEHRAN, IRAN**

Mohsen Tabasi¹, Mehri Habibi², Mohammad Reza Asadi kram³, Saeid Bouzari⁴

1. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
2. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
3. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
4. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Most urinary tract infections (UTIs) arise from one type of bacteria, Uropathogenic Escherichia coli (UPEC), which normally lives in the bowel. Symptoms of a UTI in adults may include the following: a frequent and intense urge to urinate. A painful, burning feeling in the bladder or urethra during urination. The aim of this study was to investigate the diversity levels of UPEC isolates, and to examine the relationships between diversity and different clinical symptoms of UTI.

Methods: A total of 156 UPEC samples isolated from symptomatic and asymptomatic patients in Tehran, Iran, were enrolled in this study. Pulsed-field gel electrophoresis (PFGE) was used to characterize clonal relationships among 40 representative UPEC isolates according to the Centers for Disease Control and Prevention PulseNet protocol.

Results: In the present study, 34 PFGE clonal groups were found in the UPEC genome. A majority of the isolates showed 15 to 20 bands, although the isolates with less than 10 bands had the least percentage. The similarity range had been between 46-87%. Furthermore, the maximum and minimum numbers of isolates were found in six PFGE groups, each consisting of two isolates, and twenty-eight PFGE groups, each consisting of one isolate, respectively.

Conclusion: PFGE displayed a large diversity in the UPEC strains that could be considered as an evolutionary strategy in the survival of the bacteria. Unique PFGE patterns and high degree of diversity among UPEC isolates also reported by other researchers. This may be related to the different sources of UTI in community- and hospital-acquired isolates.

Keywords: Uropathogenic Escherichia coli; Urinary tract infection; PFGE

P154 - 54: OCCURRENCE OF SEA, SEP AND SCN GENES IN METHICILIN-RESISTANT STAPHYLOCOCCUS AUREUS ISOLATES

Simin Ariyarad¹, , Seyedeh Elham Rezatofighi,² Hossein Motamedi³

1. - Department of Biology, Faculty of Science, ShahidChamran University of Ahvaz, Ahvaz, Iran
2. - Department of Biology, Faculty of Science, ShahidChamran University of Ahvaz, Ahvaz, Iran
3. - Department of Biology, Faculty of Science, ShahidChamran University of Ahvaz, Ahvaz, Iran

Background and Aim:Staphylococcus aureus is a human commensal bacterium, as well as an important pathogen that can cause infections ranging from mild to life-threatening. This is one of the most pathogenic bacteria that causes food- poisoning, generalized exfoliation and bullous impetigo afflicts.To counteract innate immunity S. aureus expresses a number of immune-modulating proteins. Two of the immune-modulating proteins are SEA (Staphylococcal enterotoxin A) and SEP (Staphylococcal enterotoxin P) belongs to a broad family of superantigens that have the capability of modulating function of chemokine receptors like CCR1, CCR2, and CCR5. SCIN (staphylococcal complement inhibitor), is a C3 convertase inhibitor that blocks the formation of C3b on the surface of the bacterium and inhibits phagocytosis of the human neutrophils. S. aureus genes are related to immune evasive cluster (IEC) which are located on bacteriophages. The IEC-carrying bacteriophages are called β -haemolysin-converting bacteriophages (BC- ϕ S).The aim of this study was to identify the percentage presence of sea

Methods:: In this study, 155 Staphylococcus aureus isolates has been collected from hospitals of Ahvaz city. After the identification by biochemical tests and antibiotic susceptibility testing, the bacterial genome was extracted using boiling method and sea, sep and scn genes were identified by PCR method.

Results:In this study among 155 samples of staphylococcus aureus,10 samples were identified as mec-sensitive bacteria and 145 samples were identified as mec-resistance. Occurrence of sea, sep and scn genes at mec-resistance bacteria was 35, 3.2 and 39% respectively.

Conclusion::These results indicated the prevalence of escape immunity genes among mec-resistance isolates.

Keywords: Staphylococcus aureus; sea, sep and scn genes; Immune evasive cluster

**P155 - 57: PREVALENCE OF THE BLACTX-M-1 GENES GROUP AND THEIR
TRANSFERABILITY IN CLINICAL ISOLATES OF SHIGELLA SEROGROUPS FROM
HOSPITALS IN TEHRAN**

Kobra Salimian rizi¹, Shahin Najar Peerayeh ², Bita Bakhshi ³, Mohammad Rahbar⁴

1. Department of Bacteriology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, IR Iran
2. Department of Bacteriology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, IR Iran
3. Department of Bacteriology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, IR Iran
4. Department of Microbiology, Reference Health Laboratories Research Center, Deputy of Health ,Ministry of Health and Medical Education, Tehran, Iran

Background and Aim:Shigella is increasingly recognized as an important food-borne pathogen. The objective of this study was to describe the antibiotic susceptibility, ESBL production and determining the prevalence of the blaCTX-M-1 group among clinical isolates of Shigella serogroups.

Methods:A total of 80 Shigella spp. isolates collected from four hospitals in Tehran during 2012-2013. Shigella species were identified by using standard biochemical tests and so the specific polyvalent Shigella antisera were used for serogrouping of Shigella isolates. Antibacterial Susceptibility was determined by disk diffusion and ESBL phenotype was confirmed by combination disk method. The blaCTX-M-1 group was identified by PCR with specific primers. The transferability of the blaCTX-1 group was tested by conjugation with broth matting-method.

Results:It was observed that 80 clinical isolates that collected were from different sources. The prevalence of Shigella serogroups consist of 78.75% serogroup D, 13.75 % serogroup B, 5 % serogroup C, and 2.5 % serogroup A and 8.75% were not react with Shigella O polyvalent antisera. Maximal resistance in Shigella isolates was noticed against trimethoprim-sulfamethoxazole (61.25%) and tetracycline (53.75%). All of isolates were susceptible to imipenem. Ten (12.5%) isolates showed ESBLs phenotype. All Shigella spp. that produce ESBLs have blaCTX-1 genes group. A conjugative plasmid containing blaCTX-1 group was found in one Shigella isolate.

Conclusion:This study demonstrates the predominant presence of the gene encoding CTX-M-1 group among ESBLs producing of Shigella spp. They can transmit to bacteria of this genus or even other genera of enteric bacteria.

Keywords:Shigella serogroups, blaCTX-M-1 group, antibiotic resistance, conjugation, broth matting.

P156 - 66: PREVALENCE OF VIRULENCE FACTORS AND VANCOMYCIN-RESISTANT GENES AMONG ENTEROCOCCUS FAECALIS AND ENTEROCOCCUS FAECIUM ISOLATED FROM CLINICAL SPECIMENS

Seyed mostafa Hosseini¹, Mohammad Reza Arabestani²

1. Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, IR Iran
2. Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, IR Iran

Background and Aim: The aim of this study was to determine the occurrence of three virulence determinants and detection vancomycin-resistant vanA, vanB and vanD genes among *Enterococcus faecalis* and *Enterococcus faecium* obtained from various clinical sources.

Methods: Identified species using conventional biochemical methods were confirmed by the PCR method. Antibiotic susceptibility testing was performed using disk diffusion and MIC (Minimum Inhibitory Concentration) methods. The presence of vancomycin-resistant genes (vanA, vanB and vanD) and virulence genes (asa1, esp, and hyl) was investigated using PCR.

Results: Of 280 enterococcal isolates, 175 (62.5%) isolates were identified as *E. faecalis*, 67 (24%) as *E. faecium* and 38 (13.5%) as *Enterococcus* spp. The results of antibiotic susceptibility testing showed resistance rates of 5% and 73% to vancomycin and teicoplanin in *E. faecalis* and *E. faecium* isolates, respectively. No resistance to linezolid and nitrofurantoin was detected among *E. faecalis* isolates. All isolates of *E. faecium* were susceptible to linezolid. Of Sixty vancomycin-resistant Enterococci (VRE) strains, Fifty-one isolates were identified as vancomycin-resistant *Enterococcus faecium* (VREfm) and Nine as *E. faecalis* (VREfs).

Conclusion: Due to the high Prevalence of Vancomycin-resistant Enterococci and also increasing resistance of *Enterococcus* than to most common antibiotics, there is a need for the application of preventive and control measures. In order to proper prescribe of antibiotics, antibiotic susceptibility testing is recommended for all patients before treatment.

Keywords: *E. faecalis*; *E. faecium*; Vancomycin-resistant Enterococci; Minimum Inhibitory Concentration

P157 - 74: EVALUATING HEPATITIS B VACCINE EFFICACY IN IRANIAN MEDICAL STUDENTS AND HEALTHCARE WORKERS- A META-ANALYSIS STUDY

Milad Azami¹, Marzieh Khataee², Kourosh Sayehmiri³

1. Medical Student, Student Research Committee, Ilam University of Medical Sciences , Ilam, Iran
2. Medical Student, Student Research Committee, Ilam University of Medical Sciences , Ilam, Iran
3. Associate Professor, Department of Biostatistics, Research Center for Prevention of Psychosocial Impairment, Ilam University of Medical Sciences , Ilam, Iran

Background and Aim: Hepatitis B is an infectious disease with significant global expansion, which is now estimated to be about 2 billion people worldwide are affected. Hepatitis B vaccine efficacy among the staff and health care workers demonstrate various results in many studies which is done in different countries and a general and comprehensive estimate is not available so far. This meta-analysis study was performed to determine the efficacy of hepatitis B vaccine in clinical students and health care workers.

Methods: This study is a systematic review based on internal and external databases including: Magiran, Iranmedex, IranDoc, SID, Medlib, Scopus, Pubmed, Science Direct, Cochrane, Embase, Web of Science, Springer, Online Library Wiley, Trials Register, index Copernicus, DOAJ and Google Scholar search engine was also used. Taken into account of inclusion criteria, all peer-reviewed papers were evaluated by statistic STATA ver.11.1 software.

Results: In 12 studies, the numbers of 1655 samples were analyzed. Hepatitis B vaccine efficacy in clinical staff and students after 1-6 months of the last dose of vaccine was 93.1% (CI 95%: 90.3- 97), the rate among males and females was 95.9% (CI 95%: 93.1- 98.6) and 91.3% (CI 95%: 87.1- 95.5), respectively.

Conclusion: Immunogenicity following hepatitis B vaccination in clinical students and staff has been pretty good and the full course of vaccinations to prevent hepatitis B injection is sufficient and need of booster dose is obviated.

Keywords: Meta-analysis, Hepatitis B, Vaccine Efficacy, Medical Students, Healthcare Workers, Iran

**P158 - 79: BRAIN ENCEPHALITIS DUE TO MELANIZED FUNGI; HOW COME WE ARE
ALIVE?**

Hamid Badali¹

1. Invasive Fungi Research Center, School of Medicine, Mazandaran University of Medical Sciences, Sari, Iran

Background and Aim: Cerebral phaeohyphomycosis is the collective name for a group of cerebral fungal infections that are characterized by black necrotic tissue or black CSF. If untreated, the infection leads to death within weeks, months, or, occasionally, years. This infection is caused by a group of black fungi, and emerging pathogens from this group are still being encountered. The thought is a bit frightening, but perfectly healthy people may suddenly die of a fungal brain infection. This type of disease is already known for 100 years. Nevertheless there has been very little progress in early diagnostics.

Methods: The disorder is often overlooked because symptoms are similar to those of cerebral carcinoma, and the option of a fungal infection will mostly not be considered by the physician. In current clinical practice a fungal brain infection is therefore mostly diagnosed at a late stage of infection or even post mortem

Results: *Rhinoctadiella mackenziei* and *Cladophialophora bantiana* are rare but very lethal neurotropic filamentous fungus related to the black yeasts. Mortality rates reach up to an impressive >75% despite therapy

Conclusion: The infection also occurs in patients with decreased immunity due to organ transplants, long-term corticosteroid use, where survival chances are even lower. For severe infections currently most clinicians would be inclined to use amphotericin B as a standard therapy, however posaconazole seems to be a good option instead of inadequate amphotericin treatment.

Keywords: Brain infection; Black yeast

**P159 - 80: DETECTION OF IINT-1,INT-2 AND CTX BETA-LACTAMASE GENES IN
ESCHERICHIA COLI ISOLATED FROM URINARY TRACT INFECTION USING
POLYMERASE CHAIN REACTION**

Mohammad Ahanjan¹, Mahya Manuchehri²

1. Mazandaran Uni of Med Sci
2. Student research center, Mazandaran university of medical sciences

Background and Aim:Background: E.Coli is a gram-negative bacteria belonging to Enterobacteriaceae family. These bacteria are the main cause of many nosocomial infections

Methods:: 200 urine samples were taken (from June to October 2013) to determine the prevalence, molecular type and antibiotic resistance patterns of beta-lactamase producing strains in E. coli compared to commonly used antibiotics in Infections and Nephrology Departments of Razi Hospital in Qaem Shahr city and Imam Khomeini Hospital in Sari city. For phenotypic detection of ESBL of E.Coli, the combined disk test was used, as suggested by CLSI organization. After full dispersion of bacterial suspension in the medium, ceftazidime disks (30 ug), ceftazidime clavulanate acid (10-30 micrograms), cefotaxime (30 mg), cefotaxime – clavulanate acid (10-30 ug were inserted in the medium with a minimum distance of 5.2 cm from each other. For DNA extraction of isolates under studies, DNA Extraction Kit (Denazist Genomic DNA kit-1) was used.

Results:: 200 urine samples tested subjects. During double synergistic test, 66 (55%) strains were found to b- lactamase producing. The frequency of ESBL production in isolated E.coli strains was 33.3% for men and 66.7% for women. In PCR test, out of 66 isolates, the frequency of TEM gene, INT Class 1 and 2 was 47 (70.8%), 48 (72.72%) and 10 (15.15%) respectively

Conclusion:: It seems that the clinical application of research results may include reporting results to the physicians in the hospitals under study as well as the percentage of ESBL and resistant and sensitive antibiotics in chemotherapy use protocol.

Keywords:: E.coli, B-lactamase genes, nephrology

P160 - 89: THE PREVALENCE OF URINARY AND ENTERIC INFECTIONS IN IMAM-KHOMEINI HOSPITAL IN SHIRVAN IN NORTH-KHORASAN PROVINCE IN 2015

Moein Hamidi hesari¹, Meead Bani Torfi², Jafar Hemmat³, Norkhoda Sadeghifard⁴

1. 1. MSC in Microbiology, Khomeini hospital in Shiravan, Iran
2. MSc student of Microbial Biotechnology, Biology Group, Islamic Azad University, Sabzevar branch, Iran;
3. Assistant Professor of Biotechnology Research Institute, Biotechnology Research Institute, Iranian Research Organization for Science and Technology, Tehran, Iran; Email: j.hemmat@gmail.com
4. Professor of microbiology, Microbiology Research Center, Ilam University of Medical Sciences, Ilam, Iran; Email: Sadeghifard@gmail.com

Background and Aim: Studies conducted in different countries have shown that gram-negative bacilli are the most common agent for urinary tract infections, of which, *E. coli* causes more than 80% of these infections. Given the importance of urinary tract infections, the present study was conducted to determine the prevalence of these infections and their causing agent in Imam Khomeini Hospital in Shirvan in 2015.

Methods: Urine samples obtained in medical laboratory of Imam Khomeini Hospital were cultured, and isolates from positive cases were identified through biochemical tests including motility, citrate, urea, bile Esculine, TSI, SIM, NaCl 6.5% tolerance, and PYR.

Results: A total of 5150 urine cultures were performed in 2015, of which, 202 cases (3.92%) were positive with CFU of over 105/ml. Of the positive cases, 64.3% were *E. coli*, 16.8% were different species of *Klebsiella*, 3.69% were *S. epidermidis*, 3.46% were *S. saprophyticus*, 3% were different species of *Proteus*, 2.5% were *Streptococcus* group D, 1.48% were *Staphylococcus aureus*, 1.48% were *Enterococcus*, 1% were *Pseudomonas aeruginosa*, 1% were *Citrobacter*, and 1% were *Enterobacter*.

Conclusion: Comparing the present and a 2013 study shows a reduction in the overall level of positive cultures. Nonetheless, *E. coli* is still the leading cause of urinary tract infection by a significant difference. The relatively low percentage of infection with *Citrobacter* and *Enterobacter* compared to *Klebsiella* and gram-positive bacteria such as *Enterococci*, *Streptococci*, and *Staphylococcus epidermidis* is indicative of gradual changes in prevalent causes of urinary tract infection from *Enterobacteriaceae* species to gram-positive bacteria, especially *Staphylococcus epidermidis*.

Keywords: Urinary tract infection, Enteric pathogens, Prevalence, Shirvan

**P161 - 106: PREVALENCE OF ESP, CYLA GENES IN CLINICAL ISOLATES OF
ENTEROCOCCUS FAECALIS**

Naeim Malekei¹, Mohammad Reza Mehrabi², Mohsen Mirzaei³

1. Department of Microbiology, Borujerd Branch, Islamic Azad University, Borujerd, Iran

Background and Aim: Enterococcus species are found in natural habitats such as soils, waters, and animals' digestive system organs. These gram-positive bacteria which are capable of growing in a highly saline environment and a wide range of pH, can acquire drug resistivity and spread among patients. The aim of this study was to investigate the occurrence of Esp and cylA genes in the clinical isolates of Enterococcus faecalis.

Methods: Therefore, 47 isolates of the bacterium were collected from Borujerd's health centers, and identified based on the growth on Bile Esculin Agar (BEA) medium, 6.5% salinity tolerance, gram test, catalase test, PYR, and sugar fermentation. Also, gene evaluation was performed using PCR method.

Results: Results showed that 41 isolates included Esp, and 37 isolates contained cylA genes with 87.23% and 78.72% occurrence, respectively.

Conclusion: These outcomes indicated the significant roles of Esp and cylA genes in biofilm formation in patients. Moreover, according to the presence of the cylA gene in samples, it is expected that acuity factors in these isolates be much more than other Enterococcus faecalis bacteria.

Keywords: Esp, cylA, E. faecalis

**P162 - 107: DISCUSSING THE ANTIBIOTIC RESISTANCE OF ESCHERICHIA COLI
BACTERIA FOUND IN URINAL INFECTION OF WOMEN**

Kamran Rahbarei¹, Kamran Rahbari², Keyvan ghoreysh³, Naghi taher tala tapeh⁴

1. Urmia Branch, Islamic Azad University, Urmia, Iran
2. Urmia Branch, Islamic Azad University, Urmia, Iran
3. Urmia Branch, Islamic Azad University, Urmia, Iran

Background and Aim: Urinal infections are considered as most prevalent types of infections and also Escherichia Coli is known as the most important agent of urinal infections. Discussing the antibiotic resistance of existing Escherichia Coli in urinal infection of women referring private and public laboratories of Mahabad was performed. This study was carried out under a sectional schema during the first six months of 2015 between 400 samples.

Methods: This study was performed under a sectional time table and during the first six months of 2015. Samples were gathered from 400 urine samples of women referring to private and public laboratories of Mahabad. For collection of samples, first the ladies participating in the research were taught how to take appropriate samples

Results: Among the 400 urine samples, 326 of them (81%) were diagnosed as positive, and after microbiological investigations, a number of 214 (53%) were isolated as Escherichia Coli infected samples. Though the comparison of dimension of lack of growth of bacteria in Antibigram test, the level of resistance of bacteria against different antibiotics was determined and shown in table

Conclusion: Results of the present study reveal the increasing resistance of strains of Escherichia Coli against Imipenem, Ciprofloxacin, ampicillin and tetracycline antibiotics. This might be the result of overuse of these antibiotics.

Keywords: Urinal infection, Escherichia Coli, Women, Antibiotic resistance

**P163 - 124: THE PREVALENCE OF CHLAMYDIA AND GONOCOCCI CERVICAL
INFECTION IN SYMPTOMATIC AND ASYMPTOMATIC WOMEN IN KASHAN-IRAN**

Shima Afrasiabi¹, mansooreh Samimi ², rezvan moniri³

1. Tehran Uni of Med Sci
2. Kashan Uni of Med Sci
3. Kashan Uni of Med Sci

Background and Aim:Chlamydia trachomatis (CT) and Neisseria gonorrhoeae (NG) are the most prevalent sexually transmitted disease

Methods:In this cross-sectional study, we enrolled 369 women attending the obstetrics and gynecology clinics between Sep 2012 and Sep 2013 of the Kashan, Iran for the detection of CT and NG infections. Endocervical specimens were collected to test for CT and NG using polymerase chain reaction. The results of symptomatic and asymptomatic groups were compared. The data was analyzed using SPSS (version 16.0). A probability value of $p \leq 0.05$ was considered as significant.

Results:Of 369 women included, 326 had symptoms of gynecological infection, and 43 were asymptomatic. Only one of the asymptomatic women was infected with CT and NG (2.3%). Among the symptomatic women, 8 were CT infected and 10 were NG infected. Chlamydia prevalence was 2.4% (95% CI 0.8 - 4%) and gonorrhea prevalence was 2.9% (95% CI 1.15 - 4.65%). One (0.27%) woman showed co-infection.

Conclusion:Prevalence of gonorrhea in women was higher than Chlamydia prevalence. Most infections were symptomatic .Young females were most likely to screen positive for CT and NG in this population. Further investigations are needed

Keywords:: prevalence, Chlamydia trachomatis, Neisseria gonorrhoeae, endocervix, Polymerase chain reaction

**P164 - 129: DESIGN OF AN INTERNAL POSITIVE CONTROL FOR MOLECULAR
DETECTION OF YERSINIA PESTIS**

Khatereh Kabiri¹, Keivan Majidzadeh- A²

1. Department of Microbiology, Islamic Azad University, Tehran North Branch, Tehran, Iran
2. Tasnim Biotechnology Research Center (TBRC), AJA University of Medical Sciences, Tehran, IR

Background and Aim: *Yersinia pestis*, a Gram negative rod belonging to the Enterobacteriaceae family, is the causative agent of plague. CDC has categorized the organism as a priority A biological agent because of its high morbidity and mortality and easy distribution through infective respiratory droplets. False negatives can occur when inhibitors are present in the sample being tested, especially if clinical samples such as blood are analyzed. To overcome this problem, an internal positive control was constructed for conventional PCR using the PCR-cloning technique.

Methods: In this study the target gene was *pla* so the specific primers were designed for it. Besides, the hybrid primers for IPC were designed then the PCR was optimized. The IPC was amplified in a stringent condition and ligated into pTZ57R plasmid vector, then transformed into *Escherichia coli* JM207 and then cloned.

Results: The analysis by PCR length of the *pla* gene and IPC were respectively 136bp and 225 bp, so there was a significant difference between their size.

Conclusion: The IPC control that is included in the same tube of the instrument that has the same primers as the specific assay and controls for the core reagents and primers, and the thermal cycling. The designed IPC assay has proven to be an effective tool for monitoring inhibitors of PCR and builds confidence in negative results obtained with agent specific assays.

Keywords: IPC, False negatives

**P165 - 130: DESIGN AND DEVELOPMENT OF A COMPETITIVE INTERNAL POSITIVE
CONTROL FOR THE DETECTION PLA AND CAF1 GENES OF YERSINIA PESTIS USING
REAL TIME PCR**

Khatereh Kabiri¹, Keivan Majidzadeh- A²

1. Department of Microbiology, Islamic Azad University, Tehran North Branch, Tehran, Iran
2. Tasnim Biotechnology Research Center (TBRC), AJA University of Medical Sciences, Tehran, IR

Background and Aim: *Y.pestis* the causative agent of the zoonotic plague infection, easy distribution through infective respiratory droplets among humans. According to WHO reported Natural foci of plague are situated in all continents except Australia. Also the Kurdistan in the Iran is foci plague. False negatives can occur when direct inhibitors are present in the clinical sample such as blood and urea or reagents such ethanol and SDS, used in nucleic acid extraction procedures. Internal positive control (IPC) needed to confirm and reliable results.

Methods: IN this study, we have designed an IPC for *pla* and *caf1* genes. For this purpose, designed hybrid primers using *Pichia pastoris* AOX1 gene sequences and Each target gene. Reverse and forward primers each containing part of the Aox1 gene and target gene. For real time PCR assay, Target gene probes with FAM dye and IPC with TET labeled.

Results: The limit of detection of the *caf1* and *pla* Real-time PCR assays was 1 fg and 4.5 fg respectively. For IPC- Real time PCR assay, Target gene probes with FAM dye and IPC with TET labeled.

Conclusion: The high sensitivity, rapidity, reproducibility and specificity of the Real time PCR with the use of IPC to monitor for false negative results can make this method suitable for diagnosis *Pla* and *caf1* genes of *Yersinia pestis*.

Keywords: *Y.pestis*, zoonotic, plague, Real time PCR

P166 - 132: THE PREVALENCE OF ANAPLASMA IN SHEEP AND CATTLE IN KURDISTAN PROVINCE, IRAN

Mohammad Khezri¹, Babak Rokhzad²

1. Veterinary Research Department, Agricultural and Natural Resources Research and Education Center, AREEO, Sanandaj, Iran
2. Veterinary Research Department, Agricultural and Natural Resources Research and Education Center, AREEO, Sanandaj, Iran

Background and Aim: Anaplasmosis is an important economic livestock disease. Limited information on its epidemiology in Iran is still lacking thus the aim of the study was to determine the seroprevalence of the disease in sheep and cattle in Kurdistan province of Western Iran. Anaplasmosis, a disease caused by various species of *Anaplasma*, poses important economic constraints to animal breeders.

Methods: A competitive enzyme-linked immunosorbent assay (c-ELISA) was performed using the *Anaplasma* Antibody Test Kit from VMRD Inc. (Pullmann, WA, USA) following the manufacturer's instructions. This assay detects serum antibodies to a major surface protein (MSP5) of *A. marginale*, *A. centrale* and *A. ovis* and *A. phagocytophilum*.

Results: The results showed that the infection rate of *Anaplasma* spp. in sheep and cattle were 6.49% and 7.62% respectively. There was no association between *Anaplasma* infection with age and sex in both sheep and cattle ($P > 0.05$).

Conclusion: This study was a preliminary study in Kurdistan province on seroprevalence of *Anaplasma* infection in sheep and cattle. The low seroprevalence observed would be due to the low tick vector population in Kurdistan province. This would be due to the geographical differences thus affecting the epidemiological pattern of the dominant vectors in the region the differences in the infection rate with *Anaplasma* from area to area may be affected by many factors like climatic condition, seasonal variation of tick vector, susceptibility of breeds, distribution of vector, system of breeding, vaccination, and strategy of prophylactic and treatment methods.

Keywords: Antibodies; *Anaplasma* spp; Cattle; C-Elisa; Sheep.

**P167 - 134: THE PREVALENCE OF THEILERIA OVIS IN SHEEP IN KURDISTAN
PROVINCE, IRAN**

Mohammad Khezri¹, Babak Rokhzad²

1. Veterinary Research Department, Agricultural and Natural Resources Research and Education Center, AREEO, Sanandaj, Iran
2. Veterinary Research Department, Agricultural and Natural Resources Research and Education Center, AREEO, Sanandaj, Iran

Background and Aim: Ticks and tick-borne diseases, including theileriosis, constitute a major constraint to livestock production. Two species, known as *Theileria lestoquardi* and *Theileria ovis*, are suspected to contribute to ovine theileriosis in Iran. However, the epidemiological aspects of ovine theileriosis are poorly understood in this country.

Methods: A total of 110 blood samples were collected from apparently healthy sheep. Genomic DNA was extracted from individual blood samples by using proteinase K method. DNA detection in *Theileria* species was performed, using specific PCR assays to amplify 18S rRNA gene sequences by utilizing a universal primer pair. The assay used a primer pair consisting of T18F2 (5'CAGATACCGTCGTAGTCC) and T18R2 (5'CCTTGTTACGACTTCTCC) to amplify both *Theileria* species. For determining the 18S rRNA gene sequence, To1 (5'gtaggg ctaatacatgttcgggaccttc) and To2 (5'tgatacatcgcatccgaagac) primers were applied to amplify 155-275 bp sequences in 18S SSU rRNA gene of *T. ovis* (AY533144). Moreover, two primers used to discriminate *T. annulata* and *T. lestoquardi* were SP1 (5'GCGAAT GTGGTCCATTCTCTCC) and SP2 (5'GAAGAATGATCCACAACATTGCG), selected to amplify bases 90-651 of *T. annulata* (AJ316248) SP gene sequence and bases 271-710 of *T. lestoquardi* (AY274335) SP gene sequence

Results: In a survey, 52 (47.27%) out of 110 blood samples were positive, based on polymerase chain reaction (PCR) results. Among 52 positive samples, 100% (52/52) were positive for *T. ovis*, while *T. lestoquardi* was not detected in any of the samples.

Conclusion: The intensity of *Theileria* infection in ruminants and infestation levels in ticks are influenced by various factors such as seasonal variations, breeding, and management systems in each region.

Keywords: Ovine theileriosis, *Theileria ovis*, *Theileria lestoquardi*, Iran

**P168 - 137: INVESTIGATING THE INCIDENCE OF BLOODSTREAM INFECTIONS IN
KHATAM-OL-ANBIA HOSPITAL IN GONBAD IN 2015**

Mahdi Samiei¹, Najime Haji Morad khani²

1. Social Security organization in Golestan ,iran
2. Social Security organization in Golestan ,iran

Background and Aim: Purpose: Septicemia or bloodstream infection is a major cause of death among hospitalized patients of different ages. This study aims at detecting the bacterial causes of bloodstream infections among the patients hospitalized in Khatam-Ol-Anbia hospital in Gonbad.

Methods:Material and method: The present study is a descriptive retrospective study which investigates 512 patients through their blood cultures. The samples were cultured on blood agar plate, EMB and chocolate agar and differential tests were performed to identify species.

Results:results: From the total of 512 blood cultures investigated in this study, 93 cases (18.1%) were reported positive in terms of growth of microorganism. These positive cases included Staphylococcus Epidermidis (64.5%), Staphylococcus Aureus (15.1%), Klebsiella (6.4%), Escherichia coli (6.41%), Enterobacter (5.4%) and Pseudomonas (2.2%).

Conclusion:Conclusion: The findings of this research shows that gram-positive cocci are the most common species causing bloodstream infections. They are associated with nosocomial (hospital-acquired) infections which can be prevented through a little more care in personal and staff hygiene as well as efficient disinfection of hospital environment.

Keywords:: Bloodstream Infection, Staphylococcus Epidermidis, Blood Culture

**P169 - 146: SURVEYING THE PREVALENCE OF VARIOUS VIRULENCE FACTORS
(ANTIBIOTIC RESISTANCE, BIOFILM FORMATION, COLONIZATION FACTORS) IN
ACINETOBACTER BAUMANNII ISOLATES RECOVERED FROM CLINICAL SOURCES, BY
PHENOTYPIC AND GENOTYPIC METHODS**

Ebrahim Babapour¹, Nour Amirmozafari², Azam Haddadi³, Reza Mirnejad⁴, Seyed-Abdolhamid Angaji⁵

1. Department of Microbiology, Ashtian Branch, Islamic Azad University, Ashtian, Iran
2. Iran University of Medical Sciences, School of Medicine, Microbiology Department, Tehran, Iran
3. Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran
4. Medical Bacteriology, Molecular Biology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran
5. Department of Cell and Molecular Biology, Faculty of Biological Sciences, Kharazmi University, Tehran, Iran

Background and Aim: *Acinetobacter baumannii* is an opportunistic bacterial pathogen responsible for many infectious diseases in humans. These bacteria take advantage of a variety of factors for colonization, resistance to different antibiotics and virulence. The aim of this study was to evaluate the prevalence of various virulence factors in *A. baumannii* isolates recovered from clinical sources.

Methods: This study was performed on clinical samples collected from patients in three hospitals of Tehran. These samples were initially screened by culture and biochemical tests for the presence of different species of *Acinetobacter*. Identifications were further confirmed by PCR assays. Their susceptibilities to 11 antibiotics of different classes were determined by disk diffusion method. The ability to produce ESBL by combination disk and biofilm were investigated using qualitative and quantitative methods. Subsequently PCR amplification of the *ompA* gene was performed for isolates

Results: From total clinical samples, 24% of specimens were confirmed to contain *A. baumannii*. The bacteria were highly resistant to most antibiotics except polymyxin B. These bacteria were highly potent to biofilm formation. At least 92% of the biofilm forming isolates were multi-drug resistant. All isolates were positive for the *ompA* gene.

Conclusion: *A. baumannii* contains *ompA* gene. Presence of this gene along with the ability of biofilm formation in bacteria can as well as the spread of MDR strains, which are considered as risk factors for hospitalized patients in hospitals. It seems necessary to provide continuous monitoring and determination of antibiotic susceptibility of clinical *A. baumannii*. This would help to select the most appropriate antibiotic for treatment.

Keywords: *Acinetobacter baumannii*, Biofilm, , Multi Drug Resistance (MDR), *ompA*

**P170 - 162: COMPARATIVE EVALUATION OF THE ANTIBACTERIAL SUSCEPTIBILITY
TEST OF RESAZURIN-PLATE AND QUICOLOR COLORIMETRIC METHODS**

Shahla Siamaki¹, Dr. Siavosh Salmanzadeh-Ahrabi², Dr.Tahereh Falsafi ³, Dr.Mahvash Seifali⁴

1. Alzahra University, Tehran, Iran
2. Alzahra University, Tehran, Iran
3. Alzahra University, Tehran, Iran
4. Alzahra University, Tehran, Iran

Background and Aim:Early and correct determination of antibacterial susceptibility patterns of clinical isolates is critical for a suitable antibacterial therapy. In this research antibacterial susceptibility of *Escherichia coli*, *Klebsiella pneumoniae*, *Enterobacter*, *Shigella sonnei*, *Salmonella typhimurium* species belonging to Enterobacteriaceae were compared in Quicolor (Salubris Inc., Massachusetts, USA) and Resazurin media (Ondokuz Mayıs University, Turkey) according to various aspects such as time, cost, repeatability, accuracy, and authenticity with CLSI standard method.

Methods:For this purpose, antimicrobial susceptibility of 100 isolates of bacterial species belonging to Enterobacteriaceae was determined for 6 different antibiotics by using standard disc Diffusion method.

Results:Their results were compared with those obtained in Quicolor and Resazurin media. The results were analyzed in SPSS software and their kappa and CV for repeatability of test in all three medium were calculated for 10 out of 100 isolates by using 10 independent experiments

Conclusion:According to our findings, Quicolor medium was preferable to Resazurin medium based on rapidity, cost, repeatability and accuracy. So it can be used as a suitable method for determining a fast and accurate antibacterial susceptibility in Enterobacteriaceae

Keywords:disk diffusion, susceptibility, rapid test, Colorimetric methods

**P171 - 163: IDENTIFICATION CAPSULAR GENES AS A SPECIFIC MARKER FOR THE
DIFFERENTIATION OF STREPTOCOCCUS PNEUMONIA STRAINS FROM VIRIDANS
GROUP**

Ramezan Ali Ataee¹, Ali Mehrabi Tavana², Mahdi Ghorbanalizadegan³, Ali Asgari⁴

1. Department of Medical Microbiology. Faculty of medicine, Baqiyatallah University of Medical Sciences, Tehran, IR Iran.
2. Department of Medical Microbiology. Faculty of medicine, Baqiyatallah University of Medical Sciences, Tehran, IR Iran.
3. Department of Medical Microbiology. Faculty of medicine, Baqiyatallah University of Medical Sciences, Tehran, IR Iran.
4. Department of Medical Microbiology. Faculty of medicine, Baqiyatallah University of Medical Sciences, Tehran, IR Iran.

Background and Aim: Rapid and accurate diagnosis of pneumococcal infections is crucial for treatment. The aim of this study was set up the PCR-based method for capsular encoding genes of *Streptococcus pneumoniae* as pathogenic biomarkers.

Methods: Based on the reference sequences of the *Streptococcus pneumoniae* cpsB, cpsD, aroE and psaA genes Specific primers pairs were designed. After bioinformatically assessment confirmation the bacterial strains were subjected to DNA preparation. Then the PCR protocol were performed. The products were sequencing.

Results: the results showed that the primers pairs against the cpsB, cpsD, aroE and psaA genes amplified 159, 202, 254 and 286 bp fragments respectively. The results of the comparison the Blast amplified sequences showed the highly homology (100%) with the reference genes.

Conclusion: the results revealed that the diagnosis of the *Streptococcus pneumoniae* virulence genes: cpsB, cpsD, aroE and psaA could be used as biomarkers to differentiation of the pathogenic *Streptococcus pneumoniae* from Nonpathogenic strains and also from virulence groups. this finding may discuss the rapid, accurate and simple method for direct diagnostic the pathogenic *Streptococcus pneumoniae* strains.

Keywords: PCR, *Streptococcus pneumoniae*, diagnosis, virulence genes

P172 - 191: RAPID DETECTION OF LEGIONELLA PNEUMOPHILA IN CLINICAL SPECIMENS OF PATIENTS WITH RESPIRATORY SYMPTOMS REFERING TO AHVAZ TEACHING HOSPITALS BY URINARY ANTIGEN AND PCR OF 16SRRNA GENE.

Mahtab Khoshkholgh Sima¹, Mahtab Khoshkholgh Sima², Mojtaba Moosavian³, Effat Abbasi Montazeri⁴

1. Dept. of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.
2. Dept. of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.
3. Health Research Institute, Infectious and Tropical Diseases Research Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.
4. Dept. of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.

Background and Aim: Legionella spp. are gram-negative bacilli which comprise 50 species and 70 serogroups. Legionella pneumophila is the most common agent of Legionnaires' disease among of the 50 recognized Legionella species and has been increasingly recognized as a pathogen causing both community- acquired and nosocomial pneumonia. Fatality rates among the elderly and immunocompromised patients may occur as a result of infection with this pathogen.

Methods: A total of 100 urine and respiratory specimens were collected from hospitalized patients with respiratory symptoms were examined in the study. The urinary antigen of Legionella pneumophila serogroup 1 was detected by Enzyme immunoassay (EIA) test using Coris Legionella V-test kit according to the manufacturer's instructions. Detection of Legionella pneumophila in respiratory samples was performed by PCR of 16SrRNA gene.

Results: Out of 100 specimens from patients with respiratory symptoms, 5% of urine specimens and 3% of respiratory specimens were positive for Legionella pneumophila by Coris Legionella V-test kit and PCR of 16SrRNA gene, respectively.

Conclusion: The detection of the soluble antigen of Legionella pneumophila serogroup 1 in urine by an enzyme immunoassay(EIA) kit has proven rapid detection, sensitive, and specific more than PCR for detection of Legionella pneumophila in sputum specimens.

Keywords: Legionella pneumophila, EIA, urinary antigen.

**P173 - 213: PREVALENCE OF CTX-M 1 EXTENDED-SPECTRUM -LACTAMASE-
PRODUCING ESCHERICHIA COLI AND KLEBSIELLA PNEUMONIAE IN PATIENTS WITH
LEUKEMIA**

Mahdane Roshani¹, Ali hashemi², Hossin goudarzi³, Aghil bahramiyan⁴, Neda yousefi⁵, zohre baseri⁶

1. Department of Medical Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran
1. Department of Medical Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran
1. Department of Medical Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran
1. Department of Medical Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran
1. Department of Medical Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran
- Shariati hospital, Tehran, Iran

Background and Aim: Patients with haematological malignancies, especially acute leukaemia, are considered as the most severely Immunodeficiency patient group, particularly during prolonged episodes of treatment-related Neutropenia. Infection is a dominant cause of post-transplantation morbidity and mortality. The extended-spectrum CTX-M β -lactamases are the most prevalent ESBLs worldwide, that first defined in Japan in 1986, CTX-M (cefotaximases) is an ESBL family including more than 60 different enzymes in five phylogenetic groups and have been mainly associated with Enterobacteriaceae, most commonly in *Escherichia coli*, *Klebsiella pneumoniae*, *Proteus mirabilis* and *Salmonella typhimurium*.

Methods: Resistance to different antibiotics was determined using the standard disk diffusion method. ESBLs, β -lactamases were detected by the combination double disk test (CDDT) method and polymerase chain reaction (PCR) was used to determine blaCTX-1 genes in the ESBLs positive isolates.

Results: The prevalence of ESBLs β -lactamase producer isolates was 51 (64%) respectively. The prevalence of blaCTX-M among isolates was 46 (90%).

Conclusion: Outbreak of isolates CTX-M1 lactamases and ESBLs can cause in patient with leukemia serious problems in the future, administration of these serious infections in these high-risk patients is becoming a clinical challenge.

Keywords: leukemia, CTX-M1, ESBL, *Klebsiella pneumoniae*, *Escherichia coli*

**P174 - 224: MUTATION SURVAY IN GYR (A) OF UREAPLASMA UREALYTICUM
ISOLATED FROM WOMEN WITH PCR AND SEQUENCING, SANANDAJ CITY, IRAN**

Amir Safari¹, Rashid Ramazanzadeh ², Samaneh Rouhi³

1. Student Research Committee, Kurdistan University of Medical Sciences, Sanandaj, Iran. Cellular & Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran. Microbiology Department, Kurdistan University of Medical Sciences, Sanandaj, Iran.
2. Cellular & Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran. Microbiology Department, Kurdistan University of Medical Sciences, Sanandaj, Iran.
3. Student Research Committee, Kurdistan University of Medical Sciences, Sanandaj, Iran. Cellular & Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran. Microbiology Department, Kurdistan University of Medical Sciences, Sanandaj, Iran

Background and Aim:Ureaplasma urealyticum is associated with pelvic inflammatory disease, bacterial vaginosis, infertility, ectopic pregnancy, as well as perinatal disorders. Macrolides and quinolones are used against infection caused by this bacterium. Point mutations in DNA gyrase are responsible for quinolones resistance in U. urealyticum. Aim of this study is mutation detection gyr (A) gene of U. urealyticum isolated from women.

Methods:During year of 2014, 100 tubes containing genital swab specimens collected from women (aged from 19-43) and referred to obstetrics and gynecology section (Beasat and Toohid Hospitals, Sanandaj, Kurdistan Province, Iran). After DNA extraction, PCR was performed and samples (30 samples) sending for sequencing. Then with NCBI website, result is compared.

Results:From 100 samples, of 30 PCR products send for sequencing, 27% (n=8/30) of them had effective point mutation.

Conclusion:In our study wide range of mutation in gyr (A) gene was found. Most of mutations were in region 104 (Q $\rightarrow$ K). Acquisition of resistance to quinolones in genital Ureaplasma is dangerous for pregnant women because it can pass from mate to fetus

Keywords: Mutation, gyr (A), Uraplasma uralyticum, Sequencing

**P175 - 246: ISOLATION AND IDENTIFICATION OF ACINETOBACTER STRAINS WITH
WIDESPREAD RESISTANCE TO VARIOUS ANTIBIOTIC FROM SPUTUM IN SHAHID
RAJAEI HOSPITAL IN SHIRAZ**

Azadeh Baoosh¹, Azadeh Baoosh^{1,2}, Dr Elham Moazamian^{2*3}, Dr Amin Edalatmanesh³

1. -
2. 1- Department of Microbiology, Faculty of Science, Science And Reserch branch, Islamic Azad University, Fars, Iran. 2- Department of Microbiology, College of Science, Agriculture and modern Technology, Shiraz Branch, Islamic Azad University, Shiraz, Iran
3. 2- Department of Microbiology, College of Science, Agriculture and modern Technology, Shiraz Branch, Islamic Azad University, Shiraz, Iran.
4. 3- Department of Physiology, College of Science, Agriculture and modern Technology, Shiraz Branch, Islamic Azad University, Shiraz, Iran.

Background and Aim: Acinetobacter Species are clinically important pathogen with widespread resistance to various antibiotic and has emerged as a major pathogen of nosocomial infection. The purpose of this study is isolated the Acinetobacter species from sputum.

Methods: Collected 50 samples from sputum of patient and culture on macconky agar, incubation of 37°C and identification by biochemical test such as Catalase, Oxidase, TSI, Citrate, MR, VP and Melting the gelatin

Results: Of 50 infected samples isolated from sputum, 9% were found to Acinetobacter species. According to this study Acinetobacter spp isolates were resistant to various antibiotic such as Cefepime, Ceftazidime, Ciprofloxacin, Trimethoprim, Ceftriaxone, Amikacin, Colistin and Gentamycin.

Conclusion: Acinetobacter spp. has emerged as a major pathogen of nosocomial infections. Acinetobacter spp. Were critical risk for hospitalization patient in ICU ward because they were important pathogen clinically with widespread resistant to various antibiotic.

Keywords: Acinetobacter, Sputum, Widespread, Resistance, pathogen, Antibigram.

P176 - 249: IS HYDROGEN PEROXIDE A CONSIDERABLE ANTIMICROBIAL AGENT OF ALL HONEY TYPES?

Elahe Mahmoodi Khaledi¹, Mehran Habibi Rezaei², Ali Akbar Moosavi-Movahedi³

1. Department of Biotechnology, School of Chemistry, University of Kashan, Kashan, Iran
2. Department of Cellular & Molecular Biology, School of Biology, College of Science, University of Tehran, Tehran, Iran
3. Institute of Biochemistry and Biophysics, University of Tehran, Tehran, Iran

Background and Aim: Honey has been used since ancient times, both as safe food and medicine. The emergence and spread of antibiotic resistance bacteria has provided the groundwork for alternative natural origin treatments such as honey. Iran has special climate and unique native flora and therefore specific honeys, but antimicrobial properties and effective compounds of Iranian honeys have been paid less attention. The aim of present study was qualitative analysis of hydrogen peroxide role, as a well-known antimicrobial component in bioactivity of Iranian honeys.

Methods: In previous study, we surveyed some Iranian honeys for their antimicrobial properties against four infection causative bacteria in wounds (*Pseudomonas aeruginosa*, *Escherichia coli*, *Staphylococcus aureus* and *Enterococcus faecalis*). In present study, a solution of the approved honeys with significant antimicrobial activity was dialyzed using 12.5 kDa membrane. The resulted dialysates and retentates were freeze dried, then their antimicrobial activities were surveyed by broth micro dilution method.

Results: For each honey, bioassay indicated the antimicrobial activity of dialysates was equivalent to honey sample before dialysis. In the other words, the retentates were not shown any antimicrobial activity. Given that the heavy proteins such as glucose oxidase were existed in retentates and glucose equilibrium was reached in two portions, the activity of hydrogen peroxide in the antimicrobial activity of the approved honey samples was negligible.

Conclusion: We conclude that hydrogen peroxide cannot be one of the most important components in surveyed honey samples. Therefore, Iranian honeys with remarkable clinical values need further studies into the identification and characterization of their bioactive constituents.

Keywords: Iranian honey, Antimicrobial activity, Bioactive constituents, Hydrogen peroxide, Wound infection

**P177 - 250: FREQUENCY OF AAC(3)-IIA GENE IN UROPATHOGENIC STRAINS OF
ESCHERICHIA COLI IN WOMENS WHIT UTI IN SHAHREKORD TEACHING HOSPITALS
USEAING PCR METHOD-2015**

Seyed Alireza Miraliakbarian¹, Behnam zamanzad²

1. M.Sc Thesis
2. Dr

Background and Aim:Antibiotic resistance is one of the main global health problems around the world; so treating serious infections like Urinary Tract Infection(UTI) as one of the most common infections worldwide which affects especially young women is becoming to be very hard. Aminoglycosides including gentamycin, kanamycin and amikacin are used broadly by clinicians to treat UTI. The objective of this study was specifying antibiotic resistance pattern among hospitalized and non-hospitalized UTI patients and also determining the presence of aac(3)II-a gene as an indicator of aminoglycoside resistance in specimens.

Methods:A total of 200 samples obtained from 100 hospitalized UTI patients and 100 non- hospitalized UTI patients were investigated. Antibiotic resistance pattern of all specimens were examined Using disk diffusion approach. Molecular analysis to investigate the presence of aac(3)II-a was accomplished by PCR method.

Results:In hospitalized group there were 45% resistance to Kanamycin, 36% to Gentamycin and 26% to Amikacin. in non-hospitalized UTI group 51% of isolates were resistant to kanamycin, 35% to gentamycin and 19% to amikacin. molecular analysis surveying the presence of aac(3)-IIa revealed that 27% and 33% of samples obtained from non-hospitalized and hospitalized patients respectively contained aac(3)-IIa gene.

Conclusion:our results demonstrated that resistance to common antibiotics like aminoglycosides among UTI patients is high so in the case of experience-based treatments, prescribing antibiotics including imipenem, nitroforantein and amikacin can be useful in treating UTI. Furthermore, regarding the high percentage of aac(3)-IIa gene presence among subjects and consequent resistance to aminoglycosides, periodic monitoring is recommended.

Keywords:Uropathogenic Escherichia Coli ; Urinary Tract Infection ; aac(3)-IIa

P178 - 252: A CLUE TO FIND THE NEW ANTIMICROBIAL PEPTIDES IN IRANIAN HONEYS.

Elahe Mahmoodi Khaledi¹, Mehran Habibi Rezaei², Ali Akbar Moosavi-Movahedi³

1. Department of Biotechnology, School of Chemistry, University of Kashan, Kashan, Iran
2. Department of Cellular & Molecular Biology, School of Biology, College of Science, University of Tehran, Tehran, Iran
3. Institute of Biochemistry and Biophysics, University of Tehran, Tehran, Iran

Background and Aim:Incidence of antibiotic-resistant bacteria is increasing, thus discovery of alternative therapeutic agents is needed. Recently, the pharmaceutical interest in honey has increased. Proteins/peptides are one of the most important constitute with 0.1- 0.5% of the honey weight. Currently the role of antimicrobial peptides (AMPs) in antimicrobial activity of honey have been paid more attention. Evaluating the role of peptides in antimicrobial activity of honey, in this study 20 Iranian honey samples were investigated.

Methods:Using 12.5 kDa permeable membrane in our previous study, we established no antimicrobial activity of dialysis retentates. In this survey, upon ultrafiltration of dialysates by Amicon Ultra 4 mL centrifugal filter with membranes NMWL of 3 and 5 kDa and concentration, three fractions were resulted. The antimicrobial activity of the resulted fractions including <3 (lower than 3 kDa), 3< <5 (between 3 and 5 kDa), 5< <12.5 (between 5 and 12.5 kDa) and the concentration of 50% (w/v) of each honey sample in sterile deionized water were determined by disc diffusion method against reference strains of *Escherichia coli* and *Staphylococcus aureus*.

Results:The results showed the significant antimicrobial effect of the 5< <12.5 kDa fractions and comparable with each honey sample alone. According to OPA (O-phthalaldehyde) method for determining of peptide concentration and their molecular weight, they represent to be antimicrobial peptides.

Conclusion:It can be concluded that the presence of antimicrobial peptides in honey and its therapeutic features can be used in determination of honey quality and provide beneficial information for future studies in this field.

Keywords:Honey, Antimicrobial peptides, Ultrafiltration, Disc diffusion.

P179 - 264: EVALUATION OF AMINOGLYCOSIDES RESISTANCE GENES AMONG BETA LACTAMASE PRODUCING ESCHERICHIA COLI

Vida Sorayaei¹, Mohammad Taghi Akhi ², Reza Ghotaslou ³, Mohammad Asgharzadeh⁴, Tahereh Pirzadeh⁵, Babak Asghari⁶, Mohammad Yousef Memar⁷, Ali Toloue Ostadgavahi⁸

1. Department of Bacteriology and Virology, School of Medicine, Tabriz University of Medical Sciences
2. Immunology Research Center, Tabriz University of Medical Sciences, Tabriz, IR Iran
3. Department of Bacteriology and Virology, School of Medicine, Tabriz University of Medical Sciences
4. Paramedical Faculty, Tabriz University of Medical Sciences, Tabriz, IR Iran
5. Department of Bacteriology and Virology, School of Medicine, Tabriz University of Medical Sciences
6. Department of Bacteriology and Virology, School of Medicine, Tabriz University of Medical Sciences, Tabriz, IR Iran
7. Department of Bacteriology and Virology, School of Medicine, Tabriz University of Medical Sciences, Tabriz, IR Iran
8. Department of Bacteriology and Virology, School of Medicine, Tabriz University of Medical Sciences, Tabriz, IR Iran

Background and Aim: Escherichia coli (E. coli) is a member of human and animals gut flora. It is also one of the major causes of nosocomial and other infections. Aminoglycosides are one of the antibiotics groups which are used for treatment of E. coli infections and yet resistance to aminoglycosides has increased in the recent years. The present study investigated the prevalence of genes encoding aminoglycoside-modifying enzymes in ESBL producing E. coli strains isolated from intestinal or extra-intestinal infections.

Methods: Antimicrobial susceptibility patterns of the 107 isolates of E. coli to different antimicrobial agents were determined by the disc diffusion method. Combined disk procedure was carried out for detection of beta lactamase production using ceftazidime and ceftazidime/clavulanic acid. The frequency of aminoglycoside modifying enzymes encoding genes aac (3)-IIa, ant(2'')-Ia, aph(3'')-IIa, aph(3')-Ia, and aac(3)-IV was analyzed by the PCR method.

Results: 107 E. coli were isolated from different clinical specimens including: urine (35), wound infections (36) and diarrheal stools (36). The susceptibility tests analysis showed that the highest resistance was towards ampicillin (50%), Trimethoprim sulphamethoxazol (50%). Out of 107 E. coli, 27 were aminoglycosides resistant which 18 of them showed beta- lactamase activities. Prevalence of aminoglycoside resistance genes among 18 ESBL producing E. coli were as follows: ant(2'')-Ia 6 (%33.33), aph(3'')-Ia 6 (%33.33), aac(3)-IIa 3 (%16.67), aph(3'')-IIa 3 (%16.67), aac(3)-IV 0 (%0).

Conclusion: The results of this study indicated that the genes encoding aminoglycoside-modifying enzymes are prevalent in E. coli isolates in the study region.

Keywords: Escherichia coli; Antimicrobial Agents; Aminoglycoside, Beta lactamase

P180 - 267: ANTIMICROBIAL RESISTANCE AND MOLECULAR PREVALENCE OF EFFLUX PUMP ENCODING GENES (ADER, ADEB) IN ACINETOBACTER BAUMANNII STRAINS ISOLATED FROM HOSPITALIZED PATIENTS IN TEHRAN

Samaneh Shabani¹, Parvaneh Saffarian², Reza Mirnejad³

1. Department of Microbiology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, Iran
2. Department of Bacteriology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, Iran.
3. Molecular Biology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran

Background and Aim: *Acinetobacter baumannii* causes variety of nosocomial infections which often lead to death. Because of wide range drug resistance amongst *A. baumannii* strains, it becomes a problem in clinical treatments. One of the main factors causing resistance in *A. baumannii* strains is the efflux pump. *Acinetobacter baumannii* causes variety of nosocomial infections which often lead to death. Because of wide range drug resistance amongst *A. baumannii* strains, it becomes a problem in clinical treatments. One of the main factors causing resistance in *A. baumannii* strains is the efflux pump. The aim of this study was to determine the prevalence of *adeR* and *adeB* genes encoding efflux pump between *A. baumannii* strains isolated from hospitalized patients in Tehran.

Methods: 300 clinical samples were collected from some main hospitals in Tehran. After strain determination through biochemical and culture method, antimicrobial resistance of *A. baumannii* isolates was evaluated with disk diffusion agar. Finally, the presence of *adeR* and *adeB* genes were examined using molecular method, PCR

Results: Out of 300 clinical samples, 100 *A. baumannii* isolates were determined. 70% of *A. baumannii* isolates showed resistance against three or more antibiotics. Moreover, molecular method assessment revealed that the prevalence of either *adeR* or *adeB* genes among antibiotic resistance *A. baumannii* strains is 96%.

Conclusion: According to results of this study, the efflux pump encoding genes (*adeR* and *adeB*) are active in between antibiotic resistance *A. baumannii* strains

Keywords: *Acinetobacter baumannii*, Efflux pump, *adeR*, *adeB*, Multidrug resistance, PCR

**P181 - 274: IMMUNOTHERAPY EFFECTS ON ENTEROCOCCUS FAECALIS (A
MICROFLORA BACTERIA) VIRULENCE GENES IN PROSTATE CANCER PATIENTS**

Tayebeh Talebzadeh¹, Fahimeh Baghbani-arani ², Massuod Houshmand³

1. Department of Microbiology, Varamin-Pishva Branch, Islamic Azad University, Varamin, Iran.
2. Department of Genetics & biotechnology, Varamin-Pishva Branch, Islamic Azad University, Varamin, Iran.
3. Department of Medical Genetics, National Institute of Genetic Engineering and Biotechnology (NIGEB), Tehran, Iran

Background and Aim: Immunotherapy is an effective and non invasive method for cancer treatment but side effects of this method is not completely clarified. An important challenge with this therapy method, is the effects of immunotherapy on induction of microflora bacteria pathogenesis. Thus, here we studied the immunotherapy effects on Enterococcus faecalis (a microflora bacteria) virulence genes in Prostate cancer patients.

Methods: To better understand the molecular mechanisms underlying these microflora pathogenesis changes, we have used the Real time PCR to analyze *gyrA* and *slyA* gene expression in the Enterococcus faecalis of three groups samples. Group A normal persons, group B prostate cancer patients before immunotherapy treatment and group C prostate cancer patients after one Immunotherapy period.

Results: Results showed significant ($P < 0.05$) over expression of *gyrA* and *slyA* in group C against group B and A. Also no significant alteration observed in expression of *gyrA* and *slyA* between group A and B.

Conclusion: It seems that Immunotherapy has side effects such as increasing the pathogenesis risk of microflora of patients. These side effects could cause further infections after ending the immunotherapy of cancer. Further gene expression studies could help to better understand of immunotherapy effects on whole body and mechanisms of patients.

Keywords: Prostate cancer, Immunotherapy, side effects, Faecalis

P182 - 275: COMBINED EFFECT OF PHOSPHOMYCIN AND B-CHLORO-L-ALANINE ON BIOFILM PRODUCTION BY METHICILLIN RESISTANT S.AUREUS

ELHAM Akbari ayezloy¹, Nima Hosseini Jazani², Saber Yousefi³

1. M.Sc. student of medical microbiology, Student's research committee, Email: akbarielham2@gmail.com, Tel: +98-9146234315, Fax: +98-441-2780800,
2. Professor of medical microbiology, Department of Microbiology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran, E-mail: n_jazani@yahoo.com.
3. Assistant Professor of bacteriology, Department of Microbiology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran E-mail: saber84@gmail.com, Tel: +88-9143415968

Background and Aim: Biofilm-forming capacity is very important for success of Methicillin-resistant *Staphylococcus aureus* (MRSA) as a pathogen. Fosfomycin is a wide spectrum bactericidal antibiotic with inhibitory effects on biofilm production and β -Chloro-L-alanine is a non toxic amino acid analog which inhibits one of the early stages of peptidoglycan biosynthesis. The aim of this study was to determine the combined effect of Phosphomycin and β -Chloro-L-alanine on biofilm production by MRSA clinical isolates.

Methods: 42 MRSA isolates were collected during a six month period and identified by the Oxacillin strip test. To determine the ability of biofilm production by bacterial isolates, microtiter plate method was used. Antibacterial activities of phosphomycin and β -Chloro-L-alanine were investigated by determining MIC and MBC values. Antibiofilm activity of phosphomycin and β -Chloro-L-alanine was measured in the presence of Sub-MIC concentrations of fosfomycin, β -Chloro-L-alanine or a combination of both.

Results: 21.4% of isolates were strong biofilm producers and 5% were moderate in this sense. The effect of fosfomycin on biofilm production was significant ($p=0.017$). However there was no significant difference between the isolates treated with β -Chloro-L-alanine and untreated ones in respect of biofilm formation ($p=0.840$). Also the effect of fosfomycin+ β -Chloro-L-alanine treatment on biofilm production was significantly different from non treated, fosfomycin and β -Chloro-L-alanine groups ($p=0.00$, 0.004 and 0.000 respectively).

Conclusion: The combination of fosfomycin and β -Chloro-L-alanine could be introduced as an excellent mixture for eradication of MRSA biofilms in vitro.

Keywords: methicillin resistant *S.aureus*, Phosphomycin, β -Chloro-L-alanine, biofilm

**P183 - 279: EVALUATION OF SERUM C-REACTIVE PROTEIN AND ITS RELATIONSHIP
WITH CAUSATIVE FACTOR IN URINARY TRACT INFECTION**

Majid Baseri Salehi¹, Saeed Shoa², Mohsen Naghmachi³

1. PhD of microbiology, Faculty member of Department of microbiology, Islamic Azad university, Kazerun Branch, Kazerun, Iran
2. PhD Student, Department of microbiology, Islamic Azad university, Shiraz Branch, Shiraz, Iran
3. MSc of Microbiology, Department of Nutrition, Yasuj University of Medical sciences, Health School, Yasuj, Iran

Background and Aim: The main purpose of this study was determination of relation between CRP level of Blood and urinary tract infections. In addition, the relation between CRP level of blood and the urinary tract infection agent was investigated.

Methods: In total 2400 samples were collected from the patient suspected to (UTI) during 5 months in 1393. For there more blood sample of all UTI patients was collected parallel with collection of urine sample collected. To continue the study CRP level of blood sample was determined using two methods. After verify testing of UTI positive of the same patient with urinary tract infection were determined by observation of 10⁵< CFU and the agents recognized by using phenotypic tests with APi kits. In addition DNA sequencing based on 16 SrRNA was carried out in order to authenticate the Identification.

Results: The results obtained indicated that out of 100 positive UTI samples 69% was Escherichia coli, 10% klebsiella, 5% enterobacter, 6% enterococcus, 2% staphylococcus and 3% the other bacteria.

Conclusion: The results obtained indicated that the level of CRP in the UTI patients increased of to 56.8%. In addition No relation was found between the level of CRP and the type of the bacterial agents. Generally, the level of CRP might be depended on the infections even urinary tract infections and the other hard, CRP level is not depended on the type of the bacterial infection.

Keywords: Bacterial infection, C-Reactive protein, Urinary tract infection

P184 - 280: INTEGRONS ASSAY IN KLEBSIELLA STRAINS ISOLATED FROM URINARY TRACT INFECTIONS

Azam Haddadi¹, Saki Hiva², Mohammadi Roya³, Shavandi Mahmoud⁴

1. Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran
2. Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran
3. Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran
4. Microbiology and Biotechnology Group, Research Institute of Petroleum Industry, Tehran, Iran.

Background and Aim: In recent years, the threat of acquisition of antibiotic resistance is growing, horizontal transfer of antibiotic resistance genes has led to the rapid emergence of antibiotic resistance among clinical isolates of bacteria. The aim of this study was to survey existence of integrons by PCR-RFLP among clinical isolates of *Klebsiella* in the immigration friendly city of Karaj, Iran.

Methods: From 129 *Klebsiella* isolates collected from Karaj hospitals and laboratories, integrons were detected using PCR with degenerate primers designed to hybridise to conserved regions of integrase genes. To detect integron classes, the amplified fragments were digested with two restriction enzymes, *RsaI* and *HinfI*.

Results: Of the 129 *Klebsiella* sample, 89% were *Klebsiella pneumoniae* and 11% were *Klebsiella oxytoca*, 107 isolates (83%) were multidrug resistant (resistant to at least two unrelated antibiotics). By amplification of *intI* gene it was revealed that 21.7% of the isolates harbour integrons. Also by PCR-RFLP it was revealed that all of them were class 1. No class 2 and 3 integrons was observed among our samples and 101 isolates did not harbor integrons. The existence of integrons was confirmed in 25 of our multidrug resistant isolates, indicating the prevalence value is high and integrons may be partly responsible for multidrug resistance.

Conclusion: Multidrug resistance suggests that strategy for treatment of patients with *Klebsiella* infections needs to be revised. The possibility of transmission of resistance genes by integrons would be decreased by treatment of patients with the appropriate antibiotics.

Keywords: *Klebsiella*, integrin, antibiotic resistance, PCR-RFLP.

P185 - 281: PREVALENCE DETERMINATION OF ESBL-PRODUCING KLEBSIELLA ISOLATES AND THEIR ANTIMICROBIAL SUSCEPTIBILITY PATTERNS ISOLATED FROM KARAJ, IRAN

Azam Haddadi¹, Mohammadi Roya², Asgari Sharafodin³, Asadi Farzaneh⁴

1. Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran, P. O. Box 313 – 31485
2. Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran, P. O. Box 313 – 31485
3. Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran, P. O. Box 313 – 31485
4. Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran, P. O. Box 313 – 31485

Background and Aim: Urinary tract infection (UTI) is the most common nosocomial infection and klebsiella is the second most common causes of UTI after E.coli. The prevalence of extended spectrum beta-lactamses (ESBLs)-producing strains and their resistance to beta-lactam antibiotic has had a daily increase. The aim of this study was to determine prevalence of ESBL-producing Klebsiella isolates and their antimicrobial susceptibility patterns.

Methods: In this descriptive study a total number of 100 isolates of Klebsiella were collected from some hospitals and clinical laboratories in Karaj. Isolates were identified based on API 20E kit. The susceptibility of the isolates to 19 different antibiotics was done by Kirby Bauer's disk diffusion method. Isolates were screened for ESBLs production by phenotypic conformatory test (PCT).

Results: Of the 100 Klebsiella sample, 86% were Klebsiella pneumoniae and 14% were Klebsiella oxytoca. Antimicrobial susceptibility testing showed the highest resistance to amoxicillin (99%), whereas ciprofloxacin, norfloxacin and ofloxacin were the most effective drugs, with only 11% resistance. Also results showed that 54 isolates were resistant to more than two unrelated antibiotics. The phenotypic confirmatory test (PCT) detected 25 isolates as ESBL producers. 23 (92%) of which were Klebsiella pneumoniae and 2 (8%) isolates were Klebsiella oxytoca.

Conclusion: As antibiotic options in the treatment of ESBL-producing organisms are extremely limited, ESBL screening by laboratories is suggested to reduce the risk of therapeutic defeat. Multi- drug resistance suggests that strategy for treatment of patients with bacterial infections needs to be revised.

Keywords: Klebsiella, antibiotic resistance, UTI, ESBLs

P186 - 283: DIAGNOSIS OF ACUTE Q FEVER IN THREE PATIENTS WITH A HISTORY OF CONSUMING UNPASTEURIZED DAIRY BY NESTED-PCR IN KHORRAMABAD CITY

Farnaz Ferdosi¹, Amin Jaydari², Nemat Shams³, Hadis Ghasemi⁴, Mahdi Hasanvand⁵

1. -Master Of Science Student In Bacteriology, Faculty Of Veterinary Medicine Lorestan University
2. Assistant Professor, Department Of Microbiology, Faculty Of Veterinary Medicine, Lorestan University
3. Assistant Professor, Department Of Microbiology, Faculty Of Veterinary Medicine, Lorestan University
4. Master Of Science Student In Microbiology, Department of Microbiology, Islamic Azad University Science and research branch tehran
5. Master Of Science Student In Microbiology, Department of Microbiology, Islamic Azad University Boroujerd

Background and Aim: Q fever is a zoonotic disease caused by the obligate intracellular gram negative bacterium, *Coxiella burnetii* and the bacterium caused various clinical symptoms in patients. There are few studies about the diagnosis of Q fever in humans in Iran. Initial serological studies in some areas of Iran revealed high seropositivity rate in patients with a history of fever associated with livestock. However consumption of unpasteurized dairy is one of the reasons for transmission the disease which is less common. This report is about three patients suspected of having brucellosis with no history of contact with animals who are resident of urban areas that for Wright and 2ME test referred to Khorramabad city laboratories. The aim of this report is consideration of Q fever as one of the probable reasons of fever among urban patients with no history of contact with animals.

Methods: Nested-PCR method was used to detect *Coxiella burnetii* genome.

Results: *Coxiella burnetii* genome was identified by molecular testing of patients' blood and further researches revealed that all three patients used traditional and unpasteurized dairy products.

Conclusion: This study reveals that Q fever might be one of the possible reasons in febrile patients that should be considered. While boiling milk is not an efficient method for eliminating bacteria, therefore consuming pasteurized dairy is recommended.

Keywords: *Coxiella burnetii*, Human, Khorramabad, Nested-PCR, Q fever

**P187 - 285: PREVALENCE OF CNA, FNBA, FNB B AND PVL AS SPREADING FACTORS
RELATED GENES IN CLINICAL ISOLATED STAPHYLOCOCCUS AUREUS BY
MULTIPLEX COLONY PCR**

Bahman Mirzaei¹, Mostafa shahmoradi², Seyed fazlollah Moosavi³

1. 2Department of Microbiology, Microbial research center, Pasteur Institute of Iran, Tehran. Microbiology Research Center (MRC) Pasteur Institute of Iran.
2. 2Department of Microbiology, Microbial research center, Pasteur Institute of Iran, Tehran. Microbiology Research Center (MRC) Pasteur Institute of Iran.
3. 2Department of Microbiology, Microbial research center, Pasteur Institute of Iran, Tehran. Microbiology Research Center (MRC) Pasteur Institute of Iran.

Background and Aim: Staphylococcus aureus is an important bacterial pathogen involved in both nosocomial and community associated infections.

Methods: Following the isolation and identification of Staphylococcus aureus using biochemical and molecular methods, profiles of cna, fnbA, fnbB and pvl genes were assessed by multiplex colony PCR procedure. Subsequently, biofilm formation and antibiotic susceptibility pattern were analyzed.

Results: A total of 50 Staphylococcus aureus were isolated from clinical specimens. Following the in vitro biofilm formation assay 3(6%) strains were detected as strong biofilm forming and 15 (30%) isolates moderately produced biofilm respectively. Among the strains frequency of targeted genes were 31(62%) for cna, 35(70%) for fnbA, 13(26%) for fnbB and 1(2%) for pvl. In 11(22%) isolated strains fnbA, fnbB and cna genes were screened. Frequency of antibiotic resistance strains were as follow: (2%) strains were determined as vancomycin resistant. 5(10%) strains were analyzed as susceptible against all antibiotics. All isolated strains were determined as penicillin, amoxicillin and clavulanic acid resistant.

Conclusion: Prevalence of the related genes for attachments and spreading in biofilm forming strains were defined and those strains with more spreading genes have more chance for colonization and pathogenesis and antibiotic resistance.

Keywords: Spreading factors, Multiplex colony PCR, Staphylococcus aureus

**P188 - 286: COMPARISON BETWEEN PHENOTYPIC AND GENOTYPIC FEATURES IN
CLINICAL ISOLATED STAPHYLOCOCCUS EPIDERMIDIS.**

Bahman Mirzaei¹, Peyman Faridi far², Seyed fazlollah Moosavi³

1. Department of Microbiology, Microbial research center, Pasteur Institute of Iran, Tehran. Microbiology Research Center (MRC) Pasteur Institute of Iran.
2. Department of Microbiology, Microbial research center, Pasteur Institute of Iran, Tehran. Microbiology Research Center (MRC) Pasteur Institute of Iran.
3. Department of Microbiology, Microbial research center, Pasteur Institute of Iran, Tehran. Microbiology Research Center (MRC) Pasteur Institute of Iran.

Background and Aim: Biofilm producing staphylococcus epidermidis, due to the undeniable role in medical device related infections are considered as hospitalized patient's health threat. Determination of biofilm forming activity and related genes in staphylococcus epidermidis were the main goals of the current study.

Methods: Following the isolation and identification of staphylococcus epidermidis strains using biochemical and molecular methods, biofilm formation pattern were assessed. Furthermore, the frequency of genes encoding polysaccharide intracellular adhesion (ica locus), in addition a fibrinogen binding adhesion (SdrG) and autolysin (atlE), was investigated.

Results: Multiplex colony PCR was accomplished to two references staphylococcus epidermidis, ATCC 12228 and 35984 as controls and to 50 (42.62%) isolated strains. All (100%) strains screened as biofilm forming. Profile of generated genes showed that in 36(72%) of isolates presence of all targeted genes. Among the isolates 36(72%) were completely ica locus, SdrG, atlE and biofilm forming positive. As well as 8(16%) strains detected as biofilm forming but mentioned genes were not discriminated. Antibiotic resistance pattern indicated that, (100%) strains as penicillin and 45(90%) amoxicillin and clavulanic acid resistant. Also cefamendole described as a best treatment choice for infections caused by these strains.

Conclusion: Biofilm formation process in Staphylococcus epidermidis has gained by presence of ica locus. Subsequently, these genes are predominant in biofilm forming Staphylococcus epidermidis

Keywords: Multiplex colony PCR, Biofilm formation, Staphylococcus epidermidis.

**P189 - 290: PREVALENCE OF BACTERIAL VAGINOSIS IN WOMEN REFERRED TO
HEALTH CENTERS IN AHAR CITY AND ITS ANTIBIOTIC SUSCEPTIBILITY PATTERN**

Arezoo Azizi¹, Behboud Jafari ², Roghaie Dargahi³

1. master of science student
2. Department of microbiology-Ahar Branch-Islamic Azad University-Ahar-Iran
3. Gynecologist, Ardabil University of Medical Sciences

Background and Aim: Bacterial vaginosis syndrome, a condition in which anaerobic bacteria, including *Gardnerella vaginalis*, *Mobiluncus* and *Mycoplasma hominis* the normal vaginal flora (mainly lactobacilli producing hydrogen peroxide) fall. In this type of vaginitis, a change in the normal vaginal bacterial flora that occurs to eliminate hydrogen peroxide-producing lactobacilli and an overgrowth of anaerobic bacteria leads. Target of this study was to determine the prevalence of bacterial vaginosis in the study population.

Methods: In this cross-sectional study, 104 women with complaints of vaginal discharge were referred to health centers in Ahar city, were randomly selected. Amsel clinical criteria for the diagnosis of bacterial vaginosis and to isolate vaginalis were cultured and isolated bacteria were AntibioGram. The average results for each group were calculated by SPSS software.

Results: The results showed that the prevalence of bacterial vaginosis in this study was 26.9 percent, the highest prevalence of bacterial vaginosis age between the ages of 20-29 years. Most of them were there with three criteria Clue cell, uniform vaginal secretions and more than 4/5 of the vaginal PH, were suffering from bacterial vaginosis. As a result Antibiotic bacteria isolated from patients, the bacteria most sensitive to chloramphenicol and tetracycline were the most resistant

Conclusion: Based on these findings the prevalence of bacterial vaginosis was 26.9 percent and among various antibiotic used, chloramphenicol has been effective. Amsel criteria as well as the use of low-cost diagnostic procedures and without spending too much time on routine examination and periodic health centers and family planning services to women in particular, it is recommended to IUD application.

Keywords: bacterial vaginosis, antibiotic sensitivity, Women

**P190 - 300: MOLECULAR DETECTION AND ANTIMICROBIAL RESISTANCE OF
INTESTINAL PATHOTYPES OF ESCHERICHIA COLI IN KHUZESTAN PROVINCE**

Atieh Mashhadikarimdarbandi¹, Saeid Bouzari², Parviz Owlia³

1. Microbiology Department, Shahed, School of Medicine University, Tehran, Iran
2. Molecular Biology Department, Pasteur Institute of Iran, Tehran, Iran
3. Molecular Microbiology Research Center, Shahed University, Tehran, Iran

Background and Aim: Pathotypes *E. coli* such as enterohaemorrhagic *E. coli* (EHEC), enteroaggregative *E. coli* (EAEC), enteropathogenic *E. coli* (EPEC), enteroinvasive *E. coli* (EIEC), enterotoxigenic *E. coli* (ETEC), diffusely adhering *E. coli* (DAEC).

Methods: Totally 1000 isolates (5 colonies of each 200 samples) were collected from patients with diarrhea in Khuzestan province of Iran. of virulence genes, i.e; eae, stx1 and stx2 for EHEC, bfp and eae for EPEC, LT and ST for ETEC, AA for EAEC, invE for EIEC, STX1 or STX2 for STEC.

Results: Of 200 stool samples, 158(79%) *E. coli* was identified. Out of 158 samples: aEPEC 49(39%), tEPEC1 (0.7%), STEC 50(39.3%), ETEC 21(16.3%), EAEC 5(4.0%), EIEC 1(0.7%) were identified. STEC and EPEC were most frequent etiological agents of diarrhea in Khuzestan province of Iran. The result showed that the highest rate of resistance were to Ampicillin 42(84%), Tetracycline 39(78%), Amoxicillin+clavulanic acid 39(78%), Cephalotin 29(58%) and also 40% were confirmed as ESBL-producers broad antibiotic resistance extending to multiple antibiotic classes, that is a frequent feature of ESBL-producing bacteria.

Conclusion: of DEC as a cause of diarrhea in Khuzestan, providing evidence that efforts should be made to estimate the burden of infection by etiology for better medical approach and should raise awareness about antibiotic resistance in diarrhea in Iran.

Keywords: *Escherichia coli*

**P191 - 303: PREVALENCE AND ANTIMICROBIAL RESISTANCE PATTERNS OF
NOSOCOMIAL INFECTIONS IN SAMPLES ABADAN WOUNDS AT TALEGHANI
HOSPITAL IN 2015**

Masoumeh Ghasemnezhad¹, alireza mazraehkar², mehdi ghasemnezhad³, zahra gorjian⁴, nabi gomeh
zadeh⁵

1. abadan university of medical sciences
2. abadan university of medical sciences
3. abadan university of medical sciences
4. abadan university of medical sciences
5. abadan university of medical sciences

Background and Aim: The highest percentage of mortality of nosocomial infections in hospitalized patients in different parts of the subject is more abundant in patients with weakened immune systems. In this study, the prevalence of antibiotic resistance and nosocomial infections are common in wounds culture here

Methods: This cross-sectional study within 6 months of 19 samples using a sterile swab culture of the ulcer was Abadan Taleghani Hospital Isolated cases of infections caused by Enterobacteriaceae family and other hospital infections studied and then sampled by a swab then transferred to the media nutrients (TSB) on blood agar plates, Mac Canky and Chocolate agar, then use to doing biochemical tests and also evaluated in terms of antibiotic resistance

Results: The results showed that a total of 19 samples isolated wounds 11 positive samples (57.9) and 8 negative samples (42.1) of which 36.8 aged less than 30 years and 63.2 were aged more than 30 years. 2 samples of the war of pediatrics, 5 sample of the, 31.6% sample of the inner man and 6 women sample from the inner part of 26.3%, 6 samples isolated from ICU 31.6 that whom of 8 men and 11 women (41.2) accounted for 57.9% allocate

Conclusion: Due to increasing antibiotic resistance, especially in patients' immune system is proposed policy of infection control perform in order to reduce the variability and infectious kind to be able treat the patients in less time and more better results

Keywords: antibiotic-resistant, wound, Taleghani Hospital

**P192 - 322: STUDY THE ANTIMICROBIAL ACTIVITY OF SEA ANEMONE AGAINST
ACINETOBACTER**

Homa Hamayeli¹, Abdolhamid Namaki Shoshtari², Mehdi Hassanshahian³, Majid Askari Hesni⁴

1. Department of Biology, Faculty of Science, Shahid Bahonar University of Kerman, Kerman, Iran
2. Department of Biology, Faculty of Science, Shahid Bahonar University of Kerman, Kerman, Iran
3. Department of Biology, Faculty of Science, Shahid Bahonar University of Kerman, Kerman, Iran
4. Department of Biology, Faculty of Science, Shahid Bahonar University of Kerman, Kerman, Iran

Background and Aim:Introduction and aims: Marine environment is a great reservoir of natural products, many of the structural features that are not found on the earth's natural products. Sedentary marine invertebrates, especially sea anemones are a rich source of bioactive metabolites, which can be used for new antimicrobial drugs, They also contain a variety of organic compounds, including some potent toxins are interesting. The aims of this study were characterization of antimicrobial activity of Sea anemone that collected from Persian Gulf against Acinetobacter.

Methods:Sea anemone collected from Persian Gulf. The crude extracts of Sea anemone were prepared with solvent methanol. Antimicrobial activities of the crude extracts against Acinetobacter were evaluated by using the disc diffusion method and hole plate method.

Results:The results of this research show that polar extract of Sea anemone have zone of inhibition 10 mm against resistant Acinetobacter. According to hole plate test the ability of Sea anemone extracts for inhibition of Acinetobacter was higher than disc diffusion method.It is means that diffusion of polar extract in agar plate method was better than paper disc.

Conclusion:The Sea anemone has optimum inhibitory effect against Acinetobacter thus the composition of this Sea anemone can be used for therapeutic purpose in the future.

Keywords:Sea anemone, Antibiotic, Acinetobacter, Persian Gulf

P193 - 324: COMPARISON BETWEEN CAPSULAR POLYSACCHARIDE (PRP) EXTRACTED FROM HAEMOPHILUS INFLUENZA TYPE-B FROM CULTURE SUPERNATANT AND PELLET

Arezoo Salahi¹, Farhad Esmaily²

1. Master of Science, Biochemistry Dep, Islamic Azad university of Damghan, Iran
2. Medical Microbiologist, Razi institute of Vaccine and Sera, Karaj, Iran

Background and Aim: Haemophilus influenzae type-b (Hib) is an important cause of serious invasive infection example meningitis in children less than five years old. Capsular polysaccharide which is made of repeating unit of ribosylribitol phosphate (PRP) is the most important virulence factor of this organism.

Methods: The aim of this study is to achieve a method for production of PRP which is economical with high purity and efficacy. We used Hib strain atf2 which is isolated from a child with meningitis and was cultivated in a bioreactor containing modified GC broth. The culture was centrifuged and PRP was extracted from both supernatant and pellet by various detergents, enzymes, ultracentrifugation and dialysis tubes.

Results: The amount of 397 µg/ml and 226 µg/ml PRP was prepared from the supernatant and pellet respectively. The amount of protein present in PRP was under 1% which is the amount recommended by WHO. The Bial and Lowry method was used for measuring PRP and protein respectively. The nucleic acid present in supernatant and pellet was 1.65 and 1.85 respectively.

Conclusion: The comparison between PRP prepared from the supernatant and pellet cultivated in bioreactor showed that supernatant is better option for PRP extraction, considering the amount of PRP and also having less contaminant to get rid of.

Keywords: Haemophilus influenza type-b (Hib), Supernatant, Pellet, PRP, Elisa, Bial

P194 - 325: MEASUREMENT OF ANTI BODY AGAINST HEAMOPHILUS INFLUENZAE TYPE B (HIB) CAPSULAR POLYSACCHARIDE CONJUGATED WITH TETANUS TOXOID BY ELISA

Arezoo Salahi¹, Farhad Esmaily²

1. Master of Science, Biochemistry Dep, Islamic Azad university of Damghan, Iran
2. Medical Microbiologist, Razi institute of Vaccine and Sera, Karaj, Iran

Background and Aim: *Haemophilus influenzae* type-b, an encapsulated bacterium, cause meningitis world wide. The capsular polysaccharide made of polyribosylribitol phosphate (PRP) is the main virulence factor and when conjugated to a carrier protein is effective in the prevention of such infection .

Methods: The aim of this study is to investigate the titer of conjugated PRP after immunization in rat in our own lab. The PRP was prepared from strain atf2 isolated from a child with meningitis by various detergents ,enzymes , ultracentrifugation and dialysetubes. The conjugation process was carried out by attaching PRP to tetanus toxoid (TT) as a protein carrier. The PRP was activated by CNBR and joined to ADH as a linker, the product then covalently attached to TT which is activated by EDAC. Sepharose CL-4B gel chromatography was used to separate PRP conjugate from PRP and protein and finally we used Sodium Deoxycholate (DOC) to separate PRP-conjugate from free PRP.

Results: The results showed the amount of 397 µg/ml PRP in PRP conjugate or 43% recovery compare to initial PRP. The amount of protein and nucleic acid was under 1% which is the amount recommended by WHO. The rat antibody titer to PRP-TT showed the highest compared to PRP only and standard PRP obtained from NIBSC.

Conclusion: The above results showed that the process which we used for PRP production or conjugation can further be used for scale up production.

Keywords: *Haemophilus influenzae* type-b (Hib) , PRP , Conjugation , immunization , Elisa

P195 - 330: IDENTIFICATION AND CHARACTERIZATION OF MUTACIN AND PUTATIVE BACTERIOCCIN GENES IN ISOLATED STREPTOCOCCUS MUTANS AND ITS ANTIMICROBIAL ACTIVITY AGAINST GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA

Mandana Salehizadeh¹

1. phd student , Islamic azad university, olom tahghighat ,tehran,iran

Background and Aim: investigate the frequency and expression of genes encoding mutacins typeI, II, III and IV and two of 8 genes in a cluster encoding the putative bacteriocins, the designated bsm 283, bsm 299, bsm 423, bsm 1889c, bsm 1892c, bsm 1896, bsm 1906c and bsm 1914, were also screened by PCR and then mutacin activity against the indicator strains determined.

Methods:Streptococcus mutans was detected using biochemical tests and molecular methods (PCR). Frequency of mutacin biosynthesis genes types I, II, III and IV, bsm299 and bsm1899 were measured by PCR.the antimicrobial spectra of Streptococcus mutans isolates against other indicators, including Staphylococcus aureus, Staphylococcus epidermidis, Enterococcus faecalis, Salmonella typhi, Pseudomonas, Escherichia coli were evaluated using well diffusion, disk diffusion and the minimal inhibitory concentrations (MICs) methods

Results: 24 strains of Streptococcus mutans 67.52% of the strains had a wide antimicrobial spectrum and 37.5% of 67.5% had a high frequency of genes with more inhibitory activity against, Staphylococcus epidermidis, Staphylococcus aureus and Enterococcus faecalis respectively.The expression frequency of the bsm gene (putative bacteriocins) was higher than that of the characterized mutacins types (I–IV). The lowest dilution rate mutacin was found against Staphylococcus epidermidis (0.0625 unit/mL).

Conclusion: These findings suggested that all putative bacteriocins may represent a large repertoire of inhibitory substances produced by Streptococcus mutans.

Keywords:Antimicrobial, Mutacin, Streptococcus mutans

P196 - 336: RAPID DIAGNOSIS OF LEPTOSPIROSIS BY PCR BASED ON LIGA GENE

Seyed mohsen Salahedin¹, Pejvak Khaki², Soheila Moradi Bidhendi³, Mehdi Gharahkhani⁴

1. Pharmaceutical Sciences Branch, Islamic Azad University
2. Department of Microbiology Razi of Vaccines and Serum Research, Karaj, Iran
3. Department of Microbiology Razi of Vaccines and Serum Research, Karaj, Iran
4. Department of Microbiology Razi of Vaccines and Serum Research, Karaj, Iran

Background and Aim: Leptospirosis is a zoonosis with global distribution that caused by pathogenic Leptospire. The incidence of leptospirosis is probably grossly underestimated, because of limited diagnostic capacity in the regions where the burden of disease greatest. Therefore the development of the reliable diagnostic method is essential. Outer membrane protein, The LigA DNA was constructed in two truncated forms as the conserved portion (LigAcon) and a variable portion (LigAvar). LigA is expressed only in pathogenic leptospires and the gene encoded of this protein is conserved among pathogenic Leptospire. So this gene may be good candidate for molecular diagnostic technique. Therefore the main aim of this study was development of the molecular technique for rapid diagnostic of pathogenic leptospire

Methods: Eight pathogenic leptospiral serovars and one saprophytic species (*L.biflexa*) were used in this study. The serovars were inoculated into the selective culture medium (EMJH) and then the genomic DNA extracted by standard Phenol-chlorophorm method. The specific primers for amplifying ligAcon gene were designed. Primer specificity and sensitivity of the DNA was confirmed by PCR.

Results: PCR amplification of the ligA gene using the designed primers resulted in a 1352 bp in all seven pathogenic serovar tested. No PCR products were amplified from the non-pathogenic *L.biflexa*.

Conclusion: Due to slow growth of leptospira, and because of limited diagnostic capacity using a rapid and accurate molecular tests like PCR is essential. Our results showed that the LigA gene may be good candidate for development of diagnostic technique

Keywords: Leptospirosis, rapid diagnosis, LigA, PCR

P197 - 340: RELATIONSHIP BETWEEN HELICOBACTER PYLORI CAGE GENE AND CAGA STATUS AND RISK OF HISTOLOGIC SUBTYPE GASTRIC ADENOCARCINOMAS IN IRAN

Shokufe Gholizade tobnagh¹, Seyedeh Zahra Bakhti², Saeid Latifi-Navid³, Saber Zahri ⁴

1. Department of Biology, Faculty of Sciences, University of Mohaghegh Ardabili, Ardabil, 56199-11367, Iran, golizades@yahoo.com
2. Department of Biology, Faculty of Sciences, University of Mohaghegh Ardabili, Ardabil, 56199-11367, Iran
3. Department of Biology, Faculty of Sciences, University of Mohaghegh Ardabili, Ardabil, 56199-11367, Iran
4. Department of Biology, Faculty of Sciences, University of Mohaghegh Ardabili, Ardabil, 56199-11367, Iran

Background and Aim:The *cag* pathogenicity island (PAI) is one of the most important determinants of *H. pylori*, mainly involved in the epithelial cell damage and chronic inflammation which could lead to cancer. Several studies have described *CagA* and *CagE* as the two important virulence determinants of *H. pylori*. The aim of present study was to analyze the relationship between *cagA*, and *cagE* genotypes of *H. pylori* *cag* PAI and the risk of histologic subtype gastric adenocarcinomas (GA) in Iranian dyspeptic patients.

Methods:A total of 151 *H. pylori* isolates from 348 patients were obtained and genotyped. Histopathological evaluations were also performed.

Results:The subjects included 114/151 with non-atrophic gastritis (NAG) and 37/151 with GA. Of the 37 GA patients, 17 (45.95%) with diffuse-, and 20 (54.05%) with intestinal- type adenocarcinomas. Statistical analysis showed no significant association between *cagA*, and *cagE* genotypes and diffuse-, and intestinal- type adenocarcinomas ($P > 0.05$). Frequency of the *cagA*, and *cagE* in patients with intestinal- type adenocarcinoma was 80.0%, and 85.0%, respectively, in patients with diffuse - type adenocarcinoma was 64.7%, and 70.6%, respectively, and in gastritis group was 61.4%, and 73.7%, respectively.

Conclusion:In this study, no genotype of *H. pylori* *cag* PAI associated with diffuse-, or intestinal- type adenocarcinomas.

Keywords:: *cagA*, *cagE*, diffuse - type adenocarcinoma, intestinal- type adenocarcinoma.

**P198 - 341: RELEVANCE OF CAGA, AND CAGE GENOTYPES OF HELICOBACTER
PYLORI CAG PATHOGENICITY ISLAND TO CARDIA- AND NON-CARDIA-CANCER**

Shokufe Gholizade tobnagh¹, Seyedeh Zahra Bakhti², Saeid Latifi-Navid³, Saber Zahri⁴

1. Department of Biology, Faculty of Sciences, University of Mohaghegh Ardabili, Ardabil, 56199-11367, Iran, golizades@yahoo.com
2. Department of Biology, Faculty of Sciences, University of Mohaghegh Ardabili, Ardabil, 56199-11367, Iran
3. Department of Biology, Faculty of Sciences, University of Mohaghegh Ardabili, Ardabil, 56199-11367, Iran
4. Department of Biology, Faculty of Sciences, University of Mohaghegh Ardabili, Ardabil, 56199-11367, Iran

Background and Aim:: *Helicobacter pylori* (*H. pylori*) is the main cause of and gastric adenocarcinoma. *H. pylori*-specific genotypes can determine the clinical consequences. The *cag* pathogenicity island (PAI) which contains genes may involve in the pathogenesis of gastrointestinal disease. In the present study, we aimed to examine the associations of *cagA*, and *cagE* genotypes of *H. pylori* *cag* PAI with risk cardia cancer (CC) and non-cardia cancer (NCC) in patients with gastric cancer (GC) in Iran.

Methods: A total of 151 *H. pylori* strains which were isolated, including 114 (75.5%) with non-atrophic gastritis (NAG) and 37 (24.5%) with GC, were genotyped. Histopathological examination and classification of subjects were then performed.

Results: Patients with GC were classified into 2 groups; CC: 14 (37.84%) and NCC: 23 (62.16%). The total frequency of *cagA* was 64.2%, and *cagE* 74.8%. The frequency of the *cagA*, and *cagE* genotypes was 10/14 (71.4%), and 9/14 (64.3%) in patients with CC, respectively; and in patients with NCC was 17/23 (73.9%), and 20/23 (87.0%), respectively, while in the control group (NAG), the frequency was 70/114 (61.4%) for *cagA*, and 84/114 (73.7%) for *cagE*. There was not a significant difference between the frequencies of *cagA* and *cagE* genotypes in isolates from CC, and NCC and those from NAG ($P > 0.05$).

Conclusion: In the present study no significant correlation was found between *H. pylori* genotypes and risk of both the CC and the NCC in Iran.

Keywords: *cagA*, *cagE*, cardia cancer, non cardia cancer.

**P199 - 350: DISCRIMINATION BETWEEN L.MONOCYTOGENES STRAINS ISOLATED
FROM DIFFERENT CLINICAL AND FOOD SOURCES USING RAPD-PCR**

Azar Hemmati¹, Lida Lotfollahi², Kambiz Diba³

1. Student Research Committee, Urmia University of Medical Sciences, Urmia, IRAN, Urmia, Iran.
2. Department of Microbiology, faculty of medicine, Urmia University of Medical Sciences, Urmia, Iran.
3. Molecular and Cellular Research Center, School of Medicine, Urmia Medical Sciences University

Background and Aim: *Listeria monocytogenes* is an ubiquitous Gram positive bacterium with intracellular localization and important food-born pathogen causing abortion, meningitis, meningoencephalitis and septicemia. It can cause human listeriosis with mortality rates up to 25% in susceptible individuals specially pregnant women , extremity of ages and immune compromised conditions. The aim of current study was to typing isolates of *L. monocytogenes* by Random Amplification of Polymorphic DNA (RAPD)-PCR.

Methods: This study was conducted using 22 strains including food (beef meet, sausage, milk and cheese) and clinical samples (blood, urine, placental tissue, fecal and vaginal swabs) collected from retail markets and women with spontaneous abortion in shariati hospital respectively . RAPD- PCR with four different primers (HLWL74, HLWL82 ,HLWL85 and OPM-01) was used to analyze and typing the isolates.

Results: From the 22 isolates assessed by RAPD-PCR , all of strains showed discriminatory patterns with all primers used except one strain that with primer OPM-01 didn't gave any amplified band. Among these four primers, OPM-01 had the most discriminatory power due to producing polymorph bands. These strains showed overall 8 different clusters.

Conclusion: RAPD –PCR is a rapid typing method with high discriminatory power; can be used as a powerful tool in the differentiation of food borne pathogens.

Keywords: *Listeria monocytogenes*, RAPD_PCR, listeriosis, typing

**P200 - 364: ISOLATION AND IDENTIFICATION OF NOCARDIA ASTEROIDS COMPLEX
FROM A PATIENT WITH KERATITIS**

Azin Ahani¹, Mehdi Fatahi Bafghi², Zeinab Yoosefy³, Seyyed Saeed Eshraghi⁴

1. Department of pathobiology, School of public Health, Tehran University of Medical Sciences
2. Department of Microbiology, Faculty of Medicine, Shahid Sadoughi University of Medical Sciences, Yazd, Iran
3. Department of Microbiology, Shahid Beheshti University of Medical Sciences, Tehran, Iran
4. Department of pathobiology, School of public Health, Tehran University of Medical Sciences

Background and Aim: The genus *Nocardia* is a gram positive and partially acid-fast bacteria which can cause various disease, known as Nocardiosis. Nocardiosis has a wide range of diseases including pulmonary, cutaneous, cerebral and ocular infection. Ocular nocardiosis is relatively a rare infection among ocular disease. Keratitis of *Nocardia* species is an aggressive ocular infection which typically followed with a corneal truma. The purpose of this study was identification of *Nocardia* species as a agent of ocular infection with phenotypic methods.

Methods: A 59-years-old man with corneal ulcer which was caused by trauma referred to Labbafinejad hospital, Tehran-Iran in August 2015. The specimen of patient was sent to laboratory and direct microscopy tests and culture was performed. Moreover for accurate identification of species, phenotypic tests such as growth in lysozyme broth, hydrolysis of casein, tyrosine, xantin, hypoxantine, utilization of citrate, urea and else was done.

Results: The isolate with characteristic including chalky white colonies with tiny areal hyphae analysis of phenotypic tests shown that our isolate is *Nocardia asteroides* complex

Conclusion: *Nocardia* species can rarely cause ocular infections specially in immunocompromised patient, because of recognition problems and also false diagnosis of this genus, use of diagnostics methods for precise and reliable diagnosis is essential.

Keywords: *Nocardia* asteroids, keratitis, ocular infection

P201 - 383: EVALUATION OF ANTIMICROBIAL ACTIVITY OF (5-NITRO-2-FURYL)&(5-NITRO-2-IMIDAZOLYL)-1,3,4-THIADIAZOLE DERIVATIVES

Mohammad Hassan Moshafi¹, Alireza Foroumadi², Ali Peymani³

1. Pharmaceutics Research Center, Kerman University of Medical Sciences, Kerman, Iran
2. Department of Medicinal Chemistry, Faculty of Pharmacy and Pharmaceutical Sciences Research Center, Tehran University of Medicinal Sciences, Tehran, Iran
3. Faculty of Pharmacy, Kerman University of Medical Sciences, Kerman, Iran

Background and Aim: Nitrofurans and nitroimidazoles are two groups of chemicals with wide range of antibacterial activity which exert their effects by damaging the DNA of bacteria. Nitrofurantoin and is a nitrofurans derivatives and metronidazole and tinidazole are two compounds of nitroimidazoles category that are now available in pharmaceutical market which have shown acceptable antibacterial activity. Regarding to the increasing microbial resistance against current antimicrobial agents and the necessity of substituting new agents, 7 new chemical compounds were synthesized and their minimum inhibitory concentration (MIC) were determined using agar dilution method. Ciprofloxacin was used as a standard compound for comparing antibacterial effects.

Methods: 6.4mg of the nitrofurans and nitroimidazole derivatives were dissolved in a minimum amount of dimethylsulfoxide and the volume was made to 10 ml using distilled water. From this solution 8 serial dilutions of 0.5 were made. Then 2 ml of each serial dilution was added to 18 ml of Muller-Hinton agar medium at 50 °C to give the final concentration ranging from 0.5 µg/ml to 64 µg/ml. The MIC of the test compounds was determined on the basis of invisible growth on the plate.

Results: After MIC examination of the synthesized compounds and comparison of the MIC results were compared by that of ciprofloxacin and it was observed that these compounds own weak antibacterial effects; in two cases the antibacterial effect was quite similar to that of positive control.

Conclusion: In sum these compounds didn't show promising antibacterial activity and further works are required to develop more efficient antimicrobials.

Keywords: Nitrofurans, Nitroimidazole, MIC

**P202 - 396: DETECTION OF ENTEROPATHOGENIC ESCHERICHIA.COLI STRAINS
ISOLATED FROM CHILDREN WITH DIARRHEA IN AHVAZ**

Mehrandokht Sirous¹, Mansour Amin², Mohammad Hashemzadeh³, Nasim Shams⁴, Mojtaba Shahin⁵,
Dorsa Koraei⁶

1. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of medical sciences, Ahvaz, Iran
2. Health research institute, Infectious and Tropical Disease Research Center, Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of medical sciences, Ahvaz, Iran
3. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of medical sciences, Ahvaz, Iran
4. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of medical sciences, Ahvaz, Iran
5. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of medical sciences, Ahvaz, Iran
6. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of medical sciences, Ahvaz, Iran

Background and Aim:Diarrhea is a major public health problem among children with high mortality rate in developing countries. Enteropathogenic Escherichia.coli (EPEC), a diarrheagenic pathotype of E.coli, is an important pathogen in children given bacterial diarrhea. Serotyping is the classical and specific method basis on O antigens for identification of EPEC strains. The aim of this study was to investigate the frequency of EPEC strains in children with diarrhea in Ahvaz.

Methods:A total of 163 strains of E.coli isolated from children under 10 years were examined. These specimens collected from two educational hospitals from April to November 2015 in Ahvaz. Colonies on MacConkey agar identified by standard biochemical tests as E.coli. Determination of EPEC serotypes was performed by agglutination tests using polyvalent antisera to the predominant O antigens.

Results:Among the 163 isolates of E.coli, 11.56% was positive by polyvalent antiserum tests. In children serogroup EPEC O26, O55, O111 (42.1%) was the most prevalent, followed by O44, O125, O126, O128 (36.8%). EPEC serogroups were isolated as a sole pathogen in 52.6% of girls & 47.4% of boys.

Conclusion:Serotyping offers an important and reliable method for EPEC strains identification. Serogrouping appears to be still the simplest and useful test for presumptive identification of EPEC strains. According to our findings, 11.56% of isolated E. coli were positive for EPEC strains. So, diagnostic tests to determine EPEC strains is necessary in medical laboratories and hospitals at Ahvaz.

Keywords:Enteropathogenic Escherichia coli (EPEC), diarrhea, serotyping

**P203 - 398: ALTERATION IN CYTOKINES RESPONSE MAY PREDICT RELAPSE IN
BRUCELLOSIS**

Siamak AsriRezaei¹, Siamak Asri-Rezaei², Zahra Nouri-Sabzikar³

1. Clinical Pathology Department, Veterinary college, Urmia University, Urmia. Iran.
2. Resident of the Clinical pathology department, Veterinary college, Mashhad University, Mashhad, Iran.

Background and Aim:Brucellosis represents a zoonotic bacterial disease, caused by a gram negative bacterium called Brucella and associated with an acute inflammatory reaction, which represents the principal local defense against spread of the infection.

Methods:This trial was conducted in 42 patients who were being followed-up with diagnosis of brucellosis. In patients whose clinical symptoms recurred within a year of treatment and exhibited infectious parameters in compliance with brucellosis, a standard tube agglutination test was performed and the diagnosis of relapse was based on brucella IgM. The status of Acute and Chronic cases was studied through Isotype specific ELISA assay. Serum samples were evaluated for IL-8 and IL-10.

Results:It was found that 28 (66.7%) of samples had high IgM antibodies while 14 (33.3%) samples were positive for IgG antibodies that were indication of Acute (Active) and Chronic (passive) cases, respectively. Also we found increased levels of serum IL-8 and IL-10 in the patients with acute form of the disease compared to the chronic form of brucellosis.

Conclusion:The results of this study shown that brucellosis by induction of released IL-8 triggered immune responses and also high levels of IL-10 that was considered a central immunoregulator antagonizing the excessive Th1 and CD8+ T cell responses could inhibits proinflammatory responses from innate and adaptive immunity, and it prevents the lesions in tissues caused by exacerbated adaptive immune responses. IL-10 is a cytokine that regulates the balance between pathogen clearance and immunopathology. These findings indicated that high serum IL-8 and IL-10 levels may predict relapse in brucellosis.

Keywords:brucella, IL-8, IL-10

P204 - 405: EPIDEMIOLOGY OF HEALTH CARE ASSOCIATED CONJUNCTIVITIS AMONG NEONATES IN AN IRANIAN HOSPITAL 1000 BED-TERTIARY CARE HOSPITAL.

Zahra sadat Mirjafari tafti¹, Mohammad Rahbar², Zahra Sadat Mirjafari Tafti^{1,3}

1. 1 Centre for Biotechnology, Institute of Science & Technology Jawaharlal Nehru Technological University-Hyderabad, Kukatpally, Hyderabad, India
2. Reference Health Laboratory Research Center, Ministry of Health and Medical Education, Tehran, Iran.
3. Research Department of Biotechnology, Mabna Toseh Bazar Co., #3, 48 Plaque, Varasteh St., Dowlat St., Tehran, Iran

Background and Aim: Conjunctivitis caused by bacteria is one of the most frequently occurring health care acquired infections. Development of conjunctivitis in neonates due to immaturity of larimic system. Immature of immune system and colonization of microorganism in conjunctivae during neonate care. The aim of present study is to determine epidemiological features, pathogenic agents and antibiotic susceptibility patterns of bacterial HCA conjunctivitis in an Iranian 1000 bed care hospital.

Methods: The study was carried out in Milad hospital of Tehran over three years, from March 2011 to January of 2014. All neonatal admitted to hospital to the NICUs of our hospital being subject of our study. Among them 42 neonatal were infected. All specimens were inoculated onto bacteriological culture media including Blood agar, Chocolate Agar and MacConkey agar. Susceptibility testing was performed by guidelines recommended by Clinical Laboratory Standards Institutes (CLSI).

Results: The most frequently isolated microorganisms included, Klebsiella pneumonia, Staphylococcus aureus and E.coli. The majority Klebsiella pneumonia isolated was resistance to Cefuroxime (100%), Cefalothin (91, 6%), Ceftizoxime (91.6%), Tobramycin (91.6%), Cefotaxime (91.6%), Cephtazidime (91.6%) and Ampicillin (83.30%). The Staphylococcus aureus was resistance to commonly used antibiotics such as penicillin (100%) and Ampicillin (50%). About 75% of E.coli isolated was resistance to cefuroxime and cefotaxime.

Conclusion: The frequency and etiological agents of conjunctivitis was determined. Our study also provides the epidemiological features of conjunctivitis in neonatal in our hospital and serves as a guideline to physics for empirical therapy.

Keywords: Epidemiology, Conjunctivitis , neonatal

P205 - 428: ANTIBIOTIC RESISTANCE OR MICROBIAL ANTAGONISM

Mohammad Ebrahim Astaneh¹, Abulqasim Avand², Mahmud Aghooli³

1. Department of Anatomy. Faculty of Medicine. Fasa University of Medical Sciences. Fasa. Iran
2. English Department Fasa University of Medical Science, IR. Iran.
3. Department of Microbiology. Faculty of Medicine. Fasa University of Medical Sciences. Fasa. Iran

Background and Aim: Antibiotics were once known to be the miracle of nature. While they were truly considered to be a great achievement for humanity, taking them became harmful over time. Although antibiotics were made to eliminate destructive bacteria inside the body, some of them can kill the healthy bacteria that live peacefully inside our bodies. Others may cause vaginal infections or disrupt our digestive system.

Methods: This study is a descriptive study. A documentary method was used to collect data. The data has been collected and analyzed indirectly through the use of archival documents either private or edited ones, specialized books and written references.

Results: The widespread use of antibiotics has become common. For example, according to the latest report by Center for Disease Control and Prevention (CDC), out of 68 percent of people with acute respiratory infections (including sinus infections), only 20 percent required antibiotics prescribed by the doctor. Although their overuse cause harm to the body, their main side effects result in antibiotic-resistant bacteria or microbial antagonism.

Conclusion: When antibiotics are not taken in such a way that a doctor prescribes, it can promote antibiotic-resistant bacteria. This is not a personal issue, but it threatens the whole community. Antibiotics are designed to kill certain species of bacteria or stop their growth, but when antibiotic resistance occurs, the species of bacteria will inevitably find ways of resisting the antibiotics developed by humans and will neutralize the drug. Methicillin-resistant *Staphylococcus aureus* (MRSA) and Vancomycin-resistant Enterococci (VRE) are two examples of bacteria that are resistant to many antibiotics.

Keywords: Antibiotic Resistance, Bacteria, Infections

**P206 - 436: INCIDENCE OF CHLAMYDIA TRACHOMATIS INFECTION AND TNFA -308 G/A
POLYMORPHISM IN MISCARRIAGE.**

FATEMEH DARVISHI KOLOR¹, Jalil Vand Yousefi², Hossein Rassi³

1. Department of Biology , Karaj Islamic Azad University
2. Department of Biology , Karaj Islamic Azad University
3. Department of Biology , Karaj Islamic Azad University

Background and Aim: *C. trachomatis* is a recognized agent of preterm labor and premature rupture of membranes. However, its role in miscarriage is unclear. the aim of this study was to evaluate Chlamydia trachomatis and its relationship with the TNF α gene polymorphisms for early detection and early treatment of abortion.

Methods: Then blood samples were taken from each of them and transferred to the laboratory, DNA extracted from each sample, then detection of Chlamydia trachomatis and TNF α -308 G / A polymorphism were determined by PCR.

Results: Among patients with clinical symptoms, 27% were positive for Chlamydia trachomatis and in the control group, 4% were positive for Chlamydia trachomatis. Statistical analysis at the -308 site showed that the frequency of AA genotype was higher in patients with vaginal infections than healthy individuals and the difference was statistically significant.

Conclusion: On the other hand, the chance of catching among carriers with genotype AA, is 6 times more than GG genotype carriers. The association was found between Chlamydia trachomatis infection and TNF α -308 G/A polymorphism in miscarriage.

Keywords: Chlamydia trachomatis , TNF α -308 G / A polymorphism, miscarriage.

**P207 - 438: THE ACTIVITY OF FOSFOMYCIN AGAINST ESCHERICHIA COLI ISOLATES
FROM URINARY TRACT INFECTIONS**

Parisa Aris¹, Mohammad Ali Boroumand², Mohammad Rahbar³, Masoumeh Douraghi⁴

1. Division of Microbiology, Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
2. Department of Pathology, Tehran Heart Center, Tehran University of Medical Sciences, Tehran, Iran
3. Department of Microbiology, Reference Health Laboratories, Ministry of Health, Tehran, Iran
4. Division of Microbiology, Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: Fosfomycin is an old antibiotic used previously in veterinary, but it has been recommended recently by CLSI for treatment of urinary tract infections caused by *Escherichia coli*. The purpose of this study was to evaluate the in vitro activity of fosfomycin against drug resistant *E. coli* isolates.

Methods: A total of 110 *E. coli* isolates from patients suffering from urinary tract infections were collected during 2008 to 2010 from a hospital in Tehran. Antibiotic susceptibility testing was performed and interpreted according to CLSI guidelines for the following antibiotics: amikacin, amoxiclav, ciprofloxacin, gentamycin, cefazolin, ceftazidim, cephalotin, imipenem, ceftriaxone, ampicillin, fosfomycin, and nitrofurantoin.

Results: The isolates were obtained from 78 (70.9%) female and 32 (29.1%) male. Patients age ranged from 3 to 92 and the mean $\pm$ SD was 63.6 ± 17.2 years. One-third (30%) of isolates were from patients admitted to CCU and followed by heart surgery unit (25.5%). More than 80% of isolates were resistant to ampicillin (96.4%), amoxiclav (88.2%), and cephalotin (80.9%). The lowest resistance rate was found for imipenem (1.8%) and nitrofurantoin (5.5%), while all isolates were susceptible to fosfomycin with inhibition zone of 18-42 mm.

Conclusion: We showed that all *E. coli* isolates were susceptible to fosfomycin, despite the high resistance rate to the majority of antibiotics tested. It seems that fosfomycin could be an effective antibiotic for treatment of urinary tract infections. Further studies need to be performed in large series of isolates.

Keywords: Antibiotic susceptibility test, *Escherichia coli*, Fosfomycin, Urinary tract infections

P208 - 442: RELATIONSHIP BETWEEN BIOFILM PRODUCTION AND FREQUENCY OF VIRULENCE GENES IN CLINICAL ISOLATES OF PSEUDOMONAS AERUGINOSA AT A UNIVERSITY HOSPITAL IN URMIA, IRAN

Saber Yousefi¹, Ehsan Shojadel², Nima Hosseini Jazani ³, Bita Zareikar⁴

1. Department of Microbiology, School of medicine, Urmia university of Medical Sciences, Urmia, Iran, Cellular and Molecular Research Center, Urmia University of Medical Sciences, Urmia, Iran
2. Department of Microbiology, School of medicine, Urmia university of Medical Sciences, Urmia, Iran, Student Research Committee, Urmia University of Medical Sciences, Urmia, Iran
3. Department of Microbiology, School of medicine, Urmia university of Medical Sciences, Urmia, Iran
4. Iman Khomeini Hospital Laboratory, Urmia University of Medical Sciences, Urmia, Iran

Background and Aim: *Pseudomonas aeruginosa* is an opportunistic gram negative rod that causes a variety of clinically important infections. The pathogenicity of *P. aeruginosa* depends on different virulence factors such as different exotoxins, enzyme, type III secretion system, biofilm production and etc. The aim of this study was to evaluate biofilm production and its relation with presence of virulence genes in clinical isolates of *Pseudomonas aeruginosa*.

Methods: During June 2015 to March 2015 all clinical isolates of *P. aeruginosa* were collected from Imam Hospital of Urmia. All bacterial isolates were identified as *Pseudomonas aeruginosa* by standard microbiological test. Biofilm formation measurement was carried out by the micro titer plate assay. Detection of virulence genes were performed by polymerase chain reaction method.

Results: A total of 127 clinical isolates of *P. aeruginosa* were included in this study. Evaluation of biofilm formation revealed that 69 isolates (54.3%) produced different level of biofilm. Detection of six different virulence genes showed that the most prevalent virulence genes among isolates were *algD* 103 (81.1%) and frequency of other virulence genes were as follows; *exoA* 95 (74.8%), *pilB* 82 (64.6%), *flicA* 57 (44.9%), *flicB* 48 (37.8%) and *flaG* 42 (33.1%).

Conclusion: Our results showed that in general the frequency of virulence genes in biofilm producer isolates were fewer than non-biofilm producer isolates but it was not statistically significant. However since biofilm producing isolates shows severe infections and are difficult to treat it's important to apply proper infection control program against these bacteria.

Keywords: *Pseudomonas aeruginosa*, Biofilm, Nosocomial infections, PCR

**P209 - 443: FREQUENCY OF ANTIBIOTIC RESISTANCE IN PSEUDOMONAS AERUGINOSA
ISOLATED FROM URINARY TRACT INFECTIONS (UTIS) IN RAJAEI HOSPITAL
PATIENTS IN WINTER SEASON**

Elnaz Bonyanpour¹, Dr Elham Moazamian², Dr Amin Edalatmanesh³

1. -Department of Microbiology, College of Science, Science and Research branch, Islamic Azad University, Fars, Iran.
2. Department of Microbiology, College of Science, Agriculture and modern Technology, Shiraz Branch, Islamic Azad University, Shiraz, Iran.
3. Department of Physiology, College of Science, Agriculture and modern Technology, Shiraz Branch, Islamic Azad University, Shiraz, Iran.

Background and Aim:: Urinary tract infections (UTIs) are a serious health problem affecting millions of people each year. Infections of the urinary tract are the second most common type of infection in the body. *P. aeruginosa* is responsible for 12% of all nosocomial urinary tract infections (UTIs), making it the third most common organism. The purpose of this study is *Pseudomonas aeruginosa* isolated from the urine of patients with urinary tract infection.

Methods: The study included fifty samples were collected from patients who suffered from UTIs. *P. aeruginosa* culture on macconky agar. Gram negative bacillus was recognized by gram staining and biochemical tests. The identified *p.aeruginosa* strains were tested against ampicillin, erythromycin, amikacin, gentamicin, imipenem, cefatoxime and ciprofloxacin.

Results:: We have analyzed 50 urine samples (12%) were positive for *Pseudomonas aeruginosa*. The prevalence of *P. aeruginosa* in male and female patients was 5 % and 7%. According to this study the most resistant antibiotic included Ampicillin, Cotrimoxazole, Nalidixic acid and Doxycycline.

Conclusion: The result shows higher prevalence of *P. aeruginosa* isolates among UTI patients, where the proportion of female patients detected positive for *P. aeruginosa* was higher than their male counterparts.

Keywords:: *Pseudomonas aeruginosa*, urinary tract infections (UTIs), Antibigram, Antibiotic resistance

P210 - 447: PREVALENCE OF PBP2B AND ALY GENES AMONG STREPTOCOCCUS PNEUMONIAE ISOLATED FROM CHILDREN BELOW 6 YEARS OF AGE

Elnaz Karimy¹, Hooman malekan², Shadi aghamohammad³, Seyed Fazlollah mousavi mousavi⁴

1. Department of microbiology, Islamic Azad university of rasht
2. Department of Microbiology Pasteur Institute of Iran
3. Department of Microbiology Pasteur Institute of Iran
4. Department of Microbiology Pasteur Institute of Iran

Background and Aim: Streptococcus pneumoniae is a Gram-positive and significant human pathogenic bacteria. S. pneumoniae resides asymptomatically in the nasopharynx of 70% healthy carriers. It is a causative agent of a variety of diseases in humans including Pneumonia, meningitis and otitis media in adults. S. pneumoniae is one of the most common causes of bacterial meningitis and Pneumonia in adults. According to previous studies resistance to betalactam drugs is frequently identified in this bacteria, including penicillin. Which is widely used in the treatment of pneumococcal infection in Iran

Methods: This study aimed to investigate genotypic resistance caused by mutation in two main genes including Aly and pbp2 which are two genes out of six genes which encoded penicillin binding protein by pcr method

Results: the frequency of Aly and pbp2 in 70 clinical strains are 80% and 60% respectively

Conclusion: Given that changes in the amino acid sequence of Aly and pbp2b are associated with reduced sensitivity to beta-lactam antibiotics. based on the findings of this study and The high prevalence of multi-resistant strains, We can say that the treatment of pneumococcal infections are at a critical stage and requires further study.

Keywords: Streptococcus pneumoniae , antibiotic resistant, Pneumonia

**P211 - 452: DETERMINATION OF ANTIBIOTIC RESISTANCE PATTERN AND
PRODUCTION OF EXTENDED-SPECTRUM BETA-LACTAMASES AMONG
DIARRHEAGENIC ESCHERICHIA COLI ISOLATES**

Sanaz Mahdavi Broojerdi¹, Mohammad Roayaei Ardakani², Seyedeh Elham Rezatofighi³

1. Msc student of Microbiology ,Department of Microbiology, Faculty of science, Shahid Chamran University of Ahvaz, Iran.
2. Associate professor in microbiology, Faculty of science, university of shahid Chamran Ahvaz, Iran
3. Associate professor in microbiology, Faculty of science, university of shahid Chamran Ahvaz, Iran

Background and Aim: Antibiotic resistance is a growing threat worldwide. In recent years, increased incidence of resistance to beta-lactams among members of the family Enterobacteriaceae has been reported worldwide. The Extended Spectrum of Beta Lactamases (ESBLs) are plasmid-mediated enzymes which are capable of hydrolyzing and inactivating a wide variety of Betelactams including third generation cephalosporins (3GC), penicillins and aztreonam. They are susceptible to Blactamase inhibitors (clavulanic acid). Majority of ESBLs producing strains are Escherichia coli, Klebsiella pneumoniae, and Klebsiella oxytoca.

Methods: A total of 208 individual stool specimens were collected from diarrheal children and analyzed by multiplex PCR to detect diarrheagenic E. coli pathotypes. Then, E. coli isolates were tested for antibiotic susceptibility to 8 antibiotics (Ceftazidime, Ceftizoxime, Cefotaxime, Ceftriaxone, Ciprofloxacin, Gentamicin, Imipenem, Amikacin) by the disk agar diffusion (DAD) method. The ESBL production was determined by combination disk method using disks containing Ceftazidim and Cefotaxim alone and in combination with Clavulanic acid.

Results: In this research fifty five strains of diarrheagenic E. coli were isolated. Most of the antibiotic resistance was reported against Ceftazidime (92.59%), Ceftizoxime (87.03%), Cefotaxime (74.07%), Ceftriaxone (33.33%), Gentamicin (31.48%) with very low resistance to Ciprofloxacin (18.5%), Imipenem (20.37%), Amikacin (22.3%). Out of 55 E. coli pathotypes detected, 43 (78.18 %) isolates were ESBL producing.

Conclusion: Organisms expressing ESBLs in this study were widely distributed, often possessing the multidrug resistance phenotype. Limiting the use of broad-spectrum cephalosporins is recommended to control this high rate of ESBL expression.

Keywords: diarrheagenic Escherichia coli, Extended- Spectrum Betalactamase, Antibiotic resistance.

**P212 - 464: DESIGN AND EVALUATION OF A NOVEL KIT FOR RAPID DETECTION OF
STREPTOCOCCUS PYOGENES FROM PHARYNGEAL SPECIMENS**

Akram Rahimi moghaddam¹, Siavosh Salmanzadeh-Ahrabi ², Tahereh Falsafi³, Mahvash Seifali⁴

1. Department of Biotechnology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
2. Department of Microbiology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
3. Department of Microbiology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
4. Department of Plant sciences, Faculty of Biological Sciences, Alzahra University, Tehran, Iran

Background and Aim: Group A beta-hemolytic Streptococcus (GAS) is the most frequent cause of bacterial pharyngitis. Patients with acute streptococcal pharyngitis should be rapidly treated with an appropriate antibiotic. Rheumatic fever and acute glomerulonephritis can develop as complications of inadequately treated strep throat. Furthermore antibiotic misuse promotes antibiotic resistance. The culturing of bacterial specimen from the pharynx is considered as the standard diagnostic method, which is time-consuming. Thus creating a new, rapid, appropriate and inexpensive kit is very important for detection of Streptococcus pyogenes from pharyngeal specimens.

Methods: In this study a new kit was designed for rapid detection of Streptococcus pyogenes from pharyngeal specimens. Designed kit consists of a three section plate containing 5% sheep blood agar in the first section, 5% sheep blood agar with bacitracin in the second section and 5% sheep blood agar with trimethoprim sulfamethoxazole in the third section. Twenty four isolates of Streptococcus pyogenes were isolated from throat of children aging from 5 to 15 years old. The isolates were tested with both latex-agglutination method (as gold standard) and our newly designed kit.

Results: Comparison of the latex-agglutination test results with those of the newly designed kit showed total consistency. The sensitivity and specificity of our new kit was 100% and 100%, respectively.

Conclusion: The new designed kit developed in this work may provide an easy and useful method to identify GAS in the period of 18 hours. This rapid detection method not only enhances rapid treatment with appropriate antibiotics but is also economical in routine diagnostic microbiology.

Keywords: Streptococcus pyogenes, Rapid detection, Pharyngitis

**P213 - 470: EVALUATION OF THE PREVALENCE OF THE HYA ,IUCD AND PAPE GENES
AMONG ISOLATED UROPATHOGENIC STAINS OF ESCHERIACHOLI FROM THE
PATIENTS OF TEHRAN MAHDIE HOSPITAL IN MEHR OF 1394.**

Amirreza Akhlaghikia¹

1. MSc in microbiology, saveh branch, islamic azad univercity, saveh,iran

Background and Aim: Uropathogenic Escheria coli are responsible for the urinary tract infections. These strains are characterized by the distinctive bacterial properties referred to as virulence factors include adhesion,toxins and iron uptake system. Virulence genes are located either on mobile genetic elements or large pieces of DNA called “pathogenicity islands”. The purpose of this study was the evaluation of the virulence development among uropathogenic strains of E.coli.

Methods: Thirty strains of uropathogenic E.coliwere isolated from Tehran Mahdie Hospital in Mehr of 1394. The biochemical and microbial testes were done according to the standard techniques and the development of the virulence factors were analyzed by using m-PCR technique.

Results:the development of PaPE ,iuCD genes were 23% and 66% respectively.The hyA gene did not exist

Conclusion:This research was indicated that PaPE and iuCD genes have the major role in urinary tract infections by the uropathogenic E.coli. Therefore these gene could be the objective of further studies in the intermediacy treatments.

Keywords:uropathogenic Escheria coli,pathogenicity island,urinary tract infection.

**P214 - 471: MOLECULAR STUDY OF THE PREVALENCE OF CTX-M1, CTX-M2, CTX-M3 IN
PSEUDOMONAS AERUGINOSA ISOLATED FROM CLINICAL SAMPLES IN TABRIZ
TOWN, IRAN**

Abolfazl Jafari sales¹, Azizeh Shadi Dizaji²

1. Young Researchers and Elite Club, Ahar Branch, Islamic Azad University, Ahar, Iran
2. Department of Microbiology, School of Medicine, Islamic Azad University, Urmia, Iran

Background and Aim: *Pseudomonas aeruginosa* is the most common pathogen causing nosocomial infections. One of the reasons for the occurrence of drug resistance in the *Pseudomonas aeruginosa* strains is the production of the enzymes of Extended-Spectrum Beta-lactamases. The aim of this study was to determine the antibiotic resistance and the frequency of the enzymes of Extended-Spectrum Beta-lactamases (CTX-M1, CTX-M2, CTX-M3) in the *Pseudomonas aeruginosa* strains isolated in hospitals of Tabriz Town.

Methods: The *Pseudomonas aeruginosa* strains were collected from different samples of patients admitted to hospitals and medical centers in Tabriz Town during a year from 26th December, 2014 to 25th December 2015 and after identifying the phenotypic and genotypic identity (Sr RNA 16) and performing antibiogram test and double-disk synergy method, the phenotype of ESBLs in the bacterium of *Pseudomonas aeruginosa* was evaluated, then the bacterial DNA was extracted and studied and evaluated by PCR method and using special primers for the frequency of genes

Results: 110 *Pseudomonas aeruginosa* strains were identified from 1500 isolates collected from the hospitals and medical centers in Tabriz Town that in them, the highest resistant was related to the antibiotics of Amikacin (81.81%), Nalidixic acid (89.09%) and Ceftriaxone (75.45%). The highest gene frequencies of ESBLs are related to the genes of CTX-M1 (27.27%), CTX-M2 (23.63%) and CTX-M3 (9.09%), respectively.

Conclusion: The gene studied in this research were all on the chromosomes of the bacterium of *Pseudomonas aeruginosa*. So, investigating the genes of ESBL like CTX-M1 which has maximum frequency in the isolates of *Pseudomonas aeruginosa* seems necessary.

Keywords: ESBL, gene of CTX-M, *Pseudomonas aeruginosa*

**P215 - 480: FREQUENCY OF TEM EXTENDED SPECTRUM BETA LACTAMASE
PRODUCING ESCHERICHIA COLI IN URINE SPECIMENS BY PHENOTYPIC AND
MOLECULAR METHODS IN KARAJ**

Shima Hamzeloo¹, Behboud Jafari²

1. Department of Biology, Ahar Branch, Islamic Azad University, Ahar, Iran
2. Department of Biology, Ahar Branch, Islamic Azad University, Ahar, Iran

Background and Aim: Urinary Tract Infection (UTI) is one the most prevalent bacterial infections and Escherichia coli is the most common causative agent of UTI. However, the incidence of community acquired UTI caused by extended spectrum beta-lactamase producing E. coli is increasing worldwide. The aim of this study was evaluation of TEM Extended Spectrum Beta lactamase producing E. coli, in clinical samples isolated from Karaj hospitals, by phenotypic and PCR methods.

Methods: In this cross-sectional study 200 clinical specimens were collected from various hospitals in Karaj. After identification of E.coli isolates by biochemical tests, the antibiotic susceptibility test (Kirby-Bauer method) was done according to CLSI advice against 12 antibiotics. The Combined Disk method was then carried out for detection of ESBLs. Finally, the blaTEM gene was determined among the ESBL producer isolates using PCR.

Results: In this study, 99 E.coli isolates were collected from urine samples. The majority of the samples (90.89%) were resistant to Amoxicillin. By contrast, Imipenem was an effective antibiotic (100% susceptibility) against all isolates. From the total of 99 isolates, the extended spectrum beta-lactamase was detected in 46 (46.50%) of the strains, and PCR determined that 20(43.50%) of ESBL producing isolates contained blaTEM gene.

Conclusion: As only about 43.50% of the isolates were positive for the blaTEM gene, it is likely that other betalactamase enzymes cause the antibiotic resistance. Because resistance agents exist on mobile genetic elements, continuous monitoring and early detection can play an important role in preventing the spread of these broad-spectrum beta-lactamase genes.

Keywords: Urinary tract infection, Escherichia coli, Extended expectrum Beta-lactamase, blaTEM

P216 - 481: EVALUATION THE RATE OF ANTIBIOTIC SUSCEPTIBILITY AND THE ANTIBIOTIC RESISTANCE OF ISOLATED ESCHERIA.COLI OF URINARY TRACT INFECTION OF THE TEHRAN MAHDIE HOSPITAL 'S IN MEHR MONTH 1394.

Amirreza Akhlaghikia¹

1. MSc in microbiology, saveh branch, islamic azad univercity, saveh,iran

Background and Aim:Escheria coli is the leading cause of urinary tract infections. This research has been done based on the evaluation of the rate of antibiotic susceptibility as well as resistance of the patients referred to the Tehran Mahdie Hospital.

Methods:This study was done sectional in autumn of the year 1394 and samples were collected sterile and were analyzed and cultured. The microbial sensivity done according to the standard operational disk diffusion method and the results were analised.

Results: Thirty strains of Escheriachia coli were identified after microbiological analysis.The high degree of susceptibility rates were to tetracyclin (76.7%),ciprofloxacin (70%)and the high resistance rates were to chlormphenicol (93.3%) and co amoxyclov (83.4%).

Conclusion: The results of this study indicated the increasing rate of antibiotic resistance of E.coli stains to chloramphenicol and co amoxyclov due to the irrlar consumption of usage of these antibiotics. Therefore it advised to avoid the unnecessary consumption of antibiotics and the production of the new generation of antibiotics are notable.

Keywords:urinary tract infection, Escherchia coli,antibiotic

P217 - 483: INVESTIGATION OF THE PRESENCE PSTS AND BLA OXA -50 RESISTANCE GENES TO ANTIBIOTICS IN P. AERUGINOSA STRAINS ISOLATED FROM DIFFERENT PARTS OF SHAHID TALEGHANI HOSPITAL OF CHALLUS USING PCR TECHNIQUE

Fatemeh Zaboli¹, Mohammad Reza Kuchaki², Abdoljalil Eiri³

1. Department of biology, Ayatollah Amoli Branch, Islamic Azad University, Amol, Iran
2. Department of microbiology, Islamic Azad university, Tonekabon, IRAN
3. Department of biology, Ayatollah Amoli Branch, Islamic Azad University, Amol, Iran

Background and Aim: *Pseudomonas aeruginosa* is common hospitalized pathogens. This organism is an important opportunistic pathogen with an innate resistance to many antibiotics. The objective of this study is to Prevalence of the presence bla oxa -50 and Psts resistance genes to antibiotics in *P. aeruginosa* strains isolated from different parts of shahid Taleghani hospital of challus using PCR technique

Methods: In this study, 35 strains of *Pseudomonas aeruginosa* were collected from different wards of the Shahid Taleghani hospital of challus within 2014-2015. In order to determine the resistance of strains, antibiogram test was carried out by the method of the disk diffusion. In order to the presence of the studied genes, the specific primers were used and the PCR technique was applied to amplification the above genes

Results: Also, they showed different levels of resistant to other antibiotics including, 44.7% to Tobramycin, 23% to Cephtazidim and 2.8% to Imipenem. All *Pseudomonas aeruginosa* isolates were sensitive 100% to Ciprofloxacin, and Amikacin, Ampicilin. Of total 40 studied strains, Psts, bla oxa -50 genes was observed, in 40 (100%) and 35 (87.5%) strains, respectively.

Conclusion: The accurate performance of the antibiogram tests before the prescription of the antibiotic in the treatment of the infections resulted from these bacteria is an unavoidable necessity.

Keywords: *Pseudomonas aeruginosa*, Antibiotics resistance, bla oxa -50 gene , Psts gene

P218 - 507: A STUDY OF THE INHIBITION OF BIOSURFACTANT ON IN VITRO BIOFILM FORMATION BY BACTERIAL PATHOGENS: APPLICATION OF MALDI-TOF MS IN STRAIN IDENTIFICATION AND CHARACTERISATION OF THE LIPOPETIDES

Shadi Khonsari¹

1. Middlesex University; Department of Natural Sciences

Background and Aim: Microbial biofilms are able to develop on many different types of surfaces including medical apparatus, implants and food preparation area; there is a need to identify an effective and sustainable means to combat and inhibit biofilm formation. Biosurfactants are nontoxic, surface-active compounds synthesized by a wide variety of microorganisms. They are molecules that have both hydrophobic and hydrophilic domains and are capable of lowering the surface tension and the interfacial tension of the growth medium. They have anti-adhesion properties that can act against biofilm of pathogenic microorganisms.

Methods: A number of previously isolated *Bacillus* strains were identified using PCR and MALDI-TOF-MS Biotyping system and their capability to produce lipopeptides (a class of biosurfactant) examined. Both the molecular and Biotype analyses identified the isolates to species level and are in 100% agreement, but the latter method required considerably shorter preparation time. Crude biosurfactant from the most promising isolate (a *Bacillus subtilis* strain) was selected for further study. The biosurfactant was purified using HPLC-RP and characterised by MALDI-TOF and MALDI-TOF-TOF.

Results: Acid precipitation followed by chloroform/methanol extraction yielded three distinct lipopeptides similar to surfactins [m/z 1016-1074], fengycins [m/z 1447-1491] and subtilosin-A [m/z 3400]. The crude biosurfactant demonstrated anti-biofilm properties against a range of bacteria including MRSA and in vitro biofilm formation on stainless steels and polyethylene plastic.

Conclusion: Biotyping analysis are faster as they required shorter preparation time and MALDI-TOF-MS analysis results are reliable as they results correlate PCR results. *Bacillus subtilis* is a promising strain with ability of producing a number of biosurfactant with property of inhibition on biofilm formation.

Keywords: Biofilms, Biosurfactant, *Bacillus*, MALDI-TOF-MS

**P219 - 512: PREVALENCE OF EXFOLIATIVE TOXIN GENES IN STAPHYLOCOCCUS
AUREUS ISOLATED FROM CLINICAL SPECIMENS**

Fariba Rafiei¹, Mojtaba Mohseni², Ezzat Allah Ghaemi³

1. Department of Molecular and Cell Biology, University of Mazandaran, Babolsar, Iran
2. Department of Molecular and Cell Biology, University of Mazandaran, Babolsar, Iran
3. Department of Microbiology, Golestan University of Medical Sciences, Gorgan, Iran

Background and Aim: Staphylococcus aureus is known as the main nosocomial pathogen due to its ability to generate a wide range of virulence factors such as extracellular protein toxins and resistance to antimicrobial compounds. Staphylococcal scalded skin syndrome refers to a spectrum of blistering skin diseases caused by S. aureus exfoliative toxins A and B. The eta gene has a chromosomal origin that is integrated by prophage, whereas the etb gene is a plasmid gene. Virulent strains of these bacteria produce exfoliative toxins (ETs) that cause the loss of keratinocyte cell-cell adhesion in the superficial epidermis. The aims of this study to investigate the prevalence of eta and etb genes in S. aureus isolated from clinical specimens.

Methods: In this descriptive study, 137 clinical samples were collected from hospitals in Sari and Babol. Then by performing standard tests, 120 samples were identified as S. aureus. polymerase chain reaction was used for detection of the eta and etb genes among the isolates.

Results: The frequency of genes eta, etb in studied strains was 10% and 6.6%, respectively.

Conclusion: The results of this study indicate that importance of these isolates circulating among community especially immunocompromised adults. there is also likely to spread and transfer these genes between strains.

Keywords: Exfoliative toxin, Staphylococcus aureus, Staphylococcal scalded skin syndrome

**P220 - 514: CROSS SECTIONAL STUDY OF ESBL PRODUCER E. COLI ISOLATES FROM
UTI PATIENTS OF PAYVAND'S LAB DURING 2014-15**

Behzad Poopak¹, Masoud Parsania², Naser Omidi³, Sepideh Ghasemshahi⁴, Afsoon Ghoudarz⁵

1. Tehran Medical Sciences Branch, Islamic Azad University Tehran-Iran
2. Tehran Medical Sciences Branch, Islamic Azad University Tehran-Iran
3. Payvand Clinical and Specialty Laboratory
4. Payvand Clinical and Specialty Laboratory
5. Payvand Clinical and Specialty Laboratory

Background and Aim:Background: E.coli, is the most important bacterial agent in urinary tract infections (UTIs) and its resistant to common antibiotics is increasing. Extended spectrum beta-lactamase (ESBL) producer E.coli isolates are capable to resist against 3th and 4th generation of cephalosporins. So, in this cross sectional study the frequency of ESBL producer E.coli isolates from UTI patients of Payvand's lab during 2014-15 were determined and compared.

Methods:During first 6 months of 2014-2015, all E.coli isolates from UTIs patients of Payvand's lab of Tehran were collected. All the bacterial isolation and identification were based on standard bacteriologic tests. Further antibiotic sensitivity test (AST) was done by CLSI 2014 protocol. Double Disk Synergy Test (DDST) were used to screen ESBL production using ceftazidime alone/ ceftazidime -clavulanic. The increased zone of inhibition ≥ 5 mm were selected as ESBL positive. E.coli ATCC25922 was tested, simultaneously.

Results:143 and 104 E.coli isolates were detected during first 6 months of 2014-2015, respectively. Based on AST all E. coli isolates were 100% sensitive to imipenem and meropenem and 100% were resistant to aztreonam, ceftriaxone, cefotaxime and cefalotin. By DDST, 60/143 and 43/104 of E.coli isolates were ESBL positive in this survey.

Conclusion:: based on the results, there is no increasing in the rate of ESBL producer E. coli isolates in this cross sectional study. Doing AST before any prescription and increasing the physician notification about ESBLs detection is recommended to control. Also, doing molecular survey is recommended to identify the responsible genes

Keywords:E.coli, ESBL, antibiotic resistance

**P221 - 524: DETECTION OF VIRULENCE GENES PRODUCING URINARY TRACT
INFECTION IN UROPATHOGENIC E. COLI ISOLATED FROM HUMAN SAMPLES**

Elaheh Salami khameshan¹, Mina Naseri²

1. MSc. in Microbiology, Department of Microbiology, Saveh Branch, Islamic Azad University, Saveh, IR Iran.
2. MSc. in Microbiology, Department of Microbiology, Saveh Branch, Islamic Azad University, Saveh, IR Iran

Background and Aim: Escherichia coli (E.coli) causes more than 80% of urinary tract infections in all age groups in society. Escherichia coli causing urinary tract infections include a large number of pathogenic virulence genes. The aim of study is to detection of virulence genes aer, pap, sfa, afa, traT producing urinary tract infection in uropathogenic E.coli isolated from patients referred to Tabriz medical clinic.

Methods: In this study, 170 sample of urine collected by standard methods and blood agar colonies were separated after Macconkey +EMB culture, Then the differential diagnosis was performed by biochemical tests. And specific primers were used to detect E.coli virulence genes by Multiplex PCR method.

Results: Finally, 60 sample contained of E.coli strains were isolated M-PCR results in determining the distribution of virulence genes in strains showed that there were respectively afa genes of 25 isolate (31/2%) , pap genes of 18 isolate (22/5%) , sfa genes of 9 isolate (11/2%), aer and traT genes (0%).

Conclusion: Our study showed that the sfa and pap virulence genes were highly prevalent among of the isolated from clinic patients; Therefore, They can play a more effective role in the occurrence of urinary tract infection compared to other virulence gene.

Keywords: Escherichia coli ,virulence gene ,urinary tract infection

P222 - 543: IDENTIFICATION OF OQXAB EFFLUX PUMPS IN EXTENDED SPECTRUM-B-LACTAMASE- PRODUCING ENTEROBACTERIACEAE ISOLATES OF PATIENTS REFERRING TO TEACHING HOSPITALS IN AHVAZ, IRAN.

Mahtab Khoshkholgh Sima¹, Mahtab Khoshkholgh Sima², Mojtaba Moosavian³, Nazanin Ahmad Khosravi⁴, Effat Abbasi Montazeri⁵

1. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.
2. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.
3. Health Research Institute, Infectious and Tropical Diseases Research Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.
4. Department of Microbiology, Faculty of Medicine, International Arvand, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.
5. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Background and Aim: Antibiotic resistance mechanisms in Enterobacteriaceae are causative agents of global health problems. Bacterial multidrug resistance (MDR) may be mediated by the overexpression of efflux pumps. In this study, we investigated the prevalence of Oqx A and Oqx B genes in extended spectrum beta-lactamase (ESBL) producing Enterobacteriaceae.

Methods: In this study, 100 Enterobacteriaceae isolates which were collected from clinical specimens of patients referring to teaching hospitals in Ahvaz, Iran were examined. Identification of the isolates was performed by standard biochemical tests and then susceptibility test of them to twelve antibiotic disks was carried out by Kirby-bauer disk diffusion method according to CLSI guidelines. Phenotypic confirmation of ESBLs producing Enterobacteriaceae isolates was done by combination disk method and finally the Oqx A and Oqx B genes were detected by PCR.

Results: Among 100 Enterobacteriaceae isolates, 53 (53%) isolates were phenotypically ESBL positive including 40 (75.5%) E. coli, 8 (15.1%) Enterobacter gergoviae, 3 (5.7%) Enterobacter cloacae and 2 (3.8%) Enterobacter aerogenes. Out of 53 Enterobacteriaceae isolates which were phenotypically ESBLs positive, 10 isolates (18.7%) were positive for at least one of Oqx A or Oqx B genes, while both of Oqx A and Oqx B genes were found among 5.7% of them.

Conclusion: The results of this study showed that ESBLs producing Enterobacteriaceae isolates with efflux pumps such as OqxAB are increasing in the world and so for prevention of spreading these MDR isolates, identification of resistant isolates and antibacterial management of patients is necessary.

Keywords: Oqx A, Oqx B, Enterobacteriaceae, ESBLs.

P223 - 547: MOLECULAR DETECTION OF BACTERIAL CAUSING URINARY TRACT INFECTION IN DIABETIC PATIENTS IN KERMANSHAH, IRAN

Farshad Yadollahi¹, Elahe Tajbakhsh²

1. Graduated of Microbiology, Shahrekord Branch, Islamic Azad University, Shahrekord-Iran
2. Department of Microbiology, Shahrekord Branch, Islamic Azad University, Shahrekord-Iran

Background and Aim: Diabetic patients are very susceptible to infection and they are endangering the infection. Due to a urinary tract infection is the most common infection in diabetics, identifying the factors that cause common infections, results in the best selection of an effective antibiotic can be an effective step in the treatment of diabetes.

Methods: In this study, urine samples were taken from 353 patients with type 2 diabetes mellitus in Kermanshah. Identification of bacteria that cause urinary tract infections were carried out by using biochemical and molecular tests. PCR reaction was performed in the presence of specific primers.

Results: According to this study, 28.33% of diabetic patients with urinary tract infections. A total of 353 diabetic patients, 100 patients were diagnosed with UTI, of which 30% men and 70% were female. 22.1% of the diabetic patients without clinical signs and only in 6.23% bacteriuria were observed. *Escherichia coli* (51.22%) was common in these patients. Infection with *K. pneumoniae*, *Proteus*, *S. saprophyticus*, *Acinetobacter*, *Citrobacter*, *Enterobacter*, *Pseudomonas* and *Providencia* was reported 15.24%, 10.98%, 7.32%, 5.49%, 4.27%, 3.04%, 1.22% and 1.22% respectively.

Conclusion: Considering that urinary tract infection in patients with diabetes happens in old age, most patients were asymptomatic bacteriuria. Therefore, urine culture should be performed in diabetic patients.

Keywords: Urinary tract infection, Diabetes mellitus, Molecular detection.

P224 - 560: A SURVEY ON THE OCCURRENCE OF VANCOMYCIN RESISTANCE IN THE STAPHYLOCOCCUS AUREUS STRAINS ISOLATED FROM CLINICAL SPECIMENS

Vedad Alekhamis¹, Seyedeh Elham Rezatofighi ², Hossein Motamedi ³

1. Senior student of microbiology, Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Ahvaz, Iran
2. Associate Professor, Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Ahvaz, Iran
3. Professor, Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Ahvaz, Iran

Background and Aim: Empiric therapy for staphylococcal infections by penicillins led to spread of penicillin resistance throughout the world. Therefore reliance on vancomycin for treatment of documented methicillin-resistant *S. aureus* (MRSA) infections, as well as for empiric therapy of infections in populations where the prevalence of MRSA is high is increased. Since 2002, nine MRSA strains that are also resistant to vancomycin (VRSA) have been reported in the United States. There is no documented evidence for investigation of vancomycin resistance among *Staphylococcus* isolates in Khuzestan.

Methods: A total of 50 MRSA isolates collected from clinical specimens of patients in hospitals of Khuzestan province and checked for presence of vancomycin resistance genes (*vanA*, *vanB*, *vanC*, and *vanD*) by PCR. Also phenotypic resistance of isolate was checked by minimum inhibition concentration (MIC) method.

Results: Among the isolates prevalence of *vanA*, *vanB*, *vanC*, and *vanD* was found 0%, 4%, 6% and 4% respectively. Two isolate showed MIC equal to 8 µg/ml.

Conclusion: The results showed that the frequency of vancomycin resistance genes is high in MRSA strains isolated from patients in south of Iran. Thus to keep the emergence and transmission of these isolates to a minimum, urgent interventions are needed.

Keywords: *Staphylococcus aureus*, vancomycin, MRSA, VRSA

**P225 - 571: DESIGN AND EXPRESSION OF RECOMBINANT CHIMERIC ANTIGEN
SEQUENCE AS POLY TROPHIC UROPATHOGENIC ESCHERICHIA COLI**

Niloufar Sadeghi¹

1. student of Islamic Azad university - Zanjan

Background and Aim: Abstract Background: Escherichia coli is one of the most important frequent causes of UTI, and is the reason of more than 85 percent of acute cystitis and pyelonephritis. Need to develop the vaccine is quite evident, considering the high prevalence of UTI and antibiotic resistance against the causes of this infection. The aim of this study was to introduce and expression of the new chimeric molecule through the evaluation of antigenic proteins by Immunoinformatics ways to design polytopic vaccine.

Methods: Material and method: Fim H, Ire A, Iut A, Pap G and Sfa proteins evaluated in the NCBI database, then appropriate regions of these genes of proteins were selected by using Immunoinformatics servers. The proper order of these gene regions selected and synthesized as a gene in the pGEM vector after optimization. The plasmid amplified in DH5 α strain. Then the target gene sub-cloned in pET-21 and expressed in the BL21 Competent E. coli. In the end, expression of recombinant proteins analysed by SDS-PAGE and confirmed by Western Blot technique.

Results: Results: After SDS-PAGE analysis of cell extract of bacteria containing the plasmid, a band was observed with molecular weight of 17.7 kDa that is correspond to the target chimeric protein. The identity of recombinant protein was confirmed by Western blotting, using anti-His-tag monoclonal antibody.

Conclusion: Conclusion: According to the results of bioinformatics analysis, it seems chimeric protein that wae studied, could be a good candidate for a vaccine against pathogenic strains of E. coli in the next phase of the study.

Keywords: Keywords: Urinary Tract Infection (UTI), SDS-PAGE, Western blotting

**P226 - 579: DETECTION OF BORRELIA MICRITI INFECTION IN MICE BY WESTERN
BLOT ANALYSIS**

Sabah Naeimi¹, Saied Reza Naddaf²

1. Dept. of Microbial Biotechnology, Faculty of Biological sciences, Islamic Azad University, North-Tehran Branch, Tehran, Iran
2. Dept. of Parasitology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Tick-borne relapsing fever (TBRF) is a disease endemic in Iran, with more 100 annual cases. The main manifestation, as the name indicates, is a recurring fever and tremors. In Iran the disease is also caused by *Borrelia microti*. Studies show the presence of GLPQ gene in relapsing fever group of spirochetes which permits the acquisition of glycerol 3phosphate from phospholipids. The purpose of this study was to produce recombinant GLPQ and evaluate its antigenicity against mice infected sera.

Methods: The DNA encoding glycerophosphodiester phosphodiesterase (GLPQ), was obtained from *B. Microti* by polymerase chain reaction amplification and cloned in the prokaryotic expression plasmid pET28b. The rGLPQ was expressed in *Escherichia coli* (*E. coli*) and purified by immobilized metal ion affinity chromatography.

Results: DNA sequencing showed 99% similarity between the cloned sequence and the similar sequences *Borrelia duttoni* and *recurrentis* in Genbank database. The sera from *B. microti* infected mice reacted with rGLPQ in Western blot analysis.

Conclusion: The rGLPQ can be used as a valuable tool for detection of relapsing fever infections by serological methods.

Keywords: *Borrelia microti*, glpQ protein, Relapsing fever

**P227 - 585: DETECTION OF HELICOBACTER PYLORI IN PATIENTS WITH
HYPERLIPIDEMIA BY PCR**

Simin Khodabakhshi¹, Hossein Rassi², Behzad Salehi³

1. Department of Biology , Karaj Islamic Azad University
2. Department of Biology , Karaj Islamic Azad University
3. Department of Biology , Karaj Islamic Azad University

Background and Aim:Hyperlipidemia is too much cholesterol in the blood and it is a major risk factor for heart disease, the leading cause of death in the US. In this matter, as multifactorial disease, genetic and environmental factors can be effective such as some bacterial infections. Relation between this disease and some infections such as *Helicobacter pylori* has been shown in several studies. The aim of this study was to investigate the relationship between *H. pylori* infection and hyperlipidemia by PCR technique.

Methods:This study is a case-control study in which 144 as cases or patients and 160 healthy peoples were studied. Of all people of venous blood prepared and arranged by age, BMI, glucose, cholesterol, LDL, HDL, urea, uric acid, triglycerides, creatinine, SGPT and SGOT determined. Then, DNA extracted and *cag A* gene of *H. pylori* detected by PCR. Statistical analysis was obtained by EPI Info software.

Results:The results showed that the prevalence of *Helicobacter pylori* infection in case and control groups was 39.58% (57 out of 144) and 18.42% (28 of 152) respectively. Significant difference was in the prevalence of *H. pylori* was achieved between the two groups ($P = 0.0001$). Also, cholesterol, triglyceride, LDL, HDL measured in both groups and data were compared between two groups.

Conclusion:Therefore, *H. pylori* can be a new risk factor for hyperlipidemia or can be exacerbate effect of other risk factors.

Keywords:hyperlipidemia, *H. pylori*, PCR

**P228 - 590: LACTAMASE GENE CODING FOR THE ENZYME AMPC IN CLINICAL
ISOLATES OF KLEBSIELLA PNEUMONIAE**

Javad Dahmardeh¹, , Shahram Sharaki Zahedani², Farokh Rokhbakhsh zamein³

1. 1. microbiology graduate student of Islamic Azad University Kerman, Kerman, Iran.
2. 2. Assistant Professor, Faculty member, University of Medical Sciences Zahedan, Department of Microbiology, Zahedan, Iran.
3. 3. Assistant Professor, Faculty, Islamic Azad University Kerman, Department of Microbiology, Kerman, Iran.

Background and Aim: Lactamase enzyme is one of the most important factors in the development of antibiotic resistance among Gram-negative bacteria. Ampc identify genes in *Klebsiella pneumoniae* strains producing ESBLs, useful information about the epidemiology and risk factors involved in this treatment and provides infections. The aim of this study was to determine antibiotic susceptibility and ESBL-producing *Klebsiella pneumoniae* strains (ESBLs) and Ampc genes in teaching hospitals in Zahedan.

Methods: In this cross sectional study in 1394 on 120 *Klebsiella pneumoniae* isolates from various clinical specimens were collected Zahedan teaching hospitals were identified by standard biochemical tests. Antibiotic susceptibility was determined by disk diffusion method CLSL guidelines. Finally ESBLs *Klebsiella pneumoniae* strains Ampc for the presence of genes by PCR and DNA sequencing were evaluated.

Results: Most of antibiotic resistance to antibiotics erythromycin and was Colistin (90 percent) while the lowest antibiotic ceftriaxone, ceftazidime and cefotaxime-related antibiotics (10 percent). *Klebsiella pneumoniae* clinical isolates of 120 isolates 95 were positive in the initial screening of ESBLs producing isolates, 23 were Ampc lactamase gene.

Conclusion: The study showed that the high incidence of *Klebsiella pneumoniae* clinical isolates lactamase producing isolates of Ampc in Zahedan teaching hospitals, antibiotic resistance has become a major concern. Hence, the policy prescription of antibiotics and infection control Reconsider be achieved.

Keywords: *Klebsiella pneumoniae*, ESBL gene Ampc, antibiotic resistance.

**P229 - 595: KELEBSIELLA RHINOSCLEROMA: A DIAGNOSTIC CHALLENGE FOR
NASAL/UPPER RESPIRATORY TRACT GRANULOMATOUS INFECTION REPORT OF
TWO CASES AND REVIEW OF THE LITERATURE**

Bahman Shafaeian¹, BAHMAN SHAFAYAN², YASAMIN SHAFAYAN³, NAHID MIRZAIE⁴

1. TEHRAN UNIVERSITY OF MEDICAL SCIENCES
2. TEHRAN UNIVERSITY OF MEDICAL SCIENCES
3. TEHRAN UNIVERSITY OF MEDICAL SCIENCES

Background and Aim:GRANULOMATOUS INFLAMMATION OF UPPER RESPIRATORY TRACT CAUSED BY KLEBSIELLA RHINOSCLEROMATIS WITH OR WITHOUT CERVICAL LYMPH NODE ENLARGEMENT IS AN UNUSUAL CHRONIC INFECTION RESEMBLING FUNGAL, MYCOBACTERIAL, LYMPHOPROLIFERATIVE AND IMMUNE VASCULAR DISEASES, TWO CASES HAVE BEEN PRESENTED.

Methods:TWO CASES “25, 37 YEAR OLD” WITH NASAL DISCOMFORT AND PARANASAL FULNESS/INFERIOR TURBINATE HYPERTROPHY WERE ADMITTED. CT SCANNING REVEALED NASAL MUCOSAL THICKENING WITH NORMAL THORACIC, ABDOMINAL-PELVIC IMAGING. LABORATORY SEROLOGIC TESTS “FOR VASCULITIS” WERE NEGATIVE.

Results:HISTOPATHOLOGICAL EXAMINATION WAS COMPATIBLE WITH GRANULOMATOUS FIBROTIC/INFLAMMATION CONTAINING PLASMA CELLS “RUSSELL BODIES” AND MICULICZ CELLS. INTERESTINGLY TISSUE CULTURES FOR KLEBSIELLA “RHINOSCLEROMA” SHOWED POSITIVE RESULTS WITH SIGNIFICANT RESPONSE TO CIPROFLOXACIN THERAPY.

Conclusion:UPPER RESPIRATORY TRACT “NASAL/MAXILLARY SINUS” GRANULOMATOUS INFECTION WITH KLEBSIELLA “RHINOSCLEROMA” IN TWO CASES HAVE BEEN PRESENTED. THIS UNUSUAL AND INFREQUENT SUBTYPE OF KLEBSIELLA MUCOSAL INFLAMMATORY DISORDER IS A DIAGNOSTIC CHALLENGE RESEMBLING MYCOBACTERIAL, FUNGAL INFECTION AND GPA “WEGENER’S” VASCULITIS. CLINICAL IMPRESSION AND TISSUE CULTURE SHOULD BE CONSIDERED.

Keywords:KLEBSIELLA RHINOSCLEROMA , NASAL GRANULOMATOUS INFECTION

**P230 - 596: AN INVESTIGATION INTO DRUG RESISTANCE AND BIOFILM FORMATION
IN ESCHERICHIA COLI SEPARATED FROM PATIENTS AFFLICTED WITH URINARY
TRACT INFECTION IN MARAGHEH.**

Elnaz Davari narj abad¹, Asghar Tanomand²

1. Department of Microbiology, Islamic Azad University, Urmia, Iran
2. Department of Microbiology, Medical University Of Maragheh, Maragheh, Iran

Background and Aim: Escherichia coli are of the most important microbial causes prevalent in urinary tract infections. Connection to epithelium of urinary system is the first phase of UTI, and this issue leads to an increase in their capability to proliferate and attack renal tissue. Additionally, as resistance to drug has increased over recent years, treating such infections has encountered some difficulties. The present study aims to determine drug resistance and formation of uropathogen Escherichia coli biofilm in patients afflicted with urinary tract infections in Maragheh, Iran.

Methods: 80 samples of Escherichia coli were isolated from patients afflicted with urinary tract infections and then were verified through biochemical tests. Possibility of UPEC biofilm formation under laboratory conditions was measured by means of microtiter plate method. In this study, $OD \geq 0.1$, $0.07 \leq OD \leq 0.09$, $0.01 \leq OD \leq 0.06$, and $OD \leq 0.009$ were considered to be strong, average, weak, and with no connected result, respectively. Additionally, disk diffusion method was employed to study drug resistance.

Results: Based on the results obtained from this study, biofilm formation in 6 separations (7.5%), in 6 separations (7.5%), in 65 separations (81.25%), and in 3 separations (3.75%) were reported to be strong, average, weak, and with no connected result, respectively. Antibigram results revealed that the highest resistance observed was to Amoxicillin and Ampicillin and the lowest resistance was to Nitrofurantoin and Amikacin.

Conclusion: Uropathogen escherichia coli separations have different abilities in biofilm formation. Further, they have a noticeable drug resistance in comparison with common antibiotics.

Keywords: biofilm, Escherichia coli, urinary tract infection, drug resistance

P231 - 599: MOLECULAR IDENTIFICATION OF MYCOPLASMA SPP ISOLATED FROM PATIENTS WITH MULTIPLE SCLEROSIS (MS) IN KERMAN PROVINCE.

Maryam Naghib¹, Babak Kheirkhah²

1. PhD student in microbiology, Islamic Azad University of Kerman, Department of microbiology, Kerman, Iran
2. Assistant Professor of Microbiology, Islamic Azad University of Kerman, Department of microbiology, Kerman, Iran

Background and Aim: Multiple Sclerosis or MS, is chronic inflammatory disease in which demyelinating nervous system is happened. This damage causes some disorders within some parts of The nervous system that are responsible for communication. Although the causes of this disease are unknown, It's main mechanism system the destruction of myelin – producing cells. The given reasons in these mechanisms include genetic factors, and environmental factors such as Infection. Chronic or recent infections in the patient affected by MS, themselves can have a major role in the start or aggravation of attacks. Among the mentioned bacteria having such effect, is Mycoplasma that has word. Wide spread. Mycoplasma pneumoniae involved in the disturbances nervous system like Encephalitis, Guillain-Barre syndrome, MS,.....

Methods: This study performed as a continuation of the studies completed to search for Mycoplasma on 30 frozen samples of cerebrospinal fluid that one night were enhanced on PPLO broth then for 7 weeks have been passaged to PPLO broth and PPLO agar until colonies has shaped. After extracting DNA by using the specific Mycoplasma primers. Nested PCR was done to increase the sensitivity and specificity of the study then PCR was used to determine species.

Results: in 1 sample Mycoplasma was certainly observed After wards. Then PCR was used to determine species.

Conclusion: Mycoplasma within cerebrospinal fluid was Mycoplasma pneumoniae.

Keywords: Mycoplasma pneumoniae, Multiple sclerosis, Demyelinating.

**P232 - 601: COMPARISON OF DOMVS AND NOMVS IMMUNIZATION AS A NEW
CHOLERA VACCINE**

Razieh Rezaei¹, seyyed latif mousavi²

1. student in shahed university
2. phd of biochemistry

Background and Aim: Cholerae caused by toxigenic *V.cholerae* as a significant health problem and an important agent in mortality of children in developing countries. Annually about 3-5 million people are being infected world wise, leading to death of 100 000-120 000. Immunization with currently available cholera vaccines has been recommended by WHO in areas where cholera is endemic or at risk of outbreaks. Outer membrane vesicles (OMVs) released from Gram-Negative bacteria is an appropriate candidate for vaccine development.

Methods: We investigated the protection conferred by this new vaccine with a nanoparticles in an experimental model of cholera in mice. OMVs were encapsulated in chitosan-TPP nanoparticles prepared by an ionic gelation and coated with Eudragit as an entric polymer

Results:. OMVs loaded into NPs (NP-OMVs) were homogeneous and spherical in shape, with a size of 390 nm. OMVs were extracted by two methods as natural or with using of detergent in two temperature conditions. BALB/c mice (male, 5-week-old, 20-24g) were immunized by intradermal (20µg) or oral route (50µg) with free or encapsulated OMV. Sixty days after administration, serum of mice were infected with a lethal dose of *V.cholerae* (107 CFU)

Conclusion: The new vaccine was able to protect fully against infection when it was administered via mucosa. By intradermal route the free OMVs formulation increased the protection against this bacteria.

Keywords: vaccine, vibrio cholerae, OMVs

**P233 - 607: MOLECULAR DIAGNOSIS OF ACUTE Q FEVER IN TWO PATIENTS WITH
POSITIVE WRIGHT TEST IN KHORRAMABAD CITY**

Farnaz Ferdosi¹, Amin Jaydari², Nemat Shams³, Lida Etemad Far⁴

1. Master Of Science Student In Bacteriology, Faculty Of Veterinary Medicine Lorestan University
2. Assistant Professor, Department Of Microbiology, Faculty Of Veterinary Medicine, Lorestan University
3. Assistant Professor, Department Of Microbiology, Faculty Of Veterinary Medicine, Lorestan University
4. Master Of Science Student In Bacteriology, Faculty Of Veterinary Medicine Lorestan University

Background and Aim: Q fever and Malta fever are zoonotic diseases caused by the obligate intracellular gram negative bacteria, *Coxiella burnetii* and *Brucella*. These bacteria caused various clinical symptoms in patients. There are few studies about the diagnosis of Q fever in humans in Iran. Initial serological studies revealed high seropositivity rate in patients with a history of fever associated with livestock. There is a high prevalence of brucellosis in some areas of Iran, including Lorestan. Wright and 2ME tests are often used for diagnosis of brucellosis in Iran; these tests have low sensitivity to diagnose (of brucellosis). The aim of this report is to study two cases that acute Q fever with positive results was diagnosed by wright and 2ME tests.

Methods: We investigated two cases of suspected brucellosis by molecular methods to diagnose the genome of *Brucella* and *Coxiella burnetii*.

Results: Wright and 2ME results were positive in both patients, but *Brucella* molecular's result was negative. The genome of *Coxiella burnetii* was identified in both patients by Molecular testing.

Conclusion: This study reveals that Q fever might be one of the possible reasons in febrile patients that should be considered. In addition, due to the low sensitivity of Wright and 2ME tests to diagnose brucellosis, using more reliable methods such as ELISA and PCR is recommended

Keywords: *Brucella*, *Coxiella burnetii*, Human, Khorramabad, Nested-PCR

**P234 - 626: ISOLATION OF ANTIBIOTIC-RESISTANT STAPHYLOCOCCUS ARGENTEUS
FROM SPUTUM SAMPLE**

Pantea Fatehfard¹, Javad Hamed², Abbas Akhavan Sepahi³

1. Department of Microbiology, Faculty of Science, Islamic Azad University, North Branch of Tehran. Microbial Technology and Products Research Center, University of Tehran.
2. Department of Microbial Biotechnology, School of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran. Microbial Technology and Products Research Center, University of Tehran.
3. Department of Microbiology, Faculty of Science, Islamic Azad University, North Branch of Tehran.

Background and Aim: *Staphylococcus argenteus* is recently introduced species, it is very similar to *S. aureus* and cannot be differentiate by conventional diagnostic tests. here is a report of *S. argenteus* isolation from clinical samples and its antibiotic resistance pattern.

Methods: Eighty-one putative *Staphylococcus aureus* isolated from sputum (Tehran's medical laboratories) identified using conventional test: Gram stain, coagulase and DNase activities, mannitol fermentation, salt resistance and novobiocin sensitivity, yellowish orange (golden) pigment production on Blood Agar and Chocolate Agar. Antibiotic susceptibility pattern was investigated using CLSI standard method. Putative *S. argenteus* colonies were subjected to 16SrRNA gene analysis.

Results: Among 81 isolates, strain FH 77 had similar characteristics to *S. aureus*, but, cannot produce golden pigment. FH77 had 100% similarity to *S. argenteus* (MSHR 1132) in 16S rDNA analysis. It was resistant to Cotrimoxazole, Clindamycin, Gentamicin, Ciprofloxacin, Erythromycin, Doxycycline, Tetracycline and Vancomycin, with no inhibition zone, but sensitive to Rifampin.

Conclusion: *S. argenteus* FH77 unable to produce golden pigment and shows high antibiotic resistance. *S. argenteus* and golden-pigment-negative-*S. aureus* variants are different in similarity in 16SrRNA gene. Therefore, golden-pigment-negative-*Staphylococcus aureus* according conventional tests, should be a subject of additional molecular diagnostic test for correct identification.

Keywords: *Staphylococcus argenteus*, *Staphylococcus aureus*, antibiotic resistance, clinical isolates.

P235 - 660: INFECTIONS AND INCREASED RATE OF DIABETES MELLITUS: IS THERE A LINK?

Abed Zahedi¹, Hamed Ebrahimzadeh leylabadlo², Hossein Samadi kafil³, Abed Zahedi bialvaei⁴

1. Department of Microbiology and Virology, faculty of Medicine, Tabriz University of Medical Science, Tabriz, Iran
2. Drug Applied Research Center, Tabriz University of Medical Sciences, Tabriz, Iran
3. Department of Microbiology, faculty of Medicine, Iran University of Medical Science, Tehran, Iran

Background and Aim:Chronic infections could be contributing to the socioeconomic gradient in chronic diseases. Although chronic infections have been associated with increased levels of inflammatory cytokines and cardiovascular disease, there is limited evidence on how infections affect risk of diabetes. In the preset study, we reviewed the association between serological evidence of chronic viral and bacterial infections and incident diabetes by searching in the main literatures

Methods:We analyzed data on more 40 paper published among 2005–2016, which blood was tested for antibodies to herpes simplex virus 1 (HSV 1), Enterovirus, varicella virus, hepatitis C virus (HCV) cytomegalovirus (CMV), *Helicobacter pylori*, and *Toxoplasma gondii*.

Results:According to the results of most published data, we found no evidence for an association between individuals seropositive for herpes simplex virus 1, varicella virus, CMV, and *T. gondii* and an increased rate of diabetes. However, in other studies conducted on *H. pylori*, enterovirus and active HCV infection, those patients who were seropositive, at enrollment were 2.7 times more likely at any given time to develop diabetes than seronegative individuals (with hazard ratio 2.69 [95% CI 1.10–6.60]).

Conclusion:The results suggest that a large proportion of diabetic patients have prolonged/persistent *H. pylori*, enterovirus and HCV infection associated with an inflammation process. Our findings implicate a potential role for antibiotic treatment in preventing diabetes.

Keywords:Infections, Diabetes mellitus, *H. pylori*, HCV, enterovirus

**P236 - 670: EVALUATION OF TOPICAL THERAPEUTIC EFFECTS OF EUCALYPTUS
ESSENTIAL OIL ON EXPERIMENTAL MASTITIS CAUSED BY STREPTOCOCCUS
AGALACTIAE**

Hasan Jafari¹

1. Employee veterinary office in qom

Background and Aim: The most economical loss in the dairy herds are occurred due to mastitis. Mastitis is treated with antibiotics which has two problems, residual in milk and bacterial resistance. So several researchers start to experience non antibiotic drugs for mastitis treatment. Topical treatment of mastitis with eucalyptus is thought to be effective, because our primary study showed that infusion of extracts of eucalyptus in bovine mastitis caused by; agalactia had hopeful results.

Methods: In this study 18 dairy cows were infected experimentally with St; agalactia they located in three groups; group 1 (six cows treated with 15% lotion of eucalyptus), group 2 (six cows treated with 10% lotion of eucalyptus), group 3 (six cows experimentally infected but not treated). Before infection CMT and culture of milks were performed to ensure that they had not any mastitis then were infected using 6×10^6 cfu st, agalactia each group were treated after milkings (2 times per day) for three consecutive days (total six times) with 150ml of lotions. Lotions were applied on skin of the udders for two minutes. After treatments CMT and culture of milks were done evaluation treatments.

Results: We concluded that topical application of 10 or 15 percent of eucalyptus essence had no therapeutic effect on experimental mastitis caused by st.agalactia.

Conclusion: We concluded that topical application of 10 or 15 percent of eucalyptus essence had no therapeutic effect on experimental mastitis caused by st.agalactia.

Keywords: streptococcus agalactiae- mastitis-eucalyptus

P237 - 675: E.COLI SECRETS RECOMBINANT HUMAN GROWTH HORMONE TO PERIPLASM BY MEANS OF XYLA SIGNAL PEPTIDE

VAJIHE AKBARI¹, ali asghar deldar², hamideh rouhani nejad³

1. Molecular Genetics department, Research Centre for Biosciences and Biotechnology, Malek -Ashtar University of Technology, Tehran, Iran
2. Molecular Genetics department, Research Centre for Biosciences and Biotechnology, Malek -Ashtar University of Technology, Tehran, Iran
3. Molecular Genetics department, Research Centre for Biosciences and Biotechnology, Malek -Ashtar University of Technology, Tehran, Iran

Background and Aim: Human growth hormone (HGH) important biological role in growth . In HGH deficiency and some other medical situations, exogenous recombinant human growth hormone could be used as an effective treatment. The active and non-Immunogenic form of rhgh should not contain formyl methionine at the N-terminus. In cytoplasmic expression of this recombinant hormone in E.coli fMet remains at the N-terminus therefore secretion into periplasm is an alternate. XylA signal peptide coding sequence linked to synthetic rhgh DNA fragment.

Methods: hgh sequence (GenBank ; AIA66930) optimized and synthesized. Fragment cloned into pet21a. Ligation product pET21a+- rhgh transformed into the Ecoli DH5- α and confirmed by PCR and restriction enzyme digestion. Thereafter pET21a+- rhgh transformed into the Ecoli BL21 and induced with IPTG. SDS PAGE used for analysis of rHGH expression

Results: Results of colony PCR and RE-digestion confirmed cloning of rhgh in the pet21a+ and its transformation to the Ecoli BL 21. rHGH expressed and observed as 22kDa protein band after induction. finally blotting technique with monoclonal antibody analysis of expressed protein accuracy .

Conclusion: XylA signal sequence successfully used for expression of rhGH protein. The efficiency of this signal sequence for secretion of rhgh will be revealed after improvement of growth and induction conditions.

Keywords: rHGH , periplasm, signal peptides

**P238 - 702: AN EVALUATION OF ASSOCIATION BETWEEN DENTAL PRACTICE AND
COLONIZATION OF CANDIDA ALBICANS IN DENTISTS' MOUTHS**

Majid Zare Bidaki¹, Faeze Saeidi², Baniasadi³

1. Paramedical Faculty, Birjand University of Medical Sciences
2. Dentistry Faculty, Birjand University of Medical Sciences
3. Dentistry Faculty, Birjand University of Medical Sciences

Background and Aim: Contamination with *Candida albicans* can provide risk of opportunistic infections with this fungus. Due to close contact of dentists with the oral cavity of patients, it seems that this group are at more risk of oral colonization of *Candida albicans* than others. This study aimed to determine the association between dentistry practicing and oral colonization of *Candida albicans*.

Methods: In this case - control study, case group was consisted of 37 dentists working in the city of Birjand and the control group consisted of 37 non-medical personnel. Using oral swab applicator and scrubbing the rear surface of the tongue, saliva sample was obtained. In the first phase, smear was prepared, and after staining with Methylene blue, microscopies were observed. In the second stage, all samples were cultures on selective media and inoculated at 37 ° C for a week. Positive cultures were tested for germ tube.

Results: From 37 dentists, 6 cases were positive (16.2%) and 29 (78.4%) were negative. In control group, only 3 samples (8.1%) were positive. Although the number of positive cases among the dentists was more than the controls, it was not statistically significant. 4 out of 6 positive samples were male, but statistically no significant correlation between gender and the prevalence of oral colonization of *Candida albicans* was found.

Conclusion: This study suggests that the dentists are at risk of oral colonization of *Candida albicans* not more than what non-medical personnel are.

Keywords: Dentistry, *Candida albicans*, Oral colonization

**P239 - 714: THE PREVALENCE OF ESBL-PRODUCING PSEUDOMONAS AERUGINOSA
ISOLATED FROM CLINICAL SAMPLES IN TABRIZ TOWN**

Azizeh Shadi Dizaji¹, abolfazl jafari sales²

1. Social Security organization shahid mokhtari clinic
2. Department of Microbiology, Ahar Branch, Islamic Azad University, Ahar, Iran

Background and Aim: Today, due to the increased use of antibiotics, the resistance of microorganisms to a variety of antibiotics can be seen. *Pseudomonas aeruginosa* bacteria are dangerous for human society because they tend to get resistance genes. So, the aim of this study is to investigate the prevalence of ESBL-producing *P. aeruginosa* in hospitals and medical centers in Tabriz Town.

Methods: in this study, in a period of one year, 892 individuals of patients admitted to hospitals and medical centers were isolated and after identification and performing antibiogram test, the phenotype of ESBLs in *Pseudomonas aeruginosa* bacteria was investigated by double disk synergy test.

Results: 98 Of 892 isolated *Pseudomonas aeruginosa* bacteria were identified that 18 of them were positive ESBL. In this bacteria, the highest resistance is related to the antibiotics of piperacillin, imipenem, cefotaxime, ceftriaxone, gentamicin and ceftazidime.

Conclusion: the results indicate the high prevalence of enzymatic resistance of ESBL in the bacteria isolated from the hospitals and medical centers in Tabriz Town. So, screening the clinical samples is very important in terms of the resistance of ESBL.

Keywords: ESBL enzymes, *Pseudomonas aeruginosa*, Antibiogram

**P240 - 723: COMPARISON OF PSEUDOMONAS AERUGINOSA VIRULENT
GENES(EXO,PHZ,LASA,LASB) IN CLINICAL SAMPLES**

Bahareh Ghobadi saki¹, fatemeh noorbakhsh², raheleh safayi javan³

1. microbiology department,islamic azad univercity varamin-pishva branch
2. microbiology department,islamic azad univercity varamin-pishva branch
3. microbiology department,islamic azad univercity varamin-pishva branch

Background and Aim: Pseudomonas aeruginosa is a Pathogen opportunistic bacteria and one of the most important causes of hospital infections. These pathogens cause a wide range of infections ranging from urinary tract infection to bacteremia. These bacteria have several pathogen factors including Tox A ,Phz H ,Las A and Las B genes. In this study, the frequency of Tox A ,Phz H ,Las A and Las B genes in Pseudomonas aeruginosa isolated from clinical samples by Polymerase Chain Reaction (PCR) have been studied.

Methods: In this study 50 isolates of P. aeruginosa were recovered from sore, pulmonary tract , urine , excrement ear ,and blood infections then extract DNA and PCR Performed with specific primers.

Results: twenty - four out of 50 (48%) male infection specimens and 26 out of 50 (52%) female infection specimens harbored P. aeruginosa. Also, 48 samples (96%) were positive for Las A and Phz H virulent genes of P. aeruginosa, which was a high rate. The genes encoding Tox A (88%) and Las B (46%) were the virulent genes found among the samples.

Conclusion: The results of this study can be concluded that the most important factors of virulence in Pseudomonas aeruginosa bacteria are Las A, Phz H genes. Urine samples (30%) and sore samples (28 %) The most infection specimens recovered from patients.

Keywords: Pseudomonas Aeruginosa, Tox A ,Phz H ,Las A , Las B genes, hospital infections

**P241 - 729: DETECTION OF CAMPYLOBACTER IN STOOL SAMPLES OF CHILDREN AND
OTHER DIARRHEIC SAMPLES IN PASTEUR MEDICAL LABORATORY FROM ARAK-
IRAN**

Marjan Salehi¹, Majid Akbari²

1. Master's graduate of Qom Islamic Azad University, Department of Microbiology, Qom, Iran
Email:marjaanii1393@gmail.com
2. Assistant Professor, Department of Microbiology and Immunology, ARAK University of Medical Sciences,
ARAK, IRAN

Background and Aim: Campylobacter is a common cause of bacterial diarrhea in many countries and because of the difficulty of diagnosis, it often overlooked in medical laboratories . Diarrhea is the most common cause of death in our country for children. In this study we determined the prevalence of Campylobacter in patients affected with diarrhea, especially children around 5 years. that have come to the Pasteur medical laboratory in the Arak city during the years 1393-1394 and early in 1395.

Methods:: We examined direct gram smear for fresh and mucosal faecal specimens . history showed that most of patients had travel and feeding of chicken or related products.

Results: In total, 438 diarrhoeic faecal samples were examined for Campylobacter that includes 255 , 5 years old and younger and 138 adults . In the cases of 112 children of 255 equal to 45 % or 25 % of all (438) patients The predominant morphologic forms of Campylobacter observed on positive smears of stool specimen were sea-gull and short spirochetel. also 13 Symptomatic patients of 138 adults or 7.1 % were involved with campylobacter .

Conclusion: The direct Gram stain method can provide a presumptive result within 30 minutes of receipt of a faecal sample with relatively high sensitivity, and at low cost. IN Laboratories with limited resources for culture should consider adopting this as a routine method.

Keywords: Campylobacter-diarrhea-gram smear

**P242 - 731: PREVALENCE OF INTESTINAL PARASITIC INFECTIONS IN
MENTALLY/PHYSICALLY DISABLED CHILDREN AND ADOLESCENTS AND THEIR
CAREGIVERS “SABZEVARAN” BOARDING CARE CENTER IN JIROFT CITY, IRAN**

Pooya Ghasemi Nejad Almani¹, Samira Salari², Majid Fasihi Harandi³, Zahra Babaei⁴, Iraj Sharifi⁵,
Ebrahim Saedi Dezaki⁶, Hossein Kamyabi⁷, Farideh Tohidi⁸, Reza Abbasi⁹

1. Department of Medical Parasitology and Mycology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran
2. Department of Medical Parasitology and Mycology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran
3. Department of Medical Parasitology and Mycology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran
4. Department of Medical Parasitology and Mycology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran
5. Leishmaniasis Research Center, Kerman University of Medical Sciences, Kerman, Iran
6. Department of Medical Parasitology and Mycology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran
7. Department of Medical Parasitology and Mycology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran
8. Department of Medical Parasitology and Mycology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran
9. State welfare organization of Kerman, Iran

Background and Aim: Infections with some intestinal parasite can interfere in absorption of nutrients and vitamins in the intestine cause decreased growth rate in children. Diagnosis and treatment of these infections can be very effective in improving children's health and development.

Methods: This study has been carried out on 82 children and teenager who are under 13 years old as well as 32 staffs who are working at Boarding care sustenance Center of infirm children in Jiroft city. Three independent stool samples were collected for each participant. Totally 342 samples have been collected. Each specimen was studied macroscopically and microscopically using Formalin-ether concentration test as well as Scotch tape. Diarrheic specimens have been considered by direct smear because of probable existence of protozoa trophozoites.

Results: In children, out of 82 persons the following parasite have been identified: Blastocystic hominis 32.9%, Giardia lamblia 30.48% , Entamoeba coli 28%, Endolimax nana 19.51% , Chilomastix mesnili 9.7%, Entamoeba hartmanni 7.31%, Iodamoeba butschlii 2.43%, Hymenolepis nana 1.21% and out of 32 caregivers Blastocystic hominis 50%, Entamoeba coli 15.62%, Endolimax nana 15%, Giardia lamblia 9.37% , Entamoeba hartmanni 6.25%, Endolimax nana 6.25%, Iodamoeba butschlii 6.25% and Chilomastix mesnili 3.12%.

Conclusion: Children and the staffs most commonly infected with Giardia lamblia. Results of the study have been submitted to center's physician for appropriate treatment.

Keywords: Intestinal Parasites, Children, Adolescents, Mental and Physical Disabilities, Jiroft

**P243 - 742: PRODUCTION OF ANTI-BREAST CANCER DNA THERAPY VECTOR USING
TOP10S**

Zahra Sadat Hashemi¹, Mehdi Forouzandeh Moghadam², Esmaeil Sadroddiny³

1. Department of Medical Biotechnology, School of Advanced Technologies in Medicine, Tehran University of Medical Science, Tehran, Iran
2. Department of Medical Biotechnology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran,
3. Department of Medical Biotechnology, School of Advanced Technologies in Medicine, Tehran University of Medical Science, Tehran, Iran

Background and Aim: Breast cancer, particularly its invasive ductal carcinoma, is the most prevalent type of cancer and the second leading cause of cancer deaths in women worldwide. One of the major causes of cancer deaths are complications aroused from metastasis. Breast cancer metastasis suppressor-1 (BRMS1) is a member of metastasis suppressor genes. A DNA therapy vector containing anti-breast metastasis genes could be an effective tool to arrest metastasis in all types of breast cancers.

Methods: The BRMS1 gene sequence has been optimized by GenScript Company in order to reach the highest possible level of expression and was cloned into pcDNA 6.2-GW/EmGFP plasmid by SalI/DraI restriction enzymes. Competent Top10 and Stb14 bacteria were transformed by physical/chemical method. Spectinomycin selection, colony PCR and sequencing were performed to confirm the cloning. Metastatic breast cells were isolated by FACS and MACS methods from the bulk of breast tumor and cultured in specific media and thereafter transfected with chimeric plasmid using Lipofectamine2000. Reduction in invasion was detected by real-time PCR and Matrigel-coated Transwell assay.

Results: The sequencing results confirmed the successful construction of therapeutic vector within the Top10 bacteria. The administration of chimeric plasmid led to significant reduction in invasive characteristic in metastatic cells compared to normal tumor cells (73.65 ± 0.02 to 24.97 ± 0.01 invasion percent).

Conclusion: Our approach resulted in a more robust and efficient inhibition of the metastatic process in the breast metastatic tumors. It suggests that constructed DNA therapy vector could prevent the invasiveness of ductal carcinoma metastatic cells carrying drug candidates.

Keywords: DNA therapy, Breast cancer, BRMS1

**P244 - 748: EFFECTS OF CENTRAL RECEPTOR OF H1 AND H2 ON THE AMOUNT OF
BROILER WATER AND FOOD USAGE**

Safoura Salahi¹, Saeed Shalbaf², Keyomarss Amini³

1. Young Researchers and Elites Club ,Saveh branch ,Islamic azad university ,Saveh ,iran
2. Young Researchers and Elite club, Central Tehran Branch, Islamic Azad University, Tehran, Iran
3. Asistans Professor of Microbiology at Islamic Azad University of Saveh

Background and Aim: This study is conducted to evaluate the effects of Determining the importance of nutrition mode, on the effect caused by histamine via intra-peritoneal injection histamine peripheral receptors in satiety and hunger on food and water of broilers.

Methods: 32 one-day-old broilers were raised to four-week-old in group and then in the 4th week as single. Data was variened in form of repeated measurments and averages were compared using LSMEANS test. Data analysis was perfomed using SAS software. Treatments included 40 mg/kg injectable chloramphenicol, 2.5 mg/kg famotidine, 1 mg/kg histamine, and saline. Total volume injected was 5.0 ml intraperitoneally.

Results: Results showed a significant difference between food intake of hungry broilers and broilers who had free access to food. Histame induced lower food intake in both satiety and hunger, but its effect was more significant in satiety. Chloramphenicol reduced food intake in both satiety and hunger. Famotidine induced lower food intake in first minutes, but had no effect in hunger. Water appetite was decreased by chloramphenicol but famotidine increased water appetite by inhibiting H2 receptor, both in satiety and hunger.

Conclusion: Generally, H1 and H2 receptors play role in food and water intake. Receptor antagonist H1 (chlorpheniramine), in both satiety and hunger modes causes significant decrease in feed intake, also receptor antagonist H2 (famotidine) at limited times significantly decreased feed intake in chickens with no limitation period, that this reduction in feed intake in satiety mode was more and total, chickens in satiety mode consume less feed than hungry chicks.

Keywords: Broiler chickens, famotidine, chlorpheniramine, histamine

**P245 - 751: STUDYING THE OUTBREAK OF ANTIBIOTIC RESISTANCE GENES OF
QUINOLONES IN ISOLATED BACTERIA OF URINARY TRACT INFECTION.**

Atousa Monavari¹, Atousa Monavari²

1. Atousa Monavari . PHD Fatemeh Norbakhsh . PHD Rozbeh yalfani
2. Atousa Monavari

Background and Aim: Urinary tract infection is one of the most common infections which if not treated, it can be cause serious problem in patients. One of the ways to treat of this f infection is antibiotic therapy. Nowadays antibiotic resistant in microorganisms is a main problem for physicians and patients in the world. The aim of this study is to evaluate the genetic resistance to quinolones antibiotics in Enterobacteriaceae isolated of urine samples.

Methods: Initially suspected sample of urinary infection were collected. After isolation, diagnostic tests performed for Enterobacteriaceae family, for evaluation of antibiotic susceptibility in bacteria. Antibigram test performed by quinolone antibiotics. Later DNA was extracted and PCR was performed by using specific primers.

Results: Hundred bacteria were isolated of clinical urine sample including 60 E.coli, 32 Klebsiella, 3 Enterobacter, and 5 Proteus. Bacterial antibiotic resistance to ciprofloxacin were 36%, nalidixic acid 45%, norfloxacin, ofloxacin 38%, levofloxacin 35% and enrofloxacin 39%. In overall antibiotic resistance were observed in 36 bacteria. Among these 33 bacteria were resistant to all antibiotic and 3 bacteria were susceptible to 1 or 2 antibiotics. This study revealed that E.coli isolates carry a mutation in gyrA, gyrB, parE genes. These mutations have an important role in antibiotic resistance in

Conclusion: Comparison between the antibiotic susceptibility test and PCR results for gyrA, gyrB, parC, parE genes are the same and Verification.

Keywords: antibiotics resistance, quinolone, gyrA, gyrB, parC, parE genes, Enterobacteraceae, PCR

P246 - 754: PREVALENCE OF UROPATHOGENS BACTERIA AND THEIR ANTIMICROBIAL SUSCEPTIBILITY PATTERNS ISOLATED FROM CHILDREN

Kiana Amiri¹, Kiana Amiri siavashani², Akbar Mirsalehian³

1. -
2. Department of Medical Microbiology, School of Medicine, Tehran University of Medical Science
3. Department of Medical Microbiology, School of Medicine, Tehran University of Medical Science

Background and Aim: Urinary tract infections (UTIs) are one of the most frequent bacterial infections in children. Prevalence of UTI agents and their antimicrobial susceptibilities patterns may vary among geographical locations. Therefore, The aim of this study was to investigate the prevalence and antimicrobial susceptibility patterns of uropathogens bacterial isolated from children.

Methods: During December 2015 to March 2016, 8202 urine samples obtained from children's medical center, which suspected to UTI. Then urine culture and standard biochemical tests performed. Also antimicrobial susceptibility testing carried out by disc diffusion method according to the CLSI guideline (2014) for trimethoprim-sulphamethoxazole, cefexime, ciprofloxacin, cephalexine, ampicillin, penicillin, amikacin, nitrofurantoin.

Results: Totally, 268 (3.2%) bacterial growth in culture media were seen. In this regard 167 (62%) strains were identified as *Escherichia coli*, 43 (16%) *Enterococcus faecalis*, 38 (14%) *Klebsiella pneumoniae*, 5 (2%) *Staphylococcus haemolyticus*, 3 (1%) *Staphylococcus epidermidis*, 4 (1.5%) *Proteus mirabilis*, 3 (1%) *Enterobacter aerogenes* and 2 (0.75%) *Enterobacter cloacae*. *E. coli* isolates showed high resistance to trimethoprim-sulphamethoxazole (72%), cephalexine (69.7%), ciprofloxacin (66.6%), cefotaxime (55.7%), cefexime (55.1%), high degree of resistance in *Klebsiella pneumoniae* to cefepime (70.8%), nitrofurantoin (61.1%) and cefotaxime (57.9%), in *Enterococcus faecalis* (85.4%) to penicillin and (59.5%) ampicillin and in *Staphylococcus haemolyticus* 100% to trimethoprim-sulphamethoxazole, cefotaxime and penicillin were observed.

Conclusion: High prevalence of drug-resistant urinary tract pathogens, particularly to commonly used antibiotics such as ampicillin and trimethoprim-sulphamethoxazole suggests that empirical antibiotic selection should be based on knowledge of the local prevalence of bacterial organisms and antibiotic sensitivities rather than on universal guidelines.

Keywords: UTI, Antimicrobial susceptibility pattern

**P247 - 764: A CASE OF HUMAN WRIST SYNOVIAL INFECTION CAUSED BY ACCIDENTAL
INJECTION OF ANIMAL VACCINE**

Mohsen Abad¹, Reza Ganji², Ebrahim Golmakani ³, Seyed AhmadHashemi⁴, Amir Azimian⁵

1. Department of Ortopedic, Anesthesia and Surgery, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
2. Department of Ortopedic, Anesthesia and Surgery, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
3. Department of Ortopedic, Anesthesia and Surgery, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
4. Department of Internal Medicine, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
5. Department of Pathobiology and Labratory Sciences, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.

Background and Aim:Brucellosis, a zoonotic disease caused by different species of Brucella. The attenuated strain B. abortus S19 has been the vaccine most widely used to prevent bovine brucellosis. Infection due to these vaccines is usually acquired from conjunctival splashes, skin cuts or, occasionally, infectious aerosols, and generally occurs in individuals involved in animal vaccination. Here we describe the case of wrist Synovial infection due to accidental self injection of Brucella vaccine.

Methods:A 35-year-old veterinarian during vaccination in cattle has accidentally injected about 0.1 ml of the vaccine suspension vaccine into the wrist. The past history of patient and the serological follow-up of animals contacted by the professional did not evidence other risk contacts. One month after accidentally self injection he consults physician because of wrist pain. He didn't have systemic symptoms of brucellosis.

Results:Microscopic examination of abscess discharge showed large number of gram negative bacilli and also large number neutrophils. PCR showed presence of Brucella Spp. in the sample. Serologic follow up after two months on blood samples was negative for brucellosis.

Conclusion:The most of cases of occupational brucellosis infected due to accidental injection, facial splashes or skin exposure. In our study blood culture was negative and vaccine strain couldn't produce systemic symptoms such as fever, sweat, ague and weight. Our patient didn't have history of brucellosis and post treatment serologic and microbiologic follow up didn't show signs of brucellosis. This could be due to different nature of live attenuated vaccine strain that was a weak strain.

Keywords:Brucella, S19, Vaccine, PCR

**P248 - 774: DISSEMINATION OF MULTIDRUG-RESISTANT ACINETOBACTER
BAUMANNII IN THE HOSPITAL ENVIRONMENT**

Nasrin Esmaeilee Torkanpoory¹, Fereshte Eftekhari²

1. Shahid Beheshti University
2. Shahid Beheshti University

Background and Aim: Multidrug-resistant (MDR) *Acinetobacter baumannii* is an important opportunistic pathogen which commonly targets critically ill patients in intensive care units (ICU) and is associated with hospital outbreaks. To prevent such outbreaks, it would be important to identify the presence of MDR *A. baumannii* strains in the hospital environment especially the ICU.

Methods: Sixty swab samples were taken from various parts of the ICU in a hospital in Tehran including patient's beds, oxygen tanks, and ventilator surfaces from June 2015 to April 2016. Nutrient agar plates were inoculated with the swabs and the resulting bacterial colonies were reported as *A. baumannii* using biochemical tests and PCR detection of the blaOXA-51 gene. Antibacterial susceptibility was determined by disc diffusion using 12 antibiotics from six different antibiotic classes.

Results: From the 60 samples, 24 isolates were identified as *A. baumannii* (40%). The disc diffusion results showed resistance rates of 100% for ceftazidime, cephepim, cephalothin, piperacillin-tazobactam, ampicillin-sulbactam, ciprofloxacin, levofloxacin, imipenem and meropenem followed by gentamicin (95%) and amikacin (90%). All isolates were susceptible to colistin.

Conclusion: Isolation of MDR *A. baumannii* from 40% of ICU samples is quite alarming. It shows that the prevalence of nosocomial ICU infections and outbreaks could be directly related to the presence of the organism in ICU environment which could then be transmitted by personnel and/or contaminated equipment.

Keywords: Multidrug-resistant (MDR), *Acinetobacter baumannii*, ICU environment

**P249 - 793: FATAL GASTROINTESTINAL AND SEPTICEMIC ANTHRAX AFTER EATING
THE CONTAMINATED GOAT MEAT, NORTH EASTERN IRAN, BOJNURD**

Sara Nojoomi¹, Seyed Ahmad Hashemi², Majid Ghafouri³, Saghar Safamanesh⁴, Amir Azimian⁵

1. Medical Diagnostic Laboratory, Emam Reza Hospital, North Khorasan University of Medical Sciences, Bojnurd, Iran.
2. Department of Internal Medicine, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
3. Department of Internal Medicine, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
4. Department of Pathobiology and Laboratory Sciences, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
5. Department of Pathobiology and Laboratory Sciences, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.

Background and Aim: *Bacillus* species are aerobic, or facultatively anaerobic, gram-positive or gram-variable spore-forming rods. They are ubiquitous in the environmental sources. *Bacillus anthracis* may usually cause three forms of anthrax: inhalation, gastrointestinal and cutaneous. The gastrointestinal (GI) anthrax develops after eating contaminated meat. Thus, in this paper were report 5 cases of intestinal anthrax.

Methods: We report an isolation of *Bacillus anthracis* from blood culture of patient with intestinal anthrax. *Bacillus anthracis* was isolated from a blood culture of a 34-year-old man who had a history of severe abdominal pain, bloody diarrhea, nausea, vomiting, Fever, sweating and lethargy within 4 to 5 days after eating the meat of domestic goat.

Results: He has evidence of severe infection and septic shock and did not response to treatments and expired 9 hours after hospitalization.

Conclusion: Gastrointestinal anthrax is characterized by rapid onset, fever and septicemia. Rapid diagnosis and prompt initiation of antibiotic therapy can help to survival. Most of previous cases of septicemic anthrax were related to injectional drug users but in our case, septicemia occurred after gastrointestinal anthrax.

Keywords: *Bacillus anthracis*, septicemia, Gastrointestinal

**P250 - 803: THE CAUSES OF BACTERIAL AND ANTIMICROBIAL RESISTANCE OF
URINARY TRACT INFECTION IN CHILDREN REFERRED TO CHILDREN'S HOSPITAL OF
TABRIZ**

Changiz Ahmadizadeh¹, Mojtaba Babaei Daylari², Rozita Tamjidifar³, Sahar Ghandehari⁴

1. Assistant Professor, Department of Microbiology, Islamic Azad University of Ahar
2. Master of Science Microbiology
3. Master of Science Microbiology
4. Master of Science Microbiology

Background and Aim: The urinary tract infection is the most common urogenital disease is the second most common infection in children three to five percent of boys in childhood are affected. On time treatment with antibiotics is an important step in healing and preventing long-term complications such as kidney scarring, uremia and hypertension. Despite repeated recommendations of the World Health Organization, pattern and extent of antibiotic use different parts of the world are not the same mother and for this reason differences in the degree of resistance of microorganisms in different.: The aim of this study was to determine the prevalence of bacteriological agents such as *Escherichia coli* and also determined the sensitivity and their antibiotic resistance in children referred to Children's Hospital laboratory Tabriz.

Methods: The study included 100 children under 12 years old was conducted urinary tract infection. Urine sample midstream urine sample, and in newborns and infants under one year in urine bags were collected

Results: The most sensitive to the antibiotic amikacin, ciprofloxacin, gentamicin, ceftizoxime, nitrofurantoin and the highest resistance to the antibiotic amoxicillin, the more you look Prem, sulfamethoxazole, cephalexin and nalidixic acid

Conclusion: The study showed that *E. coli* (7.62%) is the most common cause of urinary tract infections all age groups. after that *Klebsiella pneumoniae* (12.7%) and *Enterococcus* (8.8%) and other microorganisms (15.8%), respectively.

Keywords: urinary tract infection, bacteriological agents, *Escherichia coli*, *Klebsiella pneumoniae*, *Enterococcus*

**P251 - 812: ANTIMICROBIAL EFFECTS OF PLANT EXTRACTS ON TEUCRIUM POLIUM
RESISTANT STRAIN OF KLEBSIELLA PNEUMONIA**

Roqieh Gholizadeh¹, Roghayeh Gholizadeh doran mahalleh², Babak Kheirhah³, javad Dahmardeh⁴, Hadi Hosseini⁵

1. -
2. Faculty member, Department of Laboratory Sciences, Faculty of Medicine, Islamic Azad University Zahedan,, Zahedan, Iran.
3. Assistant Professor, Faculty, Islamic Azad University Kerman, Department of Microbiology, Kerman, Iran.
4. graduate student of Microbiology, Islamic Azad University, Kerman, Department of Microbiology, Faculty of Sciences, Kerman, Iran.
5. PhD student of Microbiology, Islamic Azad University, Kerman, Department of Microbiology, Faculty of Sciences, Kerman, Iran.

Background and Aim:lactamase enzyme is one of the most important factors in creating antibiotic resistance among Gram-negative bacteria are. Klebsiella pneumoniae is an opportunistic pathogen of the Enterobacteriaceae family in nosocomial infections such as pneumonia, sepsis, urinary tract infections and intra-abdominal infections in hospitalized patients as well as patients with underlying disease plays a major role. The aim of medicinal plant extracts antimicrobial activity of Teucrium Polium in traditional medicine is used as a lifter infections on antibiotic-resistant strains of the bacterium Klebsiella pneumoniae genes were studied.

Methods:extracts from the leaves and stems of plants through extraction and production methods were blue. The minimum inhibitory concentration (MIC) of the extracts showed Klebsiella pneumoniae resistant strains.

Results:The morphology of the bacteria were exposed to extracts showed that the strain of Klebsiella pneumoniae bacteria are exposed to smaller Teucrium Polium extract (collect more) and also destroyed the bacteria capsules. The synergistic effect of medicines and tinctures and extracts Teucrium Polium simultaneously compared with medication alone reduces a lot of changes in MIC and drug-resistant super-bacteria develop antibiotic cefotaxime MIC not just about ?g / ml64 declined.

Conclusion:From the above studies it can be concluded that the medicinal plant extracts Teucrium Polium had no effect Anti plasma.

Keywords:Teucrium extract, Klebsiella pneumoniae, drug resistance.

**P252 - 813: THE FREQUENCY OF BLA VIM GENES IN CLINICAL ISOLATES OF
PSEUDOMONAS AERUGINOSA AND BLO IMP CENTERS IN ZAHEDAN**

Roqieh Gholizadeh¹, Roghayeh Gholizadeh doran mahalleh², Farokh Rokhbakhsh zamein³, javad
Dahmardeh⁴, Hadi Hosseini⁵

1. -
2. Faculty member, Department of Laboratory Sciences, Faculty of Medicine, Islamic Azad University Zahedan,, Zahedan, Iran.
3. Assistant Professor, Faculty, Islamic Azad University Kerman, Department of Microbiology, Kerman, Iran.
4. Masters student of Microbiology, Islamic Azad University, Kerman, Department of Microbiology, Faculty of Sciences, Kerman, Iran.
5. PhD student of Microbiology, Islamic Azad University, Kerman, Department of Microbiology, Faculty of Sciences, Kerman, Iran.

Background and Aim: Pseudomonas bacteria Frsa as demand among Gram-negative bacteria are of particular importance. Class B beta-lactamases such as IMP and VIM cause of resistance in bacteria including Pseudomonas aeruginosa are considered hot. This activity due to ESBL enzymes (ESBLs) and high resistance to beta-lactamase antibiotics IMP and VIM isolates of Pseudomonas aeruginosa from burn wounds in the city of Zahedan.

Methods: In this cross - sectional study, 125 Pseudomonas aeruginosa burn wound samples collected from patients admitted to hospitals in Zahedan were cultured. Suspected colonies of P. aeruginosa were identified with biochemical methods. To assess the antibiotic susceptibility of the Kirby-Bauer method was used, the MIC of these strains were investigated. IMP and VIM lactamase gene genotype of these strains were analyzed by PCR.

Results: In this study, a total of 125 Pseudomonas aeruginosa, in 32 isolates (40%) were ESBLs producing. Determines how imipenem resistance in Pseudomonas aeruginosa to antibiotics, TETRACYCLINE, CEFOTAXIME, CEFTAZIDIME, Ceftriaxone, Levofloxacin, Ciprofloxacin , gentamicin, Carbenicillin and Streptomycin, respectively M percent, 93 percent, 98 percent, 89 percent, 97 percent, 89 percent, 81 percent, 78 percent, 96 percent, 91 percent. According to the PCR test among 32 strains of ESBLs enzymes, respectively, 75/45, 17/28 IMP and VIM was lactamase gene.

Conclusion: The prevalence of ESBLs enzymes and antibiotic resistance in hospitals in Zahedan high. The results show that most cases are drug-resistant strains producing ESBLs among many more of IMP VIM genes were found.

Keywords: clinical isolates of Pseudomonas aeruginosa, antibiotic resistance genes VIM, gene IMP.

**P253 - 815: DIAGNOSIS OF PULMONARY AND EXTRAPULMONARY TUBERCULOSIS
WITH THE XPERT MTB/RIF ASSAY AND COMPARING ACCURACY WITH THE
STANDARD CONVENTIONAL METHODS**

Afsaneh Khoshkhoo¹, Mohammad Reza Allahyar Torkaman², Dr. Gholam Reza Hamzehloo³, Sirius
Amini⁴

1. Tehran Regional Reference of Tuberculosis, Health Deputy, Tehran University of Medical Sciences
2. Tehran Regional Reference of Tuberculosis, Health Deputy, Tehran University of Medical Sciences
3. Tehran Regional Reference of Tuberculosis, Health Deputy, Tehran University of Medical Sciences
4. Tehran Regional Reference of Tuberculosis, Health Deputy, Tehran University of Medical Sciences

Background and Aim: Xpert MTB/RIF test as an advance fully automatic diagnostic method has a great advantage over conventional TB culture and direct smear in terms of time and simultaneous detection of TB and rifampicin drug resistance. Different former studies report proper sensitivity and specificity for pulmonary tuberculosis specimens with this test. However, accuracy of Xpert MTB/RIF for extrapulmonary tuberculosis (EPTB) specimens is still controversial owing to varied kinds of extrapulmonary specimens. In this study, Xpert MTB/RIF test perform for pulmonary and extrapulmonary tuberculosis suspected specimens and the result compare with the combinational CRS standard (composite reference standard) which are TB culture and direct microscopic smear to determine the sensitivity and the specificity of the test.

Methods: Xpert MTB/RIF and conventional culture and smear were conducted on 473 pulmonary and 460 extrapulmonary TB suspected specimens. The specimens were referred to the Tehran Regional Reference Laboratory of Tuberculosis from December 2014 to June 2016.

Results: Comparison of Xpert MTB/RIF and conventional methods as standard for pulmonary specimens revealed 91.1%, 98.1%, 83.6% and 99.07% of sensitivity, specificity, Positive predictive value (PPV) and negative predictive value (NPV) respectively. While result for extrapulmonary specimens were 68.1%, 95.2%, 41.7% and 98.3% of sensitivity, specificity, PPV and NPV respectively.

Conclusion: The sensitivity and specificity of Xpert MTB/RIF for pulmonary specimens has proven reliable detection of tuberculosis for pulmonary cases. Moreover, PPV and NPV for Pulmonary TB showed accurate detection of tuberculosis. However, less PPV especially for extrapulmonary samples suggest further study and redesign of Xpert MTB/RIF for detection of extrapulmonary specimens.

Keywords: Tuberculosis, Xpert MTB-RIF, Pulmonary, extrapalmunary, Culture, Sencitivity.

P254 - 841: EFFECT OF SUB-INHIBITORY VANCOMYCIN AND LINEZOLID ON CLFA AND CLFB GENES EXPRESSION AND ADHESION OF METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS

Fatemeh Asadi¹, Mohsen Mirzaee², ShahinNajarPeerayeh³

1. Dept. of Laboratory Sciences, Borujerd Branch, Islamic Azad University, Borujerd, Iran.
2. Dept. of Laboratory Sciences, Borujerd Branch, Islamic Azad University, Borujerd, Iran.
3. Dept. of Bacteriology, Faculty of Medical Sciences, TarbiatModares University, Tehran, Iran.

Background and Aim: Staphylococcus aureus is an important human pathogen that cause many infection like endocarditis. It expresses a variety of virulence factors like ClfA and ClfB. The aim of this study is investigation of effect of sub-minimum inhibitory concentrations (sub-MICs) of vancomycin and linezolid on clfA/B genes expression.

Methods: In total 87 clinical isolates were collected, to determined amounts of MIC by broth microdilution. The polymerase chain reaction (PCR) was employed to detect clfA and clfB. 3 isolates of them selected and exposure to sub-MIC of vancomycin and linezolid and observed the effect of both antibiotics on clfA/B genes expression using real time PCR method. Finally, biofilm assay performed to determine S. aureus attachment to fibrinogen.

Results: Of the 78 isolates relative to linezolid, 96.5% is resistant. 98.8% of isolates is susceptible to vancomycin and 1.2% is intermediate. Of the 3 isolates which selected, all of them showed decrease in clfA/B genes expression when treated by sub-MIC of vancomycin although, in linezolid-treated isolates, clfA gene expression in two isolates increased and clfB gene expression decreased. Biofilm formation in vancomycin treated and linezolid treated isolates decreased and increased respectively.

Conclusion: It has been demonstrated that treatment for bacterial infection should depend on their bactericidal and bacteriostatic features and pharmacokinetics and their effect on bacterial virulence. Our finding demonstrate that linezolid and vancomycin effect on gene expression and biofilm formation. Then, more investigation require to find the best way for infection treatment and inhibition of represent resistance in bacteria or induction biofilm formation.

Keywords: sub-MIC, microdilution, linezolid-treated

**P255 - 849: EVALUTION OF ANTILEISHMANIAL ACTIVITY OF THE ESSENTIAL OIL OF
MEDICAGO LUPULINA' LEAVES AGAINST LEISHMANIA MAJOR (MHOM/IR/75/ER)
PROMASTIGOTES BY USING MTT ASSAY**

Elham Gharirvand eskandari¹, monir doudi²

1. Ms student, Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran.
2. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran

Background and Aim: Leishmaniasis induced by protozoa of the genus *Leishmania* can be evaluated as a zoonotic disease. This disease created significant global health problems with high endemicity in developing countries including Iran. The prevalence of leishmaniasis has increment in the absence of a vaccine. Different medicines are exploited for treatment of Leishmaniasis but their side effects and drug resistance cause to seek new effective compounds. Traditional plants such as *Medicago lupulina* is a valuable source of new medicinal factor.

Methods: *Leishmania major* promastigotes were cultured at $25 \pm 2^{\circ}\text{C}$ in stationary phase in RPMI- 1640 medium complemented with 10% fetal calf serum and antibiotic Penicillin- Streptomycin. Then by using MTT assay, the biological activity of plant essence in analogy to glucantime on *L. major* promastigotes was evaluated. The optical density due to breaking of the tetrazolium salt MTT [3-(4, 5-dimethylthiazol-2-yl)-2, 5-diphenyl tetrazolium bromide] into a colored product formazan by the parasite was measured using ELISA reader and IC50 values were evaluated. All tests were repeated in Triplicate.

Results: IC50 of glucantime for *L. major* (MHOM/IR/75/ER) promastigotes was 27, 12 and 8 $\mu\text{gr/mL}$ and IC50 values for essence of *Medicago lupulina* against *L. major* (MHOM/IR/75/ER) was 720, 250 and 110 $\mu\text{gr/mL}$.

Conclusion: As regards, plant essence had anti- leishmanial effects in vitro, further works are required to appraise the essence effect on *Leishmania* agent in animal models.

Keywords: Leishmaniasis, , *Medicago lupulina*, MTT formazan.

P256 - 876: DETERMINATION OF CORRELATION BETWEEN BIOFILM AND EXTENDED SPECTRUM B LACTAMASES PRODUCERS OF URINARY ESCHERICHIA

Ailin Ahmadi¹, Teena Dadgar², Ania Ahani Azari³

1. MSc of Microbiology, Department of biology, Golestan Science and Research Branch, Islamic Azad University, Gorgan, Iran
2. Assistant professor of Microbiology ,Department of biology, Golestan Science and Research Branch, Islamic Azad University, Gorgan, Iran Teena Dadgar, Assistant professor of Microbiology ,Department of biology, Golestan Science and Research Branch, Islamic Azad University, Gorgan, Iran
3. Assistant professor of Microbiology ,Department of biology, Golestan Science and Research Branch, Islamic Azad University, Gorgan, Iran

Background and Aim:The aim of this study was to evaluate the differences biofilm-forming capabilities of ESBL and Non ESBL urinary Escherichia isolates

Methods:: This study was conducted on 100 isolated E.coli from urinary tract infection of out patients referring to medical laboratories in Gorgan,. The resistance to Cefotaxim (Rosco. Co.) was assessed by Kirby-Bauer disk diffusion method. The confirmatory test for detection of resistant isolates was carried out by double disk method at the presence of Cefotaxim and clavulanic acid. All the isolates were subjected for biofilm production by microtiter plate using BHI medium containing 1% sucrose

Results:of 100, 68 isolates are resistant to Cefotaxim. 85.5% of them are confirmed as ESBL producing E.coli. Biofilm production was detected in 67% of the isolates Of total 58(58%) ESBL producing uropathogenic strains of E. coli, 9 were strong biofilm producers, 4were moderate biofilm producers, 30 were weak biofilm producers and 15 were biofilm non producers. Whereas among 42(42%) ESBL non producing E. coli 5 were moderate biofilm producers, 19 were weak biofilm producers and 18 were biofilm non producers.

Conclusion:58% of E. coli isolated from urinary tract infections in Gorgan are ESBL producing. The results of our study and others emphasize that The ability of biofilm formation was found to be no significant difference in ESBL producing strains of E. coli than ESBL non producing strains .

Keywords:Escherichia coli , Extended spectrum beta lactamase, Biofilm

P257 - 878: ENTEROCOCCUS FAECALIS INFECTION AND BURN WOUND INFECTION

Mohammad Khodadad Motlagh¹, اعظم حیدر پور²

1. Shiraz university, shiraz
2. مربی میکروب شناسی، دانشکده پیراپزشکی، دانشگاه علوم پزشکی قم، قم، ایران

Background and Aim:: Burn wound are the switable environment to growing the kind of infection opportunist microorganisms. Awareness of effective microorganisms in appearing the infection and their Antibiotic Sensitivity has a fundamental role in preventing and timely and correct treatment of infection. In this study, effective bacterial factors in post burning infections and their antibiotic resistance determined in burn section of Nekuei Hospital of Qom.

Methods: In this study, the sampling carried out from 70 hospitalized patients in burn section of Nekuei hospital at 5 mounth course. After sampling and bacterial isolation, the biochemical tests performed to detect the microorganisms based on being standards. Determining the antibiotic resistance model carried out by using the Disk diffusion or Kirby Bauer method included the antibiotics of Co-Trimoxazole, Vancomycin, Ciprofloxacin, Cephalothin, Ceftazidime, Amoxycillin, Amikacin, Gentamycin, Chloramphenicol, Cefazolin, Cefotaxime, Ceftriaxone, Ampicillin, Oxacillin, Imipenem.

Results: Totally, of 70 samples have taken from hospitalized patient in burn section, 54 sample (%77.14) of wound had positive culture. Enterococcus fecalis with %9.52 that causing the hospital infrcction. Resistance of Enterococcus fecalis in this study: Oxacillin %60, Cefazolin %50, Amikacin & Cephalothin & Ceftazidime & Imipenem %40, Ampicillin, Amoxycillin, Gentamycin, Vancomycin, Ciprofloxacin, Cefotaxime, Ceftriaxone & Chloramphenicol %30, Co-Trimoxazole %20.

Conclusion: The result of this study are indicating that with regard to high prevalence of hospital infections in burn section, using the new methods is inevitable affair to preventing and transferring the infections factors and also using the infective antibiotic such as Amikacin and Gentamycin in treatment.

Keywords: Infection; Enterococcus fecalis; Burning Wound; Bacteria; Antibioti Resistance

P258 - 886: DETECTION OF ARMA,TET(39),AND THE INSERTION SEQUENCE ISABA4 GENES AMONG ACINETOBACTER BAUMANNII CLINICAL STRAINS ISOLATED FROM THE UNIVERSITY HOSPITAL IN TEHRAN BY PCR AND SEQUENCING TECHNIQUES.

Parvaneh Khiabani rad¹, Gita Eslami², Ali Hashemi³, Fatemeh Fallah⁴

1. International Branch of Shahid Beheshti University of Medical Sciences, Tehran, Iran
2. Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. Shahid Beheshti University of Medical Sciences, Tehran, Iran
4. Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: *Acinetobacter baumannii* has been involved in a wide range of hospital-acquired infections because of its high ability to develop antibiotic resistance, including resistance to β -lactams, aminoglycosides, and tetracyclines. The aims of this study were to determine the antimicrobial susceptibility pattern and prevalence of *armA*, *tet(39)*, and the insertion sequence *ISAbA4* genes in *A. baumannii* strains obtained from Iranian burn patients of Shahid Motahari hospital.

Methods: In total, ninety-two *Acinetobacter baumannii* clinical isolates from burn wound infections were collected from Motahari hospital in Tehran. The phenotypic identification of all isolates was performed by conventional microbiological tests. The confirmation of species identification was done by detecting of presence of the *blaOXA-51* gene. Antibiotics susceptibility tests were performed by disk diffusion according to CLSI guidelines. The isolates were studied for the genetic basis of resistance to antibiotics. The distribution and prevalence of *armA*, *tet(39)*, and the insertion sequence *ISAbA4* genes were investigated by PCR, and Sequencing methods.

Results: Out of 92 *A. baumannii*, 95.6% ,89.2% ,97.9% ,and 81.5% were resistant to Gentamicin, Amikacin, Imipenem, and Tetracycline respectively. All isolates were also resistant to Meropenem. PCR results for *armA* gene was detected in 63% of isolates. All strains carried *tet(39)* gene, while *ISAbA4* was only detected in only 3.2% of isolates.

Conclusion: This study detected clinical *A. baumannii* isolates harboring antibiotic resistance genes. This is the first study on the distribution of *tet(39)* among *A. baumannii* in IRAN. Therefore, the identification of drug resistance patterns in *A. baumannii* and investigation of molecular epidemiology are also critical to control the rapid spread of antimicrobial-resistant strains.

Keywords: *Acinetobacter baumannii*, antimicrobial susceptibility, resistance genes

P259 - 889: THE PREVALENCE OF HELICOBACTER PYLORI GENOTYPES ACCORDING TO CAGA, CAGM AND CAGE GENES IN IRANIAN PATIENTS WITH GASTRIC ADENOCARCINOMA

Ali Bahadori¹, Mahsa Esmaeillou², Mohammad Hossein Somi³, Suna Kızılyıldırım⁴, Basak Bedir⁵, Melda Meral⁶, Fatih Koksall⁷

1. Medical microbiology Department, Faculty of Medicine, Cukurova University, Adana, Turkey
2. Department of Biology, Faculty of Natural Sciences, University of Tabriz, Tabriz-Iran
3. Liver and Gastrointestinal Disease Research Center, Tabriz University of Medical Sciences, Tabriz, Iran
4. Medical microbiology Department, Faculty of Medicine, Cukurova University, Adana, Turkey1
5. Medical microbiology Department, Faculty of Medicine, Cukurova University, Adana, Turkey1
6. Medical microbiology Department, Faculty of Medicine, Cukurova University, Adana, Turkey1
7. Medical microbiology Department, Faculty of Medicine, Cukurova University, Adana, Turkey1

Background and Aim: Helicobacter pylori (H. pylori) is a gram negative pathogen that colonizes majority of the world's population. The pathogenicity of H. pylori is related to cag Pathogenicity Island (cag PAI) and has been associated with clinical outcome after H. pylori infection. The aim of this study was investigation of association between gene diversity of H. pylori cag PAI and clinical outcome in Iranian patient with gastric Adenocarcinoma.

Methods: Formalin Fixed Paraffin Embedded tissues (FFPE) obtained from 80 patients with gastric Adenocarcinoma in their pathology report from pathology archive of Imam Reza Hospital. H. pylori infection was confirmed by histology and PCR examination with using glmM gene primers. The prevalence of the cagA, cagE and cagM genes was studied in positive samples by using the polymerase chain reaction (PCR) method and specific primers.

Results: In this study presence of cagA, cagE and cagM genes were confirmed at 58.8%, 52.94% and 5.88% of patients with gastric adenocarcinoma respectively.

Conclusion: Our work suggests that although H. pylori infection is significantly associated with gastric adenocarcinoma and chronic gastritis, the cagA is the dominant virulence in development of gastric adenocarcinoma. Although, we found that cagE, but not only cagA, could be used as a marker for the presence of cag PAI in Iranian patients and also for determination of the role of various parts of cagPAI in clinical outcome of disease.

Keywords: Helicobacter pylori, gastric cancer, cagA, cagE, cagM

**P260 - 894: IDENTIFICATION OF ACNE RESONATOR BACTERIAL FACTORS AND CHECK
THE ANTIBIOTIC RESISTANCE OF ISOLATED STRAINS**

Iman Dehghani champiri¹, zahra bamzade², hosin hjazi³

1. Department of microbiology, Faculty of Basic Sciences , Shahrekord Branch, Islamic Azad University, Sahrekord, Iran.
2. microbiology, Shahrekord Branch, Islamic Azad University, Sahrekord, Iran.
3. Parasitology, Esfahan University,Iran.

Background and Aim: Vulgaris Acne is a common disease in adulthood. Accurate diagnosis of acne and effective use of medicines can have an important role in the treatment of acne. This laboratory study was conducted both to identify the aggravating factors of bacterial acne and to survey the antibiotic resistance of isolated strains.

Methods: In this study, the visiting patients of vulgaris acne to T. S. Skin Research Center of Isfahan and Isfahan dermatology clinic were studied. The researched group included one hundred patients. Using anas, Acne lesions were obtained from patient and then cultured in the laboratory, and then the grown bacteria were identified and studied. The early identification was achieved using colony morphology and Gram stain techniques. The final diagnosis of bacteria was achieved later using a biochemical test, such as catalase, indole, coagulase, and growth in aerobic and anaerobic conditions, and also PCR test. In addition, the resistance of sample bacteria against the common antibiotics for the treatment of acne was evaluated.

Results: Effective bacteria detected in Acne include: "Propionibacterium acnes, Staphylococcus epidermidis, and Staphylococcus aureus." The rate of antibiotic resistance as follows: "52% Streptomycin, 46% azithromycin, Erythromycin 41%, Doxycycline Saklyn 39%, Clindamycin 36%, Tetracycline 29%, Vancomycin 6%.

Conclusion: The main aggravating factor of the acne is the normal skin flora bacteria, Namely Staphylococcus epidermidis, Propionibacterium acnes, Staphylococcus aureus, which the disruption of this balance can cause excessive proliferation of the skin microflora, which lead to inflammation of the acne area; also the antibiotic-resistant of aggravating acne bacteria has gone very high.

Keywords: Acne vulgaris, Propionibacterium acnes, Staphylococcus epidermidis, Staphylococcus aureus, antibiotic resistance.

**P261 - 896: EVALUATION OF INVA AND TTRC GENES IN CLINICAL SALMONELLA
TYPHIMURIUM STRAINS BY MULTIPLEX-PCR METHOD AND DETERMINATION OF
THEIR ANTIBIOTIC RESISTANCE PROFILE**

Sareh Amiri¹, Gholamaliye Moradli²

1. Department of Microbiology, Faculty of Basic Sciences, Saveh Branch ,Islamic Azad University, Saveh, IR Iran.
2. Department of Microbiology, Assistant Professor, Medical faculty member, Saveh Branch ,Islamic Azad University, Saveh, IR Iran.

Background and Aim:: Gastroenteritis caused by salmonella is common in humans as a public health problem in the world. The aim of the current study was, detection of *invA* and *ttrC* genes in the *Salmonella* Typhimurium strains isolated from stool samples using multiplex- PCR method and determination of their antibiotic resistance patterns.

Methods:In this cross-sectional study, a total of 200 stool samples were collected from the patients admitted to the children medical center at Tehran in a period of 7 months. Antibiotic susceptibility test was performed by the disk diffusion method based on CLSI godliness. Therefore, multiplex-PCR was performed by oligonucleotide specific primers for identification of these genes.

Results:Out of all samples, 60 *Salmonella* Typhimurium isolates were obtained. The results of the disk diffusion method showed that the highest resistance rate to the Nitrofurantoin and Nalidixic acid were 85% and 70%, respectively. So, all isolates were sensitive to the Ciprofloxacin. Molecular analysis of genes under study revealed that the 48 (80%) isolates carries *ttrC* gene and 14 (23.3%) were have *invA* gene.

Conclusion:Today, increased resistance to antibiotics is a global problem that occurs due to indiscriminate use of drug. So, imipenem and ciprofloxacin can be used as a valuable drug for the treatment of infections caused by this bacterium.

Keywords:*Salmonella* Typhimurium, *invA* and *ttrC* genes, antibiotic resistance.

P262 - 922: BACTERIOLOGY OF URINARY TRACT INFECTION AND ANTIMICROBIAL SENSITIVITY AMONG DIABETIC PATIENTS AT SARI, IRAN

Fatemeh Hejazi¹, Mohammad Ahanjan², Maryam Salehian³

1. Mazandaran university of medical sciences; Microbiology department
2. Mazandaran university of medical sciences; Microbiology department
3. Mazandaran university of medical sciences; Microbiology department

Background and Aim: Urinary tract infection (UTI) is the most common infection among diabetic patients particularly unrecognized or untreated. Due to the emergence of multidrug resistant (MDR) uropathogenic strains, the choice of antimicrobial agent is restricted. This study investigated the bacterial agents of UTI, antimicrobial susceptibility, and resistance patterns of bacterial isolates from adult diabetic patients

Methods: In this cross-sectional study 302 midstream urine samples were collected and after counting WBC, cultured on MacConkey agar and blood agar for UTI diagnosis ($\geq 10^5$ colony forming units [CFU]/mL of a single bacterial species was defined as positive). Then antibiotic susceptibility was tested by Kirby-Bauer method on isolated bacteria.

Results: Of the total 302 patients, 68 positive samples were obtained which included 52 females (76.4%) and 16 male (32.6%). The most commonly isolated bacteria was Streptococcus Group B with a frequency rate of (33.3%) followed by E. coli (17.6%), Staphylococcus aureus (16%), Streptococcus viridans (8.8%), Klebsiella spp. (8.8%), Staphylococcus saprophyticus (4.4%), Diptheroid (4.4%), Pseudomonas aeruginosa (3%), Enterococcus (1.4%), Acinetobacter baumannii (1.4%), Edwardsiella tarda (1.4%) and 5 non-routine gram negative bacteria (7.3%). The conducted antibiogram on these isolates which was done by approximately 21 various antibiotics based on the type of them, shows that the most appropriate antibiotic for treatment of UTI in these patients is chloramphenicol, after that piperacillin-tazobactam and gentamycin have most effects on isolates.

Conclusion: The result indicates that the third generation of cephalosporins which are usually used for the treatment of this infection, isn't the best choice and it's better to use chloramphenicol for the most effective treatment and to perform U/C and doing antibiogram for them routinely.

Keywords: UTI ; diabetes; antibiotic resistant

P263 - 924: EVALUATION OF ANTI-BACTERIAL EFFECTS OF COLLOIDAL SILVER NANOPARTICLES ON BIOFILM PRODUCTION OF HOSPITAL ASSOCIATED METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS WITH MULTIDRUG RESISTANT

Maryam Ghahremany¹, Yaeghob Sharifi², Nima Hosseini Jazani³, Homayoun babazadeh⁴

1. M.Sc. student of medical Microbiology, Student's research committee, Urmia University of Medical Sciences, Urmia, Iran
2. Assistant Professor of Bacteriology, Department of Microbiology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran
3. Professor of Microbiology, Department of Microbiology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran
4. Urmia University of Medical Sciences, Faculty of medicine, Department of Microbiology

Background and Aim: Staphylococcus aureus produces extracellular polysaccharides that result in biofilm formation and cause the adherence of the bacteria to different surfaces. The antimicrobial effects of Silver nanoparticles on different types of organisms have been shown. The aim of this study was to investigate the inhibitory effects of Silver nanoparticles on biofilm formation by MDR HA-MRSA isolates.

Methods: A total of 150 S. aureus isolates were obtained from different clinical specimens at university teaching hospitals in Urmia, during the period from June 2014 to June 2015, and were identified by standard microbiological methods. The sensitivity of isolates to Methicillin and other commonly used antibiotics was investigated by agar disk diffusion method. Methicillin resistance was confirmed by PCR. Microtiter dish biofilm formation assay method in 3 concentrations (1, 0.5 and 0.25 mg/ml) was used to determine the amounts of biofilm formation in the presence/absence of Silver nanoparticles.

Results: Of 150 isolates, which were identified as S. aureus, 15 MRSA isolates with resistance to at least 5 beta-lactam antibiotics and biofilm producers were selected for the study. The inhibitory effect of Silver particles on biofilm formation by MDR-MRSA isolates was significant. (con 1, $P=0.000$), (con 0.5, $P=0.000$), (con 0.25, $P=0.001$)

Conclusion: Considering the inhibitory effects of Silver nanoparticles on biofilm formation of HA-MRSA isolates and the safety of Silver usage in dental materials, it may be useful for prevention of biofilm formation by MRSA isolates.

Keywords: Staphylococcus aureus, HA-MRSA, MDR, biofilm, Silver nanoparticles

P264 - 932: EVALUATION OF ANITIBIOTICAL RESISTANCE PATTERN IN ESCHERICHIA COLI ISOLATED FROM URINARY TRACT CAUSING INFECTION REFERRED TO CURE CENTERS OF LAHIJAN CITY

Mehdi Simaei¹, Roghayeh Dadras²

1. Department of Microbiology, Faculty of science, Islamic Azad University, Lahijan Branch, Lahijan, Iran
2. Central Laboratory, Health Center of Lahijan, Lahijan, Iran

Background and Aim: One of the most common reasons for recourse people to health centers is urinary tract infection. Also, it is the most common reasons of hospital infections that has a different antibiotic resistance pattern in different regions. The aim of the present study is a local outbreak of urinary tract infection and determination of *E. coli* sensitivity and antimicrobial resistance pattern in people who referred health centers of Lahijan.

Methods: In this descriptive and analytic study that was done during the 5 months (from October to February) 110 bacterial infection, including *Klebsiella*, *Proteus*, *Pseudomonas*, *Staphylococcus Epidermidis*, *Enterococcus* and... were identified out of 3531 samples that 82 cases were related to *E. coli*. Differential diagnosis tests used for urine samples and then antibiotic susceptibility test was carried out using clinical and laboratory standards institute. Data were analyzed using SPSS software.

Results: Results of antibiogram test showed that the most resistance were related to ampicillin with 80%, amoxicillin with 79.26% and nalidixic with 75.73% and less resistance was related to Nitrofurantoin with 1.2%. The most sensitivity was related to nitrofurantoin, cefotaxime and imipenem with 91.46, 54.9 and 51.22 % respectively, and the less sensitivity was related to ampicillin with 10.97%.

Conclusion: The most resistance and sensitivity to antibiotics were observed in ampicillin and nitrofurantoin respectively, and experimental treatment using ampicillin dose not appropriate for most of the patients suffer from urinary infection.

Keywords: Antibiotic, *E. coli*, Resistance pattern, Urinary tract infection

**P265 - 937: COMPARISON OF RT-PCR AND NESTED-PCR ASSAYS AND VIRUS ISOLATION
FOR DETECTION OF INFECTIOUS BRONCHITIS VIRUS IN BROILER FLOCKS WITH
RESPIRATORY TRACT SYNDROME**

Aidin Azizpour¹, Yashar azizpour²

1. Meshginshahr Faculty of Agriculture, University of mohaghegh Ardabili, Ardabil, Iran
2. Tehran University of Medical Sciences, Tehran, Iran.

Background and Aim: Infectious bronchitis virus (IBV) is a highly contagious acute viral disease affecting respiratory tract and causing economic losses in poultry industry throughout the world. The definitive and rapid diagnosis of IBV virus is important for controlling of this viral disease. The purpose of this study was to identify the infectious bronchitis virus by RT-PCR and Nested-PCR assays in comparison with conventional method of virus isolation.

Methods: 14 broiler chicken flocks with respiratory tract syndrome and suspected to IBV were selected during 2013-2014. In this study, tracheal and lung samples from selected flocks were investigated for the detection of IBV using virus isolation technique and RT-PCR and Nested-PCR assays. RNA was extracted from all samples according to the manufacturer's instruction. The RT-PCR was carried out using universal primers (XCE2- and XCE1+). The RT-PCR product was amplified by Nested-PCR with specific primers of serotype 793/B (XCE3- and BCE1+). 10 day- old SPF embryonated eggs was used for virus isolation.

Results: A fragment of 464-bp and 154-bp were observed in by RT-PCR and Nested-PCR assays, respectively. From flocks tested (n= 14), 10 flocks (71.1%) were positive in RT-PCR technique. From 10 RT-PCR positive flocks, 6 flocks (60 %) were positive in Nested-PCR assay for serotype 793/B IBV and 9 flocks (90 %) were positive in virus isolation method.

Conclusion: The Results of this study showed that molecular techniques such as RT-PCR and Nested-PCR are rapid, reliable, and sensitive methods for detection of IBV.

Keywords: Infectious Bronchitis Virus, RT-PCR, Nested-PCR, broiler flocks

P266 - 943: GENOTOXIC EFFECTS OF OUTER MEMBRANE VESICLES FROM A CLINICAL ISOLATE OF PSEUDOMONAS AERUGINOSA ON HUMAN PERIPHERAL BLOOD LYMPHOCYTES USING MICRONUCLEUS ASSAY

Faezeh Aboutalebi¹, Mansour Mashreghi², Farhang Haddad³, Seyed Davar Siadat⁴

1. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
2. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran. Cell and Molecular Research Group, Institute of Biotechnology, Ferdowsi University of Mashhad, Mashhad, Iran
3. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
4. Department of Microbiology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: *Pseudomonas aeruginosa*, an important human pathogen, is a significant cause of acute and chronic infections in patients with compromised host defenses. Outer membrane vesicles (OMVs) secreted by *P. aeruginosa* play an important role in virulence and host-pathogen interaction. Recently *Escherichia coli* OMVs were revealed as potentially genotoxic. therefore in this study, we investigated the genotoxic effects of OMVs secreted by *P. aeruginosa* on human blood lymphocytes.

Methods: OMVs were prepared as described by Siadat et al. Human lymphocytes were treated in vitro by OMV with doses of 5, 10 and 15 µg/ml. Cytokinesis-blocked lymphocytes were harvested 72 hours post culture initiation. After slide preparation and staining by Giemsa, mononuclear cells, binucleated cells without micronucleus and binucleated cells with micronucleus were scored. The data were analyzed using SPSS software and analysis of variance (ANOVA) at the level of $P < 0.05$

Results: The data showed that OMVs were able to significantly induce Micronucleus frequency in lymphocytes. The increase in micronucleus frequency were dose-dependent. So that the micronucleus frequency were 1.06% in dose 5 and 1.7% in dose 15 as the highest dose compared to the control group (0.06%).

Conclusion: Above findings indicated that OMVs are able to increase the frequency of micronucleus in human lymphocytes and induce a genotoxic response.

Keywords: *Pseudomonas aeruginosa*; outer membrane vesicles; genotoxic effect; lymphocyte; micronucleus assay

**P267 - 948: ISOLATION AND CHARACTERIZATION OF OUTER MEMBRANE VESICLES
FROM A CLINICAL ISOLATE OF PSEUDOMONAS AERUGINOSA**

Faezeh Aboutalebi¹, Mansour Mashreghi², Farhang Haddad³, Seyed Davar Siadat⁴

1. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
2. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran. Cell and Molecular Research Group, Institute of Biotechnology, Ferdowsi University of Mashhad, Mashhad, Iran
3. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
4. Department of Microbiology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: *Pseudomonas aeruginosa*, an opportunistic human bacterial pathogen, constitutively secretes outer membrane vesicles (OMVs) into the extracellular milieu. OMVs are essential for pathogenesis of *P. aeruginosa*. Also OMVs are important in virulence factor secretion, bacterial survival, and biofilm formation. Therefore In this study, *P. aeruginosa* OMVs production was investigated from a clinical isolate of Ghaem hospital in Mashhad.

Methods: OMVs were prepared as described by Siadat et al. In brief, *P. aeruginosa* strain was grown in LB, at 37°C for 10 h up to early stationary phase. OMVs were extracted in 0.1 M Tris-HCl, pH 8.6, 10 mM EDTA and 0.5%w/v deoxycholate. Purification of OMVs was done by sequential centrifugation at 20,000 g for 30 min followed by ultracentrifugation at 125,000 g for 2 h. The OMV pellet was homogenized in Sucrose 3%. Then physicochemical properties of extracted OMVs were analyzed by Electron microscopy, SDS-PAGE and NanoDrop.

Results: The results revealed that the content of protein extracted was 0.2 mg/mL. The electron microscopy showed that OMVs were in the range of 20-200 nm in size. Also several bands were observed in SDS-PAGE analysis in which strong bands with 35-100kDA was mostly an indication for OMVs production.

Conclusion: The results showed that the extracted OMVs were conformationally stable, and there were no impurity determinants in OMVs.

Keywords: *Pseudomonas aeruginosa*; outer membrane vesicle (OMV); clinical isolate; physicochemical properties

**P268 - 957: MICROTITER PLATE ASSAY FOR ASSESSMENT OF LISTERIA
MONOCYTOGENES BIOFILM FORMATION**

Seyede sara Parvin¹, Lida Lotfollahi ², Nima Hosseini Jazani³, Maryam ghahramani⁴

1. Student Research Committee, Urmia University of Medical Sciences, Urmia, Iran
2. Department of Microbiology and Virology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran
3. Professor of Microbiology, Department of Microbiology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran
4. Student Research Committee, Urmia University of Medical Sciences, Urmia, Iran

Background and Aim: *Listeria monocytogenes* is an opportunistic pathogen that causes listeriosis. In general, these bacteria due to resistance to a range of disinfectants as well as ability to produce biofilms, pose a serious threat in the food industry. The aim of present study was to evaluate biofilm formation by *Listeria monocytogenes*.

Methods: A total of 38 *Listeria monocytogenes* isolated from different clinical, food and cattle specimens were evaluated for biofilm formation. Microtiter plate assay method was used for this assessment and optical density of biofilm formers was read by ELISA-reader. $ODs \leq OD_c$ No biofilm producer $OD_c \leq ODs \leq 2 \times OD_c$ Weak biofilm producer $2 \times OD_c \leq ODs \leq 4 \times OD_c$ Moderate biofilm producer $4 \times OD_c < ODs$ Strong bio-film producer

Results: Of the 38 isolates of *Listeria monocytogenes* 17 (44/73%) had the ability to produce biofilm. Of them 12 isolates (70/60%) were weak, 3 isolates (17/64%) moderate and two isolates (11 / 76%) were strong biofilm former. A total of 26(55%) isolate lack the ability to produce biofilm. Both of strong biofilm formers belonged to clinical isolates.

Conclusion: Due to the high percentage of biofilm formation among our strains, given the importance of the formation of biofilms on surfaces of medical and food industry, the assessment of this phenomenon is important.

Keywords: *Listeria monocytogenes* biofilm Microtiter plate

**P269 - 977: DETECTION OF DIFFERENT SEROVARES OF SALMONELLA ENTRICA BY
MULTIPLEX PCR IN DIARRHEA REFERED TO HOSPITALS OF SABZEVAR**

Seyyed Mostafa Hosseini Fatemi¹, Azadeh Hadad Sabzevar², Elham Arghiani³

1. Islamic Azad University, Mashhad Branch, Department of Biology, Mashhad, Iran
2. Phd, Ferdowsi University of Mashhad, School of Veterinary Medicine, Department of Pathobiology, Mashhad, Iran
3. Islamic Azad University, Damghan Branch, Department of Biology, Damghan, Iran

Background and Aim: Salmonella infections that called food infections, maybe caused by any of the serovar. Salmonella and serotypes are important source of food contamination and strong and virulent pathogen factor in humans. The purpose of this study was to detection of different serovares of salmonella entrica by multiplex PCR in diarrhea referred to hospitals of sabzevar.

Methods: This study was a cross-sectional and descriptive - analytic. In this study, 50 stool samples of people suffering from diarrhea were collected from Sabzevar's hospitals. Primary culture media for the isolation of *Salmonella* were: Tryptone water, selenite F broth, XLD agar and SS were used. Biochemical tests were used to confirm the diagnosis of *Salmonella* using urea agar and VP, indole and citrate and the latter. Then using specific primers for each of the genes *rfb*, *ompC* and *invA* the Multiplex PCR was performed.

Results: In this study, 10 cases of *Salmonella* were isolated using the method of bacterial culture. However, the use of molecular methods Multiplex PCR, 21 cases of *Salmonella* were detected in the samples.

Conclusion: Therefore, the PCR method has higher accuracy than the culture and the traditional culture is often expensive, time consuming and boring.

Keywords: *Salmonella*, Multiplex PCR, stool.

**P270 - 982: PREVALENCE OF SEASONAL CAMPYLOBACTER COLI IN DIARRHEIC
SAMPLES BY USING PCR FROM KAZEROUN CITY**

Hossein Fattahi¹, Nastaran Abbasi², Masoud Emadi³, Abbas Hosseinizadeh Ghasemi⁴, Amir Sayahi⁵,
Fatemeh Jouibar⁶

1. Department of Pathobiology, Kazerun Branch, Islamic Azad University, Kazerun, Iran
2. Young Researchers and Elite Club, Kazerun Branch, Islamic Azad University, Kazerun, Iran
3. Young Researchers and Elite Club, Kazerun Branch, Islamic Azad University, Kazerun, Iran
4. Young Researchers and Elite Club, Kazerun Branch, Islamic Azad University, Kazerun, Iran
5. Young Researchers and Elite Club, Kazerun Branch, Islamic Azad University, Kazerun, Iran
6. Young Researchers and Elite Club, Kazerun Branch, Islamic Azad University, Kazerun, Iran

Background and Aim: Campylobacter is an important Zoonosis disease, a major role in the development of infectious gastroenteritis in humans and in many countries is the main cause of gastroenteritis and in addition to watery and bloody diarrhea, cause secondary diseases such as meningitis, cholecystitis is either.

Methods: In this study, 150 samples of diarrhea collection from Imam Ali Hospitales in both spring and autumn 1394 from Kazeroun city randomly, were prepared. Samples were transported to the laboratory in cold conditions. Then, the samples for 48 hours under microaerophilic Campylobacter enrichment broth at 42 ° C were incubated for 48 hours. Rich environments into a selective culture medium were transferred on the basis of Blood agar and again were incubated under the conditions mentioned above. Then, DNA was extracted from bacteria to phenol -chloroform. Tracking and identification of Campylobacter coli species-specific PCR analysis using gene was performed. DNA ladder 100 pb as a reference size for PCR testing was used.

Results: The PCR products for 894 bp species coli were identified by gel electrophoresis. A total of 150 samples per season in the spring, C. Coli 1.7% and in the autumn, C. Coli 0.3 percent were diagnosed.

Conclusion: The results showed that in the spring, Campylobacter coli highest prevalence in autumn and the lowest prevalence in diarrhea were demonstrated opioid city.

Keywords: Campylobacter Coli, diarrheic samples, PCR, Kazeroun city

**P271 - 995: COMPARISON OF ZNO NANOPARTICLE ANTIBACTERIAL EFFECT AGAINST
CLINICAL ISOLATED STREPTOCOCCUS MUTANS AND STREPTOCOCCUS MUTANS
PTCC 1683 USING SERIAL DILUTION METHOD**

Sarvenaz Esmaeilee¹, Khosro Issazadeh², Mirsasan Mirpour³

1. Department of Microbiology, Faculty of Basic Sciences, Islamic Azad University, Lahijan Branch, Lahijan, Iran; Esmaeili.s@liau.ac.ir
2. Department of Microbiology, Faculty of Basic Sciences, Islamic Azad University, Lahijan Branch, Lahijan, Iran, P.O.Box:1616; Issazadeh@liau.ac.ir
3. Department of Microbiology, Faculty of Basic Sciences, Islamic Azad University, Lahijan Branch, Lahijan, Iran, P.O.Box:1616; Mirpour@liau.ac.ir

Background and Aim:Dental caries and periodontal problems are among the prevalent oral diseases throughout the world. Acidogenic bacteria such as Streptococcus mutans are considered as the contributory factors of dental caries. ZnO nanoparticles have selective toxicity to bacteria but exhibit minimal effects on human cells. This study aimed to comparison of ZnO nanoparticle antibacterial effect against clinical isolate of Streptococcus mutans and Streptococcus mutans PTCC 1683.

Methods:For this experiment ZnO nanoparticle concentrations ranging from 3.90 to 4000 µg/ml were used. The MICs and with subcultures the MBCs of Streptococcus mutans and Streptococcus mutans PTCC 1683 were determined from known concentration of ZnO nanoparticle using the serial dilution method.

Results:The lowest OD against both strains, belongs to 4000 µg/ml and the highest OD, belongs to 3.90625 µg/ml of ZnO nanoparticle. MIC for both strains belongs to 125 µg/ml and MBC for both strains belongs to 250 µg/ml of ZnO nanoparticle

Conclusion:In this article we found that Clinical isolate S. mutans is more resistant than S. mutans PTCC 1683, and the effects of ZnO nanoparticle on Clinical isolate S. mutans was much more than it effects on S. mutans PTCC 1683.

Keywords:Zno nanoparticle, Dental caries bacteria, Streptococcus mutans.

**P272 - 996: STAPHYLOCOCCUS AUREUS BURN WOUND INFECTION AMONG PATIENTS
ATTENDING IMAM REZA HOSPITAL, MASHHAD, IRAN**

Alireza Sedaghat¹, Mohammadreza hajiesmaeili², Fahimeh Sadat Mostafaei³

1. Assistant professor, Fellowship of critical care medicine, Cardiac Anesthesia Research Center, Mashhad University of Medical Sciences, Mashhad, Iran. SedaghatAR@mums.ac.ir
2. Assistant Professor of Critical Care Medicine, Loghman Hakim Hospital, Shahid Beheshti University of Critical Care Medicine
3. Foodborne and Waterborne Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: Staphylococcus aureus is one of the most frequently isolated pathogens in both community and hospital practices. The objective of this study was to investigation of prevalence and antibiotic susceptibility patterns of S. aureus isolated from burn wound infections at Imam Reza Hospital, Mashhad, Iran.

Methods: Methods Patients treated at the burn ward of Imam Reza Hospital, Mashhad, Iran between March 2012 and March 2015 were included in this retrospective analysis. A total of 1163 samples from burn intensive care unit (BICU), were cultured on Blood agar and Mannitol salt agar plates. Colony counts of each culture and biochemical identification were done according to standard methods. Antimicrobial susceptibility of S. aureus isolates to 18 clinically important antibiotics was assessed on the basis of CLSI guideline by the disk diffusion method.

Results: Out of 1163 burn wound pus swab specimens processed, 1018 (87.5%) grew organism on culture. One hundred and seventy six S. aureus isolates were identified from 1163 samples. Methicillin resistant S. aureus (MRSA) isolates showed a frequency of 46.8%. Sensitivity of S. aureus isolates to vancomycin, imipenem, cefazolin and cefotaxime 99%, 77.8%, 66.7% and 100%, respectively. In another way the resistance of S. aureus isolates rates was observed to penicillin G, tetracyclin, ampicilin and erythromycin 94.9%, 80%, 75% and 61%, respectively.

Conclusion: Strict consideration for s. aureus infection and proper usage of antibiotic policy are recommended in decreasing the incidence and occurrence of multidrug resistant S. aureus infections in Imam Reza Hospital

Keywords: Staphylococcus aureus, burn wound infection, drug sensitivity

**P273 - 997: HEMAGGLUTINATION PROPERTIES OF PROTEUS MIRABILIS ISOLATED
FROM URINARY TRACT INFECTIONS**

Arezoo Mirzaei¹, Mehri Habibi², Saeid Bouzari³, Mohammad Reza Asadi Karam⁴

1. Molecular biology department, Pasteur institute of Iran, Tehran, Iran
2. Molecular biology department, Pasteur institute of Iran, Tehran, Iran
3. Molecular biology department, Pasteur institute of Iran, Tehran, Iran
4. molecular biology department, Pasteur institute of Iran, Tehran, Iran

Background and Aim: *Proteus mirabilis* is commonly associated with complicated urinary tract infections and expresses several types of fimbriae. These adhesins may cause hemagglutination (HA) of erythrocyte from different species. Correlation between HA ability, adhesion and bacterial pathogenicity for many pathogens has been shown. The objective of this study was to determine the incidence of HA phenotypes of *Proteus mirabilis* isolates between different blood origins.

Methods: 100 *P. mirabilis* were isolated from UTI patients. For HA assay, serial dilutions of the bacterial suspensions in PBS were mixed with an equal volume of 1% suspension of erythrocytes human blood group A, guinea pig and chicken in PBS in a 96-well microtiter plate and the results were read after incubation in 4°C. The HA unit was defined as the highest dilution of the bacterial suspension causing visible agglutination. For inhibitory effect of D-mannose on hemagglutination, 50 µl of 1% erythrocyte suspension containing 1% D-mannose was added to each well and after incubation, HA results recorded as described above.

Results: We detected strongest hemagglutination activity with human blood group A and guinea pig erythrocyte in the presence and absence of mannose with same pattern, and the weakest activity with chicken erythrocytes with different pattern.

Conclusion: We observed mannose resistant pilli (mrp) in all isolates and different HA pattern on different blood origins. As the adhesion ability of an enteropathogen like *P. mirabilis* is usually assessed by determining the hemagglutination ability and the erythrocyte membrane is believed to possess the homologues of the mucosal substances involved in bacterial adherence to epithelial cells, so mrp can serve as a potential virulence factor for *P. mirabilis* in UTI.

Keywords: *Proteus mirabilis*, UTI, Hemagglutination, mrp

P274 - 1012: MOLECULAR CHARACTERIZATION OF ESBLs KLEBSIELLA PNEUMONIAE ISOLATES COLLECTED FROM HOSPITALS IN ZAHEDAN

Javad Dahmardeh¹, Shahram Sharaki Zahedani², Farokh Rokhbakhsh zamein³

1. graduate student of Microbiology, Islamic Azad University, Kerman, Department of Microbiology, Faculty of Sciences, Kerman, Iran.
2. Assistant Professor, Faculty member, University of Medical Sciences, Department of Microbiology, Zahedan, Iran.
3. Assistant Professor, Faculty member, Islamic Azad University, Kerman, Department of Microbiology, Faculty of Sciences, Kerman, Iran.

Background and Aim: Klebsiella pneumoniae species are members of the Enterobacteriaceae family. In recent years many reports of a high incidence of resistance to beta-lactam drugs in the organism there. So far, various types of beta-lactamase enzymes have been identified in Klebsiella pneumoniae broad-spectrum beta-lactamase (ESBLs) hydrolysis of penicillin and cephalosporin with broad-spectrum are of particular importance. This study, the frequency of the most common ESBLs genes coding for these enzymes, CIT and MOX.

Methods: A total of 120 isolates of Klebsiella pneumoniae were collected from hospitals in Zahedan. First of all isolates using standard microbiological and biochemical methods were identified. All the isolates for the presence of ESBLs agar disk diffusion method than the three antibiotic screening and then drive phenotypic methods combined (Combined disk) were confirmed. Then ESBLs-producing isolates using specific primers for the presence of MOX genes and CIT were investigated by PCR method.

Results: Most of antibiotic resistance to antibiotics erythromycin was (92/5 percent) while the lowest antibiotic Colistin (1/7 percent), Amikacin (10 percent) and Imipenem antibiotic (9 percent). Klebsiella pneumoniae clinical isolates of 120 isolates 95 were positive in the initial screening of ESBLs producing isolates, 23 were Ampc lactamase gene.

Conclusion: This study showed noticeable frequency of ESBLs in Klebsiella pneumoniae strains isolated from clinical samples in hospitals under study. Early identification of ESBLs and implementation of appropriate infection control practices to prevent spread of the resistant organisms in different parts of the hospital are necessary.

Keywords: Klebsiella pneumoniae, broad-spectrum beta-lactamase, combined disk method.

**P275 - 1036: DESIGN, CONSTRUCTION AND EXPRESSION OF RECOMBINANT VECTOR
CONTAINING THE RABIES VIRUS NUCLEOPROTEIN IN PROKARYOTIC EXPRESSION
SYSTEM**

Zohreh Fadajan¹, Gholam Reza Javadi², Fatah Sotoodehnejadnematalahi³, Alireza Gholami ⁴, Maryam Fazeli⁵

1. Department of Biology, College of basic science, Tehran Science and Research branch, Islamic Azad University, Tehran, Iran
2. Department of Biology, College of basic science, Tehran Science and Research branch, Islamic Azad University, Tehran, Iran
3. Department of Biology, College of basic science, Tehran Science and Research branch, Islamic Azad University, Tehran, Iran
4. WHO-Collaborating Center for Reference and Research on Rabies, Pasteur Institute, Tehran, Iran
5. WHO-Collaborating Center for Reference and Research on Rabies, Pasteur Institute, Tehran, Iran

Background and Aim: Rabies is a zoonotic, endemic and fatal viral disease. Antibody against nucleoprotein (N) is used in direct fluorescent antibody (DFA) as a serologic gold standard method of the World Health Organization (WHO). Also, N protein plays an important role in the induction of protective immunity; therefore it can be base of vaccine research. The aims of this study was to design, construction and expression of the rabies virus N protein from prokaryotic system to achieve a repeatable system for production of N protein.

Methods: The complete sequence of nucleoprotein cDNA of rabies virus fixed strain, CVS, was amplified by RT-PCR and cloned into the pCDNA3.1(+) vector. The cloned gene was excised by restriction enzyme digestion and sequenced. Then, the excised N gene was sub-cloned into pET28a expression vector and expressed in Escherichia coli BL21. The expression of the NP was identified by SDS-PAGE and western blots. NP was purified by Anti His Tag Column chromatography. Finally, amount of purified proteins were evaluated using Bradford test.

Results: Restriction enzyme digestion and sequencing showed that the N gene had been successfully cloned into pCDNA3.1(+) vector. Successful sub-cloning of excised N into pET28a expression vector was confirmed using restriction enzyme digestion and electrophoresis. The expression construct was further characterized by SDS-PAGE and western blots.

Conclusion: This study showed that the N protein of rabies virus subtype CVS can be expressed in a reproducible prokaryotic expression system using the pET28a expression vector. N protein produced in this study can be used in diagnosis and research fields.

Keywords: prokaryotic expression system, Nucleoprotein, rabies virus

**P276 - 1049: EFFICACY OF DDAC ON EXTEND –SPECTRUM – BETA LACTAMASE (ESBL)
ARE PRODUCING BY E.COLI STRAINS**

Syede golchereh Mirlahiji¹, Syede Golchereh Mirlahiji², Iraj Nikokar³

1. Gilan medical university
2. Gilan medical university

Background and Aim:: Didecyldimethyl ammonium chloride (DDAC) is a Quaternary Ammonium Compound (QAC) disinfectant often used in the burn hospital. DDAC is a membrane active agent and causes the leakage of important intracellular material. Understanding the mode of action and possible resistance is important; in particular, the pending post antibiotic era that in the hospital is facing

Methods: The cross sectional study was performed to obtain disinfectant resistance genes in E. coli. One hundred E.coli strains were collected from burn hospital in Rasht city that including urine ,wound ,tracheal secretion which were subjected for production extended spectrum beta-lactamase'-(ESBL) enzyme as well as determining antibiotic sensitivity pattern with 20 antibiotics. Antibiotic and antiseptic susceptibility testing was performed according to Clinical and Laboratory Standards Institute recommendations. E.coli isolates were screened by PCR amplification qacE and qacEΔ1 genes that using specific primers and sequence analysis of the amplified regions were performed.

Results:: the presence of qacE and qacEΔ1 resistance gene were 90% , 78% , respectively and high MICs of qacE. In all of the strains, overexpression of qacE and qacEΔ1 was always associated with higher MICs of antibiotics and resistance to beta-lactams and resistance to moderate concentration of DDAC.

Conclusion: These results suggest that the mass usage of DDAC disinfectants is potentially a contributing factor for hindering antibiotic resistance and may be used of ineffective dose of DDAC to be emergence of resistance of E. coli strains.

Keywords: DDAC, beta-lactamase, qacE, qacEΔ1, disinfectant, E.coli

**P277 - 1070: GENETIC ANALYSIS OF PERTUSSIS TOXIN SUBUNIT3 AMONG
BORDETELLA PERTUSSIS ISOLATES IN IRAN**

Pouran Badiri¹, Fereshteh Shahcheraghi², Zahra Nourmohammadi³, Mojtaba Noofeli⁴, Vajiheh Sadat Nikbin⁵, Tayebe Shahbazi⁶

1. Department of Biology, Science and Research Branch, Islamic Azad university, Tehran, Iran
2. Department of Bacteriology and Microbiology, Pasteur Institute of Iran, Tehran, Iran
3. Department of Biology, Science and Research Branch, Islamic Azad university, Tehran, Iran
4. Department of Bacterial Vaccines, Razi Vaccine and Serum Research Institute, Karaj, Iran
5. Department of Bacteriology and Microbiology, Pasteur Institute of Iran, Tehran, Iran
6. Microbiology M.Sc Student, School of Medicine, Shahed University, Tehran, Iran

Background and Aim:whooping cough or pertussis, caused by *Bordetella pertussis*, is an important vaccine preventable diseases. Although the incidence of pertussis was successfully reduced after the introduction of vaccination, the resurgence of pertussis has been revealed in many countries even with high vaccination coverage. Among the several reasons for pertussis reemergence, genetic diversity in virulence factors is one of the major causes. Here genetic variation for *ptxC* gene, which encodes subunit3 of pertussis toxin, was studied in *B. pertussis* isolates from patients of different provinces of Iran and different age groups between 2008 to 2015 years.

Methods:Nasopharyngeal Dacron Swab samples were cultured on Regan-Lowe medium. Genomic DNA was extracted and *ptxC* gene was amplified using specific PCR primers.DNA sequencing was performed and data were analysed by common softwares MEGA4 and ClustaLW.

Results:Two alleles were found for *ptxC* gene in Iranian population. After data analyzing from total *B.pertussis* isolates 87.5% were *ptxS3B* and 12.5% were *ptxS3A*.

Conclusion:*ptxS3B* has been reported as dominant allele in some countries includes: the Netherlands, France, United Kingdom and Germany in recent years. These data is in accordance with our findings that *ptxS3B* is also dominant allele in our circulating *B.pertussis* population.

Keywords:*pertussis toxin subunit3, Bordetella Pertussis, sequencing*

**P278 - 1085: POLYMORPHISM OF FIMBRIAE AND PERTACTIN GENES AMONG
BORDETELLA PERTUSSIS CLINICAL ISOLATES ON 2014-2016**

Tayebe Shahbazi¹, Fereshteh Shahcheraghi², Parviz Owlia³, Farzad Badmasti⁴, Vajiheh Sadat Nikbin⁵,
Pouran Badiri⁶, Hamid Solgi⁷

1. Microbiology M.Sc Student, School of Medicine, Shahed University, Tehran, Iran
2. PhD, Pertussis Reference Laboratory, Department of Bacteriology, Pasteur Institute of Iran, shahcheraghifereshteh@yahoo.com
3. Ph.D., Molecular Microbiology Research Center, Shahed University, Tehran, Iran
4. PhD, Pertussis Reference Laboratory, Department of Bacteriology, Pasteur Institute of Iran
5. PhD student, Pertussis Reference Laboratory, Department of Bacteriology, Pasteur Institute of Iran
6. genetic M.Sc student, Departement of Genetics, Science and Research Branch, Islamic Azad university, Tehran, Iran
7. PhD student, Pertussis Reference Laboratory, Department of Bacteriology, Pasteur Institute of Iran

Background and Aim: *Bordetella pertussis* is a gram negative cocobacil bacteria and causer of whooping cough. this bacterium produces many virulence factors include of fimbriae (Fim2) and pertactin (Prn). these adhesions are the major part of vaccine. in attention to importance of these components, study of those polymorphism is important and unavoidable, specially because of pertussis recent out break in several country.

Methods: Nasopharynx samples of suspicious persons to pertussis have transferred to National Pertussis Reference Laboratory in Pasteur Institute of Iran. after the culture of total samples, finally 20 of them were positive for *Bordetella pertussis*. then DNA was extracted with use of Kit (Roche, Germany). In next step Fim2 and 2 region of Prn genes were detected with PCR method. finally the PCR products were sequenced.

Results: 14 samples (70%) had Fim2-2 allele and 6 samples (30%) had fim2-1 allele. about of 2 region of Prn, were not detection any polymorphism and total of them were equivalent of tohamma (standard strain) sequence.

Conclusion: in attention to change the predominant allele rather than previous research (Fim2-1), and importance of this results in vaccine production, we need to more study in this field.

Keywords: polymorphism, *Bordetella pertussis*, Fimbriae, Pertactin

P279 - 1096: ANTIBIOTIC RESISTANCE OF CLINICAL ISOLATES OF ACINETOBACTER BAUMANNII ISOLATED FROM PATIENTS IN A HOSPITAL IN ZAHEDAN, IRAN.⁴³

Mahnaz Sabbaghi¹, Farokh Rokhbakhsh-Zamin²

1. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran
2. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran

Background and Aim: *Acinetobacter baumannii* strains show resistance to most antibiotics at present, including broad-spectrum penicillins, cephalosporins, carbapenems, most aminoglycosides, fluoroquinolones, chloramphenicol, and tetracyclines. Different researches about antibiotic resistance patterns both in specific area and on whole country can be helpful to clarify the mode of *A. baumannii* antibiotic resistance spread. The present study aimed to elucidate the rate of antibiotic resistance of *A. baumannii* in an individual (Avicenna) hospital in Zahedan, Iran.

Methods: This research was performed in Avicenna Hospital in Zahedan, Iran. Clinical samples obtained from patients in different sections of hospital. Identification of isolates was done by biochemical tests as well as PCR method. Finally antibiotic susceptibility tests were performed.

Results: Among 30 strains of *A. baumannii* isolated from patients and according to the Antibiogram tests, multi-drug resistant (MDR), non-multidrug-resistant and extensively multi-drug resistance (XDR) was observed. On the other hand, the highest rate of antibiotic resistance was observed regarding to ceftriaxone, Ticarcillin, erythromycin antibiotics but the lowest rate was measured about minocycline.

Conclusion: Correct information about the epidemiologic patterns of different antibiotics to the agents of infectious disease is very important and critical. So, this experiment as well as the other parallel research can be a good map for physicians to use correct antibiotics in specific regions and areas of a country such great Iran.

Keywords: *Acinetobacter baumannii*, Antibiotic resistance, PCR

**P280 - 1104: EVALUATE PATIENT'S REFERRING TO THE MASSOUD LABORATORY FOR
DIAGNOSIS MYCOBACTERIUM TUBERCULOSIS THROUGH 2013**

Reza Azizian¹, Fahimeh Morteza², Saeed Zaker Boostanabad³, Shadi Habibniya⁴, Mostafa Ghalami⁵,
Amir Amini⁶, Ali Ghorbanipour⁷, Shahin Pourazar⁸

1. Dep. of Massoud Clinical Laboratory
2. Dep. of Massoud Clinical Laboratory
3. Dep. of Massoud Clinical Laboratory
4. Dep. of Massoud Clinical Laboratory
5. Dep. of Massoud Clinical Laboratory
6. Dep. of Massoud Clinical Laboratory
7. Dep. of Massoud Clinical Laboratory
8. Dep. of Massoud Clinical Laboratory

Background and Aim: Tuberculosis that caused by Mycobacterium tuberculosis is a significant public health problem in Iran. Recently various molecular methods such as PCR were used for more accurate rapid identification of these species. The aim of this study was compare a rapid and accurate diagnosis of patients referring to the Massoud laboratory who were suspected to tuberculosis during the years of 2013.

Methods: 152 patients referred to the Massoud laboratory that was investigated by direct smear and culture. Then DNA was extracted due to performing PCR.

Results: Among 152 samples, 67 ones had complete data that is included age, gender, smear and culture data. 5 samples had positive culture (7.4%) and 1 case had positive smear (1.4%). Among 5 samples just 1 case was detected by PCR that previously had positive smear.

Conclusion: Regards to our comparison, most of samples that prescribed by physicians was sputum. Bronchoalveolar lavage and biopsy samples were isolates that had PCR positive. According this study culture is accurate diagnostic method and other methods must be confirmed by culture.

Keywords: Mycobacterium tuberculosis, PCR, molecular methods

**P281 - 1106: COMPARISON BETWEEN TRADITIONAL AND MOLECULAR DIAGNOSTIC
ORDERS FOR PATIENT WHO REFER TO THE MASSOUD LABORATORY FOR
DIAGNOSIS MYCOBACTERIUM TUBERCULOSIS THROUGH 2014**

Reza Azizian¹, Saeed Zaker Boostanabad², Shadi Habibniya³, Amir Amini⁴, Ali Ghorbanipour⁵, Mostafa Ghalami⁶, Shahin Pourazar⁷, Famhimeh Morteza⁸

1. Dep. of Massoud Clinical Laboratory
2. Dep. of Massoud Clinical Laboratory
3. Dep. of Massoud Clinical Laboratory
4. Dep. of Massoud Clinical Laboratory
5. Dep. of Massoud Clinical Laboratory
6. Dep. of Massoud Clinical Laboratory
7. Dep. of Massoud Clinical Laboratory
8. Dep. of Massoud Clinical Laboratory

Background and Aim: Tuberculosis that caused by Mycobacterium tuberculosis is a significant public health problem in Iran. Recently various molecular methods such as PCR were used for more accurate rapid identification of these species. The aim of this study was compare a rapid and accurate diagnosis of patients referring to the Massoud laboratory who were suspected to tuberculosis during the years of 2014.

Methods: 64 patients referred to the Massoud laboratory that was investigated by direct smear and culture. Then DNA was extracted due to performing PCR.

Results: Among 64 samples, 25 ones had complete data that is included age, gender, smear and culture data. 88% smear was negative and 4% were Nocardia. While, 92% culture were negative therefore smear had completely accorded to culture.

Conclusion: Regards to our comparison, most of samples that prescribed by physicians was sputum. According this study culture is accurate diagnostic method and smear is mostly accorded to culture but PCR must be checked by culture.

Keywords: Mycobacterium tuberculosis, PCR, molecular methods

**P282 - 1115: PREVALENCE AND ANTIMICROBIAL RESISTANCE OF STAPHYLOCOCCI
ISOLATED FROM BLOOD CULTURES OF NEONATES ADMITTED IN PEDIATRIC WARD
IN ABADAN HOSPITALS, 2015**

Masoumeh Ghasemnezhad¹, zahra gorjian², nabi gomeh zadeh³

1. abadan university of medical sciences
2. abadan university of medical sciences
3. abadan university of medical sciences

Background and Aim:: According to sepsis is a common cause of mortality in this study to check out staphylococcal infections, antibiotic resistance and sensitivity

Methods: In this descriptive cross-sectional study using blood samples from the children on three occasions on blood agar medium and methyl red eosin incubated and the gram stain and using standard biochemical tests, such as catalase and coagulase test and then was evaluated antibiotic resistance by disk diffusion method

Results: in this study that during six months in Abadan Taleghani Hospital in 1394 carried out 121 blood culture samples taken from children hospitalized infants and children , 57 samples of the girls acting (47.1%), and 64 (52.9%) boys ,total of 13 positive blood culture (10.7%) with growth of Staphylococcus, and 108 case (89.3%) were negative Staphylococcus far more growth. 21 children with ages less than one month (18.4%) and 22 individuals aged between 1 and 6 months (19.3%) and 16 case children 6 months to a year (14%) and 33 those aged between 1 and 2 years (28.9%) and 22 children more than 2 years (19.3%), respectively.

Conclusion: The results of this study, the importance of coagulase-negative staphylococci infections uncommon blood culture child and infant effective antibiotic usage survey reveals with high efficacy

Keywords: Staphylococcus"; Abadan Taleghani Hospital "; blood culture"; infant's "; children

**P283 - 1121: EVALUATION OF DIFFERENT DEGREE OF DENTAL CARIES REGARDING
TLR2 AND TLR4**

Mohsen Afkar¹, Mandana Sattari², Masoomeh Dibaj³, Hengameh Akhavan⁴

1. Dept. Endodontics, Dental School, Azad University
2. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN
3. Dept. Endodontics, Dental School, Azad University
4. Dept. Endodontics, Dental School, Azad University

Background and Aim: Regarding to importance of pathobiology of pulpal inflammation and innovations in treatment methods the aim of this study was to evaluate relationship between different degrees of caries in reversible pulpitis with TLR2,4 gene expressions.

Methods: This study was historical cohort. The pulps of a hundred extracted premolar teeth were extirpated. They were divided into 5 groups: healthy (negative control) , superficial caries, moderate caries, deep caries and deep complicated caries (positive control). All samples were reversible pulpitis except control ones. After pulpal extirpation and homogenization of samples , we used quantitative Real time PCR for evaluate TLR2,4 gene expression. Data analysis was made by REST software (QIAGEN,2009).

Results: TLR2, gene expressions were significantly higher in deep caries group and deep complicated caries group in comparison with negative control group. $p<0.003$, $p<0.035$ respectively. TLR2 gene expression were significantly higher in deep caries groups versus superficial ones ($P<0.043$), involved groups versus superficial ones ($p<0.033$), involved group versus moderate ones ($p<0.002$). The difference in TLR4 gene expression was not significant.

Conclusion: Despite of predominance of gram negative bacteria in advancing caries the expression of TLR2 has been increased instead of TLR4.

Keywords: Dental caries, TLR2, TLR4, Innate Immunity

**P284 - 1131: EPIDEMIOLOGICAL SURVEY OF MENINGITIS IN SOUTH KHORASAN
PROVINCE IN 2011-2015**

Bita Bijari¹, Ali Abassi², Kambiz Mehdizade³, Majid Shayeste⁴

1. MD, Associate Professor, community medicine specialist, school of medicine, Birjand University of Medical Sciences ,Birjand, Iran
2. Ms of medical education, Health Department, Birjand University of Medical Sciences ,Birjand, Iran
3. MD, Health Department, Birjand University of Medical Sciences ,Birjand, Iran
4. MD, Health Department, Birjand University of Medical Sciences ,Birjand, Iran

Background and Aim: Bacterial meningitis is an important disease with high mortality and morbidity. Despite the implementation of meningitis surveillance program in the province, there are no data of the epidemiology of this disease. The aim of this study was to evaluate the epidemiology of meningitis cases in 2011-2015

Methods: In this cross-sectional study after coordination with health departments, records of patients with suspected meningitis were requested from the health centers. Information form is designed and was completed based on patient records and summary data form. Data entered SPSS (16) software and were analyzed using the chi-square test at a significance level of $\alpha=0.05$

Results: 368 suspected cases of meningitis were reported in five years. The mean age of cases was 7.6 ± 13.5 year. The majority were in the age group one year and less than one year 169 (46.3%) and were men 225 (61.3). According to the definition of surveillance system 119 (32.4%) cases were probable and 18 (4.9%) cases were confirmed. LP was performed for 284 (77.2%). Streptococcus pneumonia was the most common germ. There was no significant association between confirmed cases of meningitis and type of meningitis with age, gender, city, source and year study. $P > 0.05$

Conclusion: Reported cases of meningitis surveillance in South Khorasan province is less than expected. This can be failing to recognition or non-reporting of cases of meningitis. Pattern of probable and confirmed cases and age and sex in cases in this study was similar to reported cases based on surveillance system in the country.

Keywords: meningitis, epidemiology, surveillance

**P285 - 1132: EVALUATION OF UPEC BIOFILM FORMATION AMONG ISOLATES FROM
PATIENTS WITH UTI IN MILAD HOSPITAL ,TEHRAN**

Nafise Nosrati Sadaghiani¹

1. Department of microbiology, Islamic Azad university, Varamin- Pishva branch, Iran

Background and Aim: Bacterial biofilms are present and found everywhere in different places or niches. pathogenic bacterial biofilm on medical devices and inserted in the body tissues or host often leads to infections that are highly resistant to antimicrobial compounds and host responses. Biofilms play a major role in nosocomial infections and urinary tract infections (UTIs) that also cause recurrence and incidence of acute prostatitis. Escherichia coli is cause of more than 80% of UTIs and uropathogenic Escherichia coli (UPEC) is the first cause of 90-70% of community-acquired and 50% of hospital-acquired UTI. This bacterium is capable to make biofilm within the bladder epithelium cells and play an important role in pathogenesis. Identify UPEC strains producing biofilm to better understand of bacterial pathogenesis in UTI is important

Methods:. A total of 100 UPEC strains from patients with UTI in Milad Hospital ,Tehran were collected and diagnosed by biochemical tests and their biofilm formation were determined by TCP, TM and CRA methods. Sensitivity and specificity of methods was determined. TCP was gold standard method for biofilm formation

Results:. Among 100 isolates by TCP method 35 and 65 isolates were strong and weak biofilm producers, respectively. By CRA 2 strains was strong biofilm producers , 70 weak and 28 were negative .By TM method 27 were strong, 51 weak and 22 isolates were negative. The Sensitivity and specificity of CRA and TM methods were 6.25%, 28.12% and 97% ,79.41% ,respectively.

Conclusion: The results showed that TCP and then TM methods are important for UPEC biofilm formation determination

Keywords: UPEC, Biofilm formation, CRA, TCP, TM

**P286 - 1161: O-SEROTYPING OF ESCHERICHIA COLI ISOLATES COLLECTED FROM
BROILERS WITH COLIBACILLOSIS IN ZABOL**

Fateme Mirzayi¹, ahamd rashki²

1. student of DVM, department of veterinary medicine, zabol university
2. Ph.D, professor of microbiology and molecular genetic specialist, department of veterinary medicine, zabol university

Background and Aim: colibacillosis is one of the prevalent infections in poultry industry which is caused by escherichia bacteria. this organism possess more than 180 types of O antigens but few are of clinical importance in incidence of poultry colibacillosis. the prevalence of serogroups in poultry is different. despite of various prevalence rates of colibacillosis in different parts of iran, few studies have been conducted in the aspect of molecular detection of important serogroups of O antigen.

Methods: in this study in order to evaluate the serogroups, from 100 chickens which were infected to colibacillosis proved clinically and by necropsy, and sterile swab was taken from their peritoneal cavity. after culturing the contents of swab, biochemical discrimination of the organism was performed then. after DNA extraction of E.coli isolates, the multiplex polymerase chain reaction was accomplished on O1, O2, O4, O6, O7, O12, O15, O16, O18, O25, O75 and O157 samples.

Results: subsequently, O157, O16, O75 and O12 serotypes with 22.5%, 14.8 %, 13.8 and 5.5% were the most abundant, respectively.

Conclusion: by determination of E.coli isolates serogroups, we can more recognize the characteristics of colibacillosis forming isolates and their zoonotic significance.

Keywords: escherichia coli, colibacillosis, O-serotyping

P287 - 1173: PREVALENCE OF TEM AND PER TYPE EXTENDED SPECTRUM B-LACTAMASES IN ACINETOBACTER BAUMANNII CLINICAL ISOLATES BY PCR

Nasim Shams¹, Mojtaba Moosavian ², Mehrandokht Sirous³

1. Dept. of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
2. Health Research Institute, Infectious and Tropical Diseases Research Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.
3. Dept. of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Background and Aim: *Acinetobacter baumannii* is gram-negative bacilli that have emerged as important opportunistic pathogens, especially among critically ill patients (1). Treatment of infections due to this organism is becoming a serious clinical concern and this bacterium is frequently resistant to multiple classes of antibiotics such as family of β -lactam drugs (2). Resistance to beta-lactams among common nosocomial gram-negative pathogens evolves mainly along two genetic pathways: mutation of special intrinsic genes and acquisition of resistance genes. Extended spectrum-beta-lactamases (ESBLs) genes, represent the main mechanism of bacterial resistance to β -lactam antibiotics (3). The aim of this study was to determine the frequency of TEM and PER type genes among *A. baumannii* isolates from hospitalized patients in two hospitals in Ahvaz, Iran.

Methods: A total of 100 *Acinetobacter baumannii* isolates from clinical specimens were identified by standard chemical tests (4). To confirm the identity of *A. baumannii*, blaOXA-51-like gene was sought by PCR. These specimens were collected from the hospitalized patients in teaching hospitals of Ahvaz, Iran. TEM and PER-1 types of ESBL producing genes was detected by PCR test.

Results: Based on the results of this study, the prevalence of blaTEM and blaPER genes was 24(24%) and 17(17%), respectively.

Conclusion: According to this study, the prevalence of ESBLs -producing *A. baumannii* strains detected is a major concern and highlights the need of infection control measures.

Keywords: *Acinetobacter baumannii*, ESBL, blaTEM, blaPER

P288 - 1175: ANTIBACTERIAL ACTIVITY OF ZIZIPHORA CLINOPODIODES ESSENTIAL OIL AGAINST CLINICAL ISOLATES OF METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS (MRSA)

Nasrin Pourramezan¹

1. School of Public Health, Tehran University of medical science

Background and Aim: Staphylococcus aureus is one of the most important causes of community and hospital acquired infections. methicillin resistant S. aureus (MRSA) is a dominant pathogen in postoperative infections that is also multidrug resistant. Therefore, it is important to introduce new sources of drugs such as traditional medicinal plants with antimicrobial properties.

Methods: We determined the chemical composition of the essential oil of Ziziphora clinopodioides subsp. bungeana from the Jandagh area and its antibacterial activity against clinical isolates of S. aureus, mostly MRSA isolates as well as standard ATCC cultures. The essential oil of the aerial parts of Ziziphora clinopodioides from Jandagh area in Iran was prepared by hydrodistillation and its chemical constituents were analyzed by a combination of capillary GC and GC-MS.

Results: Thirty two components were identified of which, Pulegone (33.17 %), Alpha-terpinyl acetate (11.37%), Thymol (10.31%) and Menthone (7.28 %) were the main constituents. The antibacterial activity of the oil was determined against 10 clinical isolates of Staphylococcus aureus and 6 Gram positive and Gram negative bacterial standards by disc diffusion.

Conclusion: Minimum inhibitory and bactericidal concentrations (MIC and MBC) were determined by broth microdilution assay. Considerable inhibitory activity was shown against all test bacteria shown by disc diffusion (except P. aeruginosa) and MIC and MBC values were within the range of 0.66 - 2.64 mg/ml for the susceptible organisms.

Keywords: Antibacterial activity, Staphylococcus aureus, essential oil, Iran.

**P289 - 1176: ANTIBACTERIAL ACTIVITY OF ZATARIA MULTIFLORA BOISS ESSENCE
OIL AGAINST ESBL PRODUCING ISOLATES OF ESCHERICHIA COLI**

Nasrin Pourramezan¹

1. Department of pathobiology, School Of Public Health, Tehran University Of Medical Science,

Background and Aim: Escherichia coli is the most common pathogen of bacterial infections worldwide that most frequently associated with ESBL production. E.coli with ESBL may cause urinary tract infections that can sometimes progress to more serious infections like blood poisoning. The increase in ESBL producing E. coli among community-onset urinary tract infections is an important public health concern as these organisms are resistant to multiple antimicrobial agents. Plant essential oils rich in carvacrol and thymol have gained importance for their antimicrobial activity.

Methods: We determined the composition of Zataria multiflora essential oil of the Jandagh area in Iran and measured its activity against ESBL producing urinary isolates of Escherichia coli. The essential oil of the aerial parts of Zataria multiflora from Jandagh area in Iran was prepared by hydrodistillation and its chemical constituents were analyzed by a combination of capillary GC and GC-MS.

Results: Twenty five components were identified of which, carvacrol (50.6 %), thymol (13.4 %) and p-cymene (8.3 %) were the main constituents. The antibacterial activity of the oil was determined against 10 clinical isolates of Escherichia coli and 6 Gram positive and Gram negative bacterial standards by disc diffusion.

Conclusion: Minimum inhibitory and bactericidal concentrations (MIC and MBC) were determined by broth microdilution assay. Considerable inhibitory activity was shown against all test bacteria shown by disc diffusion (except P. aeruginosa) and MIC and MBC values were within the range of 0.015 - 2.01 mg/ml for the susceptible organisms.

Keywords: Antibacterial activity, Escherichia coli, essential oil, Iran.

P290 - 1178: EVALUATION OF THE RELATIONSHIP BETWEEN PATIENTS' AGE AND PHENOTYPIC/GENOTYPIC CHARACTERISTICS OF UROPATOGENIC E. COLI ISOLATES DERIVED FROM HOSPITALIZED WOMEN WITH URINARY TRACT INFECTION

Zohreh Ghazvini¹, Habibeh Bashiri vand fabriki², Alireza Abdollahi MD³, Mehrnaz Rasoulinejad MD⁴, Shahram Sabeti MD⁵, Masoud Mardani MD⁶, Saeid Bouzari PhD⁷, Mohammad Pooya MD, PhD⁸

1. Department of Biology, Islamic Azad University, Damghan branch
2. Department of Biology, Islamic Azad University, Damghan branch
3. Imam Khomeini Hospital Complex, Tehran University of Medical Sciences
4. Imam Khomeini Hospital Complex, Tehran University of Medical Sciences
5. Loghman Hakim Hospital, Shahid Beheshti University of Medical Sciences
6. Loghman Hakim Hospital, Shahid Beheshti University of Medical Sciences
7. Department of Molecular Biology, Pasteur Institute of Iran
8. Department of Molecular Biology, Pasteur Institute of Iran

Background and Aim: Urinary tract infection (UTI) is a significant public health problem that can affect women in all age groups; however, the uropathogen(s) causing UTI, varies over the female lifespan. This study was performed to evaluate any probable variation in phenotypic/genotypic characteristics of uropathogenic E. coli (UPEC) isolates recovered from hospitalized women with UTI at different ages.

Methods: The study was conducted on 100 UPEC isolates derived from the female patients diagnosed with UTI who hospitalized in the Loghman and Imam Khomeini hospitals. The isolates were divided into five different groups based on the patients' ages. They were subjected to antibiotic susceptibility test. Their phenotypic characteristics were evaluated and the common virulence and antibiotic resistance genes were assessed too.

Results: While in the age group below 40, none of the recovered isolates were resistant to imipenem and gentamicin and no multidrug resistance (MDR) was seen, in the other groups above this age, the isolates were significantly resistant to these antibiotics and MDR pattern were obviously detected. Similar results were seen for ceftazidime and ciprofloxacin. In contrast, the isolates in the age groups below 60 were significantly more resistant to sulfamethoxazole-trimethoprim (in opposite to presence of dfr antibiotic resistance gene) and more hydrophobe as well. Moreover, as the patients' ages increased, the isolates' resistance to serum decreased.

Conclusion: Although there is no significant difference in most of characteristics of UPEC derived from UTI patients at different ages, they are more resistant to most of antibiotics in older patients, may be due to indiscriminate use of antibiotics.

Keywords: uropathogenic Escherichia coli, patients' age, antibiotic susceptibility

**P291 - 1181: IDENTIFICATION OF ANTIMICROBIAL RESISTANCE GENES IN
SALMONELLA SPECIES ISOLATED FROM CHILDREN WITH ACUTE INFECTIOUS
DIARRHEA BY MULTIPLEX-PCR AND THEIR ANTIBIOTIC RESISTANCE PROFILE**

Sareh Amiri¹, Gholamaliye Moradli²

1. Department of Microbiology, Faculty of Basic Sciences, Saveh Branch ,Islamic Azad University, Saveh, IR Iran.
2. Department of Microbiology, Assistant Professor, Medical faculty member, Saveh Branch ,Islamic Azad University, Saveh, IR Iran.

Background and Aim:: Salmonellosis is one of vital infectious illness in both human. Drug administration in gastroenteritis caused by Salmonella are limited to acute illness particularly pediatric and immunocompromised individuals. The aim of the study, was detection of bla TEM/CTX-M/SHV in Salmonella Typhimurium isolated from children with acute infectious diarrhea using multiplex-PCR and their antibiotic resistance profile.

Methods:: In this cross-sectional study, 273 stool samples were obtained from children admitted to Children's Medical Center Hospital. The antibiotic susceptibility test was determined using the disk diffusion method agreeing with CLSI guideline. Then, M-PCR was achieved for determination of beta lactamase genes by specific oligonucleotides primers.

Results:: Of 273 collected stool samples, 18(6.5%) Salmonella spp., were obtained, which 11(61.1%) were S. typhi, 5(27.7%) S. enteritidis and 2 (11.1%) S. typhimurium. Antibiotic resistance analysis showed that the highest and lowest resistance rate were related Imipenem and Ciprofloxacin (100%) and Ofloxacin (54.5%), respectively. The MPCR results revealed that 7 (38.8%), 8 (44.4%) and 2 (11.1%) of Salmonella spp., isolates carried CTX-M, TEM and SHV genes, respectively. Only 1 isolate was positive for all tested genes.

Conclusion:: The results show the presence of antibiotic-resistant Salmonella spp. in nontyphoidal salmonellosis from children with acute infectious diarrhea in Tehran, Iran. accurate detection and fast identification of Salmonella producing ESBLs is important from the source of infection such as, foods, animals and its products and carriers

Keywords:resistance genes, Salmonella, diarrhea.

P292 - 1188: RESISTANCE AND ANTIBIOTIC SUSCEPTIBILITY PATTERN KLEBSIELLA PNEUMONIAE STRAINS ISOLATED FROM CLINICAL SPECIMENS IN EDUCATIONAL HOSPITAL IN ZAHEDAN

Maryam Ghaedi¹, Fatemh Zabuli², Shahram Sharaki Zahedani³

1. microbiology graduate student Ayatollah Amoli Islamic Azad University, Amol, Iran.
2. Assistant Professor, Faculty member, Ayatollah Amoli Islamic Azad University, Amol, Iran.
3. Assistant Professor, Faculty member, University of Medical Sciences, Department of Microbiology, Zahedan, Iran.

Background and Aim: The incidence of antibiotic resistance in *Klebsiella pneumoniae* as a nosocomial infection is important. According to different reports about the sensitivity of *Klebsiella pneumoniae* bacteria This study aimed to determine the susceptibility of *Klebsiella pneumoniae* strains isolated from patients in teaching hospitals in Zahedan.

Methods: In this study, cross - sectional hospital in the city of Zahedan 120 clinical samples were collected and cultured for the isolation of *Klebsiella pneumoniae*. Suspect isolates were confirmed by biochemical properties. Isolates were resistant to 10 antibiotics was determined by disk diffusion method.

Results: Most strains of *Klebsiella pneumoniae* isolated from samples of urine, 95 isolates (2/79 percent) and respiratory secretions isolates, 23 (19.1 percent). The highest sensitivity to Colistin, Imipenem and Amikacin and highest resistance to Cefotaxime was found.

Conclusion: The results of this study demonstrated an increase in strains of *Klebsiella pneumoniae* antibiotic Cefotaxime, which may be due to irregular use of antibiotics. Obviously, because of the growing use of antibiotics and the subsequent spread of antibiotic resistance, control of this resistance, is indispensable. It is recommended that unnecessary use of antibiotics should be avoided.

Keywords: Antibiotic resistance, *Klebsiella pneumoniae*, susceptibility.

**P293 - 1190: IDENTIFICATION OF CAMPYLOBACTER JEJUNI, AND C. COLI IN ÒURBAN
DUCKS FECES IN THE NORTH OF IRAN**

Elham Saberi nik¹, Kh.Kafshdouzan², I. Ashrafi Tamai³, E. Saberi Nik⁴, S. Rahmani Firouzjani⁵

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Background and Aim:: The incidence of Campylobacter-associated food poisoning has gradually increased, and this organism is now considered to be the leading cause of bacterial gastroenteritis worldwide. Among the pathogenic Campylobacter species, *C. jejuni*, *C. coli*, *C. fetus* and *C. lari* are important infectious pathogens. Birds, both domesticated and wild and their products are known as important sources of human campylobacteriosis. The fastidious growth requirements, complex taxonomy and unreliable biochemical tests, present significant challenge in the identification of Campylobacter spp. polymerase chain reactions based on the 16SrRNA gene, and specific genes, can be used to identify bacteria of the genus Campylobacter, and four Campylobacter species.

Methods:: Fecal samples from cloac of 75 ducks were collected and DNA extraction was performed with AccuPrep, Bioneer, kit (Korea). samples were confirmed to be Campylobacter spp., *C.jejuni* and *C.coli* using monoplex polymerase chain reaction (PCR) that targeted 16s rRNA for Campylobacter spp. and the membrane-associated protein A (mapA) for *C. jejuni* and *ceuE* for *C.coli*.

Results:out of 75 samples, overall prevalence of Campylobacter spp. in the sampled wild ducks feces was 17.33% and prevalence of *C.jejuni* and *C.coli* were 84.6% and 15.4% respectively.

Conclusion:Most of the studies on Campylobacter have focused on food sources and reports on wild birds are very scarced. Detection of Campylobacter in duck feces is important for the identification of the source of outbreaks associated with the consumption of improperly cooked meat

Keywords:Campylobacter spp., Campylobacter jejuni, Campylobacter coli, ducks

**P294 - 1204: AN ASSOCIATION STUDY BETWEEN LEWIS BLOOD GROUP PHENOTYPE
AND IL-6 PRODUCTION BY P. AERUGINOSA STIMULATED PBMC**

Samaneh Alinezhad monfared¹, Kambiz Bagheri²

1. Department of Microbiology, Kazerun Branch, Islamic Azad University, Kazerun, Iran.
2. Department of Immunology, Faculty of Medicine, Kazerun Branch, Islamic Azad University, Kazerun, Iran.

Background and Aim: There are several studies about the relationship of blood groups or secretory status with susceptibility to various diseases, particularly autoimmune diseases, infectious diseases, cancer and inflammatory problems. In addition to ABO, other subgroups such as Lewis also introduced which the phenotype (a + b-) are completely non-secretor and (a-b +) are quite secretor. The aim of this study was to measure the level of IL-6 after stimulation with an extract of *P. aeruginosa* in both Lewis phenotypes.

Methods: Lewis phenotype of volunteers was defined and their mononuclear cells were subdivided in 2 subgroups (control without any stimulation) and test (cultivation in the presence of bacteria extract of *Pseudomonas aeruginosa*). Prepared bacterial extracts was added to the culture medium and the IL-6 in were measured by ELISA.

Results: The results showed that after stimulation with bacterial extract the IL-6 level significantly increased. On the other hands, this increasing level was significantly higher in phenotype Lewis A as compared to Lewis B. This result could be a new justification for the recent findings of more prevalence of autoimmune, inflammatory and other malignancies in non-secretor group.

Conclusion: Thus, a higher prevalence of inflammatory, infectious and autoimmune diseases may be associated with overproduction of inflammatory cytokines which is higher in people with Lewis A phenotype. Although the final confirmation of this topic requires further research.

Keywords: Lewis, blood group, IL-6, *P. aeruginosa*

**P295 - 1212: BIODEGRADATION AND DECOLORIZATION (DAYS CONGO RED
INDIGOCARMINE) BY SOME SPECIES OF THE BACTERIA (BACILLUS AND
ACINETOBACTER)**

Mitra Chalabzardi¹

1. MSc in Microbiology, Faculty of Sciences, Faculty of Sciences, ILAM University, ILAM, Iran,

Background and Aim: synthetic dyes are spreadingly used in the industries, that these dye existing in wasterwater are carcinogenic and mutagenic. One of the most important microorganism used indecolorizeing theday is bacteria. The-aim of this study was to biodegradation and decolorization days congored indigoarmine by6 species of the bacteria Bacillus and A.baumannii isolated from solid.

Methods:methods In the study6 bacteria species including Bacillus-sp-(B.subtilis,- B.-megaterium,B. cereus,B.-pumilus,-B.-licheniformis and A.baumannii which were isolated from solid and standard used.Then their capability in decolorization of days congored,indigocarmine were investingated and also different condition were tested for optimize decolorization:time,-PH,-dye-deconcentration oxygen,-and temperature.It was foud that in the optimal condition B.subtilis with93%on the dye congored and B. cereus with86%indigocarmine decolorization have the most capacity. B. licheniformis with42%on the dye congored and B. megaterium with56%indigocarmine decolorization have the least.

Results:The results of this study showed that bacillos maintain their decolorization in hight dyeconcentration150mg/l,butA.-baumanni maintain decolorization rate least in the dye concentration70mg/l,the optimal PH in decolorizatio was the most decolorization in all of the bacterial use in neutral-PH in vestigating. The effect of different temperature this result was reached that37°C is optimal temperature for growhing bacteria is the most suitable temperature for decolorization.

Conclusion:Aerobic and anaerobic condition the latter one has the most suitable condition in order to decolorizae the congored dye by the B.subtilis, B. megaterium,B. cereus andA.baumani have more power to decolorizati on this dye in the aerobic and decolorizae the indigocarmine dye by the B. pumilus, B. licheniformis more power to decolorizati on this dye in the anaerobic condition.

Keywords:Biodegradation, Decolorization, Bacillus, Indigocarmine

P296 - 1213: MOLECULAR STUDY OF PER, VEB AND FOC GENS IN ACINETOBACTER BAUMANNI ISOLATED FROM PATIENS IN HOSPITAL MOSTAFA KHOMEINI IN ILAM CITY

Mitra Chalabzardi¹

1. MSc in Microbiology, Faculty of Sciences, Faculty of Sciences, ILAM University, ILAM, Iran,

Background and Aim: Acinetobacter baumannii one of the most common hospital infectious was wide. One of mechanisms of resistance to the beta-lactam antibiotics beta lactamase enzymes produced [1]. The aim of this study was to investigate the patterns of antibiotic sensitivity towards lactam antibiotics and determine the genes PER, VEB and FOC beta lactamase Acinetobacter baumannii isolated from patients in Hospital Mostafa Khomeini in Ilam City.

Methods: In whole, 89 isolates of Acinetobacter baumannii from various clinical specimens were identified by biochemical tests and the antibiotic susceptibility of the identified strains were determined using Kirby-Bauer method, the antibiotics under investigation include: Cephalothin 33/70%, Ceftriaxone 84/26%, Cefotaxime 29/21%, Cefazolin 44/94%, Ceftazidime 19/10%, Cephalixin 60/67%, Ciprofloxacin 38/20%, Trimoxazole 12/35%,. PCR was performed on the samples to evaluate the presence or absence of PER, VEB and FOC genes.

Results: The results of antibiogram showed that the highest amount of resistance is for Ceftriaxone 84/26% and the least amount of resistance is Trimoxazole 12/35%,. Phenotyping evaluation showed that 24 strains (26.96%) were beta-lactamase producers. PCR results showed that 15 strains (62.5%) gene PER and 8 strains (33.33%) gene VEB and 3 strains (12.5%) gene FOX lactamase positive strains producing enzymes

Conclusion: Frequency of Acinetobacter baumannii producing ESBL was 24% in city of Ilam and PER gene in ESBL producing Acinetobacter baumannii isolated is the high frequency gene in Ilam City.

Keywords: PER, VEB, FOC, Acinetobacter baumannii, EBSL

P297 - 1231: BACTERIAL CONTAMINATION OF TOOTH BRUSH

Zeinab Rigi¹

1. Department of biotechnology, Faculty of Basic science , Lahijan Branch, Islamic Azad University, Lahijan, Iran

Background and Aim: Tooth brushes are the most commonly used oral hygiene aid to promote oral health and prevent dental diseases. Contaminated tooth brush can dramatically transport various microorganisms. The aim of this study was to determine bacterial contamination of tooth brushes.

Methods: Eighty tooth brushes were collected. Different agar media such as blood agar and MacConkey agar were used, and incubated at 37 °C for 48 h. Different patterns of colonies were identified based on their colony morphology and standard biochemical tests.

Results: The results of study indicated that, the majority of the tooth brushes were positive for the presence of microorganisms as indicated: *Streptococcus mutans* (47.2%), *S. aureus* (16.8 %), *E. coli* (22.9%) *Pseudomonas* (13.1%).

Conclusion: According to this study, tooth brushes play a major role in retention or retrieval of microorganisms. Thus, it is mandatory for every individual to disinfect his brush at regular intervals.

Keywords: Bacterial contamination-tooth brush- dental disease

**P298 - 1253: CONSIDERATION THE REASONS OF SUPPURATION IN PEDUNCLE DORSAL
IN RAINBOW TROUT IN KERMAN**

Laleh Yazdanpanah¹, shima tasharofi²

1. laleh yazdanpanah
2. shima tasharofi

Background and Aim: Infectious diseases could engage the whole organs of fish and these diseases may be associated to different kinds of bacteria, fungi, parasites and viruses

Methods: In order to developing the knowledge of fish propagation (suppuration in peduncle dorsal) in cold culture water fishes in Kerman province, in the present study, 200 rainbow trout fishes (*Oncorhynchus mykiss*) with average weight of 50-200 g, suffering from fin necrosis, body darkness and/or newly dead, from all over aquaculture farms in Kerman were collected and evaluated for bacterial contamination.

Results: Clinical signs included: exophthalmia, body darkness, blindness, spiral swimming, fin corrosion and bloodshed. Microbiological examinations resulted in recovery of some secondary gram negative and gram positive bacteria belonging to the genera of: *Acinetobacter*, *Aeromonas*, *Citrobacter*, *Pseudomonas* (gram negative) and *Planococos*, *Staphilococos epidermis* (gram positive) which were isolated from liver, spleen and fins

Conclusion: according to this investigation, there is a correlation between environmental changes and bacterial diseases occurrence in the Rainbow trout farms in Kerman province.

Keywords: *Aeromonas hydrophila*- suppuration- peduncle dorsal

P299 - 1255: ISOLATION AND ANTIBIOTIC SUSCEPTIBILITY PATTERNS OF SHIGELLA AND SALMONELLA SPECIES AMONG CHILDREN WITH ACUTE DIARRHEA

Kiana Amiri¹, Kiana Amiri siavashani², akbar mirsalehian³, shahnaz halimi⁴

1. -
2. Department of Clinical Microbiology, School of Medicine, Tehran University of Medical Science
3. Department of Clinical Microbiology, School of Medicine, Tehran University of Medical Science
4. Department of Clinical Microbiology, School of Medicine, Tehran University of Medical Science

Background and Aim: Diarrhoeal diseases are among the most common causes of death in children in developing countries. While Shigella and Salmonella species are among the most important agents causing diarrhoea worldwide, few studies on these pathogens have been conducted in Iran. The purpose of this study was to isolate and serotype Shigella and Salmonella species and determine their resistance to antibiotics from children with acute diarrhea.

Methods: During March and June 2016, 320 samples of suspected acute diarrhoea in children's medical center were collected. Stool culture and standard biochemical tests were conducted. Also antimicrobial susceptibility testing was carried out by disc diffusion method according to the CLSI (2014) for trimethoprim-sulphamethoxazole, ampicillin, ciprofloxacin, cefotaxime and nalidixic acid.

Results: Of 15 Shigella isolates, 8 were identified as Shigella flexneri and 7 as S. sonnei. Of salmonella isolates 6 were identified as type D, 4 type C and 2 type B. (100%) resistance to ampicillin and (25%) resistance to nalidixic acid were seen in Shigella flexneri isolates whereas (28.6%) resistance to ampicillin and (100%) resistance to nalidixic acid were observed in Shigella sonnei isolates. Less than 50% of Shigella isolates were resistant to ciprofloxacin. Also high resistance (66.7%) to nalidixic acid in both salmonella type D and C were observed.

Conclusion: High resistance to two clinically important drugs, ampicillin and nalidixic acid in Shigella and salmonella isolates suggested that clinical utility of these drugs in the treatment of acute diarrhea because of these enteropathogens in children will have received limitation.

Keywords: Serotyping, Antimicrobial susceptibility pattern

**P300 - 1258: COMPARISON OF ANTIBIOTIC RESISTANCE PATTERN OF BACTERIA
CAUSING URINARY TRACT INFECTIONS IN OUTPATIENT AND INPATIENT OF
SHAHIDMOHAMMADI HOSPITAL IN BANDARABBAS**

Fatemeh Poureskandari ¹, Farzaneh Dehghan², Afsaneh Karmostaji³, Nader Zolghadri⁴

1. Student Research Committee, Hormozgan University of Medical Sciences, Bandar Abbas, Iran.
2. Infectious & Tropical Diseases Research Center , Hormozgan University of Medical Sciences, Bandar Abbas, Iran
3. Iranian Social Security Organization, Hormozgan Social Security management, Khalij Fars Hospital of Social Security, Bandar Abbas, Iran
4. Infectious & Tropical Diseases Research Center , Hormozgan University of Medical Sciences, Bandar Abbas, Iran
5. M.Sc Statistics, Department of Mathematics, Islamic Azad University, Sama college, Bandar Abbas, Iran

Background and Aim: Urinary tract infection (UTI) is the most frequent bacterial infections in humans that awareness of antibiotic resistance pattern of isolated bacterial agents in each area has a significant impact on improving infection. This study was conducted to investigate the frequency of UTI, the etiologic microorganisms, and their antibiotic resistance pattern in targeted populations.

Methods: This cross-sectional study was performed on 3300 urine samples from outpatients (1492) and inpatients (1808) admitted into different wards of Shahidmohammadi Hospital in Bandarabbas from March 2014 and July 2015. After identification of causative agents by standard biochemical test, antimicrobial susceptibility test was done by disk diffusion method. Findings were analyzed by SPSS version 22.

Results: The occurrence of UTI in inpatients was 19.6% and in outpatients was 16.1%. Amongst the samples tested, 593 positive culture, 2475 negative culture and 232 mixed growth were isolated. 355 positive cultures were from inpatient and 241 from outpatients. The most common causative pathogen was E. coli in both groups, followed by Klebsiella pneumoniae in inpatients and staphylococcus spp in outpatients. The highest resistance were observed to cotrimoxazole (65.6%) in outpatients and to Ceftriaxone (47.1%) in inpatients, while the lowest resistance were observed to imipenem in both groups.

Conclusion: Similar to those reported in other studies E. coli was the most common microorganisms in UTI in this study, the presence of resistant isolates indicated the existence of resistance mechanisms that could lead to multi-drug resistance phenotype and limits therapeutic options, if infection control policy have not been used.

Keywords: Urinary tract infection, inpatients, outpatients, antibiotic resistant

**P301 - 1263: ISOLATION AND IDENTIFICATION OF BACTEROIDES FRAGILIS FROM
CHRONIC TONSILLITIS, IRAQ**

Maitham ghaly Yousif¹, Dr.Maitham Ghaly Yousif²

1. Al-qadyssia university college of Science biology department Dewnia Iraq
2. Al-qadyssia university college of Science biology department Dewnia Iraq

Background and Aim:Chronic tonsillitis is a common diseases that Infect people of both sexes at different ages, especially in the early stages of life. This study aim to diagnose the aerobic and anaerobic bacteria that cause chronic tonsillitis.

Methods:224 tonsil collected of 112 patients with chronic tonsillitis of Diwaniya Teaching Hospital, between the first of October 2014 until the first of May 2015, patients' ages ranged from (3-40) years, it was 63 (56.25 %) case of male and 49 (43.75 %) case of females. divided tonsils into two groups, the first (112) tonsil and it got 325 bacterial isolates from the surface and core of tonsil

Results:The other groups of tonsils 112 were obtained in which the 57 isolates of B. fragilis group, diagnosed mediated by direct polymerase chain reaction technique (Direct PCR), and has both molecular methods using diagnostic gene (nanH) encoded enzyme neuraminidase. The results showed that possessing all isolates, (30 isolation) gene nanH in the technique of PCR, while the technique of Direct PCR showed (57 isolation) out of (112) tonsil possesses gene nanH, and thus technique of Direct PCR gave a higher proportion of roads bacteriological standard to isolate B.fragilis group.

Conclusion:the results of the analysis also showed a convergence of isolates of B. fragilis bacteria local number (S5 and S6) to the isolation of the B. fragilis registered in the world, USA, NCBI-BLAST B. fragilis (Af 031639.1) and Japan NCBI-BLAST B. fragilis (D28493.1), the bacterial isolates of B. fragilis local number (S4 and S8) appeared different from other isolates apparent in the genetic tree analysis .

Keywords:Isolation ,Bacteroides fragilis ,chronic tonsillitis

Drug Resistance

P302 - 19: A INVESTIGATION ON CLASS 3 INTEGRON BETWEEN ESCHERICHIA COLI CLINICAL SAMPLES, KURDISTAN PROVINCE, IRAN

Rashid Ramazanzadeh¹, Parviz Mohajeri², Samaneh Rouhi³, Sako Akhdar⁴

1. Cellular & Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran. Department of Microbiology, Kurdistan University of Medical Sciences, Sanandaj, Iran.
2. Department of Microbiology, Kermanshah University of Medical Sciences, Kermanshah, Iran.
3. Student Research Committee, Kurdistan University of Medical Sciences, Sanandaj, Iran. Cellular & Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran. Department of Microbiology, Kurdistan University of Medical Sciences, Sanandaj, Iran.
4. Student Research Committee, Kurdistan University of Medical Sciences, Sanandaj, Iran. Cellular & Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran. Department of Microbiology, Kurdistan University of Medical Sciences, Sanandaj, Iran.

Background and Aim: Bacteria may obtain resistance to different antibiotic through the transfer of resistance genes located on mobile DNA elements such as integrons. Studies showed that Multidrug resistance (MDR) in *Escherichia coli* is related to integrons. This study aimed to investigation on class 3 integron prevalence between *E. coli* strains isolated from patients in western Iran (Toohid and Besat hospitals, Sanandaj , Kurdistan Province).

Methods: 120 isolates of *E. coli* were collected from various specimens (urine, stools, blood and body fluid, November 2013 to April 2014). *E. coli* bacterium was identified using standard bacteriological procedures. Then PCR were performed on samples for class 3 integron detection (int 3 in 980 bp). Data were analyzed using SPSS16 and determining the frequency of this gene.

Results: In this study 84 (70%) and 36 (30%) *E. coli* strains were isolated from females and males, respectively. Samples were from urine (107; 89.16%), stools (2; 1.66%), blood (10; 8.33%) and cerebrospinal fluid (1; 0.83%). PCR showed int 3 gene was detected in 8 (6.66%) samples of *E. coli* strains.

Conclusion: Human clinical samples containing int3 *E. coli* and may be a reservoir for antibiotic-resistant genes. These bacteria can spread these genes in the bacteria community. A appropriate health program need for control and prevention of these genes spread.

Keywords: Class 3 Integron, *Escherichia coli*, Clinical Samples

**P303 - 33: HIGH PREVALENCE OF CLINICAL AND ENVIRONMENTAL TRIAZOLE
RESISTANT ASPERGILLUS FUMIGATUS IN IRAN: IS IT A CHALLENGING ISSUE?**

Hamid Badali¹, Mojtaba Nabili², Tahereh Shokohi³

1. Invasive Fungi Research Center, School of Medicine, Mazandaran University of Medical Sciences, Sari, Iran
2. Invasive Fungi Research Center, School of Medicine, Mazandaran University of Medical Sciences, Sari, Iran
3. Invasive Fungi Research Center, School of Medicine, Mazandaran University of Medical Sciences, Sari, Iran

Background and Aim: Triazole antifungal agents are the mainstay of aspergillosis treatment. As highlighted in numerous studies, the global increase in the prevalence of triazole resistance could hamper the management of aspergillosis

Methods: In the present three-year study, 513 samples (213 clinical and 300 environmental samples) from ten provinces of Iran were processed and screened in terms of azole resistance (4 and 1 mg/L of itraconazole and voriconazole, respectively), using selective plates. Overall, 150 *A. fumigatus* isolates (71 clinical and 79 environmental isolates) were detected. The isolates were confirmed by partial sequencing of β -tubulin gene. Afterwards, in vitro antifungal susceptibility tests against triazole agents were performed based on the Clinical and Laboratory Standards Institute (CLSI) M38-A2 document

Results: The CYP51A gene was sequenced in order to detect mutations. The minimum inhibitory concentration of itraconazole against 10 (6.6%) strains, including clinical (n=3, 4.2%) and environmental (n=7, 8.8%) strains, was higher than the breakpoint and epidemiological cut-off value. Based on the findings, the prevalence of azole-resistant *A. fumigatus* in Iran has remarkably increased from 3.3% to 6.6% in comparison with earlier epidemiological research. Among resistant isolates, TR34/L98H mutations in the cyp51A gene were the most prevalent (n=8, 80%), whereas other point mutations (F46Y, G54W, Y121F, G138C, M172V, F219C, M220I, D255E, T289F, G432C, and G448S mutations) were not detected

Conclusion: Although the number of patients affected by azole-resistant *A. fumigatus* isolates was limited, strict supervision of clinical azole-resistant *A. fumigatus* isolates and persistent environmental screening of azole resistance are vital to the development of approaches for the management of azole resistance in human pathogenic fungi

Keywords: Azole-resistant, *A. fumigatus*, Iran

**P304 - 38: FREQUENCY OF VANC GENE IN VANCOMYCIN-RESISTANT ENTEROCOCCUS
ISOLATED FROM CLINICAL SAMPLES**

Vahid Lohrasbi¹, Habib Zeighami², Fakhri Haghi³

1. Master of Science Medical Microbiology ,Zanjan Pharmaceutical Biotechnology Research Center , Zanjan University of Medical Sciences, Zanjan, Iran
2. Assistant Professor of Bacteriology ,Zanjan Pharmaceutical Biotechnology Research Center , Zanjan University of Medical Sciences, Zanjan, Iran
3. Assistant Professor of Bacteriology ,Zanjan Pharmaceutical Biotechnology Research Center , Zanjan University of Medical Sciences, Zanjan, Iran

Background and Aim:Enterococci are a part of the normal flora of the human gastrointestinal tract and play an important role in the spread of resistance genes and produce antibiotic-resistant strains. Vancomycin-resistant enterococci (VRE) are one of the major nosocomial pathogens in worldwide. The aim of this study was to investigate the frequency of phenotype and genotype of vanC gene in vancomycin resistant Enterococci isolated from clinical samples in 2015.

Methods:After isolating and identifying 100 strains of enterococci from clinical specimens ,the enterococcus isolates were identified by biochemical confirmation tests. Resistance of each isolate to vancomycin determined by disk diffusion and MIC test and was tested for the presence of the vanC genes by PCR.

Results:The results of the 100 isolates of enterococci collected from clinical specimens showed 21 (21%) enterococcus was resistant by disk diffusion method to vancomycin and using MIC test ,15 (15%) enterococci was resistant in high level to vancomycin. PCR assay of 21 samples showed 1 patients (4.7%) included vanC gene.

Conclusion:Based on the results of the present study ,the rate of isolation of vanC-containing strains was lower than other resistant genes. PCR has a high specificity compared to other phenotypic methods MIC test and disk diffusion method.

Keywords:Enterococcus, Vancomycin-Resistant Enterococci, VanC

P305 - 41: BLOODSTREAM BACTERIAL PATHOGENS AND THEIR ANTIMICROBIAL RESISTANCE PATTERN IN RASHT, IRAN

Abdol-Rasoul Sobhani¹, Mahin Mallaei², Samaneh Kazemi³

1. Department of Pharmacology, School of Medicine, Guilan University of Medical Sciences, Rasht, IR Iran
2. Vice-Chancellor of Research and Technology, Guilan University of Medical Sciences, Rasht, IR Iran
3. Vice-Chancellor of Research and Technology, Guilan University of Medical Sciences, Rasht, IR Iran

Background and Aim: The choice of antimicrobial treatment for septicemia is often empirical and based on the knowledge of local antimicrobial activity patterns of the most common bacteria causing such bloodstream infections. This study was carried to identify the microbial profile in the blood culture isolates and their antibiotic susceptibility patterns.

Methods: This retrospective cross sectional study was done at Razi Hospital, Rasht, Iran over a period of Thirteen months from August 2012 to September 2013. Bacteria were identified by various biochemical tests and antimicrobial susceptibility testing of the isolates was performed by Kirby-Bauer disc diffusion method.

Results: Out of 954 culture positive processed, Gram-negative isolates were 482 (50.58%) followed by Gram-positive isolates 471 (49.42%). Among Gram-positive organisms *Staphylococcus epidermidis* was the highest (255 (54%)) and in Gram-negative bacteria *Pseudomonas* spp. was highest (241 (50%)). There were 467 (49.0%) positive blood culture reports for males and 487 (51.0%) for females. *Pseudomonas* spp. (134 reports) and *Staphylococcus epidermidis* (162 reports) were the most common pathogens in male and woman, respectively. In 15-44 years age group, *Pseudomonas* spp. and in 45-75< years age group, *Staphylococcus epidermidis* were identified as the most common. *Staphylococcus epidermidis* strains were more resistant to Erythromycin, Oxacillin and Doxycycline. *Pseudomonas* spp. isolates had more resistant to Imipeneme, Amikacin and Cefalexin.

Conclusion: It can be concluded that resistant to majority of the antibiotics for several pathogens used in bloodstream infections can make complication in treatment of infection cause by them.

Keywords: Blood-Borne Pathogens, Anti-Bacterial Agents, Bacteria

**P306 - 46: HIGH LEVEL DISINFECTANT RESISTANCE IN CLINICALLY ISOLATED ESBL
POSITIVE E. COLI IN A TERTIARY CARE HOSPITAL**

Maryam Shafaati¹, Mohammadreza shafaati²

1. Department of Microbiology Science, Islamic Azad university_Jahrom beranch, Fars, Iran
2. Department of cellular and Molecular Biology Science, Islamic Azad university_Hamadan beranch, Hamadan, Iran.

Background and Aim: There are growing concerns about involvement of disinfectants in increased resistance to antibiotics, worldwide. This cross sectional study was designed to assess the association of commonly used disinfectant, 'didecyl di-methyl ammonium chloride' (DDAC), with antibiotics and disinfectant resistance genes in E. coli.

Methods: One hundred and two isolates of E. coli strains from the hospital of Tehran Heart Center were isolated from clinical specimens including urine, stool, blood, tracheal secretions and wounds. Sensitivity of E. coli strains to the disinfectant and sixteen antibiotics were assessed using several complementary and confirmatory methods. Then, existence of resistance genes of qacE and qacEΔ1 were identified using PCR and validated by sequencing. Finally, correlation between resistance to antibiotics, disinfectant and resistance genes were analyzed. As a result, most of the ESBL positive cells were positive for resistance genes, too.

Results: Significantly, these strains were resistance to moderate concentrations of DDAC solutions and antibiotics in comparison to qacE and qacEΔ1 negative strains. Frequency of positive cells for resistance genes were higher including 89.2 and 81.4% for qacE and qacEΔ1, respectively. These strains were also more resistant to beta-lactam antibiotics.

Conclusion: Our results indicate that resistance genes of qacE and qacEΔ1 are probably involved in development of antibiotic resistance which can be hindered by applying appropriate doses of disinfectants. Importantly, applying ineffective doses of disinfectants may be involved in occurrence of multi-drug resistant strains of E. coli.

Keywords: Escherichia coli, Quaternary ammonium compounds, qacE, qacEΔ1, antibiotic resistance, resistance to disinfectant, biocide resistance

**P307 - 47: THE PREVALENCE SURVEY AND ANTIBIOTIC RESISTANT IN ENTEROCOCCI
SPP. ISOLATED FROM DELIVERY ROOMS OF TWO UNIVERSITY HOSPITAL IN QOM,
IRAN IN 2015**

Faezeh Kabiri¹, somayeh momenyan²

1. Master of Sciences in Microbiology, Qom university of medical sciences, Qom, iran
2. PhD candidate in Biostatistics, Paramedical sciences Faculty, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim:Background and Objectives: Enterococci are generally regarded as normal flora of human body and considered as the second leading cause of nosocomial infections and the third most common cause of hospital associated bacteraemia. this study was performed to assess the prevalence and drug resistance of Enterococcus species isolated from delivery rooms through biochemical methods

Methods:two hundred sixteen samples were isolated from delivery rooms of two university hospital in Qom from june to september, 2015. The samples were cultured on blood agar, bile esculin azide agar and some special cultures of isolation of Enterococcus species. Suspension of bacteria was grown in Mueller Hinton agar and the inhibition zone diameter was determined by disk antibiogram

Results:Of 216 samples, 7(3.2%) were enterococci. In all of 7 cases, three showed resistance to ampicillin, one to gentamicin, one to ciprofloxacin, zero to chloramphenicol, three to Tetracycline, one to vancomycin, three to Erythromycin and one to Streptomycin.

Conclusion:It seems to be necessary to use drug sensitivity test for having appropriate treatment and preventing from resistance strains.

Keywords:Enterococci, Antibiotic Resistance, Antibiogram

**P308 - 61: RESISTANCE TO NALIDIXIC ACID AND AZITHROMYCIN IN SALMONELLA
ENTERIC STRAINS ISOLATED FROM BLOOD STREAM INFECTION**

Mojtaba Anvarinejad¹, Gholam Reza Pouladfar², Bahman Pourabbas³, Maneli Amin Shahidi⁴, Noroddin Rafaatpour⁵, Mohammad Ali Dehyadegari⁶, Pejman Abbasi⁷, Jalal Mardaneh⁸

1. Professor Alborzi Clinical Microbiology Research Center, Nemazee Hospital, Shiraz University of Medical Sciences, Shiraz, Iran.
2. Professor Alborzi Clinical Microbiology Research Center, Nemazee Hospital, Shiraz University of Medical Sciences, Shiraz, Iran.
3. Professor Alborzi Clinical Microbiology Research Center, Nemazee Hospital, Shiraz University of Medical Sciences, Shiraz, Iran.
4. Professor Alborzi Clinical Microbiology Research Center, Nemazee Hospital, Shiraz University of Medical Sciences, Shiraz, Iran.
5. Professor Alborzi Clinical Microbiology Research Center, Nemazee Hospital, Shiraz University of Medical Sciences, Shiraz, Iran.
6. Professor Alborzi Clinical Microbiology Research Center, Nemazee Hospital, Shiraz University of Medical Sciences, Shiraz, Iran.
7. Professor Alborzi Clinical Microbiology Research Center, Nemazee Hospital, Shiraz University of Medical Sciences, Shiraz, Iran.
8. Department of Microbiology, School of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran.

Background and Aim: Salmonellosis is a type of food poisoning caused by the *Salmonella enterica* bacterium. Antibiotic resistant of *Salmonella* is an increasing public health emergency since infections from resistant bacteria are more difficult and costly to treat. The goal of the this study was to investigate the isolation of *Salmonella* spp. from blood by BACTEC automated system, and determination resistance rate to nalidixic acid and azithromycin by disc diffusion and agar dilution methods.

Methods: A total of 19 *Salmonella* spp. isolated consecutively from blood samples of patients with BACTEC between 2008 and 2014 in Shiraz, Iran, were tested. The isolates were identified as salmonella, based on biochemical tests embedded in the API-20E system. In order to characterization of biogroups and subspecies biochemical tests were used. Susceptibility testing (disc diffusion and agar dilution) was performed according clinical and laboratory standards institute (CLSI) guidelines.

Results: Of the total 19 *Salmonella* spp. isolates recovered by BACTEC automated system, five isolates (26.5%) were resistant to azithromycin. Six (31.5%) isolates displayed resistance to nalidixic acid in disc diffusion method and 5(26.3%) isolates in agar dilution method (MIC >32 µg/ml). Three isolates were co-resistant to nalidixic acid and azithromycin.

Conclusion: These results indicate that multidrug-resistant (MDR) strains of *Salmonella* are rising, and fewer antibiotics may be useful for treating *Salmonella enterica* infections. Routine investigation and reporting of antibiotics MICs in patients presenting with *Salmonella* infections is suggested.

Keywords: Blood stream infection, BACTEC automated system, *Salmonella* spp., antimicrobial resistance, nalidixic acid, azithromycin.

**P309 - 62: THE BLACK SEED MINIMAL BACTERICIDAL CONCENTRATION AGAINST
GRAM POSITIVE BACTERIA**

Alireza Mohammadzadeh¹, Jalal Mardaneh², Hamed Biglari³, Faeze Momen⁴, Leila Mollaie Kandelus⁵

1. Department of Microbiology, School of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran.
2. Department of Microbiology, School of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran.
3. Department of Environmental Health Engineering, School of Public Health, Gonabad University of Medical Sciences, Gonabad, Iran.
4. Student Research Committee, Gonabad University of Medical Sciences, Gonabad, Iran.
5. Department of Experimental Sciences, Education and Training of Bajestan, Bajestan, Iran.

Background and Aim: The seeds of *Nigella Sativa* Linn. (Ranunculaceae), commonly known as black seed or black cumin has been used for medicinal purposes in different country. It has been traditionally used for a variety of conditions and treatments. The goal of this study was the survey antibacterial effects of black seed alcoholic extract on gram positive bacteria including methicillin-resistant *Staphylococcus aureus* (MRSA), *Streptococcus agalactiae* and *Listeria monocytogenes*.

Methods: The minimum bactericidal concentrate of black seed alcoholic extract was determined by agar dilution method. Various concentrations of grape seed extract were mixed along with Muller Hinton agar to obtain extract concentration. MHA were inoculated with 20 μ L of microbial suspension which approximately contained 10⁴ CFU/spot. The agar plates were incubated at 37°C for 18 to 24 hours and observed for subsequent microbial growth.

Results: The black seed MBC for methicillin-resistant *Staphylococcus aureus* (MRSA), *Streptococcus agalactiae* and *Listeria monocytogenes* was 100 mg/ml, 3.125 mg/ml and 200 mg/ml, respectively. In disk diffusion method for MRSA the zone inhibitor diameter around paper disks containing 40 mg/disk and 80 mg/disk was 10 mm and 15 mm respectively.

Conclusion: Our results showed that *Nigella Sativa* Linn. extract produce antimicrobial activity against a broad range of microbes and especially against multiple-antibiotic resistant bacteria. Further studies on the activity-directed fractionation for the isolation of respective pure compounds may result in interesting outcomes.

Keywords: Alcoholic extract, black seed, antibacterial effect, *Staphylococcus aureus* (MRSA), *Streptococcus agalactiae* and *Listeria monocytogenes*.

**P310 - 63: DETECTION CARBAPENEM-RESISTANT PSEUDOMONAS AERUGINOSA
ISOLATES BY PHENOTYPIC METHODS**

Jalal Mardaneh¹, Zahra Rabani²

1. Department of Microbiology, Faculty of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran.
2. Department of Microbiology, Fars Science and Research Branch, Islamic Azad University, Shiraz, Iran.

Background and Aim: *Pseudomonas aeruginosa* is a ubiquitous organism present in many diverse environmental settings, and it can be isolated from hospitalized patients. *P. aeruginosa* presents a serious therapeutic challenge for treatment of both community-acquired and nosocomial infections. The goals of this study were phenotypic detection of carbapenemase producing *Pseudomonas aeruginosa* strains isolated from hospitalized patients and determination of their resistance to carbapenems by disk diffusion and E-test.

Methods: In the present cross-sectional study, clinical samples from hospitalized patients were collected and culture was done on appropriate media. Final identification was performed using biochemical tests and API 20NE system. According to the protocol CLSI 2014 disc diffusion, modified hodge test (MHT) and E-test were used for antibiotic susceptibility, carbapenemase production, and MIC values of imipenem respectively.

Results: In the current study, 45 isolates of *Pseudomonas aeruginosa* were obtained from hospitalized patients, consisting of 19 males (42.2 %) and 26 females (57.8%). As revealed 77.8% of isolates showed response to group 2 carbapenems (imipenem, meropenem). MHT was positive for all carbapenem resistant isolates. All imipenem resistant strains had the MIC more than 32.

Conclusion: The isolation of carbapenem-resistant *P. aeruginosa* strains is alarming and requires the implementation of strict infection control measures in order to prevent the spread of carbapenemase encoding genes to unrelated clones or to other bacterial species in hospital environment.

Keywords: Hospital infection, *Pseudomonas aeruginosa*, carbapenem-resistant, disk diffusion, E-test, modified hodge test.

**P311 - 64: COMPARISON THE EFFECT OF STEVIA EXTRACT WITH GLUCOSE AND
FRUCTOSE ON DENTAL ENAMEL CARIES FORMATION**

Seyed mostafa Hosseini¹, jalal ghaderkhani², Farshid Vahdatinia³

1. Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran
2. Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran
3. Dental School, Hamadan University of Medical Sciences, Hamadan, Iran

Background and Aim: According to the sweetening effect and antibacterial activity of Stevia extracts against cariogenic bacteria, the purpose of this in-vitro study is to compare the experimental effect of Stevia extract with Glucose and Fructose on enamel demineralization.

Methods: In this laboratory study, 72 premolar teeth were divided into 6 experimental groups as experimental study as Acetone, Ethanol, Methanol and Aqueous extracts 20% and Glucose Fructose solution 20%. Each group of teeth was located in a bottle of cariogenic material for 28 days. After 28 days, a section of buccal surface of each tooth was separated and evaluated in terms of the caries depth. Data analysis was applied using SPSS version 21, analysis of variance (ANOVA) and post hoc tukey tests were used at the significant level of 0.05

Results: The mean and standard deviation of the caries depth induced by the glucose, fructose, methanol, and water extracts were 237.08 ± 26.48 , 216.08 ± 26.57 , 88 ± 16.69 , and $170.66 \pm 35/53$, respectively. Acetone and Ethanol extracts did not cause caries. The groups were statistically different in mean revealed by ANOVA test ($p\text{-value} < 0.05$). The demineralization depth induced by methanol, ethanol, acetone, and water extracts differed one from another, however, there was not observed any difference between glucose and fructose in this regard.

Conclusion: According to the results of present study, the enamel caries depth of stevia extracts, especially acetone and ethanol ones, were less than conventional sweeteners such as glucose and fructose.

Keywords: Stevia, Glucose, Fructose, Tooth caries.

**P312 - 67: SURVEY OF DISTRIBUTION RATES AND ANTIBIOTIC RESISTANCE PATTERN
OF GROUP B STREPTOCOCCI (STREPTOCOCCUS AGALACTIAE) STRAINS ISOLATED
FROM CLINICAL SPECIMENS**

Seyed mostafa Hosseini¹, farzaneh moradi², Mohammad Reza Arabestani³

1. Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran
2. Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran
3. Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran

Background and Aim: The aims of the current study were to determine their antibacterial susceptibility patterns with a special focusing on susceptible or resistant strains to macrolides and lincosamides antibiotics; and also to determine possible antibiotic resistance mechanisms occurring in GBS strains using PCR assay and disk diffusion method in Hamadan.

Methods: A total of 62 GBS clinical strains, including vaginal swabs, urine cultures and blood culture isolates were examined. Antibacterial susceptibility testing was performed using the disk diffusion method and inducible resistance test for clindamycin by standard double disk diffusion or D-zone test for all isolates to differentiate macrolide resistance phenotype (M), constitutive Macrolide-Lincosamide-Streptogramin B phenotype (cMLSB) and induced Macrolide-Lincosamide-Streptogramin B phenotype (iMLSB).

Results: All 62 isolates were susceptible to penicillin, ampicillin, linezolid, cefazoline and vancomycin. However, 93.5% (n=58) of isolates were shown an increased MIC to penicillin. The overall rate of erythromycin resistance was 35.5% (n=22). All erythromycin-resistant isolates displayed the M phenotype (100%, n=22). All the three erythromycin resistance genes (i.e. ermTR, ermB and mefA/E) were found in erythromycin-resistant isolates. There was not observed any resistance to clindamycin and quinupristin-dalfopristin antibiotics.

Conclusion: It was concluded from the present study that prescribing antibiotic without antibacterial susceptibility tests should be prevented because of the high prevalence of erythromycin-resistant GBS strains and the fact that erythromycin-resistant GBS strains has shown an increased MIC to penicillin, as the choice-drug for treating GBS infections.

Keywords: Streptococcus agalactiae; Group B Streptococci; Capsular genotyping; Polymerase Chain Reaction; Antibacterial susceptibility; Macrolide-Lincosamide-Streptogramin B

**P313 - 71: HIGH PREVALENCE OF MULTIPLE DRUG RESISTANCE (MDR) AMONG
ESBLs-PRODUCING KLEBSIELLA PNEUMONIAE ISOLATED FROM HOSPITALIZED
PATIENTS IN ISFAHAN, IRAN**

Zahra Tahanasab¹, Jamshid Faghri ², Sina Mobasherizadeh³, Mehdi Moghadampour ⁴, Aliakbar Rezaei ⁵,
Nafiseh Maleki⁶

1. Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
2. Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
3. Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
4. Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
5. Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
6. Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran

Background and Aim: This study was to evaluate the prevalence of CTX-M and TEM type ESBLs-producing *K. pneumoniae* and determination of MDR, XDR, and PDR phenotype of these isolates as well as find out the genetic relationship and molecular typing of these isolates using phenotypic and genotypic methods.

Methods: 96 non-repetitive *K. pneumoniae* isolates were isolated from hospitalized patients in Al-Zahra hospital of Isfahan, Iran. The antibiotic susceptibility testing was assessed for 20 antibiotics using Kirby-Bauer disk diffusion method. The frequency of ESBLs-producing isolates was determined by phenotypic confirmatory test. All ESBLs-producing isolates were assessed for blaTEM and blaCTX-M genes using PCR method. Molecular typing was performed by enterobacterial repetitive intergenic consensus sequence-based PCR (ERIC-PCR).

Results: Among 96 isolates, 58 isolates (60.4%) were ESBLs-producer. In this study, 85.7% and 30.3% of ESBLs-producing isolates showed MDR and XDR phenotype, respectively, while there was no isolate PDR. PCR amplification on ESBLs-producing isolates showed that 47(81%) isolates were carried blaTEM gene, while blaCTX-M gene was detected in all isolates (100%). ERIC-PCR typing was characterized the high genetic similarity among ESBLs-producing *K. pneumoniae* isolates and revealed 32 band patterns for these isolates.

Conclusion: This study showed the high prevalence of important ESBLs genes (blaCTX-M and blaTEM genes) among the *K. pneumoniae* isolated from inpatients. Constant following of ESBLs, also identification of their types, in bacteria isolated from hospitalized patients have an important clinical impact, since; it can often provide valuable information for the choice of appropriate antibacterial therapy and decrease of antibiotic resistance.

Keywords: *Klebsiella pneumoniae*, MDR, ESBLs, TEM, CTX-M, ERIC-PCR

**P314 - 75: DETECTION OF BLA NDM -1, BLA VIM AND BLA IMP GENES IN
ACINETOBACTER BAUMANNII AT TEHRAN HOSPITALS BY PCR AND GENE
SEQUENCING**

Yousef Erfani¹, Arezoo Rasti²

1. Department of Medical laboratory Sciences, School of Allied Medical Sciences, Tehran University Medical Sciences, Tehran, Iran
2. Oncopathology Research Centre, Iran University Medical Sciences, Tehran, Iran yerfani@sina.tums.ac.ir

Background and Aim: *Acinetobacter Baumannii* is one of the non-fermentative Gram-negative bacilli which cause serious infections. Because of its ability to produce β -lactamase, this organism is often resistant to β -lactam drugs. The aim of this study is to investigate the prevalence of metallo β -lactamases (MBL) genes (*bla* NDM -1, *bla* VIM and *bla* IMP) among isolated multidrug-resistant (MDR) *A. Baumannii*.

Methods: A total of 107 imipenem and meropenem resistant *A. Baumannii* isolated from patients at three hospitals in Tehran were included in the study. Antimicrobial susceptibility was determined by disk diffusion agar method according to CLSI recommendation. MBL enzyme production was performed by CDDT. Polymerase chain reaction (PCR) was performed for the detection of MBL (*bla* NDM -1, *bla* VIM and *bla* IMP) genes. Gene sequencing was performed for representative isolates.

Results: Of 107 imipenem and meropenem resistant *A. Baumannii*, 99 (92.5%) were MBL enzymes producing by CDDT phenotypic method. After conducting PCR, 64 cases (60.4%) were VIM positive. Furthermore *bla* NDM-1 and *bla*-IMP were not observed in isolated *A. Baumannii*.

Conclusion: Patients with bacteria carrying MBLs cannot be treated easily and because the genes producing these enzymes are on moving genetic elements, we should think about isolating these patients to avoid indiscriminate use of antibiotics and also reduce the costs of long-term treatment.

Keywords: *Acinetobacter Baumannii*, MBL genes, PCR

**P315 - 78: IDENTIFICATION OF DRUG RESISTANT ACINETOBACTER BAUMANNII
AMONG BURN PATIENTS**

Saeed Shoja¹, Mojtaba Moosavian², Amir Peymani³, Soodabeh Rostami⁴, Khadijeh Ahmadi⁵, Nasim Ebrahimi⁶

1. Infectious Diseases and Tropical Medicine Research Center, Hormozgan University of Medical Sciences, Bandar Abbas, Iran
2. Department of Microbiology, Faculty of Medicine, Infectious & Tropical Diseases Research Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Ir
3. Department of Microbiology, Qazvin University of Medical Sciences, Qazvin
4. Nosocomial Infections Research Center, Isfahan University of Medical Sciences, Isfahan, Iran
5. Department of Microbiology, Faculty of Medicine, Infectious & Tropical Diseases Research Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
6. Department of Microbiology, Faculty of Medicine, Infectious & Tropical Diseases Research Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Background and Aim: Burn patients are especially susceptible for infection with resistant bacteria such as carbapenem resistant *Acinetobacter baumannii*. The aim of present study was to determination of antimicrobial susceptibility profile and detection of oxacillinase genes among *A. baumannii* collected from burn patient.

Methods: During a one year period, 40 non duplicate isolates of *A. baumannii* were collected from burns patients (colonization or infection) who were hospitalized at Taleghani hospital at Ahvaz, sought west of Iran. All isolates were subjected to Antimicrobial susceptibility test. Multiplex PCR was performed for detection of blaOXA-23-like, blaOXA-24-like and blaOXA-58-like.

Results: The highest rate of resistance was observed for aztreonam (100% resistant) and ciprofloxacin (97.5% resistant). Furthermore, the rate of resistance to other antibiotics was high and 92.5% of isolates were resistant to imipenem, meropenem ceftazidime, rifampin, piperacillin, piperacillin-tazobactam cefepime and ceftriaxone. Polymyxin B, colistin and ampicillin-sulbactam were the most effective antibiotics and 100%, 97.5% and 72.5% of isolates were susceptible respectively. According to the result of multiplex PCR, 70% (28 of 40 isolates) and 20% (8 of 40 isolates) were positive for blaOXA-23-like and blaOXA-24-like respectively. All isolates were negative for blaOXA-58-like.

Conclusion: Due to high resistant rate, it seems that selection of effective antibiotics is limited. Carbapenems cannot use for treatment of these patients. Since, the vast majority of isolates were positive for blaOXA-23-like and blaOXA-24-like possibly these genes are involved in carbapenem resistance. Control and prevention of spread of *A. baumannii* in burns units is necessary.

Keywords: *Acinetobacter baumannii*, Drug Resistant, Burn patients

**P316 - 88: ANTIBIOTIC RESISTANCE OF KLEBSIELLA PNEUMONIA ISOLATES IN
URINARY TRACT INFECTIONS IN IMAM KHOMEINI HOSPITAL, SHIRVAN, IRAN, 2015**

Moein Hamidi hesari¹, Meead Bani Torfi², Jafar Hemmat³, Norkhoda Sadeghifard⁴

1. . Master of Microbiology, Imam Khomeini Hospital, Shirvan, Iran; Email: microbiologym2@gmail.com
2. MSc student of Microbial Biotechnology, Biology Group, Islamic Azad University, Sabzevar branch, Iran;
3. Assistant Professor of Biotechnology Research Institute, Biotechnology Research Institute, Iranian Research Organization for Science and Technology, Tehran, Iran; Email: j.hemmat@gmail.com
4. Professor of microbiology, Microbiology Research Center, Ilam University of Medical Sciences, Ilam, Iran; Email: Sadeghifard@gmail.com

Background and Aim: Urinary tract infection (UTI) is one of the most common infections in different age groups. *Escherichia coli*, followed by *Klebsiella pneumonia*, is the most important agent for UTI across the world. *K. pneumonia*, an opportunistic pathogen, plays a key role in 6-17% of UTIs. Observing more than 105 CFU/mL of a bacterium in urine samples indicates UTI. Given the importance of UTI and an increase in antibiotic resistance of *K. pneumonia*, its isolates were investigated in terms of antibiotic resistance in Imam Khomeini Hospital, Shirvan, Iran.

Methods: Urine samples collected were cultured in medical laboratory of Imam Khomeini Hospital. After *K. pneumonia* isolates were approved verified based on biochemical tests, the disc diffusion method was used to investigate resistance to antibiotics such as ampicillin, cephalothin, nitrofurantoin, cefazolin, trimethoprim-sulfamethoxazole, gentamicin, ofloxacin, cefotaxime, ceftriaxone, cefixime, cephalixin, ciprofloxacin, norfloxacin, ceftizoxime, ceftazidime, ceftiofloxacin based on CLSI standards

Results: A total of 202 urine cultures were positive in 2015, of which 34 (16.8%) were *K. pneumonia*. More than two thirds (70.58%) of the isolates were resistant to ampicillin; 52.9% to cephalothin, 41.1% to nitrofurantoin, 38.2% to cefazolin, 35.2% to trimethoprim-sulfamethoxazole, 32.3% to gentamicin, 29.4% to ofloxacin, 23.5% to cefotaxime, 20.5% to ceftriaxone, 17.6% to cefixime, 17.6% to cephalixin, 14.7% to ciprofloxacin, 11.7% to norfloxacin, 11.7% to ceftizoxime, 8.8% to ceftazidime and 5.88% to ceftiofloxacin.

Conclusion: *K. pneumonia* isolates; therefore, showed the highest antibiotic resistance to ampicillin and cephalothin, while the lowest resistance was observed to ceftiofloxacin. Attending to antibiotic resistance pattern is the key to adopting an efficient therapeutic method.

Keywords: Antibiotic resistance, *klebsiella*, urinary tract infection

**P317 - 109: EMERGING OF A NEW ANTIBIOTIC RESISTANCE BACTERIA PATHOGEN,
ACINETOBACTER LWOFFII IN WATER ENVIRONMENTS AND THEIR PATHOGENIC
EFFECTS**

Maryam Dadar¹, Milad Adel², Mohammad Jalil Zorriehzahra³

1. Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran.
2. Aquatic animal Health & Diseases Dept., Iranian Fisheries Science Research Institute (IFSRI), Agricultural Research Education and Extension Organization (AREEO), Tehran, I.R. Iran
3. Aquatic animal Health & Diseases Dept., Iranian Fisheries Science Research Institute (IFSRI), Agricultural Research Education and Extension Organization (AREEO), Tehran, I.R. Iran

Background and Aim: Whereas it is well documented that genus of *Acinetobacter* is associated with antibiotic resistant bacteria and human clinical infections, there are very few studies to date that report it as an emerging new pathogen for fish. The purpose of this study is to trace antibiotic resistant bacteria of water environments and to encourage immediate action to address the threat.

Methods: During a period of antibiotic resistance bacteria incidence at 2015, 100 moribund rainbow trout weighing 70 ± 30 g, originate from one farm, in Khuzestan province, (Southwest of Iran) was investigated.

Results: In the present study, *A. lwoffii* was isolated from diseased rainbow trout (*Oncorhynchus mykiss*) from Dezful farm, Khuzestan province, Iran by both biochemical tests and polymerase chain reaction (PCR)-based methods and further confirmed as the causative agent by infectivity experiment.

Conclusion: This is the first report on *A. lwoffii* as a virulent and multiresistant pathogen for farmed rainbow trout. Drug resistance of isolates and minimal inhibitory concentration (MIC) was examined and showed that *A. lwoffii* was multiresistant to 8 antimicrobial agents tested. The presence of *A. lwoffii* in farmed rainbow trout would increase the possibility of coinfection between fish and human via handling or food.

Keywords: *Acinetobacter lwoffii*, Drug resistance, *Oncorhynchus mykiss*

**P318 - 111: DESIGN AND DISCOVERY OF ANTIBACTERIALS TARGETING
RIBOSWITCHES: BACKGROUND AND PERSPECTIVES**

Elnaz Mehdizadeh Aghdam¹

1. Department of Pharmaceutical Biotechnology, Faculty of Pharmacy, Tabriz University of Medical Sciences, Tabriz, Iran

Background and Aim: In the last decades, it is confirmed that RNA is not just an intermediate molecule for making the proteins; as different types of RNA molecules play important roles in the cell surviving. Riboswitches are cis-acting RNAs usually located in the 5' untranslated region of mRNAs and regulates the transcription and/or translation of adjacent genes.

Methods: The genes are usually important in virulence or cell survival and making them down-regulated could possibly results in the inactivation or death of harmful bacteria. On the other hand, the unique characteristics of riboswitches in selective and specific bindings to small molecules without the interpretation of proteins, make them interesting targets to manipulate the gene regulation.

Results: In this way, computational approaches as well as experimental methods are utilized to design new compounds as novel antimicrobial agents.

Conclusion: Here we are going to discuss specially on the studies about the development of approaches for riboswitch-based antibiotics design and discovery.

Keywords: riboswitch, antibiotic, drug design

**P319 - 116: ANTIBIOTIC RESISTANCE IN YERSINIA ENTEROCOLITICA ISOLATED FROM
BROILER MEAT IN ARDABIL**

Somayeh Shekari¹, Mehdi ghiyamid²

1. Department of microbiology faculty of science Islamic azad university Ahar branch .Ahar Iran
2. Department of microbiology faculty of science Islamic azad university Ahar branch .Ahar Iran

Background and Aim: *Yersinia enterocolitica* is a gram negative bacteria which is in the family of *Enterobacteriaceae* which causes a wide range of diseases in human including, *Yersinia enterocolitica*, Gastroenteritis, Septicemia, Mesenteric lymphadenitis, Pharyngitis, and Appendicitis. Regarding that overuse of therapeutic antibiotics in poultry causes drug resistance and probable transmission of this resistance to human, current study aims to investigate antibiotic resistance of *Yersinia enterocolitica* separated from broiler meat in Ardabil compared to common antibiotics used in veterinary.

Methods: 264 broiler samples were randomly chosen and were examined in terms of contamination to *Yersinia enterocolitica*. Antibiotic susceptibility of strains was investigated by Kirby-Bauer Method using common antibiotic disks consuming in veterinary and local level.

Results: 59 (22.34%) broiler samples were contaminated to *Yersinia enterocolitica*. Results of AntibioGram pattern of strains showed that they were resistant to Ampicillin 84.74%, Cephalotin 64.49%, Cephalixin 64.4%, Amoxicillin 55.93%, Nalidixic Acid 33.89%, Methicillin 15.25%, Tetracycline 11.86%, Azithromycin 10.16%, and Gentamicin 3.38%. and no resistance observed to Chloramphenicol and ciprofloxacin.

Conclusion: Regarding the high percent of resistance of strains to several common antibiotics and their overuse, it is recommended to avoid unnecessary use of antibiotics in poultry and observe the period of avoidance from broiler consumption after prescription of antibiotics.

Keywords: *Yersinia enterocolitica*, antibiotic resistance, broiler meat, Ardabil

P320 - 135: EVALUATION OF SALMONELLA ENTERITIDIS RESISTANCE TO BETA-LACTAM DRUGS IN KHUZESTAN PROVINCE

Sedighe Zandi¹, Abbas Doosti²

1. own
2. Supervisor

Background and Aim: Introduction and Objectives: Salmonella Enteritidis, is a member of Enterobacteriaceae family and it gram negative bacilli and optional anaerobic. Salmonella causes different illnesses including gastroenterite and typhoid fever. Salmonella causes numerous examples of beta-lactamase enzyme expression (ESBL).

Methods: In this research, two hundred samples of chicken waste from the villages of province Khuzestan were collected. After cultivation and isolation of salmonella by using of disc diffusion method medicinal resistance towards 9 of the antibiotics was assessed.

Results: The greatest resistance belongs to drugs like Penicillin 100 %, Cephalexin 97/2%, Cephalothin 94.4%, Ampicillin 87/3%, Cefazolin 67/6%, Ceftriaxone 56/2%, Cefotaxim 49/3%, Azithromycin 36/6%, Ceftizoxime 22/6%.

Conclusion: In this study salmonella bacteria show high resistance towards antibiotic discs belonging to penicillin, Ampicillin, Cephalexin and cephalothin. Between this Beta-Lactam drug Ceftizoxime and Azithromycin showed the low resistance to treatment of a disease caused by salmonella. Better use of these drugs.

Keywords: Resistance/Bactry/ Salmonella Enteritidis/B-lactam drug / province Khuzestan

P321 - 139: PREVALENCE AND ANTIBIOTIC SUSCEPTIBILITY IN KLEBSIELLA PNEUMONIAE ISOLATES FROM PATIENTS WITH URINARY TRACT INFECTION, ISFAHAN, IRAN.

Nafiseh Maleki¹, jamshid faghri², sina mobasherizadeh³, ali akbar rezaei⁴, zahra tahananab⁵, razieh dehbanipour⁶

1. Isfahan university of medical science
2. Isfahan university of medical science
3. Isfahan university of medical science
4. Isfahan university of medical science
5. Isfahan university of medical science
6. Isfahan university of medical science

Background and Aim: Extended spectrum β -lactamase (ESBL) production is a significant resistant mechanism to β -lactams in Enterobacteriaceae specially in *Klebsiella pneumoniae*. The main objectives of this study were to genetically characterize urinary clinical isolates of *K. pneumoniae* through the investigating of blaTEM, blaCTX-M and using molecular typing by ERIC-PCR. We also determined the frequency of antibiotic resistance of *K. pneumoniae* strains to characterize the β -lactamases included.

Methods: Materials and Methods: A cross sectional study was performed to evaluate 98 strains of *K. pneumoniae* isolated from urine culture of outpatients referred to Al-Zahra hospital, Isfahan, Iran. Antibiotic susceptibility testing was performed by disc-diffusion method. Screening of ESBLs was carried out using Combination Disc Method. PCR technique was performed to detect TEM and CTX-M genes. The total DNA of each strain was tested by Enterobacterial repetitive intergenic consensus PCR.

Results: Results: In 98 *K. pneumoniae* studied clinical isolates, 25.5% were ESBL producing and % 44.9 MDR. From 25 ESBL isolates 23 (92%) cases showed MDR phenotype. In ESBL producing isolates 23(92%) were bla CTX-M and 19 (%76) bla TEM positive. The antimicrobial drug susceptibilities of ESBL isolates indicated high resistant rates for Cefotaxime, Ceftazidime. All 25 ESBL producing isolates were resistant to cefotaxime. Complex patterns of fingerprints isolates showed that %36 of the isolates were belonged to the cluster no 5.

Conclusion: Conclusion: the current study revealed high antimicrobial resistance rates among ESBL isolates. Epidemiological data collection from patients is recommended to develop the strategies to manage antibiotic resistance.

Keywords: β -lactamase; *K. pneumoniae*; MDR; antimicrobial resistance

**P322 - 147: ANTIBIOTIC RESISTANCE PATTERN OF E. COLI O157:H7/NM ISOLATES
FROM FECAL SAMPLES OF HEALTHY OSTRICH IN LORESTAN PROVINCE**

Nemat Shams¹, Sepideh Asadi²

1. 1- Assistant professor of Microbiology, Department of Microbiology, Faculty of Veterinary Medicine, Lorestan University, Khorram-Abad, Iran
2. 2. MSc in Microbiology, Faculty of Veterinary Medicine, Lorestan University, Khorram-Abad, Iran

Background and Aim: E. coli is regarded as a reservoir for antibiotic resistance in foods of animal origin. The purpose of this study was to determine the antibiotic resistance pattern of ostrich E. coli O157:H7/NM isolates in Lorestan province, Iran.

Methods: A total of 15 E. coli O157:H7/NM isolates were obtained from fecal samples of the healthy ostrich in Lorestan province, Iran. The E. coli O157:H7/NM isolates were confirmed using standard bacteriological and biochemical techniques. E. coli O157:H7 isolates were distinguished by agglutination with E. coli O157:H7 latex reagent. The isolates were tested for antibiotic resistance against 15 different antibiotic disk by disk diffusion method according to the Clinical and Laboratory Standards Institute, guidelines (CLSI).

Results: According to the disk diffusion results, the maximum rates of resistance were against tetracycline (100%), clindamycin (100%) and vancomycin (%33/93). The minimum rates of resistance were against Streptomycin (%40), erythromycin (%33/93), Co-trimaxazole (26/66%), ciprofloxacin (26/66%), ampicillin (20%), cefazolin (13/33%), and Co-amoxyclave (6/66%). All E. coli isolates were sensitiveness to gentamycin, nalidixic acid, norfloxacin, cefttriaxone, imipenem.

Conclusion: As these antimicrobial agents may cause cross-resistance with human enteric pathogens, controlled use of these antimicrobial agents in veterinary practice is recommended.

Keywords: Antibiotic Resistance Pattern; E.coli O157:H7; Ostrich

**P323 - 150: MOLECULAR CHARACTERIZATION OF THREE CATIONIC RW-RICH
ANTIMICROBIAL PEPTIDES DERIVED FROM IRANIAN SCORPION VENOM**

Masoumeh Baradaran¹, Amir Jalali², Maryam Naderi Soorki³, Hamid Galehdari⁴

1. Toxicology Research center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
2. Dept of Pharmacology and Toxicology, Toxicology Research center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
3. Genetics Department, Sciences Faculty, Ahvaz Shahid Chamran University, Ahvaz, Iran
4. Toxicology Research center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Background and Aim:Based on increasing the problem of antibiotic resistance finding new antimicrobial agents is important. Antimicrobial peptides (AMPs) are a major group of peptides that are candidate for replacement the conventional antibiotics. So finding new natural AMPs is valuable. Here we describe the molecular characterization of three novel AMPs founded in the venom gland of Iranian scorpion, *Mesobuthus eupeus*.

Methods:cDNA was constructed from RNA extracted from venom gland of *Mesobuthus eupeus*. With the cloning of cDNA in pSMART2IFD vector and transformation of vectors to *E.coli* host cells, cDNA library was constructed.

Results:In analysis of cDNA library we found three cDNA encoding 70, 74 and 103amino-acids peptides. The cDNA and peptide sequence of all identified peptides are deposited in NCBI under certain accession numbers. Despite similarity of amino acid sequences of three AMPs with some other scorpion peptides, differences between them can cause difference in their activities. Three identified peptides are cationic RW-rich AMPs; both of them are classified in NDBPs while the third one is defensin-like and cystein-rich. Secondary structures and some physiochemical properties of them were determined. According to the length, net charge and hidrophobicity index, the founded defensin-like peptide is most active AMP that can be active against biofilm microorganisms. They have a signal peptide and one transmembrane domain that in Involved in secretion of them to Endoplasmic Reticulum.

Conclusion:The overall results of this evaluation study can be a platform for drug design.

Keywords:scorpion antimicrobial peptides, RW-rich AMPs, defensin-like AMP, *Mesobuthus eupeus*

**P324 - 153: THE RATIONALE BEHIND ANTIBIOTIC RESISTANCE PATTERN IN
KLEBSIELLA PNEUMONIAE**

Sara Malekshahian¹, Bita Aalipour², Sobhan Ghafourian³

1. Clinical Microbiology Research Center, Ilam university of Medical Sciences, Ilam, Iran
2. Clinical Microbiology Research Center, Ilam university of Medical Sciences, Ilam, Iran
3. Clinical Microbiology Research Center, Ilam university of Medical Sciences, Ilam, Iran

Background and Aim: Now a days, there is an increase of antibiotic resistance in bacteria, this is because of relax prescription of antibiotics, especially in Iran. Undoubtedly, toxin antitoxin system, a toxin neutralized by antitoxin, is known as a potent antimicrobial target; but there is no extensive survey of prevalence of TA loci in large number of *Klebsiella pneumoniae*. Hence, the current study goals determining the prevalence of the most familiar TA loci and comparing with antibiotic resistance pattern in both clinical and environmental *K. pneumoniae*.

Methods: Bacterial Isolates: 97 *K. pneumoniae* clinical (n= 48) and environmental (n= 49) isolates were collected during period November 2013 to February 2014; the isolates were collected from hospital and sewage, respectively. Antimicrobial susceptibility testing: All *K. pneumoniae* were subjected to antibiotic susceptibility assay by disk diffusion method as CLSI guideline. Presence of different Toxin antitoxin loci PCR was performed to identify *mazEF*, *relEB*, and *mqsRA* (type II TA system).

Results: 48 *K. pneumoniae* clinical isolates and 49 *K. pneumoniae* environmental isolates were subjected for evaluation about antibiotic resistance pattern and presence of different TA loci. Sophisticated results indicated that, unexpectedly, there are no association between antibiotic resistances and presence of TA loci in *K. pneumoniae* clinical and environmental isolates.

Conclusion: Therefore, these data recommended more studies should be performed to explain that why TA loci are presented in *K. pneumoniae* and what is rationale behind antibiotic resistance in *K. pneumoniae*?

Keywords: *Klebsiella pneumoniae*, Antibiotic resistance, Toxin antitoxin systems

**P325 - 166: NOVEL SYNTHETIC DERIVATIVES WITH ANTISTAPHYLOCOCCAL
ACTIVITY AGAINST MRSA**

Maryam Salehi¹, seyed naser ostad², Mohsen Amini³

1. Islamic Azad University , Karaj Branch, Faculty of Basic Sciences
2. Department of Toxicology and Pharmacology Faculty of Pharmacy, Tehran University of Medical Sciences
3. Department of Medicinal Chemistry, Faculty of Pharmacy and Drug Design and Development Research Center, University of Medical Sciences

Background and Aim: Methicillin-resistant *Staphylococcus aureus* (MRSA) is the one of most commonly isolated organism from clinical samples which can cause life-threatening infection. The emergence and spread of antibiotic resistance makes the treatment of these infections more complicated. Efflux-mediated resistance has been recognized as an important contributor of fluoroquinolone resistance in bacteria especially in MRSA isolates. Since the antimicrobial effects of dichloroimidazole and triazole derivatives have been proven, we evaluated effect of 4 novel derivatives of dichloroimidazole conjugated with triazole on the minimum inhibitory concentration (MIC) of ciprofloxacin. The cytotoxicity of reagents has been evaluated using 4 cell lines.

Methods: A methicillin and ciprofloxacin resistant *S. aureus* (MCRSA) clinical isolate was used as the test strain. Identification of *S. aureus* was performed by routine microbiological test. To assess the resistance of MRSA strain, agar disk diffusion method was applied. MIC of ciprofloxacin was determined by the broth microdilution method against MCRSA. Further, the cytotoxicity of compounds was evaluated against a panel of tumor cell lines using MTT assay.

Results: MIC of ciprofloxacin decreased in the presence of novel compounds in comparison with ciprofloxacin alone. This decrease was between 2 to 46 fold. Moreover, novel compounds did not show any cytotoxic effect against all tested cell lines (HT29, Caco2, MCF7 and NIH3T3).

Conclusion: This study showed that 4 derivatives enhance the antibacterial effect of ciprofloxacin against methicillin and ciprofloxacin resistant *S. aureus*. In conclusion, these derivatives could be used as inhibitors of antibiotic resistance in combination therapies.

Keywords: ciprofloxacin, *staphylococcus aureus*, MRSA

**P326 - 175: STUDY OF ANTIBACTERIAL PROPERTIES OF SNAKE VENOM AGAINST
SOME BACTERIAL STRAINS**

Ehsan Zayerzadeh¹

1. Department of Biology, Faculty of Food Industry and Agriculture, Standard Research Institute, Karaj, Iran.

Background and Aim: Antibacterial resistance against antibiotics is an unavoidable outcome of drug overuse. Then, it is of significant interest to product antibiotics with a new mechanism of action which can potentially avoid the emergence of drug resistance. In the present study, we are looking for effective antibacterial natural venoms that have potential effects against some bacterial strains.

Methods: In the present investigation, we analyzed potential antibacterial activity of Echis carinatus snake venom against Pseudomonas aeruginosa, Escherichia coli and Staphylococcus aureus bacterial strains. Several concentrations (5, 10, 20 µg/ml) of crude venom were tested for antibacterial activity against Pseudomonas aeruginosa, Bacillus subtilis and Staphylococcus aureus by disc-diffusion susceptibility test.

Results: Our results demonstrated that all of concentrations of venom exhibited a well-recognized antibacterial activity against Pseudomonas aeruginosa following overnight incubation period. In addition, all of concentrations of venom have no antibacterial effects on Staphylococcus aureus and Bacillus subtilis.

Conclusion: In conclusion, the results of this study demonstrated Echis carinatus snake venom has antibacterial activity on Pseudomonas aeruginosa and may be use as new drug for disease induced by Pseudomonas aeruginosa.

Keywords: antibacterial activity, snake venom, Pseudomonas aeruginosa and disc-diffusion.

**P327 - 182: DETECTION OF MACROLID, LINCOSAMIDE AND STREPTOGRAMIN
RESISTANCE GENES IN STAPHYLOCOCCUS EPIDERMIDIS STRAINS ISOLATED FROM
CLINICAL SAMPLES IN ISFAHAN**

Mahtabossadat Mousavi¹

1. M.Sc. of Microbiology, Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran

Background and Aim: The increase in antibiotic resistance among nosocomial infections has made the treatment of these infections difficult. *Staphylococcus epidermidis* is also known as one of the most common causes of nosocomial infections. The aim of this study was to determine the prevalence of resistance to macrolide, Lincosamid and streptogramin antibiotics, in *Staphylococcus epidermidis* strains isolated from clinical samples and detected their related resistance genes.

Methods: For a period of 8 months, from among 250 clinical staphylococcal strains, 100 isolates of *Staphylococcus epidermidis* were separated. The antibiotic susceptibility patterns of the isolates were determined by the disc diffusion method. The MIC of erythromycin was determined by using the microdilution method. The frequency of inducible clindamycin resistance phenotype was detected by D test method. Resistance genes to 3 antibiotics, macrolide, lincosamid and streptogramin were detected in the isolates by PCR.

Results: Among of 100 *Staphylococcus epidermidis*, 41 isolates were resistant to erythromycin, of which 80/4% had MIC > 1024 µg/ml and 19/5% had MIC ? 128 µg/ml. Moreover, 9% of the 100 *Staphylococcus epidermidis* isolates had iMLSB phenotype and 7% had MS phenotype. The frequency of the resistance genes *ermC*, *msrA*, *ermA* and *ermB* among the resistant isolates were 92/6%, 14/6%, 7/3% and 0% respectively.

Conclusion: The results of this study show an increase in the MIC of erythromycin among isolates of *Staphylococcus epidermidis*. On the other hand, the high frequency of the *ermC* gene among isolates is a serious warning to health systems and use of convenient and effective treatment methods after antibiotic susceptibility tests is necessary

Keywords: inducible resistance, *erm* genes, *Staphylococcus epidermidis*, D test

**P328 - 187: INVESTIGATION OF ANTIBACTERIAL EFFECT OF POTENTILLA ANSERINA
AGAINST STAPHYLOCOCCUS AUREUS STRAINS RESISTANT TO ANTIBIOTICS OF
CHOICE**

Samad Vaseghi kale daragh¹, Sasan nikkhoo kordkandi², Nasrin hasanzadeh³, Negar Akhondzadeh⁴,
Keyvan Shafienia⁵, Darya moradi⁶

1. Department of Microbiology, I. A. U. of Ardabil Branch, Ardabil, Iran
2. Department of Microbiology, School of Medicine, Ardabil University of Medical Sciences, Ardabil, Iran
3. Department of Microbiology, I. A. U. of Ardabil Branch, Ardabil, Iran
4. Department of Microbiology, I. A. U. of sarab Branch, tabriz, Iran
5. Department of Microbiology, School of Medicine, Rasht University of Medical Sciences, Rasht Iran
6. Department of Nurse, I. A. U. of khalkhal Branch, Ardabil, Iran

Background and Aim: One of the most common problems in medical, bacterial resistance to antibiotics is to find new antimicrobial agents with minimal side effects is necessary. Develop drugs that prevent or cure bacterial infections, one of the major advances in improving the quality of life in recent years. Due to the presence of biologically active constituents in *Potentilla anserina* that the use of this plant in traditional medicine were needed, it seems that these plants have a remarkable antibacterial effect against *Staphylococcus aureus*.

Methods: The study was conducted extract and oregano. Sampling areas, nose and throat patients and 100 strains of *Staphylococcus aureus* were isolated and purified. The minimum inhibition concentration and minimal bactericidal concentration at six different concentrations of the bacteria were determined by broth dilution method. Sensitivity to the Kirby-Bauer disk diffusion antibiotic susceptibility test was evaluated using standard methods.

Results: The results showed that the MIC of oregano is used at a concentration of 10mg/ml, whereas the MBC was observed in the amount of 15 mg per ml. Evaluation of antibacterial activity of several antibiotics showed similar susceptibility to antibiotics was studied. But Cefixime lowest penicillin antibiotics showed that all the strains were resistant to vancomycin at concentrations higher *Potentilla anserina* antibacterial activity, of these compounds is thus used as a medicinal treatment.

Conclusion: This work showed that substances in the hydro-alcoholic extracts of medicinal plants prevented the growth of bacteria. So these plants with having effective ingredients can be used as an affordable and available source for medicinal purposes.

Keywords: *Staphylococcus aureus*, *Potentilla anserina*, antibacterial

P329 - 188: EVALUATION OF ANTIBIOTIC RESISTANCE IN E. COLI STRAINS ISOLATED FROM URINARY TRACT INFECTIONS

Samad Vaseghi kale daragh¹, Nasrin hasanzadeh², Sasan nikkhoo kordkandi³, Negar Akhondzadeh⁴, Keyvan Shafienia⁵

1. Department of Microbiology, I. A. U. of Ardabil Branch, Ardabil, Iran
2. Department of Microbiology, I. A. U. of Ardabil Branch, Ardabil, Iran
3. Department of Microbiology, School of Medicine, Ardabil University of Medical Sciences, Ardabil, Iran
4. Department of Microbiology, I. A. U. of sarab Branch, tabriz, Iran
5. Department of Microbiology, School of Medicine, Rasht University of Medical Sciences, Rasht Iran

Background and Aim: Escherichia coli is one of the normal microfloras in humans and animals intestine. Some of them is a well-known pathogen that cause diarrhea, hemorrhagic colitis and hemolytic uremic syndrome. Urinary tract infection is the most common disorder of the urinary system and is considered as a risk factor for kidney failure. Escherichia coli the most common cause of urinary tract infection is the cause of nearly 90% of urinary tract infections in young women. Symptoms of infection include urinary burning, blood in the urine. Urinary tract infection is along with flank pain. In this study drug resistant Escherichia coli isolated from urinary infectious agent patients referring to the province against the antibiotics used were examined.

Methods: After the isolation and confirmation of Escherichia coli isolates from urine cultures on Blood Agar and MacConkey Agar with conventional methods, antibiotic resistance by disk diffusion method according to CLSI standards using antibiotic disks, ampicillin, Nalidixic Acid, gentamicin, Ceftriaxone, Ciprofloxacin, Cefixime.

Results: A total of 220 cases, 123 cases were positive urine culture from which 85 cases were isolated E. coli strains isolated from ampicillin (39%), Nalidixic Acid (25%), gentamicin (12%), Ceftriaxone (8%), Ciprofloxacin (6%), Cefixime (10%).

Conclusion: Since Escherichia coli urinary tract infection, especially in hospitals and also because of increased antibiotic resistance, requires new treatments to reduce antibiotic resistance.

Keywords: urinary tract infection, antibiotic resistance, Antibiotics, Escherichia coli

**P330 - 189: INVESTIGATION OF ANTIBACTERIAL EFFECT OF NATIVE BLACK PEPPER
HYDRO-ALCOHOLIC EXTRACTS ON ANTIBIOTIC-RESISTANT STREPTOCOCCUS
PNEUMONIAE**

Samad Vaseghi kale daragh¹, Sasan nikkhoo kordkandi², Nasrin hasanzadeh³, Darya moradi⁴, Negar Akhondzadeh⁵, Keyvan Shafienia⁶

1. Department of Microbiology, I. A. U. of Ardabil Branch, Ardabil, Iran
2. Department of Microbiology, School of Medicine, Ardabil University of Medical Sciences, Ardabil, Iran
3. Department of Microbiology, I. A. U. of Ardabil Branch, Ardabil, Iran
4. Department of Nurse, I. A. U. of khalkhal Branch, Ardabil, Iran
5. Department of Microbiology, I. A. U. of sarab Branch, tabrize, Iran
6. Department of Microbiology, School of Medicine, Rasht University of Medical Sciences, Rasht Iran

Background and Aim: Pneumonia, respiratory tract infections, is associated with high mortality and complications in humans. Although antibiotics are used to treat this infectious disease, but lead to many problems such as unwanted side effects and resistance to antibiotics. This study investigated antibacterial activity of the hydro alcoholic extracts of the native medicinal plants, black pepper Ardabil, as a natural alternative to antibiotics, on antibiotic-resistant *Streptococcus pneumoniae*, the main bacteria that cause pneumonia.

Methods: Antibacterial activity of the hydro alcoholic extracts of medicinal part of these plants was evaluated by the disk diffusion susceptibility test method and broth dilution test method on bacteria.

Results: The rate of MIC for black pepper bacteria were 260 µg/µl (*S. pneumoniae*) and the rate of MBC were 230 µg/µl (*S. pneumoniae*) as well as the maximum amount of inhibition zone diameter were in concentration 600 µg/µl, *S. pneumoniae* (23.5, 18.6, 6.8 mm).

Conclusion: This work showed that substances in the hydro-alcoholic extracts of medicinal plants prevented the growth of bacteria. So these plants with having effective ingredients can be used as an affordable and available source for medicinal purposes.

Keywords: *Streptococcus Pneumonia*, black pepper, Ardabil, antibiotic-resistant

**P331 - 190: DETERMINING ANTIBIOTIC RESISTANCE OF CLINICAL ISOLATES OF
PSEUDOMONAS AERUGINOSA TEACHING HOSPITALS IN PARS ABAD**

Hilda Farhoomand¹, samad vaseghi daragh², Nasrin hasanzadeh³, Sasannikkhoo kordkandi⁴, Negar Akhondzadeh⁵, Keyvan Shafienia⁶

1. Department of Microbiology, I. A. U. of Lahijan Branch, Rasht, Iran
2. Department of Microbiology, I. A. U. of Ardabil Branch, Ardabil, Iran
3. Department of Microbiology, I. A. U. of Ardabil Branch, Ardabil, Iran
4. Department of Microbiology, School of Medicine, Ardabil University of Medical Sciences, Ardabil, Iran
5. Department of Microbiology, I. A. U. of Sarab Branch, Tabriz, Iran
6. Department of Microbiology, School of Medicine, Rasht University of Medical Sciences, Rasht, Iran

Background and Aim: *Pseudomonas aeruginosa* is an important opportunistic human pathogen which causes several nosocomial infections in immunocompromised patients and victims with burns. The purpose of this study was to identify and determine the frequency factors affecting the bacterial infection in burn wounds. It was the pattern of antibiotic resistance.

Methods: In this study, 140 samples of burn wound infections in hospitalized patients in Ardabil were evaluated in nine months. Samples using biochemical tests and cultivation required were identified. And discs used in this study were determined the drug sensitivity of the samples.

Results: Among the 140 samples, 94 cases related to men and 46 cases related to women. And among the 140 samples, bacterial strains were isolated only in 92 cases. That were 64.4 percent related to men and 36.6 percent related to women. The most abundant and the most common organisms isolated related to *Pseudomonas aeruginosa* with an abundance 53.6% and *Staphylococcus aureus* with an abundance 24.3% after other bacteria of 13.6 percent. According to the tests of done antibiogram, it was found that *Pseudomonas aeruginosa* is resistant 53.6 percent to cefotaxime, 46.69% to Azithromycin and 47.6% to gentamicin. Co-trimoxazole only antibiotic was showed the most resistance to *Pseudomonas aeruginosa*.

Conclusion: This study detected the clinical significance of *Pseudomonas aeruginosa* and resistance to the majority of antibiotics. As well as identifying bacteria implicated in burn shows require the use of appropriate methods for prevention of the spread of infection in hospitals.

Keywords: *Pseudomonas aeruginosa*, antibiotic resistance, infection burn

P332 - 195: THE PREVALENC OF ACRA AND ACRB GENES AMONG MULTIPLE-DRUG RESISTANCE OF UROPATHOGENIC ESCHERICHIA COLI ISOLATED FROM PATIENTS WITH UTI IN MILAD HOSPITAL, TEHRAN

Davood Maleki¹, Sahar Honarmand Jahromy², Shohreh Zare Karizi³

1. Department of microbiology, Islamic Azad university, Varamin- Pishva branch, Iran
2. Department of microbiology, Islamic Azad university, Varamin- Pishva branch, Iran
3. Department of microbiology, Islamic Azad university, Varamin- Pishva branch, Iran

Background and Aim: Urinary tract infection is one of the most common infectious diseases and nosocomial infections worldwide and uropathogenic *Escherichia coli* is the first cause of UTI. Due to increased antibiotic resistance and the emergence of UPEC multi-drug resistant clones specific, treatment of UTI associated with UPEC is difficult. The occurrence of MDR in *E. coli* has been attributed to AcrAB-TolC complex of efflux pumps. The aim of this study was to evaluate the frequency of *acrA*, *B* genes among MDR strains of uropathogenic *Escherichia coli* isolated from patients with UTI who admitted to the Milad Hospital, Tehran.

Methods: For 123 UPEC strains that were isolated and diagnosed from urine sample of patients by biochemical tests antibiotic susceptibility was carried out by disc diffusion method according to the CLSI guideline. Isolates were considered as MDR that were resistant to at least one antimicrobial agent in three or more of the categories. Presence and frequency of *acrA*, *B* genes was determined by PCR.

Results: Antibiotic resistance to ampicillin, cephalothin, tetracycline, cefazolin, ceftriaxone, ceftizoxime, ceftazidime, ciprofloxacin and SXT was 82.9%, 78.1%, 61.1%, 49.5%, 38.2%, 30.2%, 26.1%, 42.2% and 60.1%, respectively. The highest sensitivity was belong to antibiotics nitrofurantoin (95.9%), gentamicin (77.2%) and amikacin (71.5%). 78% of isolates were MDR. The frequency of *acrA* gene was 82.90% and *acrB* 95.90% and the prevalence of *acrA*+*acrB* was 95.90%.

Conclusion: Our study showed a high rate of resistant strains of *E. coli* and the emergency of multiple drug resistance to these bacteria in our patients in Milad Hospital Tehran, Iran.

Keywords: Uropathogenic *Escherichia coli*, Antibiotic resistance, Efflux pumps

**P333 - 198: GENOTYPING OF MULTIDRUG-RESISTANT STRAINS OF PSEUDOMONAS
AERUGINOSA ISOLATED FROM BURN AND WOUND INFECTIONS BY ERIC-PCR**

Hajar Hoveizavi¹, Azar Dokht Khosravi²

1. MD, Health Research Institute, Infectious and Tropical Diseases Research Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
2. Research CIMD, Health Research Institute, Infectious and Tropical Diseases center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Background and Aim: To determine the genetic diversity of MDR *P. aeruginosa* strains isolated from burn and wound infections in Ahvaz, Iran, by ERIC-PCR.

Methods: From total 99 strains of *P. aeruginosa* defined as MDR by using drug susceptibility testing, 66 were subjected to ERIC-PCR analysis, comprises 53 strains isolated from burn infection, and 13 randomly selected strains from wound infection with higher resistance to combinations of more numbers of drugs.

Results: Eight clusters (I to VIII), and 50 single clones were generated for tested MDR isolates analyzed by ERIC-PCR. The high heterogeneity was observed among the isolates from burn infections including 16 isolates which were categorized in eight clusters and 37 single clones. The isolates in clusters II, III, VI, VIII showed 100% similarity.

Conclusion: The high level of genotypic heterogeneity in *P. aeruginosa* strains demonstrated no genetic correlation between them. Extremely high drug resistance in isolates from burn, suggests that efficient control measures and proper antibiotic policy should be observed.

Keywords: Drug Resistance. Genotyping Techniques. *Pseudomonas aeruginosa*.

P334 - 200: HIGH ANTIBIOTIC SUSCEPTIBILITY OF LACTOBACILLUS SPP. ISOLATED FROM DAIRY PRODUCTS

Mina Yekani¹

1. 2 Department of Microbiology, School of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran.

Background and Aim:: Lactobacillus spp. are Gram-positive bacilli, act as a part of the normal flora of the body. Nowadays, antimicrobial resistance is one of the major health concerns. This study was conducted to evaluate the drug resistance of Lactobacillus spp. isolated from dairy products.

Methods: In this cross-sectional study, 100 various samples of traditional and pasteurized dairy products were collected and analyzed. The samples were inoculated to MRS broth and incubated for two days. After enrichment of isolates, identification and antibiotic susceptibility tests were performed according to standard guidelines.

Results: More than 90% of Lactobacillus spp. were resistance to metronidazole and oxacillin. In contrast, less than 10% of all isolates were resistant to amoxicillin, erythromycin, chloramphenicol, penicillin and ampicillin.

Conclusion: The findings of this study showed high sensitivity to most antibiotics in the Lactobacillus spp. It seems that the use of probiotics in food production, especially dairy products, in terms of drug resistance be used with caution.

Keywords: Lactobacillus, Dairy, Antibigram, Antibiotic resistance

**P335 - 201: STUDY OF DRUG-RESISTANT STAPHYLOCOCCUS AUREUS IN RAW MILK
AND CHEESE SAMPLES IN KERMAN PROVINCE**

Hamid Heydari gharaei¹, Mahla Khamar Moghadam², Elham Amani³

1. Department of Biology, Master of Science Molecular Genetic, University of Zabol, Zabol, Iran.
2. Department of Pathobiology, Doctor of Veterinary Medicine, University of Zabol, Zabol, Iran.
3. Department of Biology, Master of Science Microbiology, University of Tehran, Tehran, Iran.

Background and Aim: In consequence of previous study of bacterial propagation in milk and yogurt samples, present investigation endeavored to determine the existence of drug resistant *Staphylococcus aureus* especially the methicillin resistant *S. aureus* (MRSA) in raw milk and cheese samples collected from different areas in kerman.

Methods: The drug resistance pattern of the staphylococcal isolates was determined against six antibiotics novobiocin (30µg), ciprofloxacin (5 µg), nalidixic acid (5 µg), methicillin (5 µg), oxacillin (1 µg) and erythromycin (15 µg) by the Disk diffusion method on Muller- Hinton agar.

Results: Total 100 samples (50 raw milk and 50 cheese samples) were microbiologically analyzed through cultural and the confirmative biochemical identification. Out of 100 samples studied, 17 (9 raw milk and 8 cheese) were found to *S. aureus*. Three isolates from cheese samples and 8 isolates from raw milk samples were found to be resistant against at least two commonly used antibiotics. The highest resistance was found against methicillin (5µg, 58.82%) and oxacillin (1µg, 100%). The presence of methicillin resistant staphylococcal species as found from this study may pose a great public health threat, especially to the children.

Conclusion: The presence of methicillin-resistant *S. aureus* in milk and cheese samples is indicative of treatment failure scenario during food borne disease outbreaks. Furthermore, the current findings may provide the proper guidelines of hygienic handling and processing of raw milk and cheeses followed by proper pasteurization and fermentation

Keywords: Raw milk, Cheese, MRSA, Multi-drug resistance (MDR), Public health

P336 - 238: FREQUENCY OF TETRACYCLINE RESISTANCE GENES (TET K,TETM, TETL AND TETO) IN STAPHYLOCOCCUS AUREUS ISOLATED FROM TWO TEACHING HOSPITAL IN SOUTHWEST OF IRAN.

Samin Alipoor¹, Seyed Sajjad Khoramrooz²

1. Department of biology, Karaj branch, Islamic Azad University, Karaj Iran
2. Cellular and Molecular Research Center, Yasuj University of Medical Sciences, Yasuj, Iran

Background and Aim:Staphylococcus aureus is one of the most important nosocomial infections. Antibiotic resistance in this bacterium is a major challenge for public health system. Broad-spectrum antibiotics like Tetracyclines used for treatment and prevention of bacterial infections. The aim of the present study was to determine the prevalence of tetracycline resistance genes in clinical isolates of S. aureus.

Methods:In this study a total of 121 nonduplicated S. aureus isolated from different clinical samples in two teaching hospitals in Ahvaz city. Antimicrobial susceptibility pattern of isolates was performed by using Disk diffusion method against nine antibiotics including tetracycline, doxycycline, minocycline, erythromycin, kanamycin, gentamicin, tobramycin, amikacin and oxacillin.

Results:: Our results showed that the highest rate of resistance observed against tetracycline 47.93%. The resistance rate to doxycycline and minocycline were 20.66% and 3.3% respectively. Nearly all of the tetracycline resistance isolates harbored tetK gene 81.03% and tetM gene detected in 56.89% of isolates. None of the isolates were positive for tetL and tetO genes.

Conclusion:The resistance rate of S. aureus to tetracycline is high in this study. This study showed the importance of tetK and tetM genes in resistance to tetracycline. Regarding to the high detection of tetK gene in resistant isolates, this gene has the most important role in resistance to tetracycline in our study.

Keywords:Staphylococcus aureus, tetracycline, antibiotic resistance, tetK, tetM

**P337 - 262: FREQUENCY OF EXO Y GENE IN ISOLATES OF PSEUDOMONAS
AERUGINOSA WITH MULTI-DRUG RESISTANCE**

Shima Nazaraliyan¹, sanam nazaralian²

1. department of micribiology, faculty of science, azad university of zanzan, zanzan, iran
2. department of plant sciences, faculty of science, kharazmi university, tehran, iran

Background and Aim: Pseudomonas aeruginosa is a multidrug resistant bacterium causing systemic infections. Pseudomonas aeruginosa is a gram-negative opportunistic pathogen affecting patients with cystic fibrosis, AIDS and ocular infection. This organism due to multiple virulence factors outside the cell and connected to the cell can cause a range of serious infections. antibiotic resistance is often recommended for the treatment of multi-drug therapy. The purpose of this study was to evaluate the frequency of genes between strains of Pseudomonas aeruginosa Exo Y in multi-drug resistant strains isolated from clinical samples by PCR, respectively.

Methods: The study design was cross-sectional. 93 isolates of Pseudomonas aeruginosa from clinical samples of hospitals in the zanzan-iran between the years 1393-94 collected and identified using biochemical tests and antibiotic susceptibility test Kirby-Bauer method was performed for 13 types of antibiotics. DNA isolation using extraction kit (Bioneer ,South Korea) according to the manufacturer's protocol extraction, extracting and using specific primers for genes Exo Y, presence or absence of the gene was analyzed by PCR.

Results: From the 93 isolates of Pseudomonas aeruginosa were the most studied antibiotic resistance to erythromycin(95.6%) and the lowest percentage of resistance to amikacin(26.8%), respectively. Also(94.6%)of isolates were resistant to three or more antibiotics and the isolation of multidrug resistance(MDR). az considered among the samples, 84 isolates(93.1%)carriers ExoY, respectively. The 88 isolates with property MDR,71(80.6%) isolates were ExoY gene has.

Conclusion: The results of this study showed that the prevalence of multi-drug resistant gene Egzoenzyme Y in Pseudomonas aeruginosa strains obtained with it can be a reminder to infections from these bacteria.

Keywords: Pseudomonas aeruginosa, antibiotic resistance, multi-drug resistance, Exo Y

**P338 - 272: SURVEY OF ANTIBIOTIC-RESISTANCE PATTERNS IN E.COLI ISOLATED
FROM PATIENTS WITH URINARY TRACT INFECTION IN MASHHAD**

Gholamreza Hashemi Tabar¹, Barat. Ali. Asadi², Mehrnaz. Rad³

1. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.
2. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.
3. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.

Background and Aim: Urinary tract infection (UTI) is the second most common cause of infection in human. *Escherichia coli* is the most common (80%) cause of urinary tract infection. Increasing antibiotic resistance in *Escherichia coli* leads to treatment failure and recurrence. Due to different patterns of antibiotic resistance of *E. coli* in each area, study of antibiotic resistance is necessary. The present study was designed to determine the antimicrobial susceptibility pattern of *E. coli* isolated from urine culture of patients admitted to several hospitals and laboratories in Mashhad.

Methods: One hundred of *Escherichia coli* positive samples were isolated from urine samples of patients with urinary tract infection who had not received antibiotics and antibiotic susceptibility testing. Combined disk method was used to detect UTI *E. coli*. All data analyzed in SPSS version 19.

Results: From 100 isolated *E. coli*, 71% and 29% of strains were isolated from women and men, respectively. The most antibiotic resistance rates were as follow: Ampicillin (78%), Cephalothin (68%) and Cotrimoxazole (65%). The least resistance rate Amikacin (1%), Nitrofurantoin (5%), Gentamycin (19%) and Norfloxacin (30%) were identified.

Conclusion: In our study, the most effective antibiotic for UTI *E. coli* isolated from patients with a sensitivity of 99% , was Amikacin. In contrast, the highest resistance was to ampicillin (78%). According to results of this study, antibiogram test using proper antibiotic disks, the rational prescription indiscriminate use of antibiotics and also avoiding of use of unprescribed antibiotics are necessary.

Keywords:: Antibiotic-resistance, Urinary tract infection, *Escherichia coli*, Drug resistance.

**P339 - 278: EVALUATION OF THE ISOLATED BACTERIAL DIVERSITY FROM PATIENTS
WITH DIABETIC FOOT INFECTION AND DETERMINATION OF THEIR ANTIBIOTIC
RESISTANCE PATTERNS**

Noushin Nahid¹, Nima Bahador², Neamatollah Razmi³

1. Department of Microbiology, Faculty of Science, Science and Research Branch, Islamic Azad University, Fars, Iran; Department of Microbiology, Faculty of Science, Agriculture and Modern Technology, Shiraz Branch, Islamic Azad University, Shiraz, Iran
2. Department of Microbiology, Faculty of Science, Agriculture and Modern Technology, Shiraz Branch, Islamic Azad University, Shiraz, Iran
3. Department of Biochemistry, Faculty of Science, Science and Research Branch, Islamic Azad University, Fars, Iran

Background and Aim: Diabetes mellitus is a common metabolic disease and diabetic foot problems are cause of morbidity in patients and the most common cause of amputations in the world. Therefore, because of their importance, the aim of this study is isolation of microorganisms from infected diabetic foot ulcers and determination of antibiotic resistance patterns of the isolates to achieve a proper antibiotic for remedy

Methods: totally, 23 samples were collected from the patients with diabetic foot infection. After culturing the samples on blood agar, the bacterial screening was performed, and antibiotic patterns of the isolates were determined. Furthermore, most resistant species and antibiotic were recognized

Results: in general, 23 bacterial strains were isolated from the patients. Out of that the isolated (13) were gram negative and 10 were gram positive. Among the isolates *E. coli* and *S. aureus* were the most isolated bacteria involved in ulcer. Amongst the bacteria 17 were resistant to more than three antibiotics (MDR) and the 6 isolates were not responded to the most of selected antibiotics. The most effective antibiotics for all the isolates was Gentamicin and worthless antibiotic was Tetracycline

Conclusion: Based on the results obtained from the study, *Escherichia coli* (30.76%) and *Staphylococcus aureus* (21.73%) were the most isolated bacteria involved in the foot ulcer. Due to the importance of diabetes, accurate identification of bacteria involved in wound infection and evaluation of antibacterial susceptibility seems necessary

Keywords: Antibigram, Bacterial infections, Diabetes

**P340 - 299: DETERMINATION OF ANTIMICROBIAL RESISTANCE PATTERN AND
PHENOTYPIC DETECTION OF ESBL AMONG CLINICAL ISOLATES OF KLEBSIELLA
PNEUMONIAE**

Hiva Saki¹, Haddadi Azam², Shavandi Mahmoud³

1. Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran
2. Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran, P. O. Box 313 – 31485
3. Microbiology and Biotechnology Group, Research Institute of Petroleum Industry, Tehran, Iran.

Background and Aim: In patients with suspected urinary tract infections, antibiotic treatment is usually started empirically, before urine culture results are available. Unfortunately, because of excessive and unregulated use of antibiotics, antibacterial resistance has become an increasingly critical problem in many countries like Iran. The aim of this study was to determine the pattern of antimicrobial resistance and prevalence detection of ESBL among clinical Isolates of klebsiella pneumonia.

Methods: In this study, 182 clinical urine samples were collected from four hospitals and two private clinical laboratories of Alborz province, Karaj city and 115 isolates were identified as klebsiella pneumonia based on standard biochemical tests. Antimicrobial susceptibility was performed using Kirby-Bauer disk diffusion method against 19 common antibiotics. Isolates were also screened for the production of extended spectrum beta-lactamases (ESBLs) by phenotypic confirmatory test (PCT).

Results: Isolates showed the highest resistance to amoxicillin (99%). ciprofloxacin, norfloxacin and ofloxacin by highest susceptibility were the most effective drugs in vitro. Sixty two (53.9%) of isolates were resistant to more than two unrelated drugs and the frequency of multi drug resistance (MDR) to 19 antibiotics was 1%. ESBL screening of klebsiella pneumonia isolates by PCT showed that out of 115 samples, 27 isolates were ESBL positive.

Conclusion: With regards to change in drug resistance pattern among bacterial uropathogens, yearly determination of this pattern in populations is recommended. ESBLs producing organisms remain an important cause for failure of therapy with cephalosporins. Detection of ESBL producing isolates is a critical requirement for tracking of drug resistance in different geographic regions.

Keywords: Klebsiella pneumonia, antibiotic resistance, ESBLs

P341 - 302: EVALUATION OF ANTIBIOTIC RESISTANCE PATTERN AND SEROTYPING OF UROPATHOGENIC ESCHERICHIA COLI ISOLATED FROM HOSPITALIZED PATIENT IN BASHT,IRAN

Shamshiri sadegh¹, Raziieh Pooransari²

1. Department of microbiology, Yasooj Branch, Islamic Azad University
2. Department of microbiology, Yasooj Branch, Islamic Azad University

Background and Aim: Urinary tract infections (UTI) is the most frequent human bacterial infection all around the world, which are associated with a wide range of pathogen factors. Uropathogenic Escherichia Coli (UPEC) is one of the most important etiologic agents of UTI. Numerous use of antibiotics in treatment of UTI, resulted in increase of drug resistance in these bacteria. This study was aimed to evaluate antibiotic resistance pattern and determine serotypes of Uropathogenic Escherichia Coli isolated among patients with UTI in Shahid Beheshti Healthcare Center of Basht

Methods: This descriptive study was done in the first six months of 1394. 200 samples were collected from patients with UTI. Their identifications were done on basis of Gram-staining, colony morphology and biochemical testing for Escherichia Coli. Antibiotic resistance pattern was performed with disc diffusion tests using Kirby-Bauer method. Furthermore, serotyping was achieved by slide agglutination method

Results: A total of 200 urine samples were analyzed that out of them, 80 samples (40%) showed significant growth. The most frequently detected gram negative bacterium was E. coli in 45 cases (56.25%). The most antibiotic resistances in E. coli strains were to Nalidixic acid and Co-trimoxazole with 62.2% and 60% respectively. While all bacteria were sensitive to Ceftazidime and Imipenem (100%). In addition, the results showed that the most common serogroups of E. coli are O1, O2, O4 and O7 with 22.2, 20, 15.5 and 11.2 % respectively

Conclusion: Considering the result of antibiogram in this study, it is better in primary treatment of UTI, Nalidixic acid and Cotrimoxazole less used

Keywords: Urinary Tract Infections, Antibiotic Resistance, Uropathogenic Escherichia Coli, Serotyping

**P342 - 318: ANTIBIOTIC RESISTANCE PROFILE OF H. PYLORI IN PATIENTS WITH
UPPER GASTROINTESTINAL IN KASHAN, IRAN**

Shahrbanoo Keshavarz azizi raftar¹, Rezvan Moniri², Seyed Gholam Abbas Moosavi³

1. pasteur institute of Iran;Tehran,Iran
2. Department of Microbiology and Immunology, Kashan University of Medical Sciences, Kashan, Iran
3. Dept. of statistic , Health faculty, Kashan University of Medical Sciences, Kashan, Iran

Background and Aim:Helicobacter pylori infection is related with a range of upper gastrointestinal diseases, bacterial and host-related factors correspond in causing Helicobacter pylori eradication failure. H. pylori eradication treatment breakdown influences the outcome of a variety of diseases of the upper gastrointestinal tract. The aim of this study was to determine the ciprofloxacin and clarithromycin resistance pattern of H. pylori strains isolated from H. pylori-infected patients in Kashan, Iran.

Methods:A total of 95 H. pylori strains were isolated from the gastric mucosa of 246 patients undergoing gastroscopy with different clinical signs in Kashan. Minimum inhibitory concentrations (MICs) of ciprofloxacin and clarithromycin in H. pylori were determined by Etest, amplifying the urease gene used to confirmed H. pylori colonies.

Results:H. pylori strains isolated from 38.6% (95 out of 246) patients.166 patients 67.5% (166 out of 246) had Non-ulcer dyspepsia and 78 (31.7%) had peptic ulcer diseases. The majority of patients were females (68.3%). Statistically significant association was found between pylori infection and peptic ulcer disease ($p=0.001$). A significant difference was observed between resistance to CIP and CLR and peptic ulcer disease ($p= 0.001$).

Conclusion:We found that patients with peptic ulcer disease correlated with elevated risk of resistance to CIP and CLR. The difficulty of treatment in patients infected with H. pylori, fundamentally due to increased antimicrobial resistance as seen from the results of the present study, is a common challenge in many parts of the world. These data show the high resistance rates to ciprofloxacin and clarithromycin.

Keywords:ciprofloxacin,clarithromycin,gastrointestinal disease.

**P343 - 326: VIRULENCE GENOTYPE AND ANTIMICROBIAL SUSCEPTIBILITY PATTERN
IN CLINICAL PSEUDOMONAS AERUGINOSA ISOLATES**

Somayeh Malek mohamad¹, Dr.Sodابه Rostami², Dr.Behnam Zamanzad³

1. Cellular and Molecullar Research Center, Shahrekord University of Medical Sciences, Shahrekord, Iran
2. to Isfahan Infectious Diseases and Tropical Medicine Research Center laboratory
3. Cellular and Molecullar Research Center, Shahrekord University of Medical Sciences, Shahrekord, Iran

Background and Aim:: Pseudomonas aeruginosa is a common opportunistic pathogen that causes nosocomial infection in immunocompromised patients. Among different virulence factors, the type III secretion system (TTSS) is an important agent in virulence and development of antimicrobial resistance in P.aeruginosa. In this study we determined the TTSS effector genotype and pattern of antimicrobial susceptibility in clinical P.aeruginosa isolates.

Methods:From April to December 2015, a total of 175 P.aeruginosa isolates were collected from patients hospitalized in educational hospitals of Shahrekord and Chamran hospital of Isfahan, Iran. Antimicrobial susceptibility test was done by disk diffusion test. The TTSS effector genotype was detected by multiplex PCR of exoU and exoS genes.

Results:Antibiotic resistance rate was higher than 70% to many antibiotics. The highest rate of resistance was related to Levofloxacin and Meropenem [155(88.6%), 148 (84.6%); respectively]. The exoU gene was found in 75 (42.9%) isolates and 136(77.7%) of the isolates carried the exoS. In addition, 36(20.6%) of the isolates carried the both of gens. A statistical significance was detected between the ExoU+ genotype and resistance to Imipenem ($p<0.006$) and ExoU+/ExoS+ genotype and resistance to Pipracillin ($p<0.05$).

Conclusion:The result of this study indicated high resistance to most antibiotic classifies and a specific relationship between of virulence genotype, especially more virulent genotype of ExoU+ and antimicrobial resistance. It's proposed to prevent of spreading more virulent isolates and “antibiotic resistance crisis” molecular methods beside antibiogram tests was done.

Keywords:: Virulence factors, Genotype, Pseudomonas aeruginosa, Type III secretion systems

**P344 - 337: PREVALENCE AND DRUG RESISTANCE PATTERNS IN PSEUDOMONAS
AERUGINOSA ISOLATED FROM PATIENTS REFERRING TO HOSPITALS IN KERMAN
PROVINCE**

Hamid Heydari gharaei¹, Mahla Khamar Moghadam², Elham Amani³

1. Department of Biology, Master of Science Molecular Genetic, University of Zabol, Zabol, Iran.
2. Department of Pathobiology, Doctor of Veterinary Medicine, University of Zabol, Zabol, Iran.
3. Department of Biology, Master of Science Microbiology, University of Tehran, Tehran, Iran.

Background and Aim: *Pseudomonas aeruginosa* is one of the most common gram-negative microorganisms identified in the clinical specimens of hospital admitted patients. This study was conducted among patients admitted to hospitals in Kerman province.

Methods: The various clinical specimens included wound swab, urine, pus, aural swab, by colony morphology, microscopic examination and relevant biochemical tests according to standard laboratory methods. Antimicrobial sensitivity test was done by disk diffusion method. antimicrobials including imipenem, co-trimoxazole, ciprofloxacin, nalidixic acid, ceftazidime, doxycycline, gentamycin, ceftriaxone, cefixime, ofloxacin, amikacin and azithromycin of standard strengths.

Results: A total of 400 *P. aeruginosa* were isolated of which 280 (70.0%) were from indoor and 120 (30.0%) were from outdoor patients. Some 240 (60.0%) of the patients were males and the rest 160 (40.0%) were females. Most of the patients (164, 41.2%) were aged between 21-40 years, while 138 (34.7%) were below 20 years. The result of the study shows that imipenem is the most effective drug against *P. aeruginosa*, followed by amikacin and ciprofloxacin.

Conclusion: The number of patients admitted far exceeds the treatment facilities available in Hospital. So, it can be concluded that every effort should be made for routine microbiological surveillance to reduce infections. It is also necessary to carry out a large-scale study with newer antimicrobials.

Keywords: *Pseudomonas aeruginosa*, Antimicrobial Resistance

**P345 - 348: THE EFFECT FE₂NiO₄ NANOPARTICLES ON GRAM NEGATIVE BACTERIA
CAUSE URINARY TRACT INFECTIONS RESISTANT TO MULTIPLE ANTIBIOTICS**

NASRIN ALSADAT SEYEDGHALEHJOUZDANI¹, MONIR DOUDI²

1. MS student , Department of Microbiology, Falavarjan Branch, Islamic Azad University, Falavarjan, Isfahan, Iran
2. Assistant Professor, Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran. Email: Monirdoudi@yahoo.com

Background and Aim:Excessive consumption of prevalent antibiotics caused to increase antibacterial resistance against urinary pathogenicity .As regard of this social problem, this research has been chosen to treat the high resistance of the antibiotics by using Fe₂NiO₄ nanoparticles.

Methods:This study administrated on a clinical sample including E.coli MDR ,Klebsiella Pneumoniae MDR that cause to urinary tract infection .Experimental well plate Method was used to assess their sensitivity against Fe₂NiO₄ nanoparticles .In order to assess the toxicity of this nanoparticle in vivo should evaluate their effects on the consumption of prevalent antibiotics caused to increase antibacterial resistance against urinary pathogenicity .As regard of this social problem, this research has been chosen to treat the high resistance of the antibiotics by using Fe₂NiO₄ nanoparticles.liver enzymes and Wistar male rat's Liver tissues .Using SPSS/16 software was analyzed the statistical data.

Results:Results from Well plate method for Fe₂NiO₄ nanoparticle with 12mg/ml density indicated the most circumference for lack of development in E.coli and Klebsiella Pneumoniae bacteria was about 20 and 22/94 mm, respectively. results of mean SGOT and SGOT after intraperitoneal injection into different treatments of rats indicated that there is no different between groups.

Conclusion:Findings from this research suggested that there is a significant effect of Fe₂NiO₄ nanoparticle on bacteria in vitro ,although there is no significant effect of the mentioned nanoparticle on liver enzymes for different rat treatments in vivo.

Keywords:Urinary tract infections, Gram-negative bacillus MDR, Fe₂NiO₄ nanoparticle

**P346 - 363: PREVALENCE AND SUSCEPTIBILITY PATTERNS OF VANCOMYCIN
RESISTANT ENTEROCOCCUS FAECIUM ISOLATES IN UNIVERSITY HOSPITALS IN
AHWAZ**

Maniya Arshadi¹, Mohammadreza Pourmand², Moloud Motahhar³, Farrokh Izadpoor⁴, Mina
Moghaddam⁵, Fariba Abbasi⁶

1. Department of Pathobiology, School of Health, Tehran University of Medical Sciences, Tehran, Iran
2. Department of Pathobiology, School of Health, Tehran University of Medical Sciences, Tehran, Iran
3. Department of Microbiology, School of Medicine, Ahwaz Jundishapur University of Medical Sciences, Ahwaz, Iran
4. Department of Microbiology, Imam Khomeini hospital, Ahwaz, Iran
5. Department of Microbiology .Abouzar hospital Ahwaz,Iran
6. Department of Microbiology,Golestan hospital Ahwaz,Iran

Background and Aim: Vancomycin Resistant Enterococci (VRE) have been recognized as a leading cause of nosocomial infection. The aims of this study, were to determine the frequency of VRE faecium and their antibiotic resistant patterns from clinical, rectal and environmental specimens in university hospitals in Ahwaz.

Methods: Between January and July 2015, 2500 clinical specimen, rectal swab and environmental specimen collected. All samples were searched for the presence of enterococci strain and were identified to species level by biochemical tests and confirmed by PCR. Vancomycin resistant enterococcus were identified by disk diffusion and screening method and MIC determined by E test. van genes were determined by Multiplex PCR . Antibiotic susceptibility tests to 10 agents were performed by disk diffusion method for all VRE isolates.

Results: Out of 353(14.2%) isolates, recognized as Enterococci, 64.4% and 35.6% were identified as *Enterococcus faecium* and *Enterococcus faecalis* respectively. 26.5% and 1.1% of Enterococci were identified as VRE faecium and VRE faecalis respectively. all VRE faecium carried vanA gene. The VRE faecium from various sources in hospitals, showed closed resistant patterns. All of isolates showed multiple drug resistant pattern and all of them was sensitive to linezolid.

Conclusion:: High rate of VRE faecium isolates in Ahwaz in various sources, represent the importance of monitoring for VRE and their resistant patterns in enterococcus .At present, there are no surveillance guidelines for control of VRE in Ahwaz hospitals.

Keywords: Vancomycin Resistant Enterococcus, Antibiotic Resistant, Ahwaz

P347 - 371: ANTI- MICROBIAL RESISTANCE STAPHYLOCOCCUS EPIDERMIDIS

Hamid Reza Bitaraf¹, Rahele halabian², hamide mahmudinejad³

1. Department of Genetic, Faculty of science, Islamic Azad university, Damghan branch, Damghan , Iran
2. School of Medicine, Baqiyatallah University of Medical Sciences,Tehran, Iran
3. School of Medicine, Baqiyatallah University of Medical Sciences,Tehran, Iran

Background and Aim:Anti- microbial resistance is a trait in microorganisms that makes antimicrobial drugs are ineffective. Staphylococcus epidermidis is a normal skin flora, but occasionally cause infections and form biofilm. Biofilms, make bacteria to be resistance to antibiotics, antibodies and phagocytic cells

Methods:This includes the collection of a comprehensive set of relevant papers , which was conducted by searching electronic databases and the internet .

Results:Staphylococcus that are resistances to methicillin are called MRSA. They Cause various types of antibiotic-resistant infections. This type of staphylococcus is resistant to beta-lactam antibiotics, as these antibiotics have no effect on their infections. The prevalence of MRSA infections are more especially in hospitals, care centers for patients, open wounds, patients who have implants as well as in patients who have a weakened immune system. Their infections can even cause death in patients. So increasing antibiotic resistance is a concern and should be controlled. This fact has caused many problems in the treatment of infections caused by these bacteria and cause greater outbreak in the community

Conclusion:Due to non-uniform expression of mec-A gene diagnostic tests and typical accurately identify bacteria, the antibiotic susceptibility and resistance to methicillin fail. Therefore it is necessary for an accurate diagnosis and disease control methods smarter, faster and more specific such as PCR is used.

Keywords:Anti- microbial resistance, Staphylococcus epidermidis, MRSA, mec-A

**P348 - 377: OCCURRENCE OF HIGH LEVEL AMINOGLYCOSIDE RESISTANCE (HLAR)
AMONG THE CLINICAL ENTEROCOCCUS FAECIUM AND ENTEROCOCCUS FAECALIS
ISOLATES IN NORTH-WEST OF IRAN**

Ali Jahansepas¹, Mohammad Aghazadeh², Mohammad Ahangarzadeh Rezaee³, Alka Hasani⁴, Yaeghob Sharifi⁵, Jalal Mardaneh⁶

1. Department of Clinical Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran and Research Center of Infectious Diseases and Tropical Medicine, Tabriz University of Medical Sciences, Tabriz, Iran
2. Department of Clinical Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran
3. Department of Clinical Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran
4. Department of Clinical Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran and Research Center of Infectious Diseases and Tropical Medicine, Tabriz University of Medical Sciences, Tabriz, Iran
5. Department of Clinical Microbiology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran
6. Department of Microbiology, School of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran

Background and Aim:Enterococci are the leading cause of nosocomial infections, and are thus a persisting clinical problem globally. Enterococci can show high levels of resistance to aminoglycosides. The aim of this study was to determine high level aminoglycoside resistance (HLAR) in *E. faecium* and *E. faecalis* obtained from various clinical sources.

Methods:The susceptibility of 160 *E. faecium* and *E. faecalis* clinical isolates to high level gentamicin and streptomycin were determined using disk diffusion method. Likewise, the *aac* (6')*Ie*-*aph* (2'')*Ia* gene encoding gentamicin resistance was targeted by PCR reaction.

Results:High level resistance (HLR) to gentamicin and streptomycin among all *E. faecium* and *E. faecalis* isolates were 50.62% and 51.87% respectively. The *aac* (6')*Ie*-*aph* (2'')*Ia* gene was found in all high level gentamicin resistance isolates.

Conclusion:The results demonstrated that resistance to high level gentamicin and streptomycin are common in *E. faecium* and *E. faecalis* isolated in Northwest of Iran. Emergence of high level resistance to these antimicrobial agents shown by enterococcal strains is of concern because of the decrease in the therapeutic options for treatment of infections caused by enterococci.

Keywords:*E. faecalis*, *E. faecium*, high level aminoglycoside resistance, North-west, Iran.

P349 - 379: ANTIMICROBIAL RESISTANCE OF SALMONELLA SPP. AND ESCHERICHIA COLI ISOLATED FROM TABLE EGGS

Amirhossein Ghadiri¹, Saeed Veysi², Afshin Taravati³

1. Young Researchers and Elite Club, Rasht Branch, Islamic Azad University, Rasht, Iran
2. Young Researchers and Elite Club, Rasht Branch, Islamic Azad University, Rasht, Iran
3. Department of Veterinary science, Rasht Branch, Islamic Azad University, Rasht, Iran

Background and Aim: Foodborne disease is a major health and economic problem in the world. Eggs are early digestive and nutritious food that can affect family health. The aim of this study was to determine the occurrence and the level of antibiotic resistance patterns in *Salmonella* spp. and *Escherichia coli* isolated from table eggs.

Methods: A total of 500 eggs were randomly collected. After culturing and isolation processes, *Salmonella* and *E. coli* bacteria were isolated from shell and Contents (albumen + yolk) of eggs. Then, antibiotic resistance was determined by PCR and agar disk diffusion method.

Results: Among the 500 samples, 9.2 % of the egg shell samples were infected with *Salmonella* and 33.2% with *E. coli*, also, 12.1% of contents samples were infected with *Salmonella* and 26.5% with *E. coli*. In evaluation of antibiotic resistance patterns of bacteria *Salmonella* isolates showed resistance to all the antibiotics disks used and in *E. coli* isolates was to ampicillin, tetracycline and penicillin.

Conclusion: The relatively high prevalence of resistance to antimicrobial agents amongst isolates of *Salmonella* and *E. coli* may pose therapeutic implications, particularly in egg-borne salmonellosis. We recommend use of antibiotics in chicken food must be control to avoid the antibiotic resistance.

Keywords: Drug Resistance, *Escherichia coli*, *Salmonella*, Egg

P350 - 395: DETERMINATION OF ANTIBIOTIC RESISTANCE PATTERN AND CHECK AMINOGLYCOSIDE RESISTANCE IN PSEUDOMONAS AERUGINOSA

Faeze Mahdiun¹

1. Department of Microbiology, School of Medicine, Kerman University of Medical Sciences.

Background and Aim: *Pseudomonas aeruginosa* is opportunistic human pathogen and a cause of nosocomial infections, particularly in patients with cystic fibrosis, burns, neutropenia and immunosuppression. Several antibiotics like aminoglycosides, quinolones and beta lactams are used the treatment of its infections. Aminoglycosides are potent bactericidal agents that inhibit bacterial protein synthesis by binding to the 30S ribosomal subunit. These antibiotics are often used in combination with beta lactams as antipseudomonal agents. The main mechanism of aminoglycoside resistance in *Pseudomonas aeruginosa* is inactivation by aminoglycoside modifying enzymes (AGME).

Methods: In the present study, *Pseudomonas aeruginosa* strains were isolated from the specimen of 73 burns patients. The identify of isolates were confirmed using biochemical tests. Afterwards, for collected isolates, antibiotic resistance pattern was determined by disk diffusion method for ceftazidim, imipenem, ciprofloxacin, gentamicin, tobramycin and amikacin. At the end PCR assay was used to investigate the prevalence of *aac(6')* –I, *aac(6')* –II, *aph(3')*-VI and *ant(2'')*-I, the genes encoding the main aminoglycoside modifying enzymes in *Pseudomonas aeruginosa*.

Results: The Results of disk diffusion method were: Ceftazidim 98%, imipenem 64%, ciprofloxacin 100%, gentamicin 98% , tobramycin 100% and amikacin 97%. The results of PCR : *aac(6')* –I was the most frequent gene (66%) among the isolates the after that *ant(2'')*-I, *aph(3')*-VI and *aac(6')* –II genes were detected in 63%, 32% and 8% of the isolates

Conclusion: These result are similar to the most of the researches in different countries word wide which interroduce modifying enzymes as the major aminoglycoside resistance mechanism in *Pseudomonas aeruginosa*.

Keywords: *Pseudomonas aeruginosa*, aminoglycoside modifying enzymes, PCR.

**P351 - 397: CORRELATION BETWEEN QACE AND QACEΔ1 EFFLUX PUMP GENES,
ANTIBIOTIC AND DISINFECTANT RESISTANT AMONG CLINICAL ISOLATES OF E.COLI**

Maryam Shafaati¹

1. Maryam shafaati, PhD student Department of Microbiology Science, Islamic Azad University, of Jahrom Branch, Fars, Iran.

Background and Aim:Antiseptics and disinfectants are used extensively in hospitals and other health care settings to control the growth of these microorganisms. However, some disinfectants resistant strains were reported. The aim of this study is to evaluate correlation between the efflux pump genes, drugs and disinfectant resistant among clinical isolates of E.coli.

Methods:A total of 102 of E. coli strains were isolated from urine sample of hospitalized patients. The antibiotic susceptibility were carried out by disc diffusion method. Didecyl di-methyl ammonium chloride (DDDMAC) was used as Quaternary ammonium compounds (QAC) disinfectant which prolonged was used in Heart Center Hospital. PCR reaction carried out for detection of qacE and qacΔE efflux pump genes

Results:Almost the strains had higher resistance to Ampicillin, Ciproflaxacin, Cotrimaxazole and Cephalothin. Totally 49% (n: 50) of strains were produced ESBL. Almost the strains have MIC value between 0.00195 to 0.0078 mg/l. Correlation between presence of qacE and qacΔE genes and antibiotic resistance were perceived. Presence of qacE and qacΔE genes among strains that have high disinfectant MIC value were 96.9% and 96.3% respectively. In addition, 98% of ESBL producing strains harbored qacE gene and 94% of ESBL producing strains harbored qacΔE gene.

Conclusion:Our study indicated that there was strong correlation between presence of qacE and qacΔE genes, resistant to some antibiotics and growing in media which contain high concentration of disinfectant. In conclusion, also other mechanisms play important role in resistant to antimicrobial agents but the role of efflux pumps in resistant to antimicrobial agents should not neglected.

Keywords:Escherichia coli, Quaternary ammonium compounds, qacE, qacEΔ1, antibiotic resistance, resistance to disinfectant

**P352 - 404: DETECTION OF CLASS 1 AND 2 INTEGRONS AND GENE CASSETTES AMONG
MULTIDRUG-RESISTANT (MDR) ESCHERICHIA COLI UROPATHOGENIC STRAINS
ISOLATED FROM CLINICAL SPECIMENS IN SOUTH OF IRAN**

Mohamad Kargar¹, Sara Tootoonsaz², Akram Najafi³

1. Department of Microbiology, Jahrom Branch, Islamic Azad University, Jahrom, Iran
2. Student University of Microbiology, Jahrom Branch, Islamic Azad University, Jahrom, Iran
3. Department of Microbiology, Jahrom Branch, Islamic Azad University, Jahrom, Iran

Background and Aim: Uropathogenic strains of *Escherichia coli* (UPEC) are the second leading causes of bacterial infections. The appearance and dissemination of multidrug-resistance in *Escherichia coli* strains is a cause of importance in the treatment. Horizontal gene transfer of integrons are defined as the major mechanisms of multidrug-resistance (MDR) bacteria. This study aimed to determine the prevalence of class 1 integron among MDR *E. coli* strains from urine specimens in South of Iran.

Methods: There were 140 *E. coli* strains isolated from June 2013 to Sep 2014. Urine specimens identified as *E. coli* by the conventional methods. Subsequently the antibiotic resistance of isolates to 18 antibiotics was assessed using clinical and laboratory standard institute criteria (CLSI). The existence of class 1-2 integrons and embedded gene cassettes was verified using specific primers by single PCR assay.

Results: Among total of 140 studied sample, 82% and 80% were resistant to AMC and AMP respectively, 114 (81.43%) isolates were multidrug-resistant. Class 1 integron and class 2 integron were present in 25.41% and 7.12 MDR isolates respectively. The frequency of gene cassettes in integron class 1 was 21.91% and in integron cassettes class 2 was 5.71%.

Conclusion: Our results indicated that antibiotic resistance in different communities has a direct relationship to integrons existence and resistance of gene cassettes.

Keywords: UPEC, MDR, Integron, Gene Cassettes, PCR

**P353 - 414: PREVALENCE OF MULTI-DRUG RESISTANCE(MDR)PSEUDOMONAS IN
PATIENTS WITH URINARY TRACT INFECTION IN GORGAN, NORTH OF IRAN**

Hanieh Bagheri¹, Fereshteh Najafi ², Dr Ezzat Allah Ghaemi³

1. Golestan University Of Medical Science
2. Golestan University Of Medical Science
3. Golestan University Of Medical Science

Background and Aim:Due to the lack of a rational antibiotic policy in clinical medicine, antibiotics are misused more often than not in developing countries and less often than not in developed countries, which lead to the increased emergence of multidrug resistant (MDR) strains of pathogenic bacteria and even of commensals. The aim of this study is, Frequency of multi-drug resistance in patients with UTI in Gorgan.

Methods:This study carried out in Gorgan on 11 Pseudomonas isolate from urine with standard of microbiologic methods. Antibiotic susceptibility considered with Kirby-bauer disk diffusion methods(DDM).

Results:85/7% of patients with Pseudomonas were hospitalized. 10 classes of antibiotics(18 antibiotics) were considered, the most of antibiotics resistance in this study were seen in clindamycin (100%) and then Fleuroquinolons (92/9%) and the most sensitivity belonged to Monobactam (71.4%) and Amikacin (95.4%). 93% had resistant to multi drugs(MDR) simultaneous.43% to >7 (7-10) Classes and 16.7% was resistance to most of 3-4 classes (Clindamycin, Cephalosporin, Nitrofurantoin, Fluoroquinolone) of Antibiotics. 91/7 % of hospitalized patients were MDR. these analysis done about them, too.

Conclusion: In this study, were seen high frequent of multi drug resistant in uropathogens in both inpatients(91/7%) and outpatient(100%).

Keywords:Multi-drug resistance, Pseudomonas, Urinary tract infection, Gorgan

**P354 - 463: PHENOTYPIC DETECTION OF ESBL AND AMPC BETA-LACTAMASE IN
CLINICAL ISOLATES OF ESCHERICHIA COLI**

Maryam Dehghani¹, Azam Haddadi², Mahmoud Shavandi ³

1. Department of Biology, Karaj Branch, Islamic Azad University, Karaj, IR, Iran
2. Department of Biology, Karaj Branch, Islamic Azad University, Karaj, IR, Iran
3. Microbiology and Biotechnology Group, Environment and Biotechnology Research Division, Research Institute of Petroleum Industry, Tehran, IR, Iran

Background and Aim: Plasmid-mediated AmpC enzymes were first identified in 1980, since then, they have spread among the members of the family Enterobacteriaceae. AmpC β -lactamases are important cephalosporinases chromosomally encoded in many of Enterobacteriaceae and a few other organisms. They are not inhibited by available β -lactamase inhibitors. Infection with resistant organisms is a major public health issue. Six families of plasmid-mediated AmpC β -lactamases have been described, but no phenotypic test can discriminate among them. This study was aimed to indicate the prevalence of ESBLs and AmpC-type β -lactamase by using phenotypic test.

Methods: A total of 243 clinical urine samples were collected from Karaj city, Iran and 227 isolates were identified as *E. coli* based on standard biochemical tests. Subsequently, the isolates were screened by disk diffusion method and combined disk method for β -lactamase production.

Results: Antimicrobial susceptibility was performed using Kirby-Bauer disk diffusion method against cefepime, ceftazidime, ceftriaxone and cefotaxime. The antibiotic resistance pattern was observed as follows: cefepime (25%), ceftazidime (31%), ceftriaxone (37%), cefotaxime (38%). AmpC and ESBL Beta-lactamase screening of strains by phenotypic combined disc test showed that out of 227 samples, 12 (5.2 %) and 77 (34%) were AmpC and ESBLs producers, respectively.

Conclusion: Unfortunately, antibiotic resistance has become an increasingly critical problem in many countries like Iran and occurrence of isolates co-expressing AmpC- β -lactamases and ESBLs can create serious problems in future. As antibiotic options in the treatment of AmpC β -lactamases and ESBLs producing organisms are extremely limited, molecular screening by laboratories is suggested to reduce the risk of therapeutic defeat.

Keywords: Antibiotic Resistance; AmpC β -lactamases; ESBLs β -lactamases; *E. coli*

**P355 - 465: ANTIBIOGRAM PATTERN OF PROTEUS MIRABILIS STRAINS RETRIEVED
FROM DIGESTIVE TRACT OF LUCILIA SERICATA**

Nahid Ahmadi¹, Naseh Maleki-Ravasan², Fahimeh Nemati-Mansoor³, Navid Dinparast-jadid⁴

1. Department of biotechnology, Faculty of Advanced Sciences & Technology , Pharmaceutical Sciences Branch, Islamic Azad University ,Tehran – Iran (IAUPS)
2. Department Malaria & Vector Research Group (MVRG),Biotechnology Research Center (BRC),Pasteur Institute of Iran, Tehran, Iran
3. Department of biotechnology, Faculty of Advanced Sciences & Technology , Pharmaceutical Sciences Branch, Islamic Azad University ,Tehran – Iran (IAUPS)
4. Department Malaria & Vector Research Group (MVRG),Biotechnology Research Center (BRC),Pasteur Institute of Iran, Tehran, Iran

Background and Aim:: *Lucilia sericata* maggots are currently considered as highly skilled micro-surgeons in wound healing. Commensal bacteria found within the larval alimentary canal may play a role in maggot therapy by releasing antibacterial compounds. *Proteus mirabilis* is the key organism for antimicrobial activity of larvae and its fruitfulness can depends on the host antibiotic consumption background. This study was done to evaluate susceptibility/resistance pattern of *P.mirabilis* isolates from compartments of *L.sericata* used in maggot therapy

Methods: Larvae were micro-dissected under the sterile condition and their bacterial microflora were identified using culture based and 16srRNA sequencing methods. Using the disc diffusion method, 22 different antibiotics representing different families of antibiotics were tested on *P.mirabilis* isolates

Results: Total of 14 isolates of *P.mirabilis* were identified from 6 different parts of dissected larvae comprising salivary glands, fore/mid/hindgut, malpighian tubules and tracheae. Antibioqram results revealed the presence of four different sensitivity patterns among the studied strains. Susceptibility test results of antibiotics Ampicillin, Cefotaxime, Novobiocin, Optochin and Penicilin was more diverse in *P.mirabilis* isolates and ranged from susceptible and intermediate to resistance. This diversity was more sensible in the salivary glands and midgut isolates

Conclusion: *P.mirabilis* are distributed in intestinal tract of *L. sericata*. Salivary glands are the first part of the food canal which faced with the engorging environment and midgut is a “hot spot” for gene transfer where the large number of microbes occurs there. Knowledge of the sensitivity pattern of *P.mirabilis* is important in the wound healing and formulating rational antibiotic policy

Keywords: *Lucilia sericata*, *Proteus mirabilis*, Antibioqram

**P356 - 473: SENSITIVITY TO DOXYCYCLINE AND NITAZOXANIDE AMONG
METRONIDAZOLE RESISTANT HELICOBACTER PYLORI STRAINS IN PATIENTS WITH
GASTRITIS**

Ali Baradaran¹, Ali Baradaran Moghaddam², Shahla Mansouri³, Nour Amirmozafari⁴, Masoud Alebouyeh⁵, Nastaran Farzi⁶, Mohammad Reza Zali⁷

1. -
2. Microbiology Department, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran.
3. Microbiology Department, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran
4. Microbiology Department, School of Medicine, Iran University of Medical Sciences, Tehran, Iran,
5. Research Institute for Gastroenterology and Liver Disease, Shahid Beheshti University of Medical Sciences, Tehran, Iran
6. Research Institute for Gastroenterology and Liver Disease, Shahid Beheshti University of Medical Sciences, Tehran, Iran
7. Research Institute for Gastroenterology and Liver Disease, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim:In this investigation, the efficacy of doxycycline and nitazoxanide for *Helicobacter pylori* (*H. pylori*) isolates which were resistance to metronidazole was investigated.

Methods:A total of 122 patients who underwent endoscopy examinations at Kasra and Laleh hospitals in Tehran from November 2014 to July 2015 were enrolled. *H. pylori* strains were isolated from their endoscopy biopsies by bacteriological culture. Those bacterial isolates which were resistant to metronidazole were examined for their susceptibility to doxycycline and nitazoxanide. Serial agar dilution method was used to determine the minimum inhibitory concentrations for the antibiotics.

Results:From a total of 122 gastric biopsy specimens, 55 *H. pylori* isolates were recovered (45%). Forty of these isolates (72.7%) were resistance to metronidazole. Comparison of the MIC values of doxycycline and nitazoxanide compared with metronidazole showed significant differences ($p < 0.05$). The MIC₅₀ and MIC₉₀ values for doxycycline, nitazoxanide and metronidazole were 4, 8, 32, 8, 32, 64 $\mu\text{g/ml}$ respectively.

Conclusion:The very high levels of metronidazole resistance observed suggest that this drug may not be useful for first-line therapy in Iran. Due to its relative effectiveness, doxycycline and nitazoxanide can be considered as suitable alternatives for patients in Iran.

Keywords:*Helicobacter pylori*, Antibiotic resistance, Metronidazole, Doxycycline, Nitazoxanide, Minimum Inhibitory Concentration

P357 - 478: FAECAL CARRIAGE OF ESBL AND PLASMID-MEDIATED AMPC B-LACTAMASE GENES IN KLEBSIELLA SPP. AND SHIGELLA SPP. ISOLATED FROM INPATIENT AND OUTPATIENT CARRIERS IN TABRIZ, IRAN

Abed Zahedi¹, Mohammad Taghi Akhi², Abed Zahedi bialvaei³, Reza Ghotaslou⁴, Mohammad Asgharzadeh⁵, Tahereh Pirzadeh⁶, Hossein Samadi kafil⁷, Hamed Ebrahimzadeh Leylabadlo⁸

1. Infectious Disease and Tropical Medicine Research Center, Tabriz University of Medical Sciences, Tabriz, IR Iran
2. Infectious Disease and Tropical Medicine Research Center, Tabriz University of Medical Sciences, Tabriz, IR Iran
3. Infectious Disease and Tropical Medicine Research Center, Tabriz University of Medical Sciences, Tabriz, IR Iran
4. Biotechnology Research Center, Tabriz University of Medical Sciences, Tabriz, Iran
5. Department of bacteriology and virology, school of medicine, Tabriz University of medical sciences, IR Iran
6. Department of bacteriology and virology, school of medicine, Tabriz University of medical sciences, IR Iran
7. Department of bacteriology and virology, school of medicine, Tabriz University of medical sciences, IR Iran

Background and Aim: The growing incidence of community acquired infection due to Extended-Spectrum Beta-Lactamase (ESBL) - and plasmid-mediated AmpC β -lactamase producing bacteria represent a great concern because there are few therapeutic choices.

Methods: This study was aimed to determine the prevalence of faecal carriage of ESBL producing *Klebsiella* spp. and *Shigella* spp. among inpatient and outpatient and their phenotype-genotype resistance correlation that conveyed ESBL with or without AmpC genes at a university hospital in Tabriz, Iran. During March to May 2015, 200 faecal samples from hospitalized and non-hospitalized patients without gastrointestinal illness and diarrhea were cultured on MacConkey agar plate supplemented with 2 μ g/mL of cefotaxime. Bacterial identification, antimicrobial susceptibility testing and ESBLs confirmatory tests were performed according to the standard guidelines. Also, polymerase chain reaction (PCR) was used to identify the genetic determinants responsible for ESBL production (TEM, SHV, and CTX-M) and AmpC β -lactamase genes.

Results: Of 200 faecal samples analysed, 23 (11.5%) *Klebsiella pneumoniae*, and 4 (2%) *Shigella* spp. were isolated. The co-resistance frequencies in isolates recovered were as follows: Ciprofloxacin, 4.3%; Gentamicin, 4.3%; Ceftazidime, 13%; Cefepime, 17.4%; amoxicillin-clavulanic acid, 47.8%; and Ampicillin, 87%. Six (26.08%) of the *Klebsiella* isolates had phenotypic evidence of ESBL production, while blaSHV sequences were detected in 18 (66.6%), and blaTEM in 11 (40.7%) isolates. Also, blaCTX-M and blaCMY sequences were found in 4 (17.39%) and 5 (21.7%) *Klebsiella* isolates, respectively.

Conclusion: This study revealed that ESBL production was relatively prevalent in faecal carriage of *Klebsiella* and *Shigella* isolates in Tabriz. In addition, Persons attending hospital could be a reservoir of such bacteria and enzymes.

Keywords: *Shigella*; *Klebsiella*; ESBL; Faecal carriage; Iran

**P358 - 485: STUDY OF ANTIBIOTIC RESISTANCE PATTERNS IN KLEBSIELLA
PNEUMONIA ISOLATED FROM PATIENTS REFERRED TO HOSPITALS OF SEMNAN**

Shiva Mirkalantari¹, Farahnaz Bineshian², Mahboobeh Tayari³, Nastaran Momeni⁴

1. Dept of Microbiology, Faculty of Medicine, Semnan University of Medical Sciences, Semnan, Iran
2. Dept of Mycology, Faculty of Medicine, Semnan University of Medical Sciences, Semnan, Iran.
3. Dept of Microbiology, Damghan Branch, Islamic Azad University, Damghan, Iran
4. Dept of Microbiology, Damghan Branch, Islamic Azad University, Damghan, Iran

Background and Aim: *Klebsiella pneumoniae* is an opportunistic pathogen of the Enterobacteriaceae family and one of the most common nosocomial infections. Today, antibiotic resistance has increased due to the excessive use of antibiotics. The aim of this study was to determine frequency and resistance patterns of *Klebsiella pneumoniae* isolated from patients referred to hospitals of Semnan.

Methods: A total of eighty clinical isolates of *K. pneumoniae* were collected from three hospitals in Semnan in a cross sectional study in 2016. Isolates identified by morphological and biochemical laboratory tests. The antibiotic resistance and susceptibility of strains was determined by Disk diffusion (Kirby Bauer) method. Data were analyzed using SPSS16 software.

Results: Antibiotic resistance rates were as follows: Neomycin (1.25%), Colistin (1.25%), Ertapenem (10%), Kanamycin (33.75%), Ceftriaxone (45%), Aztreonam (47.5%), streptomycin (48.75%) respectively. Multi-drug resistance observed 47.5% and resistance to at least one antibiotic was 63.75%.

Conclusion: Our findings indicated that the highest sensitivity was related to Neomycin (98.75%), Colistin (98.75%) in all tested *Klebsiella*, therefore, these antibiotics can be recommended as the most effective antibiotic.

Keywords: *Klebsiella pneumoniae*, patients, Antibiotic Resistance

**P359 - 506: DETERMINATION OF ANTIBIOTIC SUSCEPTIBILITY PATTERNS AMONG
ESBL PRODUCING UROPATHOGENIC E.COLI**

Shiva Mirkalantari¹

1. Microbiology Department, School Of Medicine, Semnan University of Medical Sciences

Background and Aim: The antibiotic susceptibility pattern of *Escherichia coli* have been changed due to the development of new resistance mechanism such as production of Extended-Spectrum Beta-lactamase. The aim of this study was to determine the antibiotic resistance pattern of uropathogenic *E.coli* producing ESBL.

Methods: In this descriptive-sectional study, one hundred nine isolates of *E.coli* were collected from patients with urinary tract infections and identified by biochemical tests. Antimicrobial susceptibility test was performed by disk diffusion method against eight antibiotics. Screening of ESBL phenotype was performed by combination disk method.

Results: Of 109 *E.coli* isolates, 29 (26.6%) isolates were ESBL producing organisms. Antibiotic resistance was most often observed for Sulfametoxazole and Trimethoprim (82.75%). *E.coli* resistance to Ciprofloxacin, Gentamicin, Cefepime, Amikacin, Imipenem, Ceftazidime and Ceftriaxone was 55.1%, 37.93%, 10.34%, 51.72%, 93.1% respectively.

Conclusion: The findings of the present study suggest that for screening of ESBLs in clinical samples by laboratory more attention in antibiotics Prescription. The most effective antibiotic against uropathogenic *E.coli* was Imipenem.

Keywords: Imipenem, *E.coli*, UTIs, ESBL

P360 - 508: AN OVERVIEW ON CARBAPENAMASE ENZYMES

Mina Aghamali¹, Abed Zahedi bialvaei², Hossein Samadi Kafil³

1. Infectious Disease and Tropical Medicine Research Center, Tabriz University of Medical Sciences, Tabriz, Iran.
2. Department of Microbiology, Faculty of Medicine, Iran University of Medical Sciences, Tehran, Iran
3. Drug Applied Research Center, Faculty of Medical Sciences, Tabriz University of Medical Sciences, Tabriz, Iran

Background and Aim: Among the hundreds of β -lactam antibiotics, carbapenems are remarkable drugs for possessing broad-spectrum, potent activity and also resistance to most β -lactamase enzymes. Emergence of carbapenemase enzymes and also multidrug-resistant organisms, is a serious menace to carbapenems

Methods: In this review, based on studied papers from PubMed, Google scholar and Scopus, we summarize carbapenemase enzymes.

Results: Carbapenemases based on hydrolytic mechanisms and rate of hydrolysis, are broadly divided into two groups: (i) Serin-carbapenemases that contain serin at the active site (ii) Metallo- β -lactamases that are zinc dependent. Carbapenemases in Ambler classification, based upon amino acid sequence similarity, are classified into 3 groups: A, B and D. Class A carbapenemase enzymes include: SME, IMI, NMC, KPC, GES, SFC, FTU-1, FPH-1, BKC-1 and VCC-1. Enzymes of this class can be inhibited by commercially available β -lactamase inhibitors such as clavulanic acid, sulbactam and tazobactam. Class B carbapenemases, also named metallo- β -lactamases (MBLs), include: VIM, GIM-1, IMP-1, NDM, SPM-1, SIM-1. MBLs can be inhibited by zinc chelating agents like EDTA. Class D carbapenemases, also named OXAs, are classified into subgroups. The main subgroups have been known as OXA-23 like, OXA-40 like, OXA-48 like, OXA-51 like and OXA-58 like. There are limited OXA-inhibitors because of the variability in amino acid sequence of OXAs

Conclusion: Taken together, the ongoing emergence of resistance to carbapenems among Gram-negative bacteria is a worldwide concern. Due to the rapid and extensive dissemination of carbapenemases and lack of development of new antimicrobial drugs, there is a critical need to develop novel, effective and non-toxic clinical inhibitors to restore the antibacterial activity of carbapenems.

Keywords: Carbapenemase, Carbapenem resistance, Class A Carbapenemase, Metallo- β -lactamases, OXA-Carbapenemases

P361 - 509: AVIBACTAM AS A B-LACTAMASE INHIBITOR

Mina Aghamali¹, Abed Zahedi bialvaei², Hossein Samadi Kafil³

1. Infectious Disease and Tropical Medicine Research Center, Tabriz University of Medical Sciences, Tabriz, Iran.
2. Department of Microbiology, Faculty of Medicine, Iran University of Medical Sciences, Tehran, Iran
3. Drug Applied Research Center, Faculty of Medical Sciences, Tabriz University of Medical Sciences, Tabriz, Iran

Background and Aim: Beta-lactamase inhibitors play a critically important role in prevention of antibiotic resistance. Inhibitors coupled with β -lactam antibiotic, inactivate enzyme in the periplasmic space and restore the efficacy of partner antibiotic

Methods: In this study, based on studied papers from PubMed, Google scholar and Scopus, we summarize the current state of avibactam as a β -lactamase inhibitor

Results: Avibactam (NXL104) is a novel, reversible and non- β -lactam β -lactamase inhibitor which restores the activity of β -lactam antibiotics. This compound has little intrinsic antibacterial activity, but efficiently protects antibiotics from hydrolysis, when given in combination with other antibiotics. Avibactam shows more potent and broader spectrum of activity than currently available β -lactam/ β -lactamase inhibitors including clavulanic acid, sulbactam and tazobactam. This synthetic inhibitor shows potent inhibitory activity against ESBL, AmpC, Class A carbapenemases including KPC as well as some class D enzymes, which are resistant to inhibition by currently available β -lactam/ β -lactamase inhibitors. Avibactam has no activity against metallo- β -lactamase enzymes. It has been paired with two of third-generation cephalosporins, ceftazidime and ceftaroline. However, ceftazidime-avibactam resistance has been demonstrated from KPC-2 variants such as KPC-3 producer Enterobacteriaceae including *Klebsiella pneumoniae* and *Enterobacter cloacae*. In addition to ceftazidime and ceftarolin antibiotics, piperacillin and cefotaxime were evaluated in combination with avibactam against KPC-positive *K.pneumoniae*.

Conclusion: In conclusion, avibactam is a potent β -lactamase inhibitor that restores the antibacterial activity of currently available antibiotics. The combination of avibactam with extended spectrum cephalosporins could be a promising option against KPC-producer bacteria including *K.pneumoniae* which is a worldwide concern.

Keywords: Avibactam, NXL104, β -lactamase inhibitor, Carbapenemase inhibitor

**P362 - 520: ANTIBIOTIC RESISTANCE PATTERNS OF E.COLI ISOLATES COLLECTED
FROM UTI, IN SHOHADA HOSPITAL, TAKAB.**

Hadis Aliakbari¹, Hadis Aliakbari Abroodi², Sepideh Paktinat³, Pejvak Khaki⁴, Sohiela Moradi Bidhendi⁵,
Mehdi Gharakhani⁶, Hadis Aliakbari Abroodi⁷

1. -
2. Division of Microbiology, Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
3. 1-Shohada Hospital , Takab West Azerbaijan Province , Iran- 2- Department of Microbiology, Razi Vaccine and Serum Research Institute, Karaj, Iran
4. Department of Microbiology, Razi Vaccine and Serum Research Institute, Karaj, Iran
5. Department of Microbiology, Razi Vaccine and Serum Research Institute, Karaj, Iran
6. Department of Microbiology, Razi Vaccine and Serum Research Institute, Karaj, Iran
7. Division of Microbiology, Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: Escherichia coli (E.coli) strains are the major cause of urinary tract infections (UTI). Antimicrobial resistance in commensal and clinical E.coli is recognized as a global concern in human medicine.

Methods: A total of 90 E.coli isolates were collected from UTI inpatients and outpatients to the Shohada hospital, Takab, during October to March 2015. According to the Clinical Laboratory Standards Institute (CLSI) guidelines, culture and the antibiotic susceptibility test of E. coli isolates was determined using the disk diffusion method against 20 antibiotics.

Results: The isolates exhibited resistance against 1 to 20 antimicrobials with most frequent resistance to Erythromycin (95.5%), Ampicillin (88.88%), Cephalexin (82.23%), Chloramphenicol (75.56%), Nalidixic acid (73.32%) and Trimethoprim- Sulfamethoxazole (62.2%). A lower level of resistance was observed to Gentamicin (42.22%), Amikacin (42.22%), Kanamycin (46.66%), Imipenem (46.66%) and Ciprofloxacin (48.88%). Among the 90 E.coli isolates studied, 93.3% were resistant to more than three families of the antibiotics suggested by CLSI.

Conclusion: The current concern of UTIs is the prevalence of high level resistance and also a major problem in the treatment of UTIs. The present study revealed that antibiotic resistance is developing strongly. In the treatment of UTI, particularly caused by E.coli, proper selection of antimicrobial agents should be relevant to the bacterial susceptibility testing surveillance.

Keywords: UTI, Escherichia coli, antibiotic susceptibility test, resistance pattern

P363 - 525: STUDY OF ANTIMICROBIAL SUSCEPTIBILITY PROFILES OF GRAM-NEGATIVE BACTERIA CAUSING URINARY TRACT INFECTION IN TABRIZ, IRAN

Saba Nemati Ahmad Abad¹, Haedeh Mobaiyen², Nasrin Ghaem Magamei³

1. MD Student, Department of Microbiology, Tabriz Branch, Islamic Azad University, Tabriz, Iran
2. Assistant professor, Department of Microbiology, Tabriz Branch, Islamic Azad University, Tabriz, Iran
3. Lecturer, Central Laboratory of East Azarbiyjan, Tabriz, Iran

Background and Aim: Introduction: The frequency of urinary tract infections (UTI) are 2nd after respiratory infections which will be identified by urine culture. The physicians usually start an empiric therapy based on their knowledge of locally resistance pattern. On the other hand, antimicrobial resistance to Gram-negative and Gram-positive pathogens has increased considerably. This study is an overview of frequency and antimicrobial resistance in Gram-negative pathogens in UTIs.

Methods: Methods: This retrospective descriptive study used culture and susceptibility of UTIs infection pathogens data from March to October of 2015 from Ostan Laboratory, Tabriz, Iran.

Results: Results: There were 741 urinary gram-negative isolates. The frequency of isolates were 87% E.coli, 8% K. pneumoniae, 4% Enterobacter aerogenes, 1.1% Pseudomonas aeruginosa and 0.13 Acinetobacter baumannii, respectively. More than 54% of E.coli was resistant to Nalidixic acid, 44% of K. pneumoniae and 72% of E. aerogenes to Nitrofurantoin. One isolate of Acinetobacter was resistant to all of studied antibiotics and high rate of resistance to Trimetoprim-sulfamethoxazole (TMP-SMX) was reported in all of pathogens.

Conclusion: Conclusion: The empiric therapy against UTIs must be based on communities' infections data and antibiogram should be used with caution in uncomplicated UTIs. Some limitation must be applied in usage of TMP-SMX and quinolones as an alternative in treatment of UTIs.

Keywords: Urinary tract infections, Gram-negative pathogens, Antimicrobial resistance.

P364 - 535: MRSA IN SURGICAL SITE INFECTIONS; FREQUENCY AND VANCOMYCIN MIC

Mohammad yousef Memar¹, Mohammad Taghi Akhi ², Reza Ghotaslou³, Naser Alizadeh ⁴, Tahereh pirzadeh⁵, Samad Beheshtirouy⁶

1. 1- Research Center of Infectious and Tropical Disease, Tabriz University of Medical Sciences, Tabriz, IR Iran
2. 1- Research Center of Infectious and Tropical Disease, Tabriz University of Medical Sciences, Tabriz, IR Iran.
3. 1- Research Center of Infectious and Tropical Disease, Tabriz University of Medical Sciences, Tabriz, IR Iran.
4. 1- Research Center of Infectious and Tropical Disease, Tabriz University of Medical Sciences, Tabriz, IR Iran.
5. 2- Department of Bacteriology and Virology, Tabriz University of Medical Sciences, IR Iran
6. Cardiothoracic Department, Tabriz University of Medical Sciences, Tabriz, IR Iran

Background and Aim:Background: Methicillin-resistant staphylococcus aureus (MRSA) causes surgical site infections (SSIs) and complicates the treatment of these infections. Vancomycin is the drug of choice for MRSA treatment but increased MIC of vancomycin may be associated with failure in treatment. The aim of the present study was to determinate the prevalence and antibiotic susceptibility patterns of MRSA in patients suffering from SSIs and determination of vancomycin MIC in these isolates.

Methods:Methods: Detection of *S. aureus* in 100 aspirated specimens from SSIs was performed by standard microbiology tests. MRSA was detected by phenotypic and molecular methods. Disk diffusion (Kirby-Bauer test), E-test and agar dilution methods were performed for determination of antibiotic susceptibility patterns, the vancomycin MIC and oxacillin MIC. The results were interpreted according to guidelines of Clinical and Laboratory Standards Institute (CLSI).

Results:: Out of 24 *S. aureus* isolates, 20 (83.33%) were recognized as MRSA by 30 µg cefoxitin disk from 100 specimens and all were confirmed by PCR approach. High frequency of resistance was observed to clindamycin, erythromycin, gentamicin, ciprofloxacin and chloramphenicol while all isolates were susceptible to vancomycin, linezolid, and mupirocin. The range of vancomycin and oxacillin MICs were 0.5 to 128 and 0.38 to 2µg/ml respectively.

Conclusion:The findings of this study show a high frequency of MRSA in SSIs in our hospital. Due to the elevated MIC of vancomycin, we suggest consumption of other effective drugs for the treatment of SSIs.

Keywords:Methicillin resistant staphylococcus aureus, Minimum Inhibition concentration, surgical site infections, Vancomycin.

**P365 - 536: ANTIMICROBIAL RESISTANCE PATTERNS OF ESCHERICHIA COLI
ISOLATES FROM BROILER FLOCKS IN ARDABIL PROVINCE TO SIX ANTIBACTERIAL
AGENTS COMMONLY USED IN THE IRANIAN POULTRY INDUSTRY**

Aidin Azizpour¹, Zahra Amirajam²

1. Meshginshahr Faculty of Agriculture, University of mohaghegh Ardabili, Ardabil, Iran
2. Imam Khomeini hospital of Ardabil, Ardabil University of Medical Sciences, Ardabil, Iran

Background and Aim: Colibacillosis is one of the most prevalent bacterial diseases in poultry with huge economic losses that is caused by *Escherichia coli*. Antimicrobial therapy is an important tool in reducing both the incidence and mortality associated with colibacillosis. But, enormous use of antibiotics in poultry medicine has been increased the number of resistant bacterial strains in recent years. The purpose of this study was to investigate the antimicrobial resistance pattern of 178 *E. coli* isolates from 40 broiler flocks with colibacillosis clinical signs in Ardabil province, northwest of Iran.

Methods: The antimicrobial susceptibility of total isolates to six antibacterial agents commonly used in the Iranian poultry industry was tested from March 2014 to February 2015. These antibacterial agents include Colisten, Doxycycline, Sulfamethoxazole + Trimethoprim, Enrofloxacin, Florfenicol and Lincospectine.

Results: According to disk diffusion method, the maximum resistance was to Doxycycline (81.47%), Enrofloxacin (77.53%), Sulfadiazine + Trimethoprim (71.91%), Colistin (68.54%), Florfenicol (58.99%), Lincospectine (36.52%), respectively.

Conclusion: The results of this study showed the high frequency of resistance to antimicrobial agents commonly used in the Iranian poultry industry. It can be attributed to the incorrect use of antibiotics in poultry industry. So, National monitoring programs are strongly needed for antimicrobial resistance and for a rational use of antibiotics.

Keywords: *E. coli*, Broiler Flocks, Antibiotic Resistance, Ardabil Province

**P366 - 540: FREQUENCY STUDY OF DNA TOPOISOMERASE II MUTATION IN
FLUOROQUINOLONES RESISTANCE PSEUDOMONAS AERUGINOSA STRAINS
ISOLATED FROM PATIENT REFERRING TO THE IMAM REZA HOSPITAL**

nooshin abbasi¹, Dr Ramin abiri², Dr Amir Houshang alvandi³, Bahareh Cheshmenoushi⁴

1. medical student of University of Medical Sciences, Kermanshah, Iran
2. Associate Professor of Microbiology, University of Medical Sciences, Kermanshah, Iran
3. Associate Professor of Microbiology, University of Medical Sciences, Kermanshah, Iran
4. Master student of Microbiology , Student Research Committee, University of Medical Sciences, Kermanshah, Iran

Background and Aim: *Pseudomonas aeruginosa* is a gram-negative bacteria that due to a lot of the antibiotic resistance have important role in the increased mortality of patients hospitalized in hospital. Resistance caused by mutations in fluoroquinolone is increasing as one of the effective antibiotics on in bacteria

Methods: In this study, by disk diffusion method, the resistant of 200 samples of isolated *Pseudomonas aeruginosa* to fluoroquinolones were examined. Then presence of mutations were analyzed in genes *GyrA* and *GyrA* resistant isolates by PCR And samples with mutations were sequenced to identify mutation position

Results: From 250 samples been isolated, 200 samples were identified as *Pseudomonas aeruginosa*. 54 samples were resistant to fluoroquinolones, after performing PCR and sequencing, 30 samples had a mutation at position 83 *GyrA*, Instead threonine with isoleucine displacement occurred and no samples were not found with mutations in *GyrB*

Conclusion: The fluoroquinolone resistance in *P. aeruginosa* in Iran is growing. But in comparison with other countries is lower. According to the fact that one of the main causes of fluoroquinolone resistance in the bacteria is mutations in the enzyme topoisomerase II, And by increasing the resistance, to control this problem, the use of these antibiotics should be considered carefully and Alternative treatment used

Keywords: *Pseudomonas aeruginosa* , antibiotic resistance , fluoroquinolone, mutations, topoisomerase II,

**P367 - 563: CORRELATION BETWEEN VIRULENCE GENOTYPE AND SPECIMEN TYPE IN
MULTIDRUG RESISTANCE PSEUDOMONAS AERUGINOSA**

Somayeh Malek mohamad¹, Dr. Behnam Zamanzad², Dr. Sodabeh Rostami³

1. Author
2. Corresponding
3. Author

Background and Aim: *Pseudomonas aeruginosa* is an opportunistic pathogen that causes a wide spectrum of infections in hospitalized and immunocompromised patients. The type III secretion system (TTSS) is an important virulence factor of *P.aeruginosa* that has become increasing resistance to many antibiotics. Different strains of *P.aeruginosa* show a unique TTSS virulence genotype. We surveyed the relationship between the presence of ExoS & ExoU genes and specimen type in multidrug resistance *P.aeruginosa* isolates.

Methods: A total of 175 samples from different regains of body were collected from patients in educational hospitals of Shahrekord and Chamran hospital of Isfahan, Iran, from April to December 2015. Minimal inhibitory concentrations (MICs) of Ciprofloxacin, Amikacin and Imipenem were done by E.test strip and of exoU and exoS genes were detected by multiplex PCR.

Results: 136 isolates were resistance to at least two antibiotic classes. 49/6% of ExoU+ isolates and 76/5% ExoS+ isolates were multidrug resistance. A specific relationship among of ExoU genotype and specimen type existed ($P<0/001$). Analyses showed significant difference between multidrug resistance and specimen type ($P<0/003$).

Conclusion: This survey showed the high prevalence of multidrug resistance in clinical isolates of *P.aeruginosa* and significant difference between multidrug resistance and virulence genotype didn't show. Analyses showed significant difference between multidrug resistance and specimen type and presence of virulence genotype especially ExoU genotype in different infections of *P.aeruginosa* is different.

Keywords: Virulence genotype, *Pseudomonas aeruginosa*, MultiDrug Resistance

**P368 - 575: FREQUENCY AND ANTIBIOGRAM PATTERN OF PSEUDOMONAS
AERUGINOSA SPECIES ISOLATED FROM CLINICAL SPECIMENS IN SHAHID
MOHAMMADI HOSPITAL**

Sedigheh Javadpour¹, Seyede Zahra Hashemi², Yaghoob Hamed³

1. Infectious and Tropical Disease Research Center, Hormozgan University of Medical Sciences, Bandar Abbas, Iran
2. Department of Microbiology, Faculty of Medicine, Hormozgan University of Medical Sciences, Bandar Abbas, Iran
3. Department of parasitology, Faculty of Medicine, Hormozgan University of Medical Sciences, Bandar Abbas, Iran

Background and Aim: *Pseudomonas aeruginosa* is responsible for 10–15% of all hospital-acquired infections. Infections caused by multi-drug resistant (MDR) *P. aeruginosa* are hard to treat due to the natural antibiotic resistance of these species. The aims of this study were to determine the frequency and antibiogram patterns of *pseudomonas* species isolated from different clinical specimens at Shahid Mohammadi hospital, Bandar abbas.

Methods: This descriptive cross-sectional study was carried out on 1783 clinical specimens from March 2013 to March 2014. 68 strains of *pseudomonas* were isolated from different clinical specimens. Samples were collected in sterile condition, and transferred to appropriate media such as Blood agar, EMB or MacConkey agar. Suspicious colonies of *pseudomonas* species were identified by Gram staining, oxidase production, reactions in TSI and OF media, growth at 42°C and pyocyanin pigmentation. Antibiogram patterns of bacteria was determined by Kirby-Bauer method on Mueller-Hinton agar medium. Clinical and microbiological data were analyzed by SPSS19 software

Results: In the present study, 68 *pseudomonas* species with 3.8% frequency were identified. The majority of bacteria were isolated from trachea (26/5%) and ICU (35/3%). Multiple trauma with 32.3% frequency was the most reason for admission of patients. The most effective antibiotics were Meropenem (78/9%), Imipenem (77/4%). Most resistance (100%) was observed with Nalidixic acid, Nitrofurantoin, Ceftizoxime.

Conclusion: Although bacteria were most sensitive to Meropenem, Imipenem, the susceptibility rate was not high enough, to be suggested for empirical treatment.

Keywords: Antibiotic, Antibiotic resistance, *Pseudomonas aeruginosa*

**P369 - 597: MOLECULAR CHARACTERIZATION OF NDM-1 PRODUCING GRAM
NEGATIVE BACILLI ISOLATED FROM DIFFERENT HOSPITALS, IRAN**

Haedeh Mobaiyen¹, Sanaz Soltanzad², Genus Bayatmakoo³

1. Islamic Azad University, Tabriz
2. 1. MD , Department of Microbiology, Tabriz Branch, Islamic Azad University, Tabriz, Iran
3. Infections and Tropical Diseases Research Center, Tabriz University of Medical Sciences, Tabriz, Iran,
Department of Infectious Disease, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran

Background and Aim:Gram negative bacilli are as major factors in incidence of multi drug resistant infections. Detection of metallo- β -lactamases NDM-1 were serious attention in the worldwide because of these isolates to with fame as untreatable ones. This study was regarded to evaluate the presence of blaNDM-1 gene in imepenem resistant Gram negative bacilli

Methods:During a period of six months imepenem resistant Gram-negative bacilli were collected of three hospitals in Tabriz ,Uremia and Bonab cities. Antimicrobial susceptibility test were done by imepenem, ceftazidim, ciprofloxacin and gentamicin. MIC in imepenem resistant isolates were done by E- test. DNA extracted, Duplex-PCR were for NDM-1 gene and 16Sr RNA of bacteria in fellow by NDM-1 positive strain after sequencing of PCR by-product, were blast in NCBI

Results:In this study, 44 isolates including of *Pseudomonas aeruginosa*, *Acintobacter baumannii*, *Klebsiella pneumonia* and *Escherichia coli* isolates were evaluated. These isolates were resistance against ceftazidim, ciprofloxacin and gentamicin, 90.9%, 77.3% and 59.1%, respectively. In 93.1% of isolates the MIC was $>32\mu\text{g/ml}$. In 5 isolates were obtained blaNDM-1gene with 621bp. In sequencing more than 581 bp of these genes were homolog with other gene in NCBI site. Theses blaNDM-1 positive isolates were resistance to aztreonam

Conclusion:Presence of blaNDM-1gene were shown in *E.coli*, *K. pneumonia*, *P. aeruginosa* and *A. baumannii*. In these isolates were shown resistance to aztrenam which will be as indicator to production of extended-spectrum β -lactamases needed to more evaluate especially in *P. aeruginosa* and *A.baumannii*, as environmental pathogens by high colonization.

Keywords:Gram negative bacilli, Carbapenem, blaNDM-1gene.Drug resistance.

P370 - 598: MOLECULAR STUDY OF ENCODING GENES OF PER-1 AND VIM-1 TYPES β -LACTAMASES ENZYMES IN PSEUDOMONAS AERUGINOSA AND ACINTOBACTER BAUMANII ISOLATES

Haedeh Mobaiyen¹, Rehane Sedgi², Changez Ahmadi Zade³

1. Department of Microbiology, Tabriz Branch, Islamic Azad University, Tabriz, Iran
2. Msc Student, Department of Microbiology, Ahar Branch, Islamic Azad University. Ahar, Iran
3. Department of Microbiology, Ahar Branch, Islamic Azad University. Ahar, Iran

Background and Aim:: *Pseudomonas aeruginosa* and *Acintobacter baumanii* are the most important opportunistic pathogens which involved in nosocomial infections. The ability of extended-spectrum beta lactamases (ESBLs) and metallo- β -lactamases producing in these groups of bacteria as the most common resistant mechanisms has effect on efficiency of β -lactams in treatment. So, this study was purposed to evolutes antibiotic resistance pattern and frequency of bla PER-1 and bla VIM-1 types of β -lactamases in above mentioned bacteria

Methods: In this study, both the aforementioned bacteria from different wards of Ali- Nasb and Shohada hospitals in Tabriz and Imam Khomenii hospital in Uremia were isolated. Antibiotic resistance pattern were assayed by Disc Agar Diffusion Method and the ESBLs producing in these isolate were confirmed by combined disc method. DNA of isolates was extracted and bla PER-1 and bla VIM-1 type genes in these bacteria identified by PCR method.

Results: The most frequency of resistance were obtained against cefoxitin and cefotaxim in *P. aeruginosa* isolates (92.5 %, 83.5%) and in *A.baumanii* isolates (100%, 92%) respectively. The ESBLs producer bacteria were confirmed in 10 *P. areuginosa* isolates and 2 *A.baumanii* isolates (15.3%), respectively by combined disc method which in 9 isolates band of product with 643bp and in 3 isolates (3.7%) with 261bp dependent on bla PER-1 and bla VIM-1 type enzymes were obtained by PCR method, respectively.

Conclusion: This subject throw lighted upon distress concentration on proper usage of extended spectrum antibiotics and permanent control of resistance in mentioned hospitals.

Keywords: *Pseudomonas aeruginosa* , *Acintobacter baumanii*, Extended-spectrum beta lactamases, Metallo- β -lactamases, PER-1gene, VIM-1 gene

**P371 - 600: ANTIBIOTIC RESISTANCE PATTERN OF KLEBSIELLA PNEUMONIA STRAINS
ISOLATED FROM URINE SAMPLES OF CHILDREN WITH URINARY TRACT INFECTIONS
IN TABRIZ CHILDREN HOSPITAL**

Sevda Leisy azar¹, amirraza ebadi²

1. MSc Student, Department of Microbiology, Ahar Branch, Islamic Azad University, Ahar, Iran
2. Department of Microbiology, Ahar Branch, Islamic Azad University, Ahar, Iran

Background and Aim: Klebsiella pneumonia is considered as the most common causes urinary tract infections in patients. Resistant strains of Klebsiella pneumoniae, especially to antibiotics of different drug classes, have become prevalent. In most cases, this resistance exacerbates the illness. The aim of this research is to study the antibiotic resistance pattern of Klebsiella pneumonia strains isolated from the urinary tract infections.

Methods: this study is a cross-sectional and descriptive research. In this study, 120 strains of Klebsiella pneumonia were collected from patients with urinary tract infections. Firstly, the strains were selected using standard laboratory and microbiology methods and special media. In order to assess the antibiotic susceptibility patterns of strains, they were cultured on Muller Hinton agar media with sterile cotton swab in three directions and Kirby-Bauer disk diffusion method was used for antibiogram.

Results: the highest resistance level of Klebsiella pneumonia were related to amoxicillin 97.5% and cotrimoxazole 95%, respectively

Conclusion: Due to the increasing prevalence of resistance to antibiotics, quick and timely detection of resistant strains seems necessary in order to select appropriate treatment options and to prevent the increase of resistance.

Keywords: Klebsiella pneumonia, urinary tract infection, drug resistance

**P372 - 609: CHARACTERIZATION OF ANTIMICROBIAL RESISTANT UROPATHOGENIC
ESCHERICHIA COLI ISOLATED FROM IRAN**

Nooshin Kamrani Hemat¹, Mohsen Mirzaee²

1. Department of Cell and Molecular Biology, Boroujerd Branch, Islamic Azad University, Boroujerd, Iran.
2. Department of Medical Laboratory Sciences, Boroujerd Branch, Islamic Azad University, Boroujerd, Iran.

Background and Aim:Background and aims: Antibiotic resistance of urinary tract pathogens has increased worldwide. Urinary tract infections (UTIs) are one of the most common bacterial infections with global expansion. These infections are predominantly caused by uropathogenic *Escherichia coli* (UPEC). The present investigation was performed to study the characterized antimicrobial resistance of UPEC isolated from Iran.

Methods:Material and Methods: This cross sectional investigation was performed on 210 urine samples collected from hospitalized patients in Iran. Multiplex PCR was used to detect *aadA1*, *tetA*, *tetB*, *dfrA1*, *qnr*, *aac* (3)-IV, *sul1*, *blaSHV*, *CITM*, *cat1*, and *cmlA* antibiotic resistance genes. Also, antimicrobial susceptibility testing was performed using disk diffusion methodology with Mueller–Hinton agar according to the instruction of CLSI.

Results:Results: A totally, 150 samples (71.42%) were positive for *E. coli*. High resistance levels to tetracycline (68%), sulfonamide (60%) and trimethoprim (58%) were also observed. Resistance against chlor–amphenicol was low (8.66%). 7.33% of tested strains were resistant to 8 antibiotics. The incidence of genes encoding resistance against aminoglycosides (*aadA1* and *aac*(3)-IV), sulfonamide (*sul1*), beta-lactams (*blaSHV* and *CITM*), tetracycline (*tetA* and *tetB*), trimethoprim (*dfrA1*), chlor–amphenicol (*cat1* and *cmlA*) and quinolones (*qnr*) were (8%, 5.33%), 44.66%, (42.66%, 8%), (58.66%, 55.33%), 48.66%, (8%, 3.33%) and 30%, respectively.

Conclusion:Conclusion: Our results indicated that antibiotic resistance is increasing in uropathogenic *E. coli* strains in Iran. It is imperative to develop strategies for prevention and control of resistant organisms. In the current situation, it seems that the administration of tetracycline, sulfonamide and trimethoprim for the treatment of UTIs is vain.

Keywords:Uropathogenic *Escherichia coli*; Antimicrobial resistance; Multiplex PCR, UTI

**P373 - 616: PREVALENCE OF VANCOMYCIN RESISTANT STAPHYLOCOCCUS STRAINS
ISOLATED FROM URINARY TRACT INFECTIONS**

Fatemeh Abbasi¹, Nadia Kazemipoor²

1. Islamic Azad University of Kerman
2. Islamic Azad University of Kerman

Background and Aim: Vancomycin is the best choice drug for methicillin resistant *Staphylococcus aureus*. At present, continued use of vancomycin in the world is the major reason for resistance to this antibiotic. This research is going to find the prevalence of vancomycin resistant strains of *Staphylococcus* strains isolated from clinical samples of Aliebn Abitaleb in Rafsanjan city.

Methods: This project was a cross sectional study using urine samples from 150 different patients during 4 months. Identification of isolates in genus and species level was performed using different staining as well as biochemical tests. Disc diffusion and agar dilution methods were used to evaluate antibiotic resistance and Minimum inhibitory concentration for the mentioned antibiotic.

Results: 23.3% of all patients had staphylococcal urinary tract infections which 11.4% were identified as *S. epidermidis* and 88.6% *S. aureus*. In this research, it was found that all isolates were sensitive to vancomycin.

Conclusion: Although there is a worldwide different antibiotic resistance and it is a dangerous situation but according to the results of this research vancomycin is the best choice drug for Staphylococcal urinary tract infections

Keywords: *Staphylococcus aureus*, Urinary tract infections, Vancomycin

**P374 - 619: IN VITRO INHIBITORY EFFECT OF PYRAN NANOPARTICLES ON AMPC
BETA-LACTAMASE PRODUCING ESCHERICHIA COLI STRAINS**

Azadeh Noormohammadi¹, Haddadi Azam², Makarem somayeh³

1. Department of Biology, Karaj Branch, Islamic Azad University, Karaj, Iran,
2. Department of Biology, Karaj Branch, Islamic Azad University, Karaj, Iran,
3. Department of Biology, Karaj Branch, Islamic Azad University, Karaj, Iran,

Background and Aim: AmpC β -lactamases are important cephalosporinases chromosomally encoded in many of Enterobacteriaceae. The high rate of antibacterial resistance in AmpC beta-lactamase producing strain is a matter of concern. Recent years have witnessed unprecedented growth of research and applications in the area of nanotechnology. There is increasing optimism that nanotechnology, as applied to medicine, will bring significant advances in the treatment of disease.

Methods: This study was performed on 100 clinical Escherichia coli isolates. Phenotypic combined disc test was used for detection of AmpC-producing Escherichia coli isolates. MIC of pyran nanoparticles were determined using sterile 2ml 96-well plates. The tested dilutions ranged from 2500 to 9.76 $\mu\text{g/mL}$ using dimethyl sulfoxide (DMSO) as solvent. MBC was determined by subculturing the contents of wells that showed no visible growth of bacteria onto Muller Hinton agar plates and incubating at 37°C for 18 h.

Results: AmpC screening of strains by phenotypic combined disc test showed that out of 100 samples 5% (5) were AmpC positive. All AmpC-producing isolates were tested for MIC value and pyran nanoparticles showed antibacterial activity with MIC values of 2500 $\mu\text{g/mL}$. Furthermore our MIC was equal to MBC.

Conclusion: It should be mentioned that although nanoparticles is effective against bacteria in vitro, these concentrations may not have the same impacts in clinical conditions. However, further studies at the fundamental, biological, and pharmacological level are required to enable systemic administration of these antimicrobials.

Keywords: Escherichia coli, beta-lactamase AmpC, nanoparticles

**P375 - 621: EVALUATION OF ANTIBIOTICAL SENSIVITY OF URINARY TRACT
PATHOGENS IN CHILDREN REFERRED TO PEDIATRIC CLINICS IN ZAHEDAN IN YEAR
94**

Mojde Jahantigh¹, Mehdi jahantigh²

1. MSc Microbiology student, Department of Microbiology, Zahedan University of Medical Science, Iran
2. Department of Pathology, Ali Ebne Abitaleb Hospital, Zahedan University of Medical Sciences, Zahedan, Iran

Background and Aim: Urinary tract infections (UTIs) are one of the most frequent bacterial infections in children. The most commonly bacterial cause was E. coli. Other microorganisms included, Enterobacter, Klebsiella, Proteus, Staphylococcus and Pseudomonas aeruginosa, which was the last common.

Methods: This descriptive-analytical and prospective study was done in 2015-2016 on urine samples of all children 1-18 years who had been referred to pediatric clinic in Zahedan hospital and positive urine culture. Sex and age of children, kind of isolated bacteria in urine culture, susceptibility and resistance of these bacteria to current antibiotics were studied. The obtained data was analyzed by means of SPSS.

Results: 200 children (160 girls and 40 boys) with positive urine culture were studied. The most common age of urinary tract infection in boys was under 1 year and in girls was 1-7 years. E. coli was the most common cause in both sexes. The most prevalent cause of urinary tract infection in all ages was E. coli (73%), infection by Enterobacter 11.5% and Klebsiella 9.5% and Proteus 3%, and other microorganisms caused 3% of the cases. Ceftriaxone and ceftazidime and the most resistance to Cephalexin and Cotrimoxazole. Not taking the type of microorganism into consideration, the most sensitive antibiotics were Nitrofurantoin, ciprofloxacin, Gentamycin, Ceftriaxone, Cefexim; and the most resistance was against Cotrimoxazole and Ampicillin.

Conclusion: Commented for treatment of UTI first know sensitivity of antibiotic of region then start to treat with this way we can decrease the resistance.

Keywords: Urinary tract infection. Antimicrobial susceptibility

**P376 - 625: SIMPLE METHOD FOR ASSESSMENT MDR ACINETOBACTER BAUMANNII BY
AGAR ETHIDIUM BROMIDE CARTWHEEL METHOD**

Amin Sepehr¹, Nader Shahrokhi², A.Japoni-Nejad³

1. MSc student of Medical Microbiology, Molecule Biology Department, Pasteur Institute of Iran-Tehran
2. PhD of Medical biotechnology, Molecule Biology Department, Pasteur Institute of Iran-Tehran
3. PhD student of Medical Bacteriology, Mycobacteriology Department, Pasteur Institute of Iran-Tehran

Background and Aim: *Acinetobacter* spp. is known as an important nosocomial pathogen and shows continuous raise in antimicrobial resistance. Efflux genes have been reported to be existed in both gram-negative and gram-positive bacteria. Our aim was to evaluate role efflux pumps and antimicrobial susceptibility in MDR *Acinetobacter baumannii*.

Methods: The antimicrobial susceptibility pattern was determined by using the standard disk diffusion method according to CLSI guidelines. The Distribution of tetA, tetB tetM and adeABC genes were determined by polymerase chain reaction method. Minimum inhibitory concentration (MIC) of tetracycline in the presence and absence of cccp measured by microdilution method according to CLSI guidelines. Agar Ethidium bromide method was used to evaluate the overexpression of adeABC efflux pump. The methodology used is ML Agar plates containing EtBr concentrations 1mg/L.

Results: Almost all isolates were resistant to a wide range of antibiotics; tetracycline (80%), imipenem (76%), Ciprofloxacin (90%) and the lowest resistance rate was found to colistin (0 %). The tetA, tetB, tetM, adeABC genes were identified in 5(12.5%), 31(77.5) , 0 and 38 (95%) isolates respectively. MIC of tetracycline was observed in isolates in presence and absence of efflux pump inhibitor (EPI). MDR bacteria were analyzed by agar ethidium bromide (Cartwheel) method and increased activity of adeABC efflux pumps in 4 isolates were confirmed.

Conclusion: Agar ethidium bromide Cartwheel method is a fast and convenient method for assessing the ethidium bromide secretion in various bacterial genera that can be used in quickly diagnose and treatment of multidrug-resistant bacteria.

Keywords: Agar ethidium bromide Cartwheel, AdeABC, *Acinetobacter baumannii*

P377 - 630: PATTERN OF ANTIBIOTIC RESISTANCE IN PSEUDOMONAS AERUGINOSA STRAINS ISOLATED FROM BURN PATIENTS IN TALEGHANI BURN HOSPITAL OF AHVAZ, IRAN

Moloudsadat Motahar¹, Azar Dokht Khosravi², Effat Abasi montazeri³

1. Dept. of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
2. 1 Dept. of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran; 2 Health Research Institute, Infectious and Tropical Diseases Research Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
3. Dept. of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences

Background and Aim:Antimicrobial resistance in *Pseudomonas aeruginosa* has been increasing in recent years. This pathogenic agent due to its virulence abilities, is one of the main threats to burn patients. *P. aeruginosa* possesses various mechanisms to counteract with antimicrobial agents including acquired and intrinsic mechanisms which makes that a formidable nosocomial pathogen. The purpose of this study was to determine the antimicrobial susceptibility patterns of *P. aeruginosa* isolated from burn patients.

Methods:In total 92 isolates of *P. aeruginosa* were collected from burn patients in a four month period. The isolates were initially identified by culture and standard biochemical tests. The antibiotic susceptibility testing was performed using the disc diffusion method according to CLSI recommendations.

Results:The high antibiotic resistance were detected among the isolates in this study. The highest resistance was seen to gentamicin and ciprofloxacin each showed 94.57% of resistance. The resistance rates to various other antibiotics were as follows: imipenem (85.87%), meropenem (90.22%), amikacin (88.04%), Piperacillin/tazobactam (86.96%), ciprofloxacin (94.57%). The most sensitive antibiotic against *P. aeruginosa* was colistin, which none of the isolates showed resistance to that.

Conclusion:Optimization of using antimicrobial agents and control of infection is recommended to prevent the increasing population of drug resistant *P. aeruginosa* in the setting of this study.

Keywords:*Pseudomonas aeruginosa*, antibiotic resistance, burn patients

**P378 - 637: ADEABC EFFLUX PUMP GENES IN MULTIDRUG RESISTANT
ACINETOBACTER BAUMANNII ISOLATED FROM PATIENTS IN BAGHDAD, IRAQ**

Kais Kassim¹, Kais Kassim Ghaima², Shurook Mohammad K. Saadedin³, Kifah Ahmed Jassim⁴

1. Institute of Genetic Engineering and Biotechnology for Postgraduate Studies, University of Baghdad, Baghdad, Iraq.
2. Institute of Genetic Engineering and Biotechnology for Postgraduate Studies, University of Baghdad, Baghdad, Iraq.
3. Institute of Genetic Engineering and Biotechnology for Postgraduate Studies, University of Baghdad, Baghdad, Iraq.
4. Central Public Health Laboratory, Ministry of health, Baghdad, Iraq.

Background and Aim:Background: *Acinetobacter baumannii* is an opportunistic nosocomial pathogen and a cause of severe infections in hospitalized patients, owing to its ability to acquire drug resistance by the efflux pump mechanism. Objectives: The current study investigated the detection and prevalence of efflux pump genes (AdeABC) in multidrug resistant *A.baumannii* isolates and the role of these genes in multidrug and carbapenems resistance.

Methods:Materials and methods: This study was conducted on 84 multidrug resistant and 13 carbapenem-susceptible *A.baumannii* isolates collected from burns and wounds infections in Baghdad hospitals, Iraq. The AdeABC genes were detected by polymerase chain reaction (PCR) assay. Phe-arg-beta-naphthylamide (PAβN) based method was used for determination of efflux pump activity.

Results:Results: This study showed high prevalence of efflux pump genes in our local isolates. AdeB gene was present in all multidrug resistant isolates (100%) while AdeRS gene (95.2%), AdeC gene (83.3%) and AdeA gene (77.4%). By comparing the exist of these gene in carbapenem-susceptible isolates, it was demonstrated that the gene AdeB was absent in all susceptible isolates, also the regulatory gene AdeRS was not found in the most of these isolates, while the other genes (AdeA and AdeC) were detected in the most carbapenem- susceptible isolates. Susceptibility of isolates to Amikacin, Gentamicin, Ciprofloxacin, Levofloxacin, Tetracycline and Tigecycline was highly increased in the presence of efflux pump inhibitor; So that, PAβN reduced the MICs by 4 to 32 folds. Also MICs of carbapenems were reduced by the inhibitor 2 to 8 folds, while the MICs of cephalosporins and Colistin were not affected.

Conclusion:Conclusion: AdeABC efflux system plays a vital role in multidrug resistance in clinical *A.baumannii* isolates. It was noted that the most important gene responsible for multidrug resistance within this system was AdeB gene especially in carbapenems resistance.

Keywords:Key words: *Acinetobacter baumannii*, multidrug resistant, AdeABC genes.

**P379 - 640: ADEABC EFFLUX PUMP GENES IN MULTIDRUG RESISTANT
ACINETOBACTER BAUMANNII ISOLATED FROM PATIENTS IN BAGHDAD, IRAQ**

Kais Kassim¹, Kais Kassim Ghaima², Shurook Mohammad K. Saadedin³, Kifah Ahmed Jassim⁴

1. Institute of Genetic Engineering and Biotechnology for Postgraduate Studies, University of Baghdad, Baghdad, Iraq.
2. Institute of Genetic Engineering and Biotechnology for Postgraduate Studies, University of Baghdad, Baghdad, Iraq.
3. Institute of Genetic Engineering and Biotechnology for Postgraduate Studies, University of Baghdad, Baghdad, Iraq.
4. Central Public Health Laboratory, Ministry of health, Baghdad, Iraq.

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Methods:Materials and methods: This study was conducted on 84 multidrug resistant and 13 carbapenem-susceptible *A.baumannii* isolates collected from burns and wounds infections in Baghdad hospitals, Iraq. The AdeABC genes were detected by polymerase chain reaction (PCR) assay. Phe-arg-beta-naphthylamide (PAβN) based method was used for determination of efflux pump activity.

Results:Results: This study showed high prevalence of efflux pump genes in our local isolates. AdeB gene was present in all multidrug resistant isolates (100%) while AdeRS gene (95.2%), AdeC gene (83.3%) and AdeA gene (77.4%). By comparing the exist of these gene in carbapenem-susceptible isolates, it was demonstrated that the gene AdeB was absent in all susceptible isolates, also the regulatory gene AdeRS was not found in the most of these isolates, while the other genes (AdeA and AdeC) were detected in the most carbapenem- susceptible isolates. Susceptibility of isolates to Amikacin, Gentamicin, Ciprofloxacin, Levofloxacin, Tetracycline and Tigecycline was highly increased in the presence of efflux pump inhibitor; So that, PAβN reduced the MICs by 4 to 32 folds. Also MICs of carbapenems were reduced by the inhibitor 2 to 8 folds, while the MICs of cephalosporins and Colistin were not affected.

Conclusion:Conclusion: AdeABC efflux system plays a vital role in multidrug resistance in clinical *A.baumannii* isolates. It was noted that the most important gene responsible for multidrug resistance within this system was AdeB gene especially in carbapenems resistance.

Keywords:Key words: *Acinetobacter baumannii*, multidrug resistant, AdeABC genes.

**P380 - 655: ANTIBIOTIC RESISTANCE PROFILE OF MULTIDRUG RESISTANT GRAM
NEGATIVE BACTERIA ISOLATED FROM AND PLASMID HOSPITAL EFFLUENTS**

Raziye Khanpoor zarengye¹, Raziye Khanpoor zarenjye², Maryam Ghane ³

1. -
2. M. Sc in Environmental sea, Islamic Azad University, Islamshahr Branch, Islamshahr, Iran
3. Assistant Professor, Department of Microbiology, Faculty of Basic Sciences, Islamic Azad University, Islamshahr Branch, Islamshahr, Iran.

Background and Aim:Waste effluent from hospitals contain high numbers of resistant bacteria. Among resistant strains, Gram negative bacilli are able to survive for a long time in the environment and act as natural reservoirs of resistant genes. The aim of this study was to determine the prevalence of antibiotic resistant gram negative bacilli and the plasmid profile of multi resistant bacteria in hospital effluents.

Methods:The antibiotic resistance patterns of the isolated strains were assayed by disc diffusion method. The isolates were identified in accordance with Bergey's Manual of Systematic Bacteriology. Plasmid extraction was carried out by alkaline lysis technique.

Results:A total of 320 bacterial isolates were picked from the sewage samples. Gram-negative rods represented the main bulk (62.5%) followed by Gram-positive rods (34.4%) and Gram positive cocci (3.1%). The most common isolates were *Escherichia coli* (33%) followed by *Pseudomonas aeruginosa* (17 %). The Gram-negative rods were tested for their susceptibility for eight antibiotics. The results showed that Gentamicin and Ceftriaxone was the most effective antibiotics and the least effective was ampicillin. The results also showed that all of the isolates were multi-drug resistant and 6% of them were resistant to all of the tested antibiotics. Isolates with high multi-drug resistance profiles were found to possess multiple plasmids with sizes in the range of 1.5 to 24.5 KB.

Conclusion:The results show that the multi-drug resistant bacteria are present in the hospital waste and could be threat for public health.

Keywords:multidrug resistance, hospital sewage, plasmid.

P381 - 656: MIC DETERMINATION AND QUALITATIVE ASSESSMENT OF ANTIBIOTIC SUSCEPTIBILITY AMONG CLINICAL, FOOD AND CATTLE BASED L.MONOCYTOGENES ISOLATES.

Lida Lotfollahi¹, ardalan chaharbalesh², Lida Lotfollahi³, Mohammad Ahangarzadeh Rezaee^{3,4}, Alka Hasani^{3,5}

1. 2Immunology Research Center, Tabriz University of Medical Sciences, Tabriz, IR Iran
2. 1Department of Microbiology, faculty of medicine, Urmia university of Medical Sciences, Urmia, Iran,
3. 3Tabriz Infectious and Tropical Diseases Research Center, Tabriz University of Medical Sciences, Tabriz, IR Iran
4. 3Tabriz Infectious and Tropical Diseases Research Center, Tabriz University of Medical Sciences, Tabriz, IR Iran

Background and Aim: Listeriosis is an important disease due to infection of *Listeria monocytogenes*. The aim of current study was determination of antibiotic resistance in isolated bacteria.

Methods: for evaluation of antibiotic resistance among 22 isolates of *L.monocytogenes* recovered from clinical, food and cattle samples, disk diffusion agar method (ampicillin , penicillin G, gentamicin , sulphamethoxazole-trimethoprim , tetracycline , rifampicin , kanamycin, linezolid , chloramphenicol , amoxicillin-clavulanic-acid and clindamycin) and determination of minimum inhibitory concentration were done using antibiotic disks and E-test (Penicillin G , clindamycin , gentamicin and ampicillin (0.016-256mg/l)

Results: 6 isolates were resistant to penicillin G. The intermediate rate was as below: All of the isolates, were intermediate to clindamycin and 2(9%) were intermediate to rifampicin. All 22 *L.monocytogenes* isolates tested against 2 antimicrobial agents (ampicillin and gentamicin) using the E-test were sensitive. 16 isolates were intermediate to clindamycin and 6 strains were resistant to penicillin G.

Conclusion: resistance to penicillin as one of therapeutic agents for listeriosis is important and physicians must be aware of that.

Keywords: *Listeria monocytogenes*, resistance, MIC

**P382 - 672: INVESTIGATION ANTIFUNGAL ACTIVITIES OF THE EXTRACT ALGAE
SARGASSUM GLAUCESCENS AGAINST HUMAN PATHOGENS**

Maryam Amirsharifi¹, Shahla Jamili², KambizLarijani³, Ali MashinchianMoradi⁴, Kummars Amini⁵

1. Department of Marine Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran.
2. Iranian Fisheries Science Research Institute, Agricultural Research, Education and Extension Organization, Tehran, Iran
3. Department of Chemistry, Faculty of Basic Science and Research Branch, Islamic Azad University, Tehran, Iran
4. Department of Microbiology, School of Basic Sciences, Saveh Branch, Islamic Azad University, Saveh, Iran
5. Department of Microbiology, School of Basic Sciences, Saveh Branch, Islamic Azad University, Saveh, Iran

Background and Aim: Considering the increasing rate of drug-resistant strains of microorganisms, antifungal compounds from natural materials certainly have fewer side effects, have long been of interest to researchers, this study aimed to evaluate the antifungal activity of methanol extracts, ethyl acetate, hexane and chloroform brown seaweed *Sargassum glaucescens* against pathogenic fungi were evaluated.

Methods: After collecting and extracting algae *Sargassum glaucescens* antifungal activity on two fungal pathogen *Candida albicans* ATCC 10231 and *Aspergillus fumigatus* PTCC 5009 Using microdilution method was studied.

Results: Two fungal pathogens were susceptible to all four types of seaweed *Sargassum glaucescens* the methanol extract of seaweed *Sargassum glaucescens* has antifungal activity and potentially more.

Conclusion: The results showed that the methanol extract of seaweed *Sargassum glaucescens* can be considered as a natural resource for use in the treatment of diseases. Therefore, further to the isolation, purification and identification of effective and active with anti-fungal properties for pharmaceutical formulation is suggested.

Keywords: Antifungal activity, *Sargassum glaucescens*, extract, microdilution.

**P383 - 682: IN VITRO INHIBITORY EFFECT OF ALCOHOLIC EXTRACT OF PHYSALIS
ALKEKENGII ON AMPC BETA-LACTAMASE PRODUCING ESCHERICHIA COLI STRAINS
ISOLATED FROM DIFFERENT CLINICAL SPECIMENS IN KARAJ**

Ziba Zafari¹, Haddadi Azam², Parvin Torabzadeh³

1. Karaj Branch, Islamic Azad University, Karaj, Iran,
2. Department of Biology, Karaj Branch, Islamic Azad University, Karaj, Iran,
3. Department of Biology, Karaj Branch, Islamic Azad University, Karaj, Iran,

Background and Aim: Unfortunately, antibiotic resistance has become an increasingly critical problem among Enterobacteriaceae in many countries like Iran. The expense for the use of traditional medicine is growing exponentially in many parts of the world. Plants with potential medicinal activity have recently come to the attention of Western scientists, and studies have reported that some are bioactive. This study aimed to evaluate the antibacterial effect of ethanol extracts of *Physalis alkekengi* against AmpC producing *Escherichia coli* isolates, one of the major causes of UTIs.

Methods: This study was performed on 100 clinical *Escherichia coli* isolates. Phenotypic combined disc test (CDT) was used for detection of AmpC beta-lactamase producing *Escherichia coli* isolates. MICs of ethanol extracts of *Physalis alkekengi* were determined using sterile 2ml 96-well plates. The tested dilutions ranged from 600 to 1.17 µg/mL. MBC was determined by subculturing the contents of wells that showed no visible growth of bacteria onto Muller Hinton agar plates and incubating at 37°C for 18 h.

Results: AmpC screening of strains by phenotypic combined disc test showed that out of 100 samples 5% (5) were AmpC positive. All AmpC-producing isolates were tested for MIC value and ethanol extracts of *Physalis alkekengi* showed antibacterial activity with MIC values of 300 µg/mL. Furthermore our MIC was equal to MBC.

Conclusion: The presence of antibacterial activity could be confirmed in most plant species used in traditional medicine in Iran which was investigated in this study for *Physalis alkekengi*.

Keywords: antibacterial activity, *Escherichia coli*, *Physalis alkekengi*

P384 - 694: MULTIDRUG RESISTANCE IN CLOSTRIDIUM ISOLATES FROM BROILER CHICKENS

Mojtaba Alimolaei¹, Majid Ezatkhah²

1. Department of Molecular Microbiology, Kerman branch, Razi Vaccine and Serum Research Institute, Kerman branch, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran
2. Department of Anaerobic Bacterial Vaccine Research and Production, Kerman branch, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran

Background and Aim: Clostridium species are gram-positive, anaerobic, and spore forming bacteria. The use of antibiotic growth promotants in poultry rearing is a public health concern due to antibiotic resistance and the harborage of resistance genes. The aim of this study was to determine the antimicrobial susceptibility in clostridial isolates from broiler chickens.

Methods: A total of 79 Clostridium isolates (50 *C. perfringens* isolates, 13 *C. clostridioforme* isolates, 9 *C. leptum* isolates, 3 *C. baratii* isolates, 3 *C. novyi* isolates, and one *C. Celatum* isolate) were used that confirmed previously by biochemical and molecular tests. These were screened for antibiotic resistance profiles with fourteen antimicrobial discs by Kirby-Bauer disc diffusion method as described by the National Committee for Clinical Laboratory Standards (NCCLS).

Results: Results were shown resistancy to many of the tested antibiotics. The high resistance rates were observed for tetracycline, gentamicin, ciprofloxacin, and trimethoprim/sulfamethoxazole. Moreover, different and diverse resistant patterns were seen among isolates.

Conclusion: These variable resistance patterns demonstrate a challenge for veterinarians in the field. Further researches for resistance genes and resistance profiles in clostridial isolates of broiler chickens were suggested.

Keywords: Clostridium, Broiler chickens, Resistance profiles

**P385 - 705: ISOLATION AND CHARACTERIZATION OF PHAGE AGAINST SALMONELLA
TYPHIMURIUM IN RASHT**

Pegah Panahi¹, Ali mojtahedi², Mohammadali Khan Mirzaei³, Mohammad Shenagari⁴

1. MSc student of Medical Microbiology, Microbiology Department, Faculty of Medicine, Guilan University of Medical Sciences, Rasht- Iran
2. Assistant Professor, Microbiology Department, Faculty of Medicine, Guilan University of Medical Sciences, Rasht- Iran
3. Assistant Professor, Department of Microbiology and Immunology, McGill University, Duff Medical Building, Montreal- Canada
4. Assistant Professor, Microbiology Department, Faculty of Medicine, Guilan University of Medical Sciences, Rasht- Iran

Background and Aim:Salmonella.spp. are important in medicine. Most related infections are self-limited. Antibiotics are used for high risk patients such as children, elder individuals and immune-compromised people. Overuse of antibiotics has led to increased multi-drug resistant bacteria which are life-threatening. Phage therapy is one of the embedment ways to reduce antibiotic prescribing

Methods:Waste waters of Rasht city were collected twice in a month. Prepared suspension of Salmonella reference collection A (SARA) number 1 (S. typhimurium) and Double LB broth were mixed with filtrated waste water. After centrifugation and filtration, serial dilution was done and phage was isolated. Phage enrichment was done and stored at -80°C. Morphologic characteristics were determined using TEM. Finally, cross host was performed against 5 SARA (No. 1, 6, 19, 51 and 54) strains to determine its spectrum effect

Results:Clear plaque formation on double layer LB agar indicated that SARA number 1 has been lysed with isolated phage. The first and last plaque formation was observed at concentration of 10⁻⁶ and 10⁻⁸ respectively. Cross host results showed that SARA number 6 (S. typhimurium) and 51 (S. paratyphi B) were lysed by isolated phage. Imaging with TEM showed that the isolate phage was belonging to podoviridae

Conclusion:It was the first report of phage isolation against Salmonella reference collection in Iran. Interestingly, SARA no. 51 (S. paratyphi B) was lysed by S. typhimurium phage. It means that the isolated phage may lyse S. typhi, a human pathogen, which important in severe diseases

Keywords:Salmonella reference collection, Bacteriophage, cross host, TEM

P386 - 706: ASSESSMENT OF ANTIBIOTIC RESISTANCE OF STAPHYLOCOCCUS SPECIES ISOLATED OF NEONATAL INTENSIVE CARE UNIT (NICU) OF MOBINI HOSPITAL IN SABZEVAR.

Faezeh Haghighi¹, Hassan salehipour², Mohammad Mohammad-Zadeh³, Ali Hosseinzadeh⁴, Morteza Haghighi Hasanabad⁵

1. Cellular and Molecular Research Center, Sabzevar University of Medical Sciences, Sabzevar, Iran
2. Department of pediatrician, Sabzevar University of medical sciences, Sabzevar, Iran
3. Cellular and Molecular Research Center, Sabzevar University of Medical Sciences, Sabzevar, Iran
4. Department of Epidemiology and Biostatistics, Sabzevar University of Medical Sciences, Sabzevar, Iran
5. Children & Pediatric Infection Diseases Research Center, Iran University of Medical Sciences, Tehran, Iran

Background and Aim: Nosocomial infections increase patients' mortality and duration of hospital stay particularly in neonatal intensive care units (NICUs). Staphylococcus species is of the important factors causing nosocomial infections. The emergence of antibiotic-resistant Staphylococcus strains has brought about several problems in treatment of the infections caused by Staphylococcus strains. Hence, the aim of this study was to detect antibiotic resistance of Staphylococcus aureus and coagulase-negative staphylococci isolated of Neonatal Intensive Care Unit (NICU) of Mobini Hospital in Sabzevar to current antibiotics.

Methods: Two hundred and twenty samples from medical equipment available at NICU were studied. For identification of staphylococcus species, the major tests of catalase, coagulase, DNase were done. Antibiotic-resistant of Staphylococcus strains was assessed by antibiogram and disk diffusion, in accordance with CLSI standards. Qualitative control was performed by staphylococcus aureus ATCC12600 and data were analyzed using SPSS.

Results: The findings of this study suggested that among total 220 samples surveyed, the most common bacteria isolated from NICU were coagulase-negative staphylococci (57.14%) and Staphylococcus aureus (22.85%). Based on antibiogram, 65.30% of specimens are resistant to Ceftazidime, 85.71% to Ampicillin, 34.69% to Cefalotin and Carbenicillin, 40.81% to Trimethoprim Sulfamethoxazole, 83.67% to Penicillin, 30.61 to Cefotaxime and Gentamicin, 16.32% to Amikacin, 38.77% to Oxacillin.

Conclusion: Our findings show that the neonatal intensive care unit of Mobini hospital has relatively high nosocomial infections. With due regard to the differences in antibiotics sensitivity and resistance rate in different strains, evaluation of antibiotic resistance is necessary for treatment of microbial infections.

Keywords: Nosocomial infections, Antibiotic resistance, Staphylococcus aureus, Coagulase-negative staphylococci

**P387 - 707: THE INCREASING EMERGENCE OF VANCOMYCIN RESISTANCE IN
METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS**

Marjan Shekarabi¹, Fereshteh Eftekhari², Mehdi Goudarzi³

1. Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University G.C., Velenjak, Tehran, Iran
2. Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University G.C., Velenjak, Tehran, Iran
3. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: Vancomycin has become the antimicrobial choice for serious infections caused by methicillin resistant *Staphylococcus aureus* (MRSA). Contrary to considerable vancomycin usage, the first vancomycin intermediately-resistant *S. aureus* (VISA) isolate was described in 1996. Since then, VRSA isolates and reports of treatment failure with vancomycin started to appear. The aim of this study was to investigate the prevalence of VRSA among clinical isolates of MRSA.

Methods: A total 97 clinical isolates of *S. aureus* were collected from June 2014 to July 2016 from 10 hospitals in Tehran. Antibacterial susceptibility was determined to 12 antibiotics by disc diffusion. Presence of *mecA* gene was detected using specific primers and PCR. Measurement of vancomycin minimum inhibitory concentrations (MIC) was carried out using broth microdilution.

Results: PCR amplification showed that 78 isolates (80.41%) carried the *mecA* gene. The highest rate of resistance was observed for ceftazidime and oxacillin (100%) followed by erythromycin (93.8%), ciprofloxacin (89.7%), clindamycin (87.6%), gentamicin (88.7%), tobramycin (85.6%), rifampin (79.4%), linezolid (35%), trimethoprim-sulfamethoxazole (21.6 %) and teicoplanin (6.2%). MIC results showed that 4.1% of MRSA were resistant ($\geq 16 \mu\text{g/ml}$) and 3.1% were intermediately resistant to vancomycin (4-8 $\mu\text{g/ml}$).

Conclusion: Our results show a high rate of vancomycin resistance among clinical isolates of MRSA.

Keywords: MRSA, VRSA, MIC, *mecA*

**P388 - 734: DETERMINATION OF RESISTANCE PATTERN IN KLEBSIELLA PNEUMONIA
ISOLATED FROM URINARY TRACT INFECTIONS IN QOM**

Saghar Shahbazi¹, Dr.Mohsen Zargar²

1. MA student of Islamic Azad University of Qom
2. Professor-Department of Microbiology , Islamic Azad University of Qom-Advisor

Background and Aim:: Antibiotic resistance has always been considered one of the serious Problem for the man health. Antibiotic resistance, indeed, is the ability of microbes to resist against the effects of antibiotics with use of different mechanisms. Klebsiella pneumonia is a negative gram pathogen and is one of the prevalent factors of urinary infections. Increasing appearance of resistance to several drugs among the hospital isolated of Klebsiella pneumonia, has limited the treatment options for infections to be existed. So performing the drug resistance tests before prescribing antibiotic, seems to be necessary. One the aim of this study is determining sample of antibiotic resistance of Klebsiella pneumonia species from clinical samples of the patients.

Methods:This study collected the sample making of 200 referred outpatients to the laboratories of Qom province in the years 1394 -1395 and then transferred to the laboratory of Azad university in Qom. Finally, about 100 number of bacteria from Klebsiella pneumonia to be recognized and separated. For determining of antibiotic sensibility, the method called disk diffusing of Kirby-Bauer according to instruction CLSI has been performed.

Results:: Results out coming of anti-microbe's sensibility test revealed that separations were in turn 74%,75%,72%,82%,81%,100%,100% sensitive to Imipenem, Meropenem, Tetracycline, Gentamycin, Nalidixic ACID, Ciprofloxacin and Amikacin. Also They were in turn 45%, 56%, 58%, 68%,100%,100% resistant to Aztreonam, Cefotaxime, Ceftazidime, Cephalexin, Ampicillin and Amoxicillin.

Conclusion:Having knowledge of Klebsiella pneumonia species to resist against the drugs is very important; because in the case of not controlling organisms which are resistant against the drug, these bacteria threatening the health of mankind.

Keywords:: Klebsiella pneumonia- urinary infections- Antibiotic resistance

**P389 - 770: THE PATTERN OF DRUG RESISTANCE IN ESCHERICHIA COLI STRAINS
ISOLATED FROM PATIENTS REFERRED TO THE HOSPITAL, ALI IBN ABI TALIB (AS)
ZAHEDAN**

Masomeh Mazaheri¹, narges badi²

1. Microbiology graduate student, Ayatollah Amoli Branch, Department of Biology, Tehran, Iran
2. Microbiology graduate student, Ayatollah Amoli Branch, Department of Biology, Tehran, Iran

Background and Aim:Background: Antibiotic resistance due to widespread use of antibiotics, one of the major reasons for failure in treatment Gtryn antibiotics. The aim of this study was to investigate the roots of antibiotic resistance in E. coli to some common antibiotics used.

Methods:This cross-sectional study within 4 months on clinical specimens sent from the hospital, Ali ibn Abi Talib (AS) Zahedan, 83 isolates of E. coli, in 1394 the microbiology laboratory samples after inoculation of clinical specimens into the culture medium on blood agar and incubated Vmk Cancan macroscopic and microscopic examination of colonies was performed. Then, using a sterile swab bacteria were cultured on Mueller-Hinton Agar medium. Resistance to six common antibiotics in the treatment of E. coli include imipenem discs, Syprvflvksasyn, Sftazydym, ceftriaxone, cefotaxime, Sfalvtyn with sterile forceps 2cm at a distance from the wall plate placed in culture. Plates were placed at 37 degrees, the demographic characteristics of patients included patient name, patient ID number, hospital ward, sampling location, sample type and other characteristics required by SPSS software were recorded.

Results:A total of 83 samples of isolated E. coli (8/57%) are resistant to ceftazidime (6/56%) were resistant to ceftriaxone. (42.1%) were resistant to cefotaxime (50.6%) are resistant to ciprofloxacin (45.7%) are resistant to cephalothin (37.3%) were resistant to imipenem

Conclusion:These results indicate increased resistance of E. coli to antibiotics imipenem and ciprofloxacin Vsfazydym compared to previous studies. More research in this field, to increase our knowledge and to deal more effectively with antibiotic-resistant microorganisms wastes will be patient.

Keywords:different clinical specimens, Escherichia coli, antibiotic resistance, Zahedan

**P390 - 773: IDENTIFICATION OF GLYCOPEPTIDE RESISTANCE ENTEROCOCCUS(GRE)
SPECIES FROM CLINICAL SPECIMENS OF PATIENTS IN AHWAZ TEACHING
HOSPITALS**

HAJAR HAMIDI¹, Ahmad Farajzadeh Sheikh², Mojtaba Shahin³

1. Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
2. Department of Microbiology, Medicine Faculty, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
3. Department of Microbiology, Medicine Faculty, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Background and Aim: Enterococci are Gram-positive, catalase-negative, non-spore-forming, facultative anaerobic bacteria, which usually inhabit the alimentary tract of humans in addition to being isolated from environmental and animal sources. The nosocomial pathogenicity of enterococci has emerged in recent years, as well as increasing resistance to glycopeptide antibiotics. There are various phenotypic and genotypic methods of detection of glycopeptide resistance in enterococci. This study for detection of various glycopeptides resistance in *Enterococcus*.

Methods: From November 2015 to May 2016, a total of 83 isolates of enterococci from various clinical samples were analyzed. GRE were identified by Kirby Bauer disc diffusion method with Clinical and Laboratory Standards Institute (CLSI) guidelines.

Results: The results of this study showed, *Enterococcus faecalis* (10 of 83) resistance to vancomycin, teicoplanin, nitrofurantoin, linezolid, fosfomicin, gentamicin, were found to be 0%, 0%, 0%, 20%, 0% and 60%, *Enterococcus faecium* (48 of 83) resistance were found to be 27.08%, 22.91%, 14.91%, 35.41%, 4.1% and 77.08%, *Enterococcus gallinarum* (2 of 83) resistance were found to be 50%, 50%, 0%, 0%, 0% and 50%, other species (23 of 83) resistance were found to be 13.04%, 8.69%, 8.69%, 43.47%, 13.04% and 78.26%, respectively

Conclusion: Resistance to glycopeptides is disseminating rapidly. Rapid identification of patients infected or colonized with VRE is essential for hospitalization patients of appropriate control measures to prevent their spread.

Keywords: Antibiotic resistance, *Enterococcus*, disc diffusion test

P391 - 788: HIGH PREVALENCE OF TRIMETHOPRIM RESISTANCE IN E. COLI ISOLATES FROM THALASSEMIA INFECTED PATIENTS IN KERMAN, IRAN

Hesam Alizade¹, Mohammad Reza Aflatoonian², Farnaz Nabavinia³

1. Department of Microbiology, Sirjan Faculty of Medical Sciences, Kerman University of Medical Sciences, Kerman, Iran; Research Center for Tropical and Infectious Diseases, Kerman University of Medical Sciences, Kerman, Iran
2. Research Center for Tropical and Infectious Diseases, Kerman University of Medical Sciences, Kerman, Iran
3. School of Pharmacy, Kerman University of Medical Sciences, Kerman, Iran

Background and Aim: In the most recent estimates of global antibiotic resistance published by the World Health Organization in 2014, *E. coli* was named as the one of greatest concern and is associated with hospital and community acquired infections. The most prevalent of *dhfr* genes, mediate high level resistance to trimethoprim and are most frequently found in gram-negative enteric bacteria. The present study was carried out to evaluate the prevalence of *dhfrI* in *E. coli* isolates from thalassemia patients in the south-east of Iran (Kerman).

Methods: This study was done with 62 *E. coli* isolates from healthy fecal samples of thalassemia infected patients. The *E. coli* isolates were confirmed using biochemical API 20E identification system. The DNA of the *E. coli* isolates was extracted by lysis method. The confirmed isolates were studied to prevalence *dhfrI* gene by PCR.

Results: Among the thalassemia patients *E. coli* isolates, 37 (59.7%) isolates were positive for *dhfrI* gene.

Conclusion: Our study indicated a high frequency of trimethoprim resistance gene in *E. coli* isolates from thalassemia patients *E. coli* isolates in Kerman.

Keywords: *Escherichia coli*, thalassemia, antibiotic resistance gene

**P392 - 789: SURVEY OF RESISTANT TO AMINOGLYCOSIDE IN ESCHERICHIA COLI
ISOLATES FROM HIV PATIENTS IN SOUTHEAST OF IRAN (KERMAN)**

Hesam Alizade¹, Farnaz Nabavinia², Mohammad Reza Aflatoonian³

1. Department of Microbiology, Sirjan Faculty of Medical Sciences, Kerman University of Medical Sciences, Kerman, Iran; Research Center for Tropical and Infectious Diseases, Kerman University of Medical Sciences, Kerman, Iran
2. School of Pharmacy, Kerman University of Medical Sciences, Kerman, Iran
3. Research Center for Tropical and Infectious Diseases, Kerman University of Medical Sciences, Kerman, Iran

Background and Aim: Bacterial infections have been detected as leading cause of death in patients with HIV. Since bacterial infections in these patients are very common, high consumption of antibiotics can result in antibiotic resistance. The goal of present study was to occurrence of aad and aacA genes in *E. coli* isolates from HIV infected patients in Kerman, Iran.

Methods: The *E. coli* isolates were obtained from HIV-infected patients (44 isolates; 39 male and five female) from September to November 2014 from the Voluntary Counseling and Testing Center in Kerman, Iran. The *E. coli* isolates of HIV patients were recovered from fecal samples. The *E. coli* isolates were confirmed using biochemical API 20E identification system. The confirmed isolates were examined to detect the aminoglycoside resistance genes including aad and aacA by PCR.

Results: Of 44 *E. coli* isolates, two (4.5%) isolates and one (2.2%) isolate were positive for aacA and aad genes, respectively. Furthermore, one isolate possessed both aacA and aad genes.

Conclusion: The results of this study revealed the low prevalence of aacA and aad genes in *E. coli* isolates from HIV patients.

Keywords: *Escherichia coli*, HIV, antibiotic resistance gene

P393 - 790: PHENOTYPIC AND MOLECULAR CHARACTERIZATION OF TEM EXTENDED SPECTRUM BETA LACTAMASE IN URINARY E.COLI ISOLATES.

Fariba Adham¹, Maryam Ghane²

1. M.Sc of Microbiology, Islamic Azad University Islamshahr Branch, Tehran, Iran
2. Assistant Professor of Microbiology, Islamic Azad University Islamshahr Branch, Tehran, Iran.

Background and Aim: Extended spectrum beta lactamases (ESBLs) are a group of β -lactamase enzymes which have the ability to hydrolyze all cephalosporins and monobactams, but are inhibited by β -lactamase inhibitors, such as clavulanic acid. This study was aimed to determine the prevalence of bla TEM gene among ESBL producing E. coli strains which can provide applicable information about their epidemiology and risk factors related to their infections

Methods: In this study, the isolated strains were identified by biochemical methods in accordance with Bergey's Manual of Systematic Bacteriology. Screening and phenotypic confirmatory test for ESBL production were performed using standard double disc diffusion methods. Each of the initial ESBL screening test isolate was investigated for the presence of bla TEM gene via polymerase chain reaction (PCR) using gene-specific primers.

Results: A total of 500 E. coli isolates were obtained from urine specimens of patients from various hospitals in Karaj, Iran. 180 (36%) of them were phenotypically ESBL-positive and 54.4% of those isolates harbored bla TEM gene. The highest rates of resistance in E. coli isolates were observed for; cefotaxime (100%), penicillin (96.25) and erythromycin (93.75%) and the lowest rate was for amikacin (20%).

Conclusion: The results show that bla TEM gene are present with high prevalence in urinary E. coli isolates in Karaj. The global dissemination of TEM producing E. coli isolates highlights the need for their epidemiological monitoring and prudent use of antibiotics in Alborz province.

Keywords: ESBL, bla TEM, E. coli. PCR

P394 - 832: CORRELATION OF ANTIBIOTIC RESISTANCE PROFILE AND BIOFILM PRODUCTION LEVEL AMONG CLINICAL ISOLATES OF PSEUDOMONAS AERUGINOSA IN URMIA, IRAN

Ehsan Shojadel¹, Saber Yousefi², Nima Hosseini Jazani³, Sadeg Asghari⁴

1. Student Research Committee, Urmia University of Medical Sciences, Urmia, Iran
2. Department of Microbiology and Virology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran - Cellular and Molecular Research Center, Urmia University of Medical Sciences, Urmia, Iran
3. Department of Microbiology and Virology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran
4. Iman Khomeini Hospital Laboratory, Urmia university of Medical Sciences, Urmia, Iran

Background and Aim: *Pseudomonas aeruginosa* is an opportunistic pathogen that can cause a wide spectrum of infections especially in hospitalized patients. Recently increasing the nosocomial infection and antimicrobial resistance besides biofilm formation among *P. aeruginosa* isolates has appeared as a grate problem in healthcare settings. This study was performed to study the relationship between antimicrobial resistance profile and biofilm production among clinical isolates of *Pseudomonas aeruginosa*.

Methods: During June 2015 to March 2015 clinical isolates of *P. aeruginosa* were collected from a university Hospital of Urmia, Iran. Identification of bacterial isolates were carried out by standard microbiological test. Antimicrobial susceptibility testing was done by disk diffusion method and biofilm formation measurement was performed by the microtiter plate assay. All data analysis was done by SPSS 16 and p value less than 0.05 was considered statistically significant.

Results: One hundred and twenty seven isolates of *P. aeruginosa* were included in this study. Evaluation of biofilm formation revealed that 69 isolates (54.3%) produced different level of biofilm. Antibiotic susceptibility testing showed that 92 isolates (72.4%) belonged to multiple drug resistant and strong correlation between biofilm formation and antimicrobial resistance was seen in most tested antibiotics.

Conclusion: Our results showed that in general the rate of antimicrobial resistant among biofilm producer was higher than non-biofilm producer isolates and in some antibiotics it was statistically significant. As mentioned in previous studies biofilm producing isolates shows more resistance to antibiotics and are difficult to treat, so it's important to early detection and eradication of biofilm producing isolates especially in hospital settings.

Keywords: *Pseudomonas aeruginosa*, Multiple drug resistant, Biofilm

**P395 - 839: HIGH PREVALENCE OF MACROLID RESISTANCE AMONG
CAMPYLOBACTERS ISOLATED FROM DYSENTERY PATIENTS IN MARKAZI PROVINCE
- 2015**

Elnaz Abbasi¹, Behzad Khansari-nejad², Hamid Abtahi³, Ehsanollah Ghaznavi-Rad⁴

1. Department of Microbiology & Immunology, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran
2. Department of Microbiology & Immunology, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran
3. Molecular and Medicine Research Center, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran
4. Department of Microbiology & Immunology, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran

Background and Aim: Campylobacter species, especially *C. jejuni* and *C. coli*, are the most common bacterial causes of gastroenteritis in humans (1). In these cases, Erythromycin is drug of choice for treatment (2). Increased macrolide resistance in campylobacter is a major concern (3). In Iran, limited studies have been done antibiotic resistance of these bacteria, so investigating macrolide resistance in them is necessary. This study aimed to determine the frequency of macrolid resistance and to investigate genotypic determinant of macrolid resistance in campylobacters isolated from the stools of the dysenteric patients admitted to educational and medical centers in Arak, Iran.

Methods: In this descriptive cross-sectional study, diarrheal stool specimens of the patients admitted to educational and medical centers in Arak in the period from May 2015 to Sep. 2015 were collected and after phenotypic and genotypic investigation of campylobacter, resistance to Erythromycin was assessed using disk diffusion method. In addition, 23srRNA genes contributing to macrolide resistance in campylobacter were also investigated according to method described elsewhere.

Results: Out of 108 dysenteric stool specimens, 28 (25.92%) campylobacter were isolated of which 26 (24.07%) were *C. jejuni* and 2 (1.85%) were *C. coli*. Phenotypic resistance prevalence in *C. jejuni* was obtained as 18 (64.28%) and in *C. coli* as 2 (7.1%). Frequency of 23srRNA macrolide resistance gene was found as 16 (57.14%) and 1 (3.57%) in *C. jejuni* and *C. coli*, respectively.

Conclusion: This study showed high macrolide resistance in campylobacter. For understanding the relationship between suitable antimicrobial usage and antimicrobial resistance we should study locally in every region.

Keywords: Campylobacter, Macrolides, Drug Resistance, Bacterial, Iran

**P396 - 853: FLORA BACTERIAL CONTAMINATION OF ANNUAL STOOL SAMPLES IN
ZAHEDAN TEACHING HOSPITALS TO COMPARE THE DISTRIBUTION OF THE
SAMPLES SHIGELLA, SALMONELLA, ANTIBIOTIC SENSITIVITY AND ANTIBODY TITER**

Hadi Hosseini¹, iman hormozi², neda koroshzadeh³

1. Young Researchers and Elite Club, zahedan Branch, Islamic Azad university, zahedan, Iran.
2. microbiology bs
3. microbiology ms

Background and Aim: To evaluate bacterial contamination in samples Stoll in patients referred to the teaching hospital in Zahedan one-year period between January 2014 to December 2015 laboratory study conducted on samples and antibiotic sensitivity Salmonella was conducted obtained. 30253 samples in this interval Stoll sent to the lab, which then cultures the culture positive samples were 4537, positive cultures were sent to the microbiology laboratory of Islamic Azad University of Zahedan.

Methods: Methods: Gram stain action on positive samples and then to the imvic (Environment Gallery bacteriological testing citrate, gas, motion, indole, etc.) were transferred. identification was completed. To search for sick or carrier individuals as well as sampling of Salmonella positive samples environments SS agar, selenit F, XLD agar were transferred, as well as complementary test for Salmonella detection kit using serological and continue with the dilution suitable compared to half Antibiotic susceptibility testing was performed McFarland.

Results: bacreia Name and presence of bacteria Salmonella Paratyphi A 64 Salmonella Paratyphi B 17 Salmonella Paratyphi D 12 Shigella flexneri 6 Other 1 Antibiotic Name and sensitivity testing percent Nitrofurantoin 65 Ciprofloxacin 60 Nalidixic acid 30 Cotrimoxazole 30 Norfloxacin 25 Cefixime 80 Amikacin 55

Conclusion: Due to Salmonella bacteria can travel one reason for that may be the way to avoid using the food prestigious centers (As well as non-use of yogurt and onions with food the way it has been stressed many books, food microbiology) is worth noting These patients as well as other bacterial diseases in warm seasons (greater compatibility with bacteria) raised (August - September). Due to the low age of personal hygiene and lack of education in schools as well as factors enhancing the statistics.

Keywords: zahedan, salmonela, shigela, antibiotic sensitivity

**P397 - 862: FREQUENCY AND ANTIBIOTIC SUSCEPTIBILITY PATTERN OF
STAPHYLOCOCCUS AUREUS ISOLATED FROM WOUND INFECTIONS**

Mina Yekani¹, Tahereh Pirzadeh², Mohammad Yousef Memar³

1. 1- Department of Bacteriology and Virology, Tabriz University of Medical Sciences, IR Iran
2. 1- Department of Bacteriology and Virology, Tabriz University of Medical Sciences, IR Iran
3. 1- Department of Bacteriology and Virology, Tabriz University of Medical Sciences, IR Iran

Background and Aim: Wound infection is one of the health troubles that are caused by the offensive of pathogenic organisms. Staphylococcus aureus is the most common organism isolated from these infections. Information of bacterial agent and susceptibility to antimicrobial drugs is essential for management of wounds. The aim of this study is to investigate of the antibiotic susceptibility of S. aureus, assessment the MRSA prevalence in wound infection

Methods: Identification of S. aureus in 200 specimens from wound infection was performed by standard biochemical testes. MRSA were detected by cefoxitin disk. Disk diffusion method was used for determination of antibiotic susceptibility patterns and the results were interpreted according to CLSI guideline

Results: In the present study S. aureus isolated from 28.5%(57 isolates) of specimens. High frequency of resistance was observed to β -lactamas, fluoroquinolones, macrolides and aminoglycosides while all isolates were susceptible to vancomycin. According to cefoxitin disk, 29(50.8%) of isolates were MRSA

Conclusion: S. aureus is highly prevalent and more resistant in our setting. Our findings emphasize the necessary of antibiotic susceptibility pattern and identification of MRSA for appropriate antibiotic therapy in wound infection

Keywords: Staphylococcus aureus, cefoxitin disk, wound infection

**P398 - 872: CHARECTERIZATION CARBAPENEM RESISTANT PSEUDOMONAS
AERUGINOSA STRAINS ISOLATED FROM HOSPITALIZED PATIENTS IN GONABAD,
IRAN**

Jalal Mardaneh¹, Alireza Mohammadzadeh²

1. Department of Microbiology, School of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran.
2. Department of Microbiology, School of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran.

Background and Aim: Because of its ubiquitous nature, ability to survive in moist environments, and innate resistance to many antibiotics and antiseptics, *P. aeruginosa* is a common pathogen in hospitals. The goals of this study was charecterization carbapenem resistant pseudomonas aeruginosa strains isolated from hospitalized patients in gonabad, Iran.

Methods: In the present cross-sectional study, clinical samples from hospitalized patients (Gonabad, Iran) were collected, and culture was done on microbiological media. For final identification, biochemical tests. Disc diffusion, was used for antibiotic susceptibility testing, according to CLSI 2014 recommendations.

Results: In the current study, 96 isolates of *Pseudomonas aeruginosa* were obtained from hospitalized patients. As observed, 10.41% (10 strains) of isolates showing resistance to imipenem and 13.54% (13 strains) were resistant to meropenem.

Conclusion: This study is important from a practical point of view. We believe that the use of imipenem for the treatment of *P. aeruginosa* should be reserved for situations where the infection is polymicrobial, particularly when anaerobic bacteria are present, or for pseudomonal isolates resistant to other antibiotics.

Keywords: Hospital infection, *Pseudomonas aeruginosa*, antibiotic susceptibility, carbapenems.

**P399 - 877: COMPARISON STUDY OF ANTIMICROBIAL AGENT ON BACTERIAL
ISOLATED FROM HOSPITALIZED PATIENTS IN QOM**

Mohammad Khodadad Motlagh¹, اعظم حیدر پور²

1. Shiraz university, shiraz
2. مربی میکروب شناسی، دانشکده پیراپزشکی، دانشگاه علوم پزشکی قم، قم، ایران

Background and Aim: Burn wounds are suitable environments for the growth of various opportunistic infections. The knowledge of the common microorganisms in these infections and their antibiotic resistance are fundamental. We studied common microorganisms and their antibiotic resistance in burn ward of Nekuei Hospital, Qom, Iran.

Methods: In this study, during 5 months, 70 patients admitted to the burn ward of Nekuei hospital were examined. After Sampling and isolation of bacteria, biochemical standard tests for determination of microorganisms were done. Determination of antibiotic resistance was done by using disc diffusion or Kirby Bauer using these antibiotics: co-trimoxazole, vancomycin, ciprofloxacin, cephalothin, ceftazidime, amoxicillin, amikacin, gentamicin, chloramphenicol, cefazolin, cefotaxime, ceftriaxone, ampicillin, oxacillin, and imipenem.

Results: Totally, the cultures of 54 cases (77.14%) of a total of 70 samples were positive. The most common isolated bacteria were *Pseudomonas aeruginosa* (38.9%), *Staphylococcus aureus*, and *staphylococcus epidermidis* (11.42%), and *Enterococcus faecalis* (9.59%). The results of the Antibiotic resistance of *Pseudomonas aeruginosa* are as follows: amoxicillin 94.73%, amikacin 25.64%, gentamicin 30.77%, co-trimoxazole 84.62%, ciprofloxacin 48.72%, ceftazidime 51.28%, cefotaxime 58.97%, Chloramphenicol 86.84%, ceftriaxone 55.26%, and imipenem 50%

Conclusion: The most common bacteria in infection of burn wound was *pseudomonas aeruginosa*, which was mostly susceptible to amikacin and gentamicin.

Keywords: infection, burn wound, bacteria, antibiotic resistance

P400 - 884: DETERMINATION ANTIBIOTIC RESISTANCE PROFILE OF PSEUDOMONAS AERUGINOSA STRAINS ISOLATED FROM HOSPITALIZED PATIENTS IN SOUTHWEST HOSPITALS OF IRAN.

IMAN BAHRAMI ABDEHGAH¹, Alireza Khodavandi phd²

1. Department of Microbiology, Islamic Azad University, Yasouj, Iran
2. Department of Microbiology, Islamic Azad University, Shiraz, Iran

Background and Aim: *Pseudomonas aeruginosa* was considered as an opportunistic pathogen. The emergence of strains with multi drug resistant was widely considered in the past 20 years. Acquired infections caused by resistance against Anti-pseudomonas antibiotics were a serious problem. The aim of this study was to evaluate antibiotic resistance of *Pseudomonas aeruginosa* strains isolated from hospitalized patients in southwest hospitals of Iran by disk diffusion method.

Methods: In this cross-sectional study, were collected on 40 *Pseudomonas aeruginosa* isolates from the patients. Identification of strains was done according to standard methods. Subsequently, antibiotic resistance pattern was determined by performing disk diffusion test according to the instructions of clinical laboratory standards institute.

Results: The analysis of the patterns of the isolates showed that the resistance rates to gentamicin, imipenem, meropenem, piperacillin, carbenicillin, ciprofloxacin, cefotaxime, tobramycin, ceftazidime and amikacin were 75%, 75%, 75%, 75%, 72.5%, 65%, 62.5%, 62.5%, 60% and 50% respectively.

Conclusion: The results showed the high rate of multi drug resistant in *Pseudomonas aeruginosa* strains to different groups of antibiotics. So in order to control infection and prevent the spread of resistant strains it is necessary to find more appropriate solutions.

Keywords: Multi drug resistant, *Pseudomonas Aeruginosa*, Disk diffusion

**P401 - 887: IN VITRO ACTIVITY OF GENTAMICIN IN COMBINATION WITH IMIPENEM
AND PIPERACILLIN AGAINST RESISTANT ISOLATES OF PSEUDOMONAS AERUGINOSA**

IMAN BAHRAMI ABDEHGAH¹, Alireza Khodavandi ²

1. Department of Microbiology, Islamic Azad University, Yasouj, Iran
2. Department of Microbiology, Islamic Azad University, Shiraz, Iran

Background and Aim: *Pseudomonas aeruginosa* is recognized as one of the leading causes of severe hospital-acquired infections. *Pseudomonas* infections have a high rate of morbidity and mortality, Thus combination therapy is often recommended. The aim of this study was to investigate the Activity of Gentamicin in Combination with Imipenem and Piperacillin against Resistant Isolates of *Pseudomonas aeruginosa*.

Methods: Antibacterial effects of Piperacillin/Gentamicin and Imipenem/Gentamicin compounds against 30 resistant isolates and 10 sensitive isolates of *Pseudomonas aeruginosa* were measured using disk diffusion agar and microdilution broth techniques and analyzed as the single dose and in combination.

Results: Fifteen percent of resistant isolates were treated by Piperacillin/Gentamicin were able to show complete or partial synergistic effects while only 0.16% (one sample) of the resistant isolates presented partial synergistic effects against Imipenem/Gentamicin. Most of the resistant isolates (77%) presented different effects and did not show any additive effect. On the other hand, almost 27% of the resistant isolates showed antagonistic effects to the antibacterial compounds tested

Conclusion: The results of this study while confirming the previous comments present a rapid growth of resistance to the standard antibiotics in *Pseudomonas aeruginosa*. While combination therapy such as Imipenem/Gentamicin or Piperacillin/Gentamicin could be one of the best strategies resulting in the dramatic reduction of resistance to antibacterial agents.

Keywords: Imipenem/Gentamicin, Piperacillin/Gentamicin, *Pseudomonas aeruginosa*

**P402 - 897: GREEN SYNTHESIS OF SILVER NANOPARTICLES USING EXTRACT OF
ECHIUM AMOENUM CAPPED WITH L-CYSTEINE**

Najme Mirabi¹, rahele safaei javan², massumeh mahdavi ortakand³

1. student

Background and Aim: Antibiotic resistance for many human bacterial pathogens is a growing problem in the treatment of infectious diseases. Nanotechnology allowing the synthesis of nanoparticles that can be assembled into complex architectures. Biosynthesis of silver nanoparticles (AgNPs) using plant extract is economically cost-effective and also because of don't use of the toxic materials are environmentally friendly. This study demonstrated that silver nanoparticles produced using the Echium amoenum for the first time as well as surface modification of cysteine also by increasing the stability and interaction of our silver nanoparticles.

Methods: Silver nanoparticles was synthesized using an extract of Echium amoenum as a reducing agent. The silver nanoparticles were characterized by colour changes in medium, uv- visible spectrum in 200-800 nm and X-ray diffraction. Surface morphology of AgNPs were studied by SEM. The interaction between cysteine and silver nanoparticles was studied by FTIR analysis.

Results: The results showed biosynthesis of silver nanoparticles by aqueous extract of Echium amoenum nanoparticles to produce in sufficient qualities and appropriate dimensions are within a short time. Capping of the silver nanoparticles with cysteine provides stability to nanoparticles.

Conclusion:: This study demonstrated that silver nanoparticles produced using the Echium amoenum for the first time. Capping of the silver nanoparticles with cysteine provides stability to nanoparticles by a thiolate bound between the amino acid and the nanoparticles surface and hydrogen bonding among the Cys-AgNPs.

Keywords: bacterial pathogens, biosynthesis silver nanoparticles, capping silver nanoparticles,

P403 - 898: PHENOTYPIC EVALUATION OF EFFLUX PUMPS ACTIVITY OF UPEC AND KLEBSIELLA MDR ISOLATES BY CARTWHEEL METHOD

Shervin Gooyandeh¹, Sahar Honarmand Jahromy², Fatemeh Noorbakhsh³

1. Department of microbiology, Islamic Azad university, Varamin- Pishva branch, Iran
2. Department of microbiology, Islamic Azad university, Varamin- Pishva branch, Iran
3. Department of microbiology, Islamic Azad university, Varamin- Pishva branch, Iran

Background and Aim: Antibiotic resistance is a phenomenon in which antibiotic used to treat a particular bacteria becomes useless due to resistance mechanism. Increased drug resistance and occurrence of MDR in bacteria specificity nosocomial and UTI bacteria has dramatically reduced the possibilities of treating infectious diseases caused by them. Efflux pumps are one of the major causes of multidrug resistance in bacteria which effluxes out the drugs accumulated. Efflux-mediated resistance towards antimicrobial compounds is increasingly recognized as an important resistance mechanism in Gram negative and Gram-positive bacteria. Various multidrug resistance (MDR) phenotypes that confer active protection against environmental toxic compounds by efflux mechanisms have been described in Enterobacteriaceae. The aim of this study was phenotypic evaluation of efflux pumps in UPEC and Klebsiella strains

Methods: 47 UPEC and 42 Klebsiella MDR strains that were isolated from urine sample and identified by biochemical tests were determined by disc diffusion method according to CLSI. The ETBr-agar cartwheel method with different concentrations of Ethidium bromide was used to assess the presence of efflux activity in all MDR strains.

Results: Our results showed that among klebsiella isolates 32% had efflux activity and 45.2% had no activity. Among UPEC isolates 44.7% and 55.3% had efflux activity and no activity, respectively. Also the frequency of UPEC bacteria with over expression of efflux pumps was 90% but for Klebsiella isolates 52.2% was reported.

Conclusion: These results demonstrated that Multidrug-resistant (MDR) phenotypes of UPEC clinical isolates have been shown to be related to over expression of efflux pump systems.

Keywords: MDR, UPEC, Klebsiella, efflux pumps, Cartwheel

P404 - 905: IDENTIFICATION MRSA AND MSSA STRAINS AND THEIR ANTIBIOTIC SENSITIVITY PATTERN

Saeed Shahmohammadi¹, Ahmad Farajzadeh Sheikh², Mojtaba Shahin³

1. MSc student in Microbiology, Student Research Committee, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
2. Assistant Professor, Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
3. Ph.D student in Microbiology, Student Research Committee, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Background and Aim: staphylococcus aureus based on sensitivity to methicillin is divided to two clusters: Methicillin sensitive staphylococcus aureus (MSSA) and Methicillin resistant staphylococcus aureus (MRSA). MRSA is an opportunist bacteria that could be seen as a common cause of human disease. This study aims to investigate the comparison antibiotic susceptibility patterns in MSSA and MRSA isolates in Ahwaz teaching hospitals.

Methods: Antimicrobial resistance test was performed on 140 various clinical samples with disk diffusion method. All *S. aureus* isolates were screened for cefoxitin resistance using agar screening method. For molecular tests, DNA was extracted and Methicillin resistance was further confirmed by detection of *mecA* gene using PCR method.

Results: The results of this study showed, MSSA resistance to vancomycin, ticoplanin, rifampin, linezolid, ciprofloxacin, gentamicin, minocycline, novobiocin, polymyxin B and mupirocin was found to be 1.4%, 0%, 7.5%, 1.5%, 35.8%, 4.5%, 29.9%, 0%, 95.5% and all isolates had absent high level mupirocin resistance and MRSA resistance to vancomycin, ticoplanin, linezolid, ciprofloxacin, gentamicin, minocycline, novobiocin, polymyxin B, rifampin and mupirocin was found to be 3%, 0%, 2.7%, 74%, 74%, 24.7%, 82.2%, 46.6% and 2.7% isolates had high level mupirocin resistance respectively (based on CLSI recommendation). 73 of the 140 isolates identified as *S. aureus* were confirmed to be MRSA using the PCR method.

Conclusion: The present study showed prevalence of MRSA isolates in Ahwaz teaching hospitals were more than MSSA isolates. MRSA isolates had more resistance to vancomycin, linezolid, ciprofloxacin, gentamicin, rifampin and mupirocin in comparison to MSSA.

Keywords: staphylococcus aureus, MRSA, antibiotic susceptibility patterns

**P405 - 906: DETERMINATION OF ANTIMICROBIAL RESISTANCE PATTERN OF
ACINETOBACTER BAUMANII ISOLATED FROM TEHRAN HOSPITALS**

Akram sadat Mousavi sani¹, Reza Ranjbar², Shahram Hossein Zadeh³

1. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. Molecular Biology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran
3. School of Medicine, Kermanshah University of Medical Sciences, Kermanshah, Iran.

Background and Aim: *Acinetobacter baumannii* survives for prolonged periods under a wide range of environmental conditions. The organism causes outbreaks of infection and health care-associated infections, including bacteremia, pneumonia, meningitis, urinary tract infection, and wound infection. Emergence and spread of *Acinetobacter* species, resistant to most of the available antimicrobial agents, is an area of great concern and increasing antibiotic-resistance cause a lot of problems for patients.

Methods: This cross-sectional descriptive study was performed on 116 *A. baumannii* isolated from sections surgery, emergency and intensive care wards in Tehran hospitals. After *A. baumannii* diagnosis and confirming, their susceptibility rate was determined to the following 12 antibiotics via the antibiogram method (disk diffusion) using bacteriological standard tests.

Results: According to the antibiotic susceptibility testing, from 116 *Acinetobacter baumannii* isolates the highest resistance was against ceftazidime (97%), aztreonam (93%), cefotaxime (90%) and cotrimoxazole (81%) antibiotics, respectively. The highest susceptibility was observed for polymyxin (100%) and colistin (97%) respectively.

Conclusion: In the present study, *A. baumannii* isolates in Tehran hospitals showed high resistance to different antibiotics, therefore the antibiotic susceptibility test is necessary before prescribing antibiotics and the correct use of antibiotics should be considered.

Keywords: *Acinetobacter baumannii*, antibiotic, resistance, antibiogram

**P406 - 907: PREVALENCE OF OXA-TYPE B-LACTAMASES GENES AMONG
ACINETOBACTER BUMANNII ISOLATED FROM TEHRAN HOSPITALS**

Akram sadat Mousavi sani¹, Reza Ranjbar², Shahram Hossein Zadeh³

1. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. Molecular Biology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran
3. School of Medicine, Kermanshah University of Medical Sciences, Kermanshah, Iran.

Background and Aim: *Acinetobacter baumannii* is the most important agent of nosocomial infections within the *Acinetobacter* genus, and it has become an important hospital-acquired pathogen worldwide, such as pneumonia, septicemia and urinary tract as well as wound infections. Carbapenem-resistant *Acinetobacter baumannii* (CRAB) presents a serious therapeutic and infection control challenge. In this study, we investigated the prevalence of OXA-Type β -Lactamases genes among *Acinetobacter baumannii* isolated from Tehran hospitals.

Methods: A total number of 120 clinical specimens were collected from nosocomial infections and evaluated in order to isolate *A. baumannii* strains. After identification of the isolates, the antibiotic sensitivity to imipenem and meropenem was assessed using disk diffusion method. The resistance genes of bla OXA-23, 24, 51, and 58 were detected by multiplex PCR method.

Results: 116 *A. baumannii* isolates were isolated from clinical specimens. 52 and 77 percent of the isolates showed phenotypic resistance to the imipenem and meropenem, respectively. According to PCR results, the frequency of resistant isolates bearing blaOXA-23, blaOXA-24 and blaOXA-58 were 83%, 7% and 2% respectively.

Conclusion: The increasing incidence of *A. baumannii* is a serious concern, therefore control of this pathogen and taking preventive measures are emphasized. The high rate presence of class D carbapenemase-encoding genes, mainly blaOXA-23 carbapenemases, is worrying and alarming as an emerging threat in hospitals.

Keywords: *Acinetobacter baumannii*, β -Lactamases, OXA-Type genes, multiplex PCR.

P407 - 918: RECA GENE EXPRESSION IN CIPROFLOXACIN RESISTANT ESCHERICHIA COLI DINI- MUTANTS

Sareh Mohammadi¹, Razieh Pourahmad²

1. MSc student in Genetics at university of shahrekord
2. Associate Professor of Genetics at university of shahrekord and corresponding author

Background and Aim: Microorganisms in response to drug development, acquire resistance to them through a variety of mechanisms. The prevalence of fluoroquinolone (FQ) resistance in *Escherichia coli* has increased markedly in recent years. In *Escherichia coli*, the SOS response is induced upon DNA damage and results in increasing expression of a set of genes involved in DNA repair and other functions. A member of the SOS regulon is the *dinI* gene. *dinI* acts as positive modulator of RecA performance. Previous studies showed *recA* gene expression in ciprofloxacin resistant *Escherichia coli* *dinI*⁺ mutants increased. The aim of this study was to investigate *recA* gene expression in *dinI*⁻ mutants resistant to ciprofloxacin.

Methods: For this purpose, *recA* gene expression was determined by real time PCR.

Results: The results showed that *recA* gene expression in mutants with low and medium resistance increased.

Conclusion: This indicates that *dinI* gene expression has no effect on *recA* gene expression.

Keywords: Ciprofloxacin, SOS response *Escherichia coli*, Real Time PCR

P408 - 936: ANTIBACTERIAL EFFECTS OF LOCAL ANALGESICS AND ANESTHETICS

Mehri Noori¹, marjan khoda bakhshi², mohammadreza bojari nasrabadi³

1. iran university of medical sciences
2. iran university of medical sciences
3. professor at iran university of medical sciences

Background and Aim: The findings of a multitude of both animal and human studies could substantiate an additive role of both local and general anesthetic agents in inhibiting bacterial growth. The present study attempted to assess antimicrobial effects of local analgesics and general anesthetics including lidocaine, bupivacaine, pethidine, midazolam, and sufentanil citrate.

Methods: A bacterial suspension containing of studied nine bacterial species was prepared. The bacteria growth was assessed through culturing each solution (containing bacterial suspension and anesthetic drug) on media culture. Antibacterial characteristics of anesthetics were assessed at different time points of culturing the bacterial solution (exposure to anesthetics) and countering the bacterial colonies and compared to the controls.

Results: We showed high efficacy of Sufentanil Citrate (50 µg/ml) on reducing colony count of *Staphylococcus aureus* and also *Streptococcus pneumoniae* with high response rate within 24 hours of exposure to antibiotic. Also, midazolam (1 mg/ml) could effectively reduce colony count of *Staphylococcus aureus* and *Streptococcus pneumoniae*. Moreover, by exposing pethidine with the dose of 50 mg/ml. the count of *Pseudomonas aeruginosa* and *Enterococcus faecalis* was successfully reduced in media. Colony counting at different time points after exposure to lidocaine 1.0% and also bupivacaine 0.5% showed reduced count of all bacterial species with high response rate.

Conclusion: Sufentanil Citrate, midazolam, and pethidine have appropriate inhibitory effect on *Staphylococcus aureus*, *Streptococcus pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. Lidocaine and bupivacaine have a strong effect on inhibiting growth of nine bacterial species studied in our survey.

Keywords: various bacteria, bacterial suspension, anesthetic drug.

**P409 - 942: ANTIMICROBIAL RESISTANCE PATTERN OF URINARY TRACT INFECTIONS
PATHOGENS IN HOSPITALIZED PATIENTS FROM SHAHID MADANI HOSPITAL OF
KHORRAMABAD, IRAN**

Sakineh Omidimajd¹, Gholamreza Goudarzi², Fhatemeh pakmehr³, Mehrnoush Ramtin⁴, Nouredin Heydari⁵

1. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Department of Microbiology, School of Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
4. Clinical Laboratory, ,Shahid Madani Hospital, Lorestan University of Medical Sciences, Khorramabad, Iran
5. Clinical Laboratory, ,Shahid Madani Hospital, Lorestan University of Medical Sciences, Khorramabad, Iran

Background and Aim: Urinary tract infections (UTIs) affect about 150 million people, and have nearly 6 billion dollar cost each year. One of the important problems , is the growing antibiotic resistance of pathogenic bacteria due to mutations and horizontal acquisition of new resistance genes. Because clinicians access to result of microbial tests at least for 48 hours, and also the regional variations of bacterial resistance patterns, , the antibiotics were often prescribed empirically. The aim of this study was to investigate the antibiotic resistance pattern among the bacterial strains isolated from hospitalized patients of Shahid Madani hospital of Khorramabad.

Methods: This cross-sectional study was performed on 2415 urine culture specimens from May 2015 to April 2016. After identifying the isolates at the species level, disk diffusion method (Kirby-Bauer) and CLSI guidelines were used to determine antibiotic resistance profile.

Results: Of total 247(10.22%) positive culture, 135 female (54.65%) and 112cases (45.35%) were male. *Escherichia coli* and *Enterococcus fecalis* with a frequency rate of 107(43.31%) and 82 (33.19%) cases , respectively, were the most prevalent, and *Staphylococcus aureus*, with a prevalence of 1 (0.4%) case was the lowest etiological agent of UTIs in this study. The most resistance amongst *Escherichia coli* and *Enterococcus fecalis* strains was demonstrated toward ampicillin and penicillinG with an accuracy of 90.6% and 78.0%, respectively.

Conclusion: This study showed that *Escherichia coli* is the most common cause of UTIs and nitroforantoin could be an appropriate antibiotic for empiric treating of UTIs caused by this bacterium.

Keywords: urinary tract infection, antimicrobial resistance, *Escherchia coli*

**P410 - 944: MOLECULAR ANALYSIS OF METALLO BETA-LACTAMASE RESISTANCE
GENES AMONG UROPATHOGENIC ESCHERICHIA COLI ISOLATED FROM URINE OF
PATIENTS WITH URINARY TRACT INFECTION**

Shahla Shahbazi¹, Mohammad Reza Asadi Karam², Saeid Bouzari³, Mehri Habibi⁴

1. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
2. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
3. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
4. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran; m_habibi1362@yahoo.com

Background and Aim: Urinary tract infections (UTIs) caused by Uropathogenic Escherichia coli (UPEC) are among the most common infectious diseases. Improper use of antibiotics results in the drug resistance in UPEC and difficult the clinical management of UTIs. Occurrence of enzymes capable of inactivating all Metallobetalactams including carbapenem beta-lactam antibiotics is a new problem in treatment of UTI patients. Metallo β -lactamases (IMP, VIM, and NDM) are a diverse set of enzymes that catalyze the hydrolysis of a broad range of β -lactam drugs including carbapenems. The objective of this study was to investigate the prevalence of MBL enzyme blaVIM, blaIPM and blaNDM in UPEC isolated from different hospitals in Tehran, Iran.

Methods: In this study, 50 UPEC isolates were collected from UTI patients from different hospitals in Tehran, Iran. After bacteriological and biochemical confirmation of the isolates in Department of Molecular Biology, Pasteur Institute of Iran, the isolates were subjected to Polymerase Chain Reaction (PCR) of uspA gene in order to confirm the UPEC strains. Finally, PCR assay was used to determine the prevalence of blaVIM, blaIPM and blaNDM genes using specific primers.

Results: According to the results, all of the UPEC strains had uspA gene. Of the 50 isolates, 4% (n =2) harbored bla-VIM, whereas the bla-IMP and bla-NDM genes were not found in any of the strains.

Conclusion: Fortunately, MBL prevalence is still low in our hospitals. However, to prescribe suitable antimicrobial therapy and to prevent resistant dissemination, early detection of MBL-producing organisms is crucial. Study of other MBL coding genes is under study.

Keywords: Urinary Tract Infection, Uropathogenic Escherichia coli, Antimicrobial Resistance, Metallo β -lactamases

**P411 - 952: ANTIBIOGRAM AND VIRULENCE GENES PROFILE OF E. COLI ISOLATED
FROM HEALTHY CAT'S FECAL**

Shima Shakeri khamseh¹, Kumars Amini², Farnoush Arfaei³

1. Small animal and Radiology department, Veterinary faculty, Science and research branch, Islamic azad university, Tehran, Iran
2. Veterinary faculty, Saveh branch, Islamic azad university, Saveh, Iran
3. Small animal and Radiology department, Veterinary faculty, Science and research branch, Islamic azad university, Tehran, Iran

Background and Aim: The normal bacterial flora contains antibiotic resistance genes to various degrees. Several factors increase the number of antibiotic-resistant bacteria in feces. One important factor is the exposure of the intestinal flora to antibacterial drugs. Due to the limited number of anti-bacterial drug, resistance is considered as a significant problem. Drug resistance in bacteria can be transferred to other strains of bacteria, which caused the numbers are increasing every day. Drug resistant strains among humans and animals are exchange.

Methods: Escherichia coli were isolated from 101 fecal samples collected from healthy cats referred to Tehran veterinary clinics. Isolated bacteria confirmed by biochemical test. STX1 and STX2 genes were analyzed by multiplex-PCR. Antibioqram was performed by Kirby-Bauer method according to NCCLS standard against Tetracycline, Ampicillin, Enrofloxacin, Gentamicin, Ceftriaxone, Cotrimoxazole and Cefazolin antibiotics. Questionnaire data and test results were statistically analyzed.

Results: 23.8% of cats were carried E.coli with virulence genes. ST and STX2 genes were found in 17(16.8%) and 7(6.9%) fecal samples respectively. About 60% of isolates were resistant to Cotrimoxazole and about 80% of isolates were sensitive to gentamicin. There was significant relationship between ST gene and antibiotic resistance. But there was not any significant relationship between STX gene and antibiotic resistance. Antibiotic resistance in isolates with virulence genes was significantly higher than non-Virulence isolated.

Conclusion: Cats can be an important reservoir of pathogenic E. coli. Due to the close relationship between cats and humans, these animals can be a danger to public health.

Keywords: Escherichia coli, drug resistance, cats, virulence factor

**P412 - 966: INCREASING TREND OF IMPENEM-RESISTANCE AMONG
ACINETOBACTER BAUMANNII ISOLATED FROM HOSPITAL ACQUIRED PNEUMONIA
IN NORTHEAST OF IRAN**

Kiarash Ghazvini¹, Azad Khaledi², Omid Elahifar³

1. 1. Antimicrobial resistance research center, Avicenna research institute, Department of Microbiology and virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
2. 1. Antimicrobial resistance research center, Avicenna research institute, Department of Microbiology and virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
3. 1. Antimicrobial resistance research center, Avicenna research institute, Department of Microbiology and virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Background and Aim: Nosocomial infections due to high mortality and economic cost are one of the most important challenges that hospitals face with around the world, most of them caused by gram-negative bacteria, including *Acinetobacter baumannii*. So, the aim was to study the frequency and resistance pattern of *A. baumannii* against imipenem.

Methods: This cross-sectional study conducted for two years on patients with nosocomial pneumonia caused by *A. baumannii* in 2 major university hospitals (Ghaem and Imam Reza) in Mashhad, Iran. After detection and identification, data about mortality and length of hospital stay and treatment were collected. Then the pattern of antibiotic resistance was investigated in *A. baumannii* against imipenem

Results: In this study among 700 patients with nosocomial pneumonia, 364 people were males and 336 were females. All of these patients received imipenem. Eighty four percent (84%) of these patients were cured and the remaining 16% were expired in spite of receiving imipenem. *A. baumannii* resistance to the imipenem antibiotic in both hospitals had an increasing rate. The resistance rate in Ghaem hospital had increased 96.6% at the end of the period compared to beginning of study. Also, similar increase (94.7%) in imipenem resistance was observed in Imam Reza hospital.

Conclusion: According to the results our study, Excessive use of imipenem caused antibiotic resistance. So appropriate selection of antibiotic should be considered. And other antibiotics such as new generations of cephalosporins should be chosen for empirical treatment of *A. baumannii*, at first.

Keywords: Antimicrobial resistance, *Acinetobacter baumannii*, imipenem

P413 - 976: PHENOTYPIC HODGE TEST APPLICATION FOR GRAM POSITIVE AND GRAM NEGATIVE BACILLI BACTERIA CARBAPENEMASE ENZYME PRODUCER ISOLATED FROM NON-BIOLOGICAL ENVIRONMENTS OF HOSPITAL

Samaneh Rouhi¹, Rashid Ramazanzadeh², Masoud Heydarifar³, Pegah Shakib⁴

1. Student Research Committee, Kurdistan University of Medical Sciences, Sanandaj, Iran. Cellular & Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran.
2. Cellular & Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran. Microbiology Department, Kurdistan University of Medical Sciences, Sanandaj, Iran.
3. Student Research Committee, Kurdistan University of Medical Sciences, Sanandaj, Iran.
4. Student Research Committee, Kurdistan University of Medical Sciences, Sanandaj, Iran. Cellular & Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran.

Background and Aim:Environmental sanitation in treatment centers is an important step in controlling the spread of disease-causing bacteria that are resistant to antibiotics. The aim of this study was to determine the prevalence of gram positive and gram negative bacilli bacteria carbapenemase enzyme-producing from Besat hospital in Sanandaj city (Kurdistan province, Iran, 2016 January to March).

Methods:In this cross-sectional study, samples were taken from hospital surfaces and equipment. 158 swab samples collected, and then on blood agar and eosin methylene blue agar were cultured. Gram staining and biochemical tests to identify the bacteria and phenotypic Hodge test in accordance with CLSI guidelines used to detect carbapenemase-producing strains. SPSS16 software with Chi-square and t- test was used for the analysis ($p < 0.05$).

Results:201 isolates of bacteria were isolated. Of these, 28 (13.93%) genus *Bacillus*, 7 (3.48%) related to other spore-forming Gram-positive bacilli, 6 (2.98%) genus *Klebsiella* and 1 (0.49%) of *E. coli* (gram-negative bacilli) were detected. There was a significant relationship between the cleaning of different parts of the hospital environment and bacterial isolation ($p < 0.05$). Hodge test results showed that only 3 (8.57%) Gram-positive bacilli were carbapenemase-producing strain and leaf clover halo around it was observed. None of the Gram-negative bacilli in the test were positive.

Conclusion:Gram-positive bacilli are rarely carbapenemase-producing. But the presence of this enzyme in the bacteria in our study was also observed. Hospital environment and hygiene is very important in this regard and should be more careful in hospital environmental sanitation.

Keywords:Phenotypic Hodge Test, Bacilli Bacteria, Carbapenemase Enzyme, Environments

**P414 - 993: METALLO-BETA-LACTAMASE BLAVIM AND BLAIMP GENES AMONG
KLEBSIELLA PNEUMONIAE ISOLATED FROM HOSPITALS OF KHORRAMABAD, IRAN**

Gholamreza Goudarzi¹, Sahar Karami², Pegah Shakib³, Reza Mohammadrezaei Khorramabadi⁴

1. Razi Herbal Medicines Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Razi Herbal Medicines Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Razi Herbal Medicines Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran
4. Razi Herbal Medicines Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran

Background and Aim: Carbapenems are commonly used as last-line antibiotics for the treatment of infections caused by multidrug-resistant *Klebsiella pneumoniae* isolates in nosocomial infections. The production of carbapenemase enzymes and the acquisition of metallo-beta-lactamases (MBLs, inhibiting by EDTA) constitute two carbapenem-hydrolyzing mechanisms. Carbapenemases and MBLs can be detected by phenotypic as well as genotypic methods. Among phenotypic tests, Modified Hodge test (MHT) and combined EDTA disk test (CEDT, imipenem disk and imipenem disk plus EDTA) are relatively easy and simple tests which have been recommended by CLSI. MBLs such as blaVIM and blaIMP cause hydrolysis of a variety of beta lactams except aztreonam, which vary between different regions. The present study was conducted to investigate the blaVIM and blaIMP genes among the *K. pneumoniae* strains isolated from patients admitted to the selected hospitals of Khorramabad, Iran.

Methods: In this cross-sectional study, 93 *K. pneumoniae* isolates were collected from various clinical samples. All of the isolates were screened for the presence of carbapenemases and MBLs by using MHT and CEDT, respectively. To detect the blaVIM and blaIMP genes, the isolates were subjected PCR.

Results: Out of the 93 strains of *K. pneumoniae* isolated, 22(23.7%) and 12(12.9%) isolates were positive for MHT (carbapenemase-producer) and CEDT (MBLs-harboring), respectively. While, one (1.07%) isolate harboured blaVIM, none of them carried the blaIMP gene using the PCR assay.

Conclusion: The screening, confirmatory and molecular methods should be routinely included and used to determine carbapenemase-producing species in clinical laboratories.

Keywords: *Klebsiella pneumoniae*, blaVIM, blaIMP, carbapenemase

P415 - 998: PREVALENCE AND ANTIMICROBIAL SUSCEPTIBILITY PATTERNS OF BACTERIA ISOLATED FROM URINARY TRACT INFECTIONS IN FULAD-SHAHR, IRAN

Fahimeh Ghanbari¹, Farzad Khademi², Masoumeh Madhi³

1. Department of Molecular Medicine, School of Medicine, Yazd University of Medical Sciences, Yazd, Iran.
2. Antimicrobial Resistance Research Center, Department of Medical Bacteriology and Virology, Qaem University Hospital, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran.
3. Department of Microbiology, School of Medicine, Tabriz University of Medical science, Tabriz, Iran.

Background and Aim: Urinary Tract Infection (UTI) is one of the most common bacterial diseases in outpatient and inpatients worldwide that, has become difficult to treat due to appearance of pathogens with increasing resistance to antimicrobial agents. The main objective of this study was to determine the prevalence and antimicrobial resistance profiles of the main bacteria which are responsible for UTI.

Methods: This study described 326 patients with UTI in Shahid Mottahari hospital in Fulad-Shahr, Iran between Mars 2015 and February 2016. The isolated bacteria were identified by biochemical tests. Disk diffusion susceptibility test was performed to determine susceptibility of bacterial agents.

Results: In this study 326 positive urine culture were survey of which, 273(83.74%) were female and 53(16.25%) were males. The most isolated bacteria were *E. coli* (58.28%), *Klebsiella* (11.65%), *Staphylococcus* spp (11.65%), *Enterobacter* spp (7.05%), *Streptococci* (3.68%), *Enterococcus* (2.45%), *Proteus* spp. (1.22%), *Pseudomonas* spp. (0.61%), *Citrobacter* spp. (0.61%), respectively. Results of antimicrobial susceptibility analysis for *E. coli*, as the predominant cause of UTI, are as follows: gentamicin (28.6%), ciprofloxacin (48.4%), nitrofurantoin (12.2%), nalidixic acid (63.7%), trimethoprim-sulfamethoxazole (67.9%), cephalotin (60%), Cefotaxim (44.8%), Imipenem (9.5%), Amikacin (66.7%), and ampicillin (85.3%).

Conclusion: This survey indicate that *E.coli* isolates were the predominant pathogens in UTI and it is more prevalent in women than in men. In our study the frequency of UTI pathogens were comparable to previous studies and showed increasing resistance pattern to the commonly prescribed antibiotics.

Keywords: Urinary tract infection, *E. coli*, antimicrobial resistance

**P416 - 999: A COMPARATIVE STUDY OF VARIOUS METHODS FOR DETECTION OF
DRUG SUSCEPTIBILITY TEST IN PATIENTS WITH SUSPECTED TB REFERRED TO
PASTEUR INSTITUTE OF IRAN**

Fatemeh Sakhaee¹, Dr. Abolfazl Fateh², Dr. Seyed Davar Siadat³, Morteza ghazanfari⁴, Dr. Farzam Vaziri⁵,
Sharareh khanipour⁶, Nayereh ebrahimzadeh⁷, Ali nour nematollahi⁸, Shahin pourazar⁹, Farid
abdollahimi¹⁰

1. - M.Sc of Genetic, Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran.
2. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran.
3. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran.
4. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran.
5. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran.
6. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran.
7. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran.
8. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran.
9. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran.
10. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran.

Background and Aim: Tuberculosis remains a disease with an enormous impact on public health worldwide due to the emergence of multi-drug resistant *Mycobacterium tuberculosis* (MDR-TB). The most common method for detection of drug-resistant-Tuberculosis (DR-TB) is indirect susceptibility testing on Lowenstein-Jensen (LJ) medium after 2-3 months. Detecting drug resistance by direct Nitrate Reductase Assay (NRA) expedites tuberculosis management.

Methods: 395 clinical isolates with positive microscopy results for acid-fast bacilli with more than 10 AFB per high-power field were used. The samples were decontaminated using N-acetyl cysteine method. The results were compared with the reference indirect proportion and PCR methods.

Results: The sensitivity and specificity were 99% and 98%, 82% and 90%, 100% and 99%, and 96% and 98% for rifampin, isoniazid, streptomycin, and ethambutol, respectively. The results were in most cases available in 18 days. 13 INH-resistant isolates (59%) had a mutation at codon 315, 6 (22.4%) at codon 141, 5 (18.6%) at codon 326 of *katG*. 12 rifampin-resistant isolates (50%) had a mutation at codon 531, 5 (20.83%) at codon 526, 6 (25%) at codon 525, 1 (4.17%) at codon 511 of *rpoB*. 10 kanamycin-resistant isolates (41.6%) had a mutation from A to T at position 1401. 14 fluoroquinolones-resistant isolates (54.5%) had a mutation at codon 94 of *gyrA*, at codon 495 of *gyrB*. 12 capreomycin-resistant isolates (58.3%) had a mutation at codon 118.

Conclusion: The NRA could be used as a rapid, inexpensive, and accurate method to determine rifampin and isoniazid susceptibility directly. The technique might become a valid alternative to traditional methods, especially in low-income countries.

Keywords: *Mycobacterium tuberculosis*, Multi-drug resistant, Nitrate reductase assay, proportion method

**P417 - 1001: STUDY THE DEPENDENCE OF CIPROFLOXACIN-INDUCED MUTAGENESIS ON
UMUC IN ESCHERICHIA COLI**

Sayyede Marzieh Nourbakhsh rezaei¹, Raziieh Pourahmad²

1. MSc student in Genetics at university of shahrekord
2. Associate Professor of Genetics at university of shahrekord

Background and Aim: Fluoroquinolone antibiotics such as ciprofloxacin are effective agents against Gram-negative bacteria. In *Escherichia coli* exposure to ciprofloxacin resulted in mutagenesis and antibiotic resistance. In addition, exposure to UV radiation induces the transcription of *umuC* by ciprofloxacin. UmuC, a subunit of the PolV is required for mutagenesis caused by UV rays. Previous studies showed that in *Streptococcus uberis* exposure to the ciprofloxacin will lead to mutagenesis and antibiotic resistance. However, UmuC is not essential for this process. In another study it was found that in the *Escherichia coli* ciprofloxacin resistance mutants the expression of *recA*, *umuC* genes increased.

Methods: For this purpose, *Escherichia coli* UmuC - mutant was used. Resistance to ciprofloxacin was created stepwise.

Results: The results showed that clones with low and medium resistance can be produced from UmuC - mutant.

Conclusion: In conclusion, UmuC is required to create mutants with high resistance and plays a role in the mutagenesis

Keywords: Ciprofloxacin, UmuC, *Escherichia coli*, mutagenesis

P418 - 1009: PHENOTYPIC AND GENOTYPIC STUDY OF BIOFILM FORMATION IN STAPHYLOCOCCUS AUREUS ISOLATED FROM URINARY TRACT INFECTIONS

Masoud Yousefi¹, Fatemeh Fallah², Mohammad Reza Pourmand³, Mohammad Hasan Namaei⁴, Ali Nazari Alam⁵, Davoud Afshar⁶

1. Faculty of Medicine, Birjand University of Medical Sciences, Birjand, Iran
2. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. Department of Pathobiology, Faculty of Public Health, Tehran University of Medical Sciences, Tehran, Iran.
4. Faculty of Medicine, Birjand University of Medical Sciences, Birjand, Iran
5. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran
6. Department of Microbiology, Zanjan University of Medical Sciences; Zanjan, Iran

Background and Aim: Emergence of multidrug resistance *S. aureus* has become a public health problem. Untreated UTI caused by *S. aureus* may lead to severe health-threatening condition. Identification of bacterial biofilm formation in UTI may prevent recurrent consequence of the infection.

Methods: In this study, a total of 39 isolates of *S. aureus* were collected from patients with UTI. The antibiotic susceptibility patterns of the isolates were determined by the Kirby-Bauer disk-diffusion. We used the Modified Congo red agar (MCRA) and Microtiter plate methods to assess the ability of biofilm formation. All isolates were examined for determination of biofilm related genes, *icaA*, *fnbA*, *clfA* and *bap* using PCR method.

Results: Linezolid, quinupristin/dalfopristin and chloramphenicol were the most effective agents against *S. aureus* isolated from UTI. Overall, 69.2% of *S. aureus* isolates were biofilm producers. Resistance to four antibiotics such as nitrofurantoin (71.4% vs. 28.6%, $P=0.001$), tetracycline (57.7% vs. 42.3%, $P=0.028$), erythromycin and ciprofloxacin (56% vs. 44%, $P=0.017$) was higher among biofilm producers than non-biofilm producers. The *icaA*, *fnbA* and *clfA* genes were present in all *S. aureus* isolates. However, *bap* gene was not detected in any of the isolates.

Conclusion: Our findings reinforce the role of biofilm formation in resistance to antimicrobial agents. Rifampin, Trimethoprim-sulfamethoxazole and doxycycline may be used as an effective treatment for UTI caused by biofilm producers *S. aureus*. Our results suggest that biofilm formation is not dependent to just *icaA*, *fnbA*, *clfA* and *bap* genes in *S. aureus* strains.

Keywords: Urinary tract infection, *Staphylococcus aureus*, Biofilm formation, Antibiotic resistance.

**P419 - 1016: INVESTIGATION OF ANTIBACTERIAL EFFECTS OF SPIRULINA PLATENSIS
EXTRACTS**

Fatemeh Yaghoobizadeh¹

1. Shahid Chamran University of Ahwaz

Background and Aim: Microalgae have been explored for their bioactive compounds with promising applications encompassing antibacterial, antiviral, antifungal and antialgal activities. Considering the present status of widely used treatment therapies and their limitations to tackle their adverse effects, the application of bioactive compounds derived from algae will prove beneficial and much more effective as compared with traditional treatment methods. Due to the emerging infectious diseases, viral infections and raise in antibiotic resistant bacteria, there is an urgent need for development of alternative treatment therapies against infectious diseases.

Methods: *Spirulina platensis* was grown in Zarrouk medium at 30°C, 150rpm and 16/8 photoperiod. *Escherichia coli* O157:H7, *Staphylococcus aureus*, *Vibrio cholera*, *Pseudomonas aeruginosa* PTCC, *Bacillus subtilis* PTCC, *Streptococcus pneumoniae* PTCC, *Salmonella typhi* PTCC, *Shigella dysenteriae* PTCC, *Listeria monocytogenes* PTCC were grown in LB at 37°C (set to 0.5 McFarland). After 21 days, antibacterial effects of ethanol, acetone and water extracts were investigated using disc diffusion method. Gentamycin and Streptomycin were used as standard discs.

Results: Disc diffusion method showed that among various extracts of microalgae, ethanol extract was effective against all pathogenic bacteria.

Conclusion: It has been reported that algae are a very interesting natural source of new compounds and many of them possess antimicrobial activities. These organisms live in habitats exposed to extreme conditions, and therefore they must adapt rapidly and efficiently, and as a consequence, produce a great variety of biologically active secondary metabolites that participate in the natural defense mechanisms.

Keywords: Microalgae, extracts, spirulina, antibacterial

P420 - 1022: THE PREVALENCE OF RESISTANCE GENES BETA-LACTAMASE CTX / PER / AMPC (CMY 2) IN ESCHERICHIA COLI ISOLATED FROM URINARY TRACT INFECTIONS IN KARAJ

Sansz Hosseini¹, Sanaz Hosseini(MSc)², Qolam ali Moradli(PHD)³, zohreh Sharifi(PHD)⁴

1. Department of Microbiology, Faculty of Science, Saveh Branch, Islamic Azad University
2. Department of Microbiology, Faculty of Science, Saveh Branch, Islamic Azad University
3. Department of Virology, Iranian Blood Transfusion Organization

Background and Aim: Beta-lactam antibiotics are currently the most common treatment for bacterial infections. The production of beta-lactamase enzymes are the most important reason of bacterial resistance to these antibiotics. The aim of this study was to investigate the presence of CTX/ PER/ AMPC(CMY2) genes in E. coli isolated from urin.

Methods:: A total of 400 clinical strains of E.coli were isolated from clinical specimens and their antibiotic susceptibility was determined by disk diffusion method. ESBL production was determined using the combined disk method with CAZ and CTX with clavulanic acid and alone. Minimum concentration inhibition (MIC) for CAZ and CTX with clavulanic acid and alone was determined by agar dilution method. Finally, PCR with specific primers was used for determining the presence of CTX/ PER/ AMPC(CMY2) genes.

Results: In this study, the highest antibiotic resistance was observed against Ceftriaxone , Ceftazidime ,Cefotaxime Penicillin, and Erythromycin (100% ,100%,100%,96.25% and 93.75%, respectively), while the highest susceptibility was reported for Nitrofurantoin and Amikacin (100% and 80%) 400E. coli isolates (20%) were ESBL positive. . Out of 80 samples, 38(47. 5%) had the CTX gene, and AMPC(CMY2) gene was detected in 8 (10%) samples. The PER gene was not detected in any of the samples. while in 31 samples (38.75%), neither of these genes were present.

Conclusion: Our results revealed that using the molecular methods with phenotype methods is very essential for complete detection of Beta- lactamases. There is the need for updating the treatment protocol because the prevalence of this resistance is increasing

Keywords: Escherichia coli, extended spectrum, beta- lactamase, CTX, PER, AmpC

**P421 - 1031: IN VITRO ACTIVITY OF CEFOPRAZONE AND CEFTRIAXONE IN
VANCOMYCIN RESISTANT ENTEROCOCCI**

ALKA HASANI¹, Mojaba Varshochi², Masoume Madhi³, Akbar Hasani⁴

1. Tabriz Uni of Med Sci
2. Professor , Department of Infectious Diseases, Tabriz University of Medical Sciences, Tabriz, I. R. Iran
3. 3. Ph.D Fellow, Department of Bacteriology and Virology, Tabriz University of Medical Sciences, Tabriz, I. R. Iran
4. 4. Assistant Professor, Department of Biochemistry and Laboratory Sciences, Tabriz University of Medical Sciences, Tabriz, I. R. Iran

Background and Aim: The emergence of enterococcal strains with multidrug-resistant determinants has significantly complicated the management of enterococcal infections. Vancomycin is used to treat infections with strains that exhibit high-level resistance to ampicillin, however, resistance towards this antibiotic has led to base the treatment using other therapeutic options and prolonged synergy therapy with high doses of ampicillin plus ceftriaxone is considered. In this study we tested activity of cefoprazone and ceftriaxone on vancomycin resistant enterococci.

Methods: Enterococci spp were isolated from various clinical specimens submitted to division of Microbiology, Sina Hospital, Tabriz. These isolates were identified to species level by standard biochemical and molecular methods. Their susceptibilities to antibiotics were determined by disc diffusion method according to CLSI guideline. Minimum inhibitory concentration (MIC) of vancomycin, cefoprazone and ceftriaxone were determined by E-test method. Vancomycin resistance was confirmed by PCR.

Results: A total of sixty enterococci were isolated during the study period. Of these 38 were from urine, 10 from wounds and others from various clinical specimens. From all isolates, 20% was *E. faecium* and 80% *E. faecalis*. Twenty seven isolates were found as VRE. All isolates were positive for *vanA* gene. The effect of ceftriaxone was 46.6% and cefoperazone was 78.3% on disk diffusion but with consideration of MIC for each species, there was no significant difference between two species (26.6% vs 28.3%, respectively).

Conclusion: As cefperazone was found more active than ceftriaxone, it can be suggested to use as an option for synergistic antibiotic usage for VRE infections.

Keywords: Enterococci, Vancomycin resistance, Cefoprazone, Ceftriaxone

P422 - 1032: THE PREVALENCE OF RESISTANCE GENES BETA-LACTAMASETEM/VEB/SHV IN ESCHERICHIA COLI ISOLATED FROM URINARY TRACT INFECTIONS IN KARAJ

Sansz Hosseini¹, Sanaz Hosseini(MSc)², Qolam ali Moradli(PHD)³, zohreh Sharifi(PHD)⁴

1. Department of Microbiology, Faculty of Science, Saveh Branch, Islamic Azad University
2. Department of Microbiology, Faculty of Science, Saveh Branch, Islamic Azad University
3. Department of Virology, Iranian Blood Transfusion Organization

Background and Aim: Extended-spectrum beta-lactamase (ESBL) enzymes hydrolyze cephalosporins and penicillins. This study aimed to determine the frequency of Escherichia coli strains producing SHV, TEM and VEB β -lactamase genes and their association by inducing antibiotic resistance.

Methods: A total of 400 clinical strains of E.coli were isolated from clinical specimens and their antibiotic susceptibility was determined by disk diffusion method. ESBL production was determined using the combined disk method with CAZ and CTX with clavulanic acid and alone. Minimum concentration inhibition (MIC) for CAZ and CTX with clavulanic acid and alone was determined by agar dilution method. Finally, PCR with specific primers was used for determining the presence of blaTEM, blaPER, and blaVEB genes.

Results: In this study, the highest antibiotic resistance was observed against, Ceftriaxone , Ceftazidime, Cefotaxime, Penicillin and Erythromycin (100% ,100%,100%,96.25% and 93.75%, respectively), while the highest susceptibility was reported for Nitrofurantoin and Amikacin (100% and 80%). 400E. coli isolates (20%) were ESBL positive. . Out of 80 samples, 41(51.25%) had the TEM gene, and SHV gene was detected in 8 (10%) samples. The VEB gene was not detected in any of the samples. while in 31 samples (38.75%), neither of these genes were present.

Conclusion: According to the results of this study, the production of ESBL was identified in 49% of the investigated E. coli isolates. Therefore, accurate and timely medical care, as well as the use of appropriate antibiotics, is required to prevent the outbreak of ESBL-producing E. coli strains.

Keywords: Escherichia coli, Extended-Spectrum Beta-Lactamase (ESBL) , VEB, TEM, SHV

**P423 - 1045: UTILITY OF BLOOD CULTURES AND ANTIBIOTIC RESISTANCE IN
PATIENTS ADMITTED TO INTENSIVE CARE UNITS**

Elghar Soltani¹, Alka Hasani², Arezoo Noie oskouei³, Akbar Hasani ⁴, Leila Dehghani⁵

1. MSc fellow, Department of Bacteriology and Virology, Tabriz University of Medical Sciences, Tabriz, I. R. Iran
2. Associate Professor, Department of Bacteriology and Virology, Tabriz University of Medical Sciences, Tabriz, I. R. Iran
3. MSc fellow, Department of Bacteriology and Virology, Tabriz University of Medical Sciences, Tabriz, I. R. Iran
4. Assistant Professor, Department of Biochemistry and Laboratory Sciences, Tabriz University of Medical Sciences, Tabriz, I. R. Iran
5. MSc fellow, Department of Bacteriology and Virology, Tabriz University of Medical Sciences, Tabriz, I. R. Iran

Background and Aim:Sometimes clinical parameters alone does not serve as useful guides for the identification of patients from whom blood samples should be obtained for culture in patients admitted to intensive care units (ICUs) and blood cultures serve as a vital tool in diagnoses and tailoring antibiotic therapy.

Methods:This study was done at ICU of Sina Hospital, a university-based tertiary-care hospital in Tabriz. Patients were required to have 2 sets of blood samples obtained for culture both before and during administration of antibiotic therapy and outcome of blood cultures were analyzed according to standard microbiological guidelines. All blood cultures were performed by use of the BacT/Alert microbial detection system.

Results:Of 157 patients studied, 104 patients had blood cultures that were either contaminated or revealed negative results, while 54 patients were positive for pathogens. Twenty six patients were positive for bacterial pathogens irrespective of receiving antibiotic therapy. *P.aeruginosa* was the most prevalent organism (15%) followed by *A. baumannii* (11%). Other pathogens were as follows: *Staphylococcus aureus* (12%), *E.coli* (11%), *Enterobacter* spp. (9%), *K.pneumoniae* (7%), *Enterococci* spp. (9%), *P.aeruginosa* (7%) and *A.baumannii* (7%). Of *E.coli*, *Enterobacter* spp and *K.pneumoniae* isolates, 66, 50 and 40% respectively were found as ESBL producers and among *P. aeruginosa* 25% each were found as either MDR or XDR. Among *A.baumannii* 50% were found as MDR and 50% as XDR.

Conclusion:The cautious culture technique and proper selection of antibiotics can manage the patient's longer stay and cost of treatment.

Keywords:Blood cultures, Antibiotic therapy, Bacteremia, Intensive care Unit

**P424 - 1052: PREVALENCE AND ANTIBIOTIC-RESISTANT BACTERIA CAUSING
URINARY TRACT INFECTIONS (UTI) AMONG LABORATORIES, HOSPITALIZED
PATIENTS AND OUTPATIENTS IN SHAHREZA, ISFAHAN, IRAN**

Mahdiye Sadat Tayebi¹, Monir Doudi², Nasrin Talebian³

1. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Falavarjan, Isfahan, Iran
2. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Falavarjan, Isfahan, Iran
3. Department of Chemistry, Shahreza Branch, Islamic Azad University, Shahreza, Isfahan, Iran

Background and Aim: The aim of this study was to determine the prevalence and patterns of antimicrobial resistance uropathogens isolated from community-acquired UTIs from different age and sex distributions in Shahreza, Isfahan province, Iran.

Methods: This descriptive study was conducted in the different clinical laboratory centers from January 2016 to June 2016. Urine samples (n=450) were collected from patients with UTIs clinical symptoms. The isolated strains were identified by differentiate tests, then, the isolates' susceptibility patterns to antibiotics were determined by the Bauer et al. method and the zone diameters of each drug are interpreted using the criteria published by Clinical and Laboratory Standards Institute (CLSI) guidelines.

Results: Among the urine specimens, 7 bacterial genus isolates were recovered and the biochemical tests revealed that, these isolates belong to 10 species. The rate of *Escherichia coli* (77%) isolation was highest followed by *Enterococcus* (5%), *Klebsiella pneumoniae* (4%), *Citrobacter freundii* (4%), *Citrobacter koseri* (3%), *Streptococcus* sp. (2%), *Staphylococcus epidermidis* (2%), *Staphylococcus aureus* (1%), *Enterobacter cloacae* (1%), *Proteus mirabilis* (1%). *E. coli* isolates were the predominant pathogens in UTI. *E. coli* were highly resistant to Ampicillin (72.72%), Cephalothin (68.83%), Nalidixic acid (61.03%) and Co-trimoxazole (59.74%).

Conclusion: Due to the very serious side effects of the most commonly used antibiotics for severe UTIs specially for pregnant women and children as well as observed some multidrug-resistant patterns for isolated strains, antibiotic therapy in the future must consider the requirements for unexpected Challenges.

Keywords: Prevalence, Urinary tract infections, Antibacterial susceptibility.

P425 - 1055: DRUG RESISTANT BACTERIA IN UNCOMPLICATED URINARY TRACT INFECTIONS RAISES CONCERN: SHOULD NITROFURANTOIN BE OPTED AS FIRST LINE THERAPY

Arezoo Noie oskouie¹, Alka Hasani², Elghar Soltani³, Akbar Hasani⁴, Leila Dehghani⁵

1. 1. MSc fellow, Department of Bacteriology and Virology, Tabriz University of Medical Sciences, Tabriz, I. R. Iran
2. 2. Associate Professor, Department of Bacteriology and Virology, Tabriz University of Medical Sciences, Tabriz, I. R. Iran
3. 3. MSc fellow, Department of Bacteriology and Virology, Tabriz University of Medical Sciences, Tabriz, I. R. Iran
4. 4. Assistant Professor, Department of Biochemistry and Laboratory Sciences, Tabriz University of Medical Sciences, Tabriz, I. R. Iran
5. 5. MSc fellow, Department of Bacteriology and Virology, Tabriz University of Medical Sciences, Tabriz, I. R. Iran

Background and Aim: Uncomplicated urinary tract infections (UTIs), despite their significant prevalence, cost, morbidity, and increasing management problems, is usually not given much clinical and microbiological importance, primarily because of our perception that uncomplicated UTIs are common but not a serious problem, easy to diagnose and simple to treat. Another therapeutic aspect is high rates of antibiotic use in hospitals and community which may contribute to emergence of resistant bacterial strains. Though antibiotic resistance cannot be eradicated, but it can be reduced by prudent use of antibiotics.

Methods: We performed urine cultures in microbiology laboratory, Sina Hospital, Tabriz for etiology and antibiotic resistance from uncomplicated urinary tract infections in year 1394-95. These patients were admitted in urology and infectious wards. Patients with relapse and complicated UTI were not enrolled in the study.

Results: E.coli and K.pneumoniae were the most prevalent microbes followed by gram positive bacteria and non-fermenters in our study. Among E.coli and K.pneumoniae, 32% and 42% respectively, were genetically confirmed as ESBL producers and 73% and 28% respectively were multi drug resistant (MDR). Non- fermenters were found as extensive drug resistant (XDR). MDR bacteria were resistant to various antibiotic categories namely, quinolones (48-69%), trimethoprim- sulphamethoxazole (34%), cephalosporins (12-42%), however, nitrofurantoin resistance was found the least (2%).

Conclusion: Though fluoroquinolone is used as first line therapy, but our results suggests that its usage should be constrained. Referring to antibiotic guidelines to good prescribing practice, nitrofurantoin provides an alternative option in uncomplicated urinary tract infections.

Keywords: Uncomplicated UTI, Antibiotic usage, ESBL, MDR, Nitrofurantoin

**P426 - 1059: INVESTIGATION OF THE REMAINING ASSESS DIAGNOSTIC ACCURACY OF
TETRACYCLINE IN GARMSAR CITY MILK AND PASTEURIZED MILK FARMS WITH
DIFFERENT BRANDS OF MILK COLLECTION CENTERS WITH HIGH PERFORMANCE
LIQUID CHROMATOGRAPHY**

Zahra Kherghepoush¹, Ali Davarzani²

1. Student of veterinary medicine, Islamic Azad University of Garmsar, Garmsar, Iran
2. Student of veterinary medicine, Islamic Azad University of Garmsar, Garmsar, Iran

Background and Aim:Hygiene Milk, one of the major constituent of the human diet is of particular importance. The use of antibiotics to ensure optimal growth and development, systemic and local disease control mastitis in dairy herds is common. This study aimed to determine the amount of tetracyclines, in industrial dairies supplied to the city of Garmsar and pasteurized milk with different brands due to incorrect use of antibiotics was done.

Methods:A total of 90 samples (30 samples from industrial cattle around Garmsar and 60 samples of pasteurized milk with different brands) are quota-randomly collected and tested was placed. Evaluation of antibiotic residues in samples using CMT Test Kit and then set the family remaining beta-lactamase antibiotics and tetracycline residues lactamas and Tetracyclines combo test β was conducted with the kit.

Results:2 samples (6.6%) of 30 industrial dairies around Garmsar the presence of residual antibiotics in the tetracycline family of beta-lactamase positive and debris were observed.

Conclusion:In both experiments to determine antibiotic residues in milk samples were negative.

Keywords:tetracycline, milk, chromatography

**P427 - 1067: ANTIBIOTIC RESISTANT BACTERIA ISOLATED FROM YOLK SACCULITIS
OF OSTRICH EGGS**

Abdolreza Nabinejad¹

1. Isfahan Res center of Agriculture

Background and Aim: Ostrich meat is going to become a good alternative or first choice for people, so the ostrich breeding is going to increase now a days, Ostrich eggs should be incubated about 6 weeks and this time is suitable for any bacterial growing and youlksacculitis which not only cause embryonic death but also could be a risk for developing pathogenic zoonotic bacteria

Methods: In current study some ostrich death embryos during incubation period were examined for bacterial identification and antibiotic resistant investigation in Spring and Summer of 2015

Results: The technical method were based on yolk swab culture on the enriching and differentiating media (Broth and Agar) for all G+ and G- and continuously the antibiotic susceptibility test were carried out by disk diffusion method based on the Mc Farland Method

Conclusion: The most popular isolated bacteria were 73% coliform and 25% fecal enterococcus. The antibiotic resistant test for current routine antibiotics exhibit resistant increasing comparing to the same last period, the most resistation were for Tetracyclines, Cephalosporines (first and second generation), Aminoglycosides, Sulfamids but the most sensitivity were for Fosbac and for Fluroquinolons

Keywords: Ostrich, Yolk sacculitis, Antibiotic, Resistant

**P428 - 1074: DETECTION AND CLONING OF A HYPOTHETICAL PROTEIN GENE FROM
MRSA IN PRESENCE OF OXACILLIN**

Mohammad Neshvan Hoorijani¹, Abbas Bahador²

1. Department of Microbiology, Kurdistan Science and Research Branch, Islamic Azad University, Sanandaj, IR Iran
2. 2Department of Medical Microbiology, School of Medecine, Tehran University of Medical Sciences, Tehran, IR Iran

Background and Aim: Methicillin-resistant *Staphylococcus aureus* (MRSA) is one of the most important causes of nosocomial infections. Treatment of infections of MRSA is difficult because of resistance to other antibiotics. The aim of this study was compression of expression profile between MRSA and MSSA.

Methods: To compare the genes expression, cDNA-AFLP technique was used. For this purpose, MSSA and MRSA standard strains bacterial suspension grown in the presence and absence of oxacillin were prepared. Then extraction of RNA, cDNA synthesis and double stranding were carried out. Then it was digested by MseI and MboI enzymes, and was ligated by T4 ligase. Finally, PCR was performed using specific primers for adapters. Then PCR bands were analyzed by vertical electrophoresis. Bands of MRSA strains grown in the presence of oxacillin and the absence of oxacillin and in MSSA were extracted from the gel and were cloned in pTZ57R/T vector, *E. coli* (Fermentas). Then after amplification these elements were sequenced and analyzed.

Results: The results of the analysis showed that coding gene of conserved hypothetical protein is expressed in MRSA grown in the presence of Oxacillin while MSSA and MRSA grown in the absence of methicillin had no expressions

Conclusion: The results of this study suggest the role of hypothetical protein coding gene in the development of resistance to beta-lactam antibiotics in *Staphylococcus aureus* and more studies to identify the function and inhibition of these factors can even be useful in the control of MRSA strains

Keywords: *Staphylococcus aureus*, methicillin resistant *Staphylococcus aureus*, cDNA-AFLP

**P429 - 1075: DETECTION OF SERINE HYDROLASE EXPRESSION AMONG METHICILLIN
RESISTANT STAPHYLOCOCCUS AUREUS BY CDNA-AFLP**

Mohammad Neshvan Hoorijani¹, Abbas Bahador²

1. Department of Microbiology, Kurdistan Science and Research Branch, Islamic Azad University, Sanandaj, IR Iran
2. 2Department of Medical Microbiology, School of Medecine, Tehran University of Medical Sciences, Tehran, IR Iran

Background and Aim: Nowadays, methicillin-resistant *Staphylococcus aureus* bacteria due to resistant to antimicrobial agents and drugs has become a major public health concern. The aim of this study was to investigate the expression profile of the two MRSA and MSSA strains using cDNA-AFLP.

Methods:: Standard MSSA and MRSA strains suspension grown in the presence and absence of oxacillin was prepared. Then extraction of RNA, cDNA synthesis and double stranding were carried out. Then it was digested by MseI and MboI enzymes, and was ligated by T4 ligase. Finally, PCR was performed using specific primers for adapters. Then PCR bands were analyzed by vertical electrophoresis. Bands of MRSA strains grown in the presence of oxacillin, the absence of oxacillin and in MSSA were extracted from the gel and was cloned in pTZ57R/T vector, *E.coli*(Fermentas). then after amplification it was sequenced and analyzed.

Results: The results of this study showed that serine hydrolase protein gene in MRSA, grown in the presence of Methicillin is expressed but it is not expressed in MSSA and MRSA grown in absence of oxacillin.

Conclusion: The results of this study showed that the expression of serine hydrolase is effective in *Staphylococcus aureus* strains resistant to methicillin. Therefore, more research in this area is needed, to be used as a new target for treatment.

Keywords: *Staphylococcus aureus*, methicillin resistant *Staphylococcus aureus*, cDNA-AFLP

**P430 - 1084: ANTIMICROBIAL SUSCEPTIBILITY ASSAY AND PFGE TYPING OF
S.MALTOPHILIA CLINICAL AND ENVIRONMENTAL ISOLATES FROM BLOOD
SAMPLES**

Amir Hesam Nemati¹, Hamid Solgi², Farzad badmasti³, Fereshteh shahcheraghi⁴

1. Bacteriology department, Pasteur institute of Iran, Tehran, Iran
2. Bacteriology department, Pasteur institute of Iran, Tehran, Iran
3. Bacteriology department, Pasteur institute of Iran, Tehran, Iran
4. Bacteriology department, Pasteur institute of Iran, Tehran, Iran

Background and Aim: *Stenotrophomonas maltophilia* is a widespread environmental, multidrug resistant bacterium. It is the third most common nosocomial non-fermenting Gram-negative bacterium. Clinical isolates of *S. maltophilia* are often highly resistant to most of the currently used antimicrobial agents, including carbapenems, and therapy of *S. maltophilia* infection presents a significant challenge both for clinicians and microbiologists. Our objectives are determining antimicrobial susceptibility and investigation of relationship between isolates with PFGE typing.

Methods: 63 clinical and environmental isolates studied. Clinical isolates identified by biochemical tests and environmental samples first, cultured on VIA agar and then suspected colonies identified by biochemical tests. Susceptibility to co-trimoxazole, levofloxacin, minocycline, ticarcillin/clavulanic acid, chloramphenicol and ceftazidime were determined by disk diffusion and Minimum inhibitory concentration (MIC) of ticarcillin/clavulanic acid tested by E-test according to clinical and laboratory standards institute (CLSI). Isolates were typed using PFGE with XbaI restriction enzyme according to Shueh's protocol.

Results: All of isolates detected as *S. maltophilia* by biochemical tests. The most of isolates (92.06%) were resistant to ceftazidime and totally were susceptible to co-trimoxazole, levofloxacin and minocycline. MIC of ticarcillin/clavulanic acid for resistant isolates which detected by disk diffusion were ranged from 128 to 256 µg/ml and all of them were resistant. The PFGE revealed 14 different pulsotypes among 61 isolates. Type A was the most common with 48 clinical isolates.

Conclusion: The least effective drugs were ceftazidime and chloramphenicol. In our study less drug resistance observed in environmental isolates which may be related to less exposure to antibiotic. 48 clinical isolates belonged to a unique pulsotype. It suggested that one isolate distributed in several wards and can be considered as an outbreak strain.

Keywords: *Stenotrophomonas maltophilia*, antimicrobial susceptibility, MIC, PFGE

P431 - 1095: CLASS 1 INTEGRON DISTRIBUTION IN S.MALTOPHILIA CLINICAL AND ENVIRONMENTAL ISOLATES

Amir Hesam Nemati¹, Hamid Solgi², Fereshteh shahcheraghi³

1. Bacteriology department, Pasteur Institute of Iran, Tehran, Iran
2. Bacteriology department, Pasteur Institute of Iran, Tehran, Iran
3. Bacteriology department, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: In the last decade *Stenotrophomonas maltophilia* has emerged as a nosocomial pathogen related to a significant case/fatality ratio in immunocompromised populations. With help of some molecular mechanisms such as β -lactamases and integrons, *S. maltophilia* can become resistant to large number of antimicrobials. Class 1 integrons have been found in *S. maltophilia* isolates in North and South America, Australia, Asia, and Europe. The aim of this study was molecular identification and detection of class 1 integron in *S. maltophilia* isolates.

Methods: 49 clinical isolates from blood samples and 76 environmental samples collected from wards. Environmental samples after cultivation on VIA agar identified by biochemical tests along with clinical ones. Isolates tested by 23S rRNA PCR for confirmation as previously described. Susceptibility to co-trimoxazole, levofloxacin, minocycline, ticarcillin/clavulanic acid, chloramphenicol and ceftazidime determined by disk diffusion and MIC of ticarcillin/clavulanic acid tested by E-test. Class 1 integrons were detected with class I integrase specific primers as previously described

Results: All of clinical and 14 (18.42%) environmental isolates detected as *S. maltophilia* by biochemical tests confirmed by PCR. Ceftazidime and co-trimoxazole were the least and most effective antibiotics against *S. maltophilia* isolates respectively. Ticarcillin/clavulanic acid MIC for resistant isolates was ranged from 128 to 256 $\mu\text{g/ml}$ and all of them were resistant. 52 isolates harbored class 1 integron

Conclusion: *S. maltophilia* is a ubiquitous bacteria and tends to wet places. In our study 71.42% of environmental isolates were collected from wet places. Although we didn't detect co-trimoxazole resistance in class 1 integron positive isolates, but these isolates may acquire drug resistance gene cassettes in future and be multi drug resistant

Keywords: *Stenotrophomonas maltophilia*, integron, 23S rRNA, MIC

**P432 - 1109: STUDY OF EXTENDED SPECTRUM BETA-LACTAMASE (ESBL) E.COLI
ISOLATED FROM PATIENTS WITH URINARY TRACT INFECTION BY DOUBLE DISC
SYNERGY TEST IN MASHHAD**

Vajihe, Abdollahian¹, Gholamreza Hashemi Tabar², Mehrnaz. Rad³

1. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.
2. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.
3. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.

Background and Aim:Enterobacteriaceae are the largest and the most diverse family of Gram-negative bacteria in medicine. These bacteria can cause more than 70% urinary tract infections (UTI). Lactam antibiotics families are the first choice in the treatment of infections caused by pathogenic Escherichia coli strains. The present study was designed to determine the antimicrobial susceptibility pattern of E.coli isolated from urine culture of patients admitted to several hospitals and laboratories in Mashhad.

Methods:One hundred of Escherichia coli isolates from patients (50 samples from patients in laboratories and 50 samples from hospitalized patients) with urinary tract infection producing broad-spectrum beta-lactamase were examined. Double disc synergy test was used with Sftazydym 30M g, Ceftriaxone 30 µg, Aztreonam 30 µg, Cefotaxime 30 µg, Cefpodoxime 10 µg and amoxicillin clavulanate 30 µg discs to detect UTI E-coli. All data analyzed in SPSS version 19.

Results:From 100 isolated E.coli, 69% and 31% of strains were isolated from women and men, respectively. The highest rate of infection were found in patients older than 60 years with abundance 20% and 10% in men and in women, respectively. In these patients the highest antibiotic resistance was observed by Cefotaxime (40%). ESBL-producing strains were found 48.1% and 26.08% in men and women, respectively.

Conclusion:Due to the beta-lactam group of antibiotics are the most common drugs used in urinary tract infections, so data of resistance to these antibiotics is important. This can help in the treatment of patients.

Keywords:: Antibiotic-resistance, Urinary tract infection, Escherichia coli, ESBL.

**P433 - 1143: PREVALENCE OF DRUG-RESISTANT PSEUDOMONAS AERUGINOSA IN
IRANIAN BURNED PATIENTS: SYSTEMATIC REVIEW AND META-ANALYSIS**

Samira Tarashi¹, Mohsen Heidary², Hossein Dabiri³, Mohammad Javad Nasiri⁴, Fazlollah Shokri⁵,
Alireza Mohammadzadeh⁶, Negar Souod⁷

1. Department of Medical Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
2. Department of Medical Microbiology, School of Medicine, Iran University of Medical Sciences, Tehran, Iran
3. Department of Medical Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
4. Department of Medical Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
5. Department of Medical Genetics, Shahid Beheshti University of Medical Sciences, Tehran, Iran
6. Department of Medical Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
7. Department of Medical Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.

Background and Aim: The increasing prevalence of drug-resistant *Pseudomonas aeruginosa* in burned patients is one of the main public health problems worldwide. Although drug-resistant *P. aeruginosa* in burn units is frequent in some countries and unusual in others, the level of this condition is not precisely known in Iran. The aim of this study was determining the prevalence of drug-resistant *P. aeruginosa* in Iranian burned patients by using a systematic review and according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses statement.

Methods: Several databases including Web of Science, Scopus, PubMed Scientific Information Database, Magiran, Iranmedex, and Science Direct were searched to get studies addressing drug-resistant *P. aeruginosa* in burned patients in Iran. A total of 34 reports available from different areas of Iran from March 2006 and May 2015 were included in the current study.

Results: The meta-analysis revealed that 54.9% (95% confidence interval [CI], 46.9-62.7) of *P. aeruginosa* were resistant to imipenem. The most common resistance was seen against Ceftazidime (66.9%) followed by Ciprofloxacin (52.9%), and Cefepime (52.3%).

Conclusion: The high incidence of drug-resistant *P. aeruginosa* isolates in Iran emphasizes the need for further implementation of *P. aeruginosa* control strategies especially in burn units. Drug susceptibility testing and continuous monitoring of drug resistance are suggested for decrease and prevention of resistance *P. aeruginosa*.

Keywords: *Pseudomonas aeruginosa*, imipenem, Iran, Burn

**P434 - 1145: EPIDEMIOLOGY OF DRUG-RESISTANT KLEBSIELLA PNEUMONIAE IN
IRAN: A SYSTEMATIC REVIEW**

Saeed Khoshnood¹, Mohsen Heidary², Hossein Dabiri³, Mohammad Javad Nasiri⁴, Fazlollah Shokri⁵

1. Department of Medical Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.
2. Department of Medical Microbiology, School of Medicine, Iran University of Medical Sciences, Tehran, Iran
3. Department of Medical Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
4. Department of Medical Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
5. Department of Medical Genetics, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: The spread of drug-resistant *Klebsiella pneumoniae* is a major public health problem worldwide. There are numerous reports on antimicrobial resistance of *Klebsiella pneumoniae* in Iran. Many of these studies have offered local statistics, but so far not carried out a comprehensive analysis on antibiotic-resistant *Klebsiella pneumoniae* from different parts of Iran. This study aimed to determine the incidence of drug-resistant strains of *Klebsiella pneumoniae* in Iran using a systematic review and meta-analysis was designed.

Methods: We have searched several databases including PubMed, Web of Science, Scopus, Magiran, Iran Medex and Scientific Information Database to identify antibiotic-resistant *Klebsiella pneumoniae* in Iran. A total of 27 published reports from different parts of Iran from January 1998 to November 2014 were enrolled in this study.

Results: The results of the meta-analysis showed that the prevalence of resistance to imipenem and ceftazidime in the *Klebsiella pneumoniae* isolates, were, 3.2% (95% confidence interval (1.5 to 6.5) and 55.7% (95%) and confidence interval (46.9 to 64.1) respectively. The highest resistance in *Klebsiella pneumoniae* isolates was against ampicillin (82.2%).

Conclusion: The results of this study indicate the need further implementation of control measures in *Klebsiella pneumoniae* clinical isolate. Susceptibility testing to antibiotics, a high degree of awareness among doctors and microbiologists, and uninterrupted monitoring on antibiotic resistance for the prevention and control of drug-resistant *Klebsiella pneumoniae* are recommended.

Keywords: *Klebsiella pneumoniae*, Iran, systematic review, Epidemiology.

**P435 - 1148: THE BLAKPC AND BLAGES CARBAPENEMASE GENES AND INTEGRON
CLASS 1 IN KLEBSIELLA PNEUMONIAE ISOLATES IN KASHAN**

Farzaneh Firoozeh¹, Mehdi Aga-Seyed Hosseini ², Ahmad Piroozmand ³, Mohammad Zibaei ⁴

1. Department of Microbiology and Immunology, School of Medicine, Kashan University of Medical Sciences, Kashan, I.R. Iran.
2. Department of Microbiology and Immunology, School of Medicine, Kashan University of Medical Sciences, Kashan, I.R. Iran.
3. Department of Microbiology and Immunology, School of Medicine, Kashan University of Medical Sciences, Kashan, I.R. Iran.
4. Department of Parasitology and Mycology, School of Medicine, Alborz University of Medical Sciences, Karaj, I.R. Iran.

Background and Aim: Carbapenemase (KPC)-producing *Klebsiella pneumoniae* are among highly antimicrobial resistant gram negative bacteria and infections due to them are an increasingly major health problem worldwide. In this study we have detected the blaKPC and blaGES carbapenemase genes and integron class 1 in *Klebsiella pneumoniae* isolated from hospitalized patient in Kashan, Iran.

Methods: In a cross-sectional study, a total of 181 *K. pneumoniae* isolates were recovered from clinical specimens during November 2013 to October 2014. Antimicrobial susceptibility profiles were determined using disk diffusion method according to CLSI guidelines. Carbapenem resistant *K. pneumoniae* isolates were identified. PCR method and sequencing were used for detection of integron class 1 and blaKPC and blaGES carbapenemase genes.

Results: Of the 181 *K. pneumoniae* isolates, 150 (82.9%) identified as MDR strains. Among carbapenems, the most resistance rate 39 (21.5%) was seen against ertapenem using disk diffusion method. All MDR *K. pneumoniae* isolates carried integron class 1 and 21 (43.7%) and 42 (87.5%) carbapenem resistant *K. pneumoniae* isolates carried blaKPC and blaGES genes respectively.

Conclusion: The data of this investigation revealed that the prevalence of GES type carbapenemase was higher than KPC type among clinical isolates of *K. pneumoniae* in Kashan, Iran. Also presence of integron class 1 in all isolates highlight the risk of rapid spread of resistance genes especially in clinical settings.

Keywords: Carbapenemases, KPC, GES, class 1 integron, *Klebsiella pneumoniae*

**P436 - 1154: THE INACTIVATION EFFECT OF CSP A GENE ON RESISTANCE TO
CIPROFLOXACIN IN ESCHERICHIA COLI CSP A-**

Hoda Akhavan armaki¹, Razieh Pourahmad²

1. MSc student in Genetics at university of shahrekord
2. Associate Professor of Genetics at university of shahrekord and corresponding author

Background and Aim: CspA is the cold shock protein in Escherichia coli. This protein is a transcriptional activator for genes, such as gyrA and hns. The target of ciprofloxacin is DNA gyrase, an essential bacterial enzyme, which consists of two subunits, gyrA and gyrB. The aim of study was to investigate the effect of the cspA gene inactivation on resistance to ciprofloxacin.

Methods: For this purpose, resistance to ciprofloxacin was produced stepwise and MIC was determined by serial dilution method

Results: The results showed that only mutants with low resistance to ciprofloxacin were produced in Escherichia coli cspA-.

Conclusion: In conclusion, it seems that the presence of cspA gene has a role in the production of ciprofloxacin high resistant mutants

Keywords: cspA-ciprofloxacin-Escherichia coli - gyrA

**P437 - 1157: ANTIBIOTIC SUSCEPTIBILITY PATTERN OF MRSA FROM HOSPITALIZED
NASAL CARRIAGE IN CARDIOTHORACIC CENTER**

Mohammad Aghazade¹, Mohammad Yousef Memar², Fatemeh Yeganeh³, Leila Yousefi⁴, Firouzeh Safaeeyan⁵, Mina Yekani⁶

1. Cardiovascular Research Center, Tabriz University of Medical Sciences, Tabriz, Iran
2. Department of Bacteriology and Virology, Tabriz University of Medical Sciences, IR Iran
3. Department of Bacteriology and Virology, Tabriz University of Medical Sciences, IR Iran
4. Department of Bacteriology and Virology, Tabriz University of Medical Sciences, IR Iran
5. Department of Bacteriology and Virology, Tabriz University of Medical Sciences, IR Iran
6. Department of Bacteriology and Virology, Tabriz University of Medical Sciences, IR Iran

Background and Aim:: The understanding of frequency of MRSA and their existing antibiotic susceptibility pattern is necessary in the selection of appropriate empirical therapy of these infections. The aim of present study was investigation of frequency and antibiotic susceptibility patterns of MRSA in the Shahid Madani cardiothoracic center (Tabriz University of medical sciences)

Methods: Two hundred and fifty five nasal swap samples were obtained from hospitalized patients in surgery, pediatric and medical Wards. MRSA were detected by phenotypic and PCR methods. Disk diffusion and agar dilution methods were performed for determination of antibiotic susceptibility patterns and results were interpreted according to guidelines of Clinical and Laboratory Standards Institute (CLSI)

Results: In the present study, MRSA was detected from 8.2% of all hospitalized patients by 30µg cefoxitin disk from 255 specimens and all were confirmed as MRSA by PCR methods. All isolates were vancomycin, linezolid and mupirocin susceptible. High frequency of resistance was observed among MRSA isolates to clindamycin, ciprofloxacin, erythromycin gentamicin

Conclusion: The nasal colonization by *S. aureus* was common in hospitalized patients in our setting and representing the need of stable monitoring of the antimicrobial susceptibility pattern of *S. aureus* isolates for the option of proper antibiotic therapy. To limit infections caused by MRSA, hospitalized nasal carriers should be screened and correctly treated

Keywords: Antibiotic susceptibility pattern, Methicillin resistant staphylococcus aureus, Minimum Inhibition Concentration and nasal carriage

**P438 - 1158: PREVALENCE OF EXTENDED SPECTRUM BETA-LACTAMASE (SHV)
PRODUCING ESCHERICHIA COLI IN POULTRY COLIBACILLOSIS BY POLYMERASE
CHAIN REACTION**

Khatereh Kafshdouzan¹, sara Alie², Hamid Staji³, Omid pazhand⁴

1. Under Supervision
2. presenter
3. consulting supervisor
4. consulting supervisor

Background and Aim: Presence of Extended-Spectrum β -lactamase (ESBL) such as (Sulphydril Variable) is a major reason for resistance of Enterobacteriaceae to β -lactam antibiotics in poultry industry. Since there is no detailed description in prevalence of SHV in Escherichia coli isolates in Semnan, Iran, the purpose of this study was determination of prevalence of ESBL producing Escherichia coli and blaSHV type gene in broiler chicken farms in Semnan.

Methods: In this study, Of 200 isolates collected from poultry farms and veterinary laboratories 70 E. coli isolated from cloac of apparently healthy broilers and 70 E. coli isolated from viscera of broilers suspected to colibacillosis

Results: The frequency of blaSHV among ESBL producing isolates was 31.4%. The frequency of ESBL in visceral samples (25.71) were significantly higher than cecal sample (11.43).

Conclusion: According to the results, the prevalence of blaSHV producing E. coli is relatively high in both studied groups. This finding provides evidence that healthy broilers in Semnan poultry farms could be as an important reservoir for dissemination of antimicrobial resistance by contaminating food chain. Therefore it is essential to plan on continuous surveillance of livestock-rearing and our food industries to monitor the ESBLs producing microorganisms

Keywords: antimicrobial resistance, , Escherichia coli, , PCR

**P439 - 1159: COLONIZATION OF METHICILLIN RESISTANT STAPHYLOCOCCUS
AUREUS (MRSA) STRAINS IN PATIENTS OF WOMEN SURGICAL WARD IN
BENTOLHODA HOSPITAL IN BOJNURD**

Sepideh Gholami¹, Reza Besharati², Hosein Lashkardoost³, Maryam Besharati⁴

1. MSc of Nursing, faculty member, North Khorasan University of Medical Science, Bojnurd, Iran
2. MSc of microbiology, faculty member, North Khorasan University of Medical Science, Bojnurd, Iran
3. MSc of Epidemiology, faculty member, North Khorasan University of Medical Science, Bojnurd, Iran
4. PhD student of microbial biotechnology, Tehran university, Tehran, Iran

Background and Aim: The major problem of different wards of hospitals is Methicillin-resistant *Staphylococcus aureus* (MRSA). Regarding the global importance of this strain to create nosocomial infections, it is necessary to determine the rate of infection in different wards of hospitals. This study aimed to determine the prevalence of Methicillin-resistant *Staphylococcus aureus* colonization in patients admitted to the women Surgical ward in Bentolhoda in Bojnurd.

Methods: A cross-sectional study was conducted on a total of 120 patients in the women Surgical ward in Bentolhoda hospital. Methicillin disk diffusion method was applied for detection of methicillin-resistant strains. Susceptibility of Methicillin-resistant strains to commonly used antibiotics was determined by disk diffusion method.

Results: From 120 patients, 16 (13.3%) were nasal carrier of *Staphylococcus aureus*, and 4 of cases (25%) were resistant to Methicillin.

Conclusion: Presence of nasal carriers, indicated presence of Methicillin resistant *S. aureus* in patients of Bentolhoda hospital. Although the prevalence of *Staphylococcus aureus* was not significant, most of the isolates were MRSA that could potentially distribute widely.

Keywords: Colonization, *Staphylococcus aureus*, MRSA, women Surgical ward

**P440 - 1193: FREQUENCY OF STAPHYLOCOCCUS AUREUS NASAL CARRIAGE IN
HEALTHY STUDENTS OF URMIA UNIVERSITY**

Solyman Abroo¹, yaehgob sharifi², Nima hosseini jazani³

1. Student Research Committee, Urmia University of Medical Sciences, Urmia. Iran
2. Assistant Professor of Microbiology, Faculty of medicine, Urmia University of Medical Sciences
3. Professor of Microbiology, Faculty of medicine, Urmia University of Medical Sciences

Background and Aim: Staphylococcus aureus is a species of the genus Staphylococcus that is found everywhere, including in the respiratory tract and on the skin of many adults and children, and that is considered one of the main pathogens in nosocomial and community acquired infections. The number of Methicillin-Resistant Staphylococcus aureus (MRSA) strains has increased globally over the past two decades. The aim of this study was to determine the prevalence of nasal carriage S. aureus among students of Urmia University.

Methods: This cross-sectional study was conducted from June 2015 to March 2016. Nasal swabs were taken from 700 randomly selected students. The isolates were identified as S. aureus based on morphology, Gram stain, catalase test, coagulase test, and mannitol salt agar fermentation. Disk diffusion agar method used to analyze sensitivity patterns of S. aureus isolates. Phenotypically isolated S. aureus was confirmed by detection of genus- species specific gene (spa) using PCR.

Results: Of total 700 collected swabs the prevalence of nasal carriage of S. aureus was 137 isolates (19.57%). Antibiotic susceptibility testing using disk diffusion revealed high resistance to penicillin (94.9%) and erythromycin (27%). All isolates that identified by phenotypical method has been carried spa gene and confirmed as S. aureus.

Conclusion: The results of this study indicate that nasal carriage of S. aureus exists in healthy students of Urmia University. The higher prevalence of nasal carriage needs close attention to prevent its transmission more especially in health-care settings.

Keywords: Staphylococcus aureus; MRSA; Nasal carriage; Urmia University

P441 - 1197: ANTIBIOTIC RESISTANCE PATTERNS OF UROPATHOGENIC KLEBSIELLA PNEUMONIA STRAINS ISOLATED FROM PREGNANT WOMEN IN KERMAN HOSPITALS

Atefe Rajabi pour¹, Atefe Rajabi - pour², Nadia Kazemi-Pour³, Farokh Rokhbakhsh-Zamin⁴

1. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
2. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran
3. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran

Background and Aim: *Klebsiella pneumoniae* is one of the causative agents for urinary tract infections (UTI) especially in pregnant women; failure diagnosis and treatment can be followed by dangerous consequences for both mother and fetus.

Methods: 132 urine samples were collected from pregnant women referring to Kerman hospitals and different bacterial strains were isolated. Antibigram tests by disc diffusion method were performed for 19 antibiotics; then, the Minimum inhibitory concentration of 8 antibiotics for all strains was evaluated by agar dilution method.

Results: Among different bacteria isolated from all urine samples, only 20 strains were identified as *Klebsiella pneumoniae*. All experiments were focused on isolated *Klebsiella pneumoniae* strains. Resistance of isolates to antibiotics was observed as follows: cephalosporin (42.8%), quinolones (26.4%), aminoglycosides (30%), sulfonamides (46.5%), tetracyclines (32.7%), carbapenems (5.6%), and penicillins (98%). Minimum inhibitory concentration of 8 selected antibiotics (with exception: imipenem) were detected to be more than 64 micrograms per milliliter and in comparison imipenem was the most effective antibiotics with 94.4% of the bacterial strains sensitivity.

Conclusion: *Klebsiella pneumoniae* strains are one of the most common causative agents of urinary tract infections but their patterns of antibiotic resistance are different. So, it is very important to have a good data base of their resistance in different parts of each country.

Keywords: *Klebsiella*, Urinary tract infection, pregnant women, Antibiotic resistance, MIC.

**P442 - 1200: ANTIBACTERIAL EFFECTS OF VANCOMYCIN/METHICILIN
COMBINATIONS AGAINST METHICILLIN-RESISTANT STAPHYLOCOCCUS
AUREUS(MRSA)**

Ali Abdolahi¹, Alireza Khodavandi ²

1. Department of Microbiology, Islamic Azad University, Yasouj, Iran
2. Department of Microbiology, Islamic Azad University, Shiraz, Iran

Background and Aim:Introduction: Methicillin-resistant Staphylococcus aureus(MRSA) is a significant cause of hospital-associated pneumonia (HAP). The combined treatments prevent rapid with MRSA by providing higher antibacterial effects. In this study we were aimed to evaluate the combined antibacterial effects of Vancomycin with Meticilin against MRSA

Methods:Method: Antibacterial effects to Vancomycin and Meticilin alone and in combination were performed using the disk diffusion agar and microdilution broth techniques, against 30 MRSA isolates and 10 sensitive isolates of Staphylococcus aureus

Results:Results:)38/75% (of isolates were treated by vancomycin/methicilin were able to show complete or partial synergistic effects while Most of the isolates (52/5%) presented indifferent effects and (8/75%) presented additive effects. On the other hand, did not show any antagonism effects

Conclusion:Conclusion: These results suggest that the combination of vancomycin with methicilin would be one of the best methods resulting in the appropriate reduction of resistance to antibacterial drugs.

Keywords:Keywords: Vancomycin/Meticilin combinations, Methicillin-Resistant Staphylococcus aureus

**P443 - 1206: DETERMINATION OF TETRACYCLINE RESISTANCE GENES IN FECAL
ESCHERICHIA COLI ISOLATED FROM PIGEON (COLUMBA LIVIA)**

Sajad Shobeiri¹, Nasrin Askari², Reza Ghanbarpour³

1. 1) MSc Student of Bacteriology, Shahid Bahonar University of Kerman
2. 2) PhD Student of Bacteriology, Faculty of Veterinary Medicine, Shahid Bahonar University of Kerman
3. 3) Professor of Microbiology, Faculty of Veterinary Medicine, Shahid Bahonar University of Kerman

Background and Aim: Tetracyclines have been widely used for the past forty years as therapeutic agent in human and veterinary medicine. Urban birds especially pigeons coexist with humans in urban environments and are considered to be important reservoirs and vectors of pathogenic and antibiotic-resistant bacterial strains. This study was set to determine Tetracycline resistance genes in fecal *Escherichia coli* isolated from pigeon (*Columba livia*)

Methods: One hundred fifty-two fresh fecal samples were obtained from trapped pigeons in southeast of Iran and were cultured for isolation of *E. coli*. The isolates were examined to determine the prevalence of tetracycline resistance genes including TetA, TetB, by PCR method. Resistance to above mentioned antibiotic was determined by disc diffusion method according to the Clinical and Laboratory Standards Institute guidelines.

Results: The results showed that ten isolates (6.57%) were positive for Tet A, ten (6.57%) for Tet B. Disk diffusion method showed 98.02% of isolates were resistance to Tetracycline phenotypically

Conclusion: According to the results, *E. coli* isolates of pigeon feces increase the potential of these birds to act as a reservoir of Tetracyclines resistant genes.

Keywords: Tetracycline resistance, *Escherichia coli*, Pigeon

P444 - 1207: ANTIBIOTIC RESISTANCE OF UROPATHOGENS

Sima Pooyan¹

1. Nadia Kazemi-poor

Background and Aim: The synthesis of large numbers of antibiotics over the past decades has caused complacency about the threat of bacterial resistance. Bacteria have become resistant to antimicrobial agents. organisms that cause, urinary infection are now resistant to virtually all of the older antibiotics. The extensive use of antibiotics in the community and hospitals has fueled this crisis. Now, clinical microbiologists increasingly agree that multidrug-resistant bacteria pose the greatest risk to public health.

Methods: Single disc diffusion method was used to examine bacterial susceptibility to antimicrobial agents. A single colony was inoculated into Mueller–Hinton broth and incubated at 37°C for 24 hours. The culture was adjusted to a 0.5 McFarland standard. Then spread the suspension over the entire surface of the plate of Mueller–Hinton agar. After 5-10 minutes Antibiotic discs were applied to the surface of the plates with and incubated at 37°C. After 16 to 18 hours of incubation, the plates were examined, and the diameters of the zones of complete inhibition were measured.

Results: The resistance of isolated bacteria was to Amikacine (4%) , Gentamycine(8%), Piperacillin(48%), Amoxicillin(80%), Nalidixic acid(40%), Kanamycin(28%), Ceftazidim(8%), Nitrofurantoin(4 %), Imipenem(40%), Trimethoprim(48%).

Conclusion: In this study, resistance to Amoxicillin, Trimethoprim and Piperacillin, were found in alarming rates. Somehow these drugs have lost their capability to inhibit uropathogens. In addition, Imipenem, Nalidixic acid show trends of resistance. Gentamycine, Amikacin, Ceftazidim and Nitrofurantoin are relatively satisfactory and effective in treating UTIs. Therefore, it is important to study these resistant uropathogens, including mechanisms of resistance, in order to develop effective future drugs.

Keywords: uropathogen

**P445 - 1209: PHYLOGROUPS DETERMINATION OF ESCHERICHIA COLI ISOLATED
FROM PIGEON (COLUMBA LIVIA)**

Sajad Shobeiri¹, Nasrin Askari², Reza Ghanbarpour³

1. 1) MSc Student of Bacteriology, Shahid Bahonar University of Kerman
2. 2) PhD Student of Bacteriology, Faculty of Veterinary Medicine, Shahid Bahonar University of Kerman
3. 3) Professor of Microbiology, Faculty of Veterinary Medicine, Shahid Bahonar University of Kerman

Background and Aim: According to the phylogenetic analysis, *E. coli* strains are distributed in four phylogroups A, B1, B2, and D. The presence of pigeon's feces in public areas has contributed to the spread of infectious agents in the environments. So, the aim of the present study was to determine phylogenetic group of *Escherichia coli* isolated from pigeon.

Methods: One hundred fifty-two fresh fecal samples were obtained from trapped pigeons in southeast of Iran and were cultured for isolation of *E. coli*. DNA was extracted by lysis method and PCR assay was used to determine the presence of *yjaA* and *chuA* gene and *TspE4.C2* for phylotyping.

Results: PCR assay indicated that *E. coli* isolates fell into four (A, B1, B2, D) groups with prevalence of 69.07% (105 isolates), 17.11% (26 isolates), 2.63% (4 isolates), 11.18% (17 isolates) respectively.

Conclusion: Phylogenetic study on human diarrheagenic *E. coli* isolates showed that EHEC strains were distributed in phylogroups A and B1. Pigeons are widely distributed in public places and are potential reservoirs for several pathogenic microorganisms and phylogenetic studies on *E. coli* isolated from this bird should be considered in epidemiological studies to determine the role of these isolates to act and spread of them to human.

Keywords: Phylotyping, *Escherichia coli*, Pigeon

P446 - 1211: DETERMINE ANTIBIOTIC SUSCEPTIBILITY RATE OF STAPHYLOCOCCUS AUREUS (MRSA) BACTERIA ISOLATED FROM CLINICAL INFECTIONS OF PATIENTS IN EMAM HOSSEIN HOSPITAL

Bahareh Ghobadi saki¹, Mehran Dolati², Bahare ghobadi saki³, BEHZAD BEHNAM⁴

1. -
2. Department of Biology, Varamin-Pishva Branch, Islamic Azad University, Pishva, Iran
3. Department of Biology, Varamin-Pishva Branch, Islamic Azad University, Pishva, Iran
4. Department of Biology, qom Branch, Islamic Azad University, qom, Iran

Background and Aim:Background and Aim:Methicillin-resistant Staphylococcus aureus is the most important causes of hospital acquired infections.Resistance to antibiotics and failure in successful treatment of such infections leads to death of large number of patients worldwide.

Methods:Methods: This study was performed on 4767 clinical samples from patients who were referred to the Emam hossein hospital. For diagnosis of bacteria, following tests were used: Gram staining, Catalase, Coagulase,Mannitol salt agar and Novobiocin susceptibility.Antibiotic resistance of bacteria was determined by disc diffusion method according to CLSI 2014.

Results:Results:In our study 58 Staphylococcus aureus were isolated from urine, blood, skin chips and spatium samples. the most Methicillin-resistant Staphylococcus aureus(MRSA) had 100% resistance to Gentamycin-Tetracyclin- Erythromycin- Cefoxitin- Oxacillin.

Conclusion:Conclusion: Conclusion:This study showed that the rate of antibiotic resistance in Staphylococcus aureus in the clinical infections has increased, and this may be due to the indiscriminate use of antibiotic and lack of performed antibiotic sensitivity test before antibiotic prescription.

Keywords:Methicillin resistant Staphylococcus aureus -MRSA-clinical infection

**P447 - 1242: FREQUENCY OF MULTI-DRUG RESISTANCE AND MORE RAISED ESBLs IN
SALMONELLA ISOLATES FROM HUMANS , LIVESTOCK AND POULTRY**

Mehdi Gharekhani¹, Mehdi Gharakhani², Pejvak Khaki³, Soheila Moradi Bidhendi⁴, Maryam Sadat Soltani⁵

1. Department of Microbiology, Razi Vaccine & Serum Research Institute, Karaj, Iran
2. Department of Microbiology, Razi Vaccine & Serum Research Institute, Karaj, Iran
3. Department of Microbiology, Razi Vaccine & Serum Research Institute, Karaj, Iran
4. Department of Microbiology, Razi Vaccine & Serum Research Institute, Karaj, Iran

Background and Aim: Salmonella is one of the most important causes of gastroenteritis in human and poultry are mentioned as a zoonotic reservoir for this agent. Use of uncontrolled antimicrobial agents in human and animal have been increased drug resistance in the different serotypes of Salmonella. The aim of this study was determining antibiotic resistant patterns and detection of ESBL producing isolates of Salmonellae spp. Isolated from different sources including human, poultry and cattle

Methods: A total of 100 isolates were examined for susceptibility to 30 antimicrobial agents. Antibiotic susceptibility testing was performed using the Kirby-Bauer disk diffusion method (Based on CLSI guidelines). Isolates were considered as MDR that were resistant to at least one antimicrobial agent in three or more of the categories. The Distribution of blaSHV, blaTEM and blaCTX-M genes were determined by PCR.

Results: Thirty-two (46%) isolates were found to be MDR isolates. The share of human isolates was 59.4%. Resistance was most often observed for Cephalexin, Nitrofurantoin. PCR amplification showed that 11 isolates carried the blaSHV, 17 isolates have blaTEM and blaCTX-M was found in 23 isolates. The highest rate of resistance genes was observed in human isolates (21.9%, 40.6% and 37.5% respectively).

Conclusion: This study revealed that multidrug-resistant and ESBL production in Salmonella strains were relatively prevalent in human source. Therefore, accurate and timely medical care, as well as the use of appropriate antibiotics, is required to prevent the outbreak of ESBL-producing Salmonella strains.

Keywords: Salmonella, MDR, ESBLs

**P448 - 1259: EVALUATION OF PLASMID MEDIATED ANTIBIOTIC RESISTANT PATTERN
IN LACTOBACILLUS SPP ISOLATED FROM DRUG PRODUCTS AVAILABLE IN IRAN**

Fatemeh Shafiei seifabadi¹, Shafiei seifabadi F *¹², Baseri salehi M¹³

1. -
2. Department of Microbiology, Faculty of Sciences, Islamic Azad University, kazeroon, Iran
3. Department of Microbiology, Faculty of Sciences, Islamic Azad University, kazeroon, Iran

Background and Aim:Background: Probiotics are living microorganisms, which when used in sufficient quantities, they were benefited from human health. The aims of the present study are determination of plasmid mediated antibiotic resistant pattern in lactobacillus spp isolated from drug products available in iran.

Methods:methods: To perform in the investigate 5 samples drug products were collected. these samples were cultivated on MRS medium. the isolates were phenotypic and genotypic identified. and the isolates were assessed for their antimicrobial resistance to prevalent antibiotics like tetracycline, erythromycin, ampicillin, vancomycin, gentamicin and streptomycin with disk diffusion method. Furthermore, plasmid or chromosomally mediated of antibiotic resistant chracters were evaluated by plasmid curing using acridine orange.

Results:Results: The results indicated that The result obtained indicated that 7 lactobacillus strains were isolated and they were Lactobacillus acidophilus, bulgaricus, reuteri, Rhamnosus, gasseri, Plantarm and casei. Based on the finding vancomycin, streptomycin and gentamicin were chromosomally mediated.

Conclusion:Conclusions: Nowadays antibiotic resistant of bacteria considered as problematic from human being. it is became this characters could transmit to among bacteria and reach to humanity. These present study suggested that antibiotic resistant genes in Lactobacillus in drug products were chromosomally mediated and therefor could not transfer amoung the bacteria speciallying in intestinal tract ecosystem.

Keywords:Key words: probiotics, Lactobacillus, plasmid mediated antibiotic resistant

Food and Water Microbiology

P449 - 4: THE INFECTION RATE OF ESCHERICHIA COLI O157: H7 IN RAW MILK OF URMIA CITY DURING 2014-2015 YEARS

Elham Hajilouyan¹, Naghi Taher Talatpeh², Moslem Neyriz Nagadehi³

1. Faculty of Sciences, Biology Department, Islamic Azad University, Urmia Branch, Urmia, Iran
2. Iran Faculty of Veterinary, Microbiology Department, Islamic Azad University Urmia Branch, Urmia, Iran
3. Faculty of Veterinary, Food Hygiene and Quality Control Department Islamic Azad University, Urmia Branch, Urmia

Background and Aim: E. coli O157: H7, a cause of food poisoning such as diarrhea, colitis disease, Hemolytic Uremic Syndrome, thrombocytopenic purpura, hemorrhage and even death of the human. Animal sources, especially cow's milk, is one of the main foci of the infection to humans. Objective of this study was to evaluate the prevalence of bacterial strains isolated from raw milk in Urmia city during 2014-2015 years.

Methods: In this study, 100 samples of raw milk collected from different parts of the city of Urmia on microbial tests of samples according to standard methods using E. coli broth enrichment media Novobiocin then cultured on agar containing sorbitol with MacConkey to evaluate the fermentation. Sorbitol and lactose were streaked. Suspected colonies were isolated and tested on them. Finally, IMViC was performed using specific antiserum for the isolation of bacteria E. coli O157: H7.

Results: From the 100 samples tested, 9 were confirmed raw milk suspected serotype O157: H7 identified. Finally, E. coli O157 was isolated in 3 cases that all 3 O157: H7 were. From the results it can be concluded that contamination of raw milk E. coli Urmia city O157: H7 is low.

Conclusion: The presence of E. coli producing Shiga toxin (O157: H7) products. Animal represents the ability of the bacteria to endanger human health. Constant monitoring of O157: H7, particularly in raw milk, may play a protective role in the health of the consumer.

Keywords: raw milk, bacteria O157: H7, the city of Urmia

**P450 - 16: ANTIBIOTIC SUSCEPTIBILITY PROFILE OF E. COLI SEROTYPE O157:H7 IN
URMIA ,IRAN**

Elham Hajilouyan¹, Naghi Taher Talatpeh², Moslem Neyriz Nagadehi³

1. Faculty of Sciences, Biology Department, Islamic Azad University, Urmia Branch, Urmia, Iran
2. IranFaculty of Veterinary , Microbiology Department, Islamic Azad UniversityUrmia Branch, Urmia, Ira
3. Faculty of Veterinary, Food Hygiene and Quality Control Department Islamic Azad University, Urmia Branch, Urmia

Background and Aim:The emergence and re-emergence of new strains of microorganisms with high virulent traits and resistant to even new generation antibiotics are significant limiting factor to patients' recovery in clinical settings. This has indeed created a lot of economic burdens and loss of productive activitiesat work places especially in developing countries.

Methods:This study was conducted to evaluate the presence of E. coli serotype O157:H7 in URMIA the antibiotics resistance pattern of the isolates. Out of the 150 samples submitted for bacteriological diagnosis at the Food Hygiene and Quality ControlIslamic Azad University, Urmia,for the period of 6months,60% of the isolates obtained were identified as E. coli.

Results: The incidence of E. coli serotype O157:H7 was 36.7% while the antibiotic susceptibility profile of the isolates to 14 antibiotic commonly prescribed at Urmia showed that the isolates were 70% resistant to Ceftazidine, 60% to tetracycline, Ampicillin-Sulbactam, Amoxicillin-Clavulanic acid, 40% to Amoxicillin, Cefuroxime, Nalidixic acid and Cefalexin, 30% to Nitrofurantoin,20% to floxacine,Chloramphenicol and Ciprofloxacin, 10% to Ceftriaxone and all the isolates were sensitive to Gentamicin.

Conclusion:We conclude that there is an incidence of E. coli serotype O157:H7 with varying resistant pattern in urmia metropolis which has influenced the results obtained from clinical samples in urmia . This calls for significant antibiotic surveillance and good hygiene practices to prevent food/water born outbreak of diarrhea associated with E. coli serotype O157:H7, as the identified serotype has been implicated in several deaths around the glob

Keywords:Food/water borne disease; E. coli O157:H7; antibiotics; urmia metropolis.

P451 - 17: SURVEILLANCE OF DAIRY PRODUCTION HOLDINGS SUPPLYING RAW MILK TO FARMHOUSE CHEESE MAKERS FOR VEROCYTOTOXIN PRODUCING E. COLI O157 AND OTHER VTEC.

Elham Hajilouyan¹, Naghi Taher Talatpeh², Moslem Neyriz Nagadehi³

1. Faculty of Sciences, Biology Department, Islamic Azad University, Urmia Branch, Urmia, Iran
2. IranFaculty of Veterinary , Microbiology Department, Islamic Azad UniversityUrmia Branch, Urmia, Ira
3. Faculty of Veterinary, Food Hygiene and Quality Control Department Islamic Azad University, Urmia Branch, Urmia

Background and Aim:Escherichia coli (E. coli) O157 is but one of a group of verocytotoxinproducing E. coli (VTEC) associated with severe disease in humans. Milk infection may result in bloody or non-bloody diarrhoea but in acute cases serious complications like haemolytic uremic syndrome (HUS) may developAlthough, E. coli O157 is the most renowned VTEC, other serogroups, including O26, O111, O103, O145 and O121 have the potential to cause serious human illness

Methods:This surveillance project involved seventy-four milk production holdings,throughout Ireland. Fifty-six bovine, 13 caprine and 5 ovine herds participated in the project. Cáis members, individual cheese producers and the local authority veterinary officers facilitated in herd participation and with sample collection. The sampling programme was divided into three cycles thereby each farm was tested on three separate occasions

Results:In this study, five verocytotoxigenic E. coli O157 isolates were detected.Another twenty-one E. coli O157 isolates were found but these were deficient for the verocytotoxin genes. Seventeen E. coli O26 isolates have been detected, four of which were verocytotoxigenic, seven isolates contained the attaching and effacement gene (eae) only, and six isolates expressed none of the virulence factors examined.NoE.coli O111 isolates were detected in this study

Conclusion:An unexpected finding in this study has been the number of E. coli O157 isolates that were VTEC deficient and the number of O26 isolates that were VTEC negative, but showed other virulence factors.Adatabase of these isolates has been established and these strains will be further characterised, to establish their potential pathogenicity and their flagellar gene status.

Keywords:Raw Milk,Verocytotoxin producing,E. coli O157

**P452 - 24: THE USE OF PROBOTIC LACTOBACILLI AS A PROPER CANDIDATE TO
TREAT URINARY TRACT INFECTION CAUSED BY UPEC**

Nazila Arbab Soleimani¹, Mahsa sadri², Mohammad Mahdi Forghanifard³

1. Department of Microbiology, Damghan Branch, Islamic Azad University, Damghan, Iran
2. Department of Microbiology, Damghan Branch, Islamic Azad University, Damghan, Iran
3. Department of Microbiology, Damghan Branch, Islamic Azad University, Damghan, Iran

Background and Aim: Scientists are of the conviction that attachment and biofilm formation of Uropathogenic Escherichia coli (UPEC) are one of the most important factors in Urinary Tract Infection, thus inhibition of bacterial attachment is the appropriate action to prevent infection. The aim of this study was to use probiotic lactobacilli to reach this goal.

Methods: In this study 40 UPEC were collected from Semnan province hospitals and two strains of Lactobacillus acidophilus PTCC 1643 and Lactobacillus casei PTCC 1608 were purchased from Persian Type Culture Collection. Microtitre plate method was done to study biofilm formation of UPEC. Existence of pap gene involved in biofilm formation was investigated by the use of specific primer and PCR assay. To evaluate the antimicrobial activity of complete culture and supernatant of probiotic lactobacilli, modified double layer method and dilution of supernatant were used, respectively. The mechanism of co-aggregation of lactobacilli with pathogens was examined. The microtitre plate method was used to detect anti-adhesion activity of Lactobacilli supernatant.

Results: Biofilm formation and the existence of pap gene were seen in all UPEC. The antimicrobial and anti-adhesive effects of probiotic lactobacilli on UPEC were confirmed in all tests. In this study, Lactobacillus casei with the growth inhibitory (42/7 mm) and anti-adhesion (46/7%) effects was reported as a proper probiotic bacterium.

Conclusion: According to the results, the probiotic lactobacilli have spectacular effects to prevent attachment, biofilm formation and pathogenicity of UPEC, so using them to prevent and treat Urinary tract infection is a practical, reasonable and acceptable method.

Keywords: UPEC, Probiotic lactobacilli, urinary tract infection

P453 - 52: INVESTIGATION OF PSEUDOMONAS AERUGINOSA, AS A SOURCE OF NOSOCOMIAL INFECTIONS, IN DRINKING WATER DISTRIBUTION SYSTEM OF SELECTED HOSPITALS IN TEHRAN CITY

Giti Kashi¹, Mahmoodi N², Nasere F³

1. *Department of Environmental Health, Islamic Azad University, Tehran Medical Sciences Branch, Tehran, Iran (E-mail: g.kashi@yahoo.com)
2. Buchler of Environmental Health, Islamic Azad University, Tehran Medical Sciences Branch, Tehran, Iran
3. Buchler of Environmental Health, Islamic Azad University, Tehran Medical Sciences Branch, Tehran, Iran

Background and Aim: The drinking water quality must obey strict regulations about microbial and chemical pollutants. *Pseudomonas aeruginosa*, opportunistic bacterium, remained in hospital water source for long periods, and resulted in nosocomial outbreak. Nosocomial waterborne infections such as *P. aeruginosa* are caused by bacteria tolerant to at least 2 classes of antibacterial agents. The main goal of this study was to investigate the *Pseudomonas aeruginosa*, as a source of nosocomial infections, in drinking water distribution system of selected hospitals in Tehran city.

Methods: This study is descriptive-analytical. In this study 17 samples are collected from drinking water distribution systems in Tehran city during winter season in the year of 2016. We compare the results with World Health Organization standard values of drinking water. The *P. aeruginosa* is measured by standard method 9213F. This method reports the number of microorganisms as most probable number (MPN). Asparagine broth and set amid broth are applied for culturing *P. aeruginosa*. Samples are incubated for 48 h at 37 °C after culturing.

Results: *P. aeruginosa* is not detected in 17 samples.

Conclusion: This research shows the unpolluted condition of the drinking water distribution systems. It is concluded that drinking water distribution system is not considered as an infective source.

Keywords: Drinking water distribution system, Hospital, *Pseudomonas aeruginosa*, Tehran city

P454 - 56: INVESTIGATING THE MICROBIAL CONTAMINATION OF TRADITIONAL ICE CREAMS IN RAFSANJAN CITY IN 2015

Ozra Hosseininavh¹, Ozra Hosseini naveh², Ashraf Kariminik³

1. -
2. Department of Microbiology, Kerman Branch, Islamic Azad University, Kerman, Iran.
3. Department of Microbiology, Kerman Branch, Islamic Azad University, Kerman, Iran.

Background and Aim:Ice-cream is a frozen dairy product that is easily contaminated and causes food poisoning. This research conducted to screen ice-cream for bacterial contamination in Rafsanjan city.

Methods:All producing and distributing of traditional ice-creams were screened. The samples were collected in hygienic conditions. A total of 40 samples of traditional ice creams were obtained randomly from the retail stores.

Results:All the samples were analyzed for microbial contaminations such as *Escherichia coli* and *Staphylococcus aureus* according to the Iran national standard No. 2406 .The results showed that 29 Samples (72.5%) with coliforms, 6 cases (15%) by *Escherichia coli* and 2 cases (5%) with *Staphylococcus aureus* were contaminated and thus contamination of traditional ice-creams was notable.

Conclusion:However pasteurization of ice-cream raw materials by sufficient heat, regarding health principles in several stages of producing and preparing health materials and controlling ice-cream producing and distributing centers are necessary to decrease contamination.

Keywords:Microbial contamination, *Staphylococcus aureus* , *Escherichia coli* , Traditional ice cream.

**P455 - 65: PRESENCE OF VIRULENCE FACTORS AND ANTIBIOTIC RESISTANCES IN
ENTEROCOCCUS SP**

Seyed mostafa Hosseini¹, Mohammad Reza Arabestani², Behruz Zeyni³

1. 1Research Center for Molecular Medicine, Department of Microbiology, School of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran
2. 1Research Center for Molecular Medicine, Department of Microbiology, School of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran
3. 1Research Center for Molecular Medicine, Department of Microbiology, School of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran

Background and Aim:Enterococci are ubiquitous bacteria present in the environment and in the gastrointestinal tract of healthy animals and humans and may be present in soil, surface waters on plants and vegetables and also they can occur in foods, especially in those of animal origin such as meat, fermented sausages and cheeses. The aim of this study was to determine the occurrence of virulence determinants and vancomycin- resistant genes among *Enterococcus faecalis* and *Enterococcus faecium* obtained from various clinical sources.

Methods:The study was performed on the 200samples collected from dairy food and meat in Hamden. Antibiotic susceptibility testing was performed using disk diffusion methods. The presence of vancomycin-resistant genes and virulence genes was investigated using PCR.

Results:Of 135 enterococcal isolates, (48.1%) were identified as *E. faecalis*, (43.7%) as *E. faecium*, *E. avium* (6.6%) and *E. gallinarum* (1.5%). The results of antibiotic susceptibility testing showed that of the total 135 isolates, 100 (74.1%) were resistance to tetracycline. Lower antibiotic resistance was seen with Nitrofurantoin 2 (1.5%). None of the isolates was found to be resistant to Teicoplanin. Prevalence of *esp*, *hyl*, and *asa1* genes were reported 48.9%, 20%, and 89.6, respectively in *Enterococcus* strains. Totally, *van* genes were identified in 70 (51.6%) *Enterococcus* strains.

Conclusion:This study indicates a high prevalence of multidrug resistance among enterococci isolated from meat and milk products that may serve as a vehicle to transport these resistant bacteria and genes from food to humans and become a serious threat to public health in the future.

Keywords:*Enterococcus faecium*; *Enterococcus faecalis*; *Enterococcus avium*; *Enterococcus gallinarum*;

**P456 - 94: DETERMINATION OF FREQUENCY VIBRIO SPP. IN FISHES DISTRIBUTED IN
SHIRAZ**

Ali Sharifzadeh¹, Maasoomah VatanDoost²

1. 1-Department of Microbiology, Faculty of Veterinary Medicine, Shahrekord Branch, Islamic Azad University, Shahrekord, Iran
2. 2-Department of Microbiology, Faculty of Pharmacy Shahreza Branch, Islamic Azad University, Shahreza, Iran

Background and Aim: Sea foods are prone to bacterial contamination and could cause health risk to the consumers.

Methods: To examine fish distributed in Shiraz, 100 samples of fish collected were tested for possible presence of *Vibrio* spp. Twenty-five grams of homogenized sample diluted with 225 ml of alkaline peptone water and remained at 37°C for 6-8 h. After primary enrichment, TCBS was used as selective medium for separation of *Vibrio* colonies.

Results: *Vibrio* spp. were separated from 53.6% samples.

Conclusion: Although *Vibrio* spp. are very sensitive to heat and readily killed by well cooking of food, consuming raw or not well-cooked seafood could be dangerous.

Keywords: *Vibrio*, culture, Frequency

**P457 - 95: THE EFFECTS OF THE HERBAL ESSENCES(URTICA DIOICA) ON THE
CLOSTRIDIUM AND E.COLI**

Ali Sharifzadeh¹, Hoda Mootamednejad²

1. Department of Microbiology, Faculty of Veterinary Medicine, Shahrekord Branch, Islamic Azad University, Shahrekord, Iran
2. 2-Department of Microbiology, Faculty of Pharmacy Shahreza Branch, Islamic Azad University, Shahreza, Iran

Background and Aim: Complications due to chemical usage and the artificial preservatives of food stuffs, an increase in microbial infections resistant to antibiotics.

Methods:In this experimental study, herbal Essences which include *Urtica dioica* were selected and collected during the year 2015. Then, their essential oils (essences) were extracted by hydro-distillation procedure. By applying Broth Micro Dilution technique and four times of repetition, the mean of Minimum Inhibitory Concentration (MIC90) and Minimum Bactericidal Concentration (MBC) of the above-mentioned essences was certified against *Clostridium* and *E.Coli*. The testing Bacteria were observed from growth level point of view after being cultured in 37 degrees centigrade in Muller Hinton broth media. Then, their MIC and MBC were determined by being sub-cultured in Muller Hinton Agar .

Results: In general, after repeating the test 4 times, the mean of MIC90 and MBC of the above mentioned essences against of Bacteria was determined . According to the results of this survey, the essential oils of *Urtica dioica* showed the best and most tonic activity against of *E.Coli* and *Clostridium* respectively

Conclusion:The findings of this study showed that *Urtica dioica* have Bacteriosttical against *Clostridium* and *E.Coli* .Therefore, that can be used in medical pharmacology, veterinary, food industries,aromatherapy and health affairs as drugs and anti-bacterial elements.

Keywords:Essences, *Urtica dioica*, *Clostridium*, *E.Coli*

**P458 - 105: EFFECT OF BENZALKONIUM CHLORIDE AND PERACETIC ACID ON
LISTERIA MONOCYTOGENES BIOFILM IN RAW MILK**

Naser Bagery¹, Mehran Moradi²

1. Faculty of Sciences, food industry Department, Islamic Azad University, Mamagan Branch, Mamagan , Iran
2. Faculty of Veterinary, Food Hygiene and Quality Control Department, Urmia, University,

Background and Aim: This study was undertaken to examine the efficacy of the disinfectants including benzalkonium chloride and peracetic acid on *Listeria monocytogenes* biofilm produced at polystyrene surface in cow, sheep and buffalo raw milk at different incubations (8, 22 and 37 °C).

Methods: A preliminary biofilm screening test were conducted among 9 different clinically and standard strains of *L. monocytogenes* according to microtiter method. *L. monocytogenes* RITCC 1293 was chosen because of strong biofilm ability and its cell surface hydrophobicity was achieved by microbial adhesion to xylene and the value was 82 %. Biofilm biomass of *L.*

Results: *L. monocytogenes* were influenced by incubation temperatures which significantly ($P < 0.05$) higher at 37°C than at 22 and 8°C. Biofilm biomass of bacteria were greater at sheep raw milk than buffalo and com milk. The results showed that benzalkonium chloride and peracetic acid at commercial concentrations reduced 90-100% of biofilm cells formed in raw milk. The type of raw milk did not significantly affect the sanitizing activity of sanitizers.

Conclusion: Overall, peracetic acid was effective than benzalkonium chloride and reached greater reduction of cells of 2 days biofilm. It concluded that both commercial disinfectants are completely effective on 2 days old biofilm of *L. monocytogenes* formed on polystyrene surface.

Keywords: biofilm; raw milk; disinfectant.

**P459 - 112: EVALUATION OF ESCHERICHIA .COLI CONTAMINATION IN LIQUID SUGAR
PALM BY USING LS+**

Masomeh Atharinia¹

1. Standard Res Institute, Iran

Background and Aim: Honey or natural substance derived from the extraction of palm and palm sugar has no additives and Looks clear and their colors vary from bright to dark yellow. It is expected that this products have a great popularity in domestic and foreign markets due to its significant features.

Methods: Liquid sugar palm is concentrated of sap palm that after extraction and purification of compounds is produced by removing palm extract pectin, protein, fiber and color that similar sugar composition of honey and high fructose corn syrup.

Results: 30 bottles of liquid palm sugar were randomly sampled from the distribution centers and tested. For the detection of E.coli, LS+ (Lauryl sulfate broth) agar was used.

Conclusion: After the evaluation of results, none of the samples showed E.coli contamination

Keywords: Liquid palm sugar, E.coli, contamination

**P460 - 115: THE PREVALENCE OF YERSINIA ENTEROCOLITICA IN BROILER MEAT
SUPPLIED IN ARDABIL**

Somayeh Shekari¹, Mehdi ghiyamid²

1. Department of microbiology faculty of science Islamic azad university Ahar branch .Ahar Iran
2. Department of microbiology faculty of science Islamic azad university Ahar branch .Ahar Iran

Background and Aim: *Yersinia enterocolitica* is a gram negative bacteria of family of Enterobacteriaceae which causes a wide range of diseases in human including, Yersiniosis, Gastroenteritis, Septicemia, Mesenteric lymphadenitis, Pharyngitis, and Appendicitis. current study aims to investigate the contamination rate of broiler meat in Ardabil contaminated to *Yersinia enterocolitica*.

Methods: In current descriptive-sectional research , 246 samples including 132 samples in spring and 132 samples in summer were selected as random cluster from different regions of city supermarkets that supply broiler meat in Ardabil. Samples were examined with Iranian National Standard Method 4556 and investigated in PBS for 14 days in terms of contamination to *Yersinia enterocolitica*. It should be noted that sampling in summer was performed from the same supermarkets which were sampled in spring and all the broilers were selected from packaged ones.

Results: 22.34 per cent of the broiler samples were contaminated to *Yersinia enterocolitica*, Contamination in spring 23.48% and summer were 21.21% , respectively.

Conclusion: Regarding to the 22.34% contamination of broiler contaminated to *Yersinia enterocolitica* in Ardabil and its importance in pathogenicity of human and the probable growth of microbes in refrigerator temperature, It is necessary to hygienic approaches to reduce the rate of contamination .

Keywords: *Yersinia enterocolitica*, Broiler meat, Ardabil

**P461 - 145: PREVALENCE OF E.COLI O157:H7 FROM FROZEN CHICKEN SAMPLES
USING CULTURE AND MULTIPLEX PCR IN SLAUGHTERHOUSES OF KERMANSHAH
PROVINCE**

Sonya Seifi¹, Nemat Shams², Mohamad Hussein Gharouni^{1,3}, Sonya Seifi^{2,4}

1. Department of Microbiology, Faculty of Veterinary Medicine, Lorestan University, Khorram-Abad, Iran
2. 1Department of Microbiology, Faculty of Veterinary Medicine, Lorestan University, Khorram-Abad, Iran
3. 1Department of Microbiology, Faculty of Veterinary Medicine, Lorestan University, Khorram-Abad, Iran

Background and Aim:: E.coli O157:H7 is recognized globally as pathogen that cause diarrhea, hemorrhagic colitis (HC) and haemolytic uremic syndrome (HUS) in humans. Currently, little information is available about the contamination level of E. coli O157:H7 from poultry in Iran. The aim of the present study was to assess the prevalence of E. coli O157:H7 in frozen chicken samples using culture and multiplex PCR from poultry slaughterhouses in Kermanshah province.

Methods:In this study, at all 235 chicken meat samples were collected from poultry slaughterhouses in Kermanshah province during March to May 2015. A 10-g portion of sample was added to 90 ml of Trypticase soya broth containing novobiocin (20 mg l⁻¹) and homogenized and incubated overnight at 37°C as an E. coli enrichment-step. One loop of each enrichment sample was streaked on selective sorbitol Macconkey agar plates supplemented with Cefixime (2.5 mg/L) and tellurite (0.05 mg/L) (CT-SMAC) for screening test. Diagnostic E. coli- O157 antisera were used for serological identification of E. coli O157:HNM. After biochemical and serological identifications, E. coli O157:HNM isolates were subjected to multiplex PCR.

Results:From 235 chicken meat samples, nonsorbitol fermenting (NSF) colonies were isolated from 11(4/68%) samples after enrichment and selective plating and Serotyping. In m-PCR assay, using specific primers for rfb O157 and flic H7 genes, only 5(2/12%) isolates were confirmed as E. coli O157:H7.

Conclusion:This study shows the importance of chicken meat as potential sources of human E. coli O157:H7/NM infection.

Keywords:E.coli O157:H7 -frozen chicken- culture and multiplex PCR- , nonsorbitol fermenting

P462 - 158: EVALUATION OF CHITOSAN MODIFIED ZEOLITE AS AN ADSORBENT FOR NITRATE REMOVAL AND ITS ANTIBACTERIAL CHARACTERISTICS

Fatemeh Yazdian¹, Darzian Rostami Arash², Yazdian Fatemeh³, Rasekh Behnam⁴, Hasani-nejad mohammadrez⁵

1. Department of Life Science Engineering, Faculty of New Science and Technologies, University of Tehran
2. Department of Life Science Engineering, Faculty of New Science and Technologies, University of Tehran
3. Department of Petroleum Biotechnology, Biotechnology Research Center, Research Institute of Petroleum Industry, Tehran, Iran
4. Department of Petroleum Biotechnology, Biotechnology Research Center, Research Institute of Petroleum Industry, Tehran, Iran

Background and Aim: Overuse of nitrogenous fertilizers in agricultural and inappropriate disposal of humans and animals wastes may lead to nitrate contamination of surface and ground waters. Nitrate can cause methemoglobinemia and could cause carcinoma, malformation and mutation when transformed into nitrosoamines. It has also been demonstrated that chitosan beads are a promising material for nitrate sorption. A disadvantage of these beads is their reported weak mechanical strength. Particle break up alters hydraulic conductivity, resulting in a negative impact to nitrate uptake.

Methods: In this study, chitosan extracted from shrimp waste and used to coat a zeolite material. Surface modifications of natural zeolite were performed by coating it with a chitosan layer. The chitosan coated zeolite (Ch-Z) was protonated with hydrochloric acid and tested for its suitability to capture nitrate from water at 25°C. Nitrate adsorption tests were conducted with 0.5 g of protonated Ch-Z was placed in a 50 ml centrifuge cell with 40 mL sodium nitrate solution 100 ppm NO₃⁻ ion. Each sample was filtered with filter paper, prior to nitrate analysis. Also the antibacterial activity of Ch-Z particles was investigated on *Escherichia coli*. The surface characterization of the Ch-Z was done by SEM and FTIR tests.

Results: The results of these tests showed significance nitrate adsorption of chitosan coating onto zeolite particles and, in addition, antibacterial effects observed.

Conclusion: The use of Ch-Z, to treat water, showed positive results. Nitrate removal was significant. It may prove useful for application in remediation systems where nitrate concentrations are expected to be high.

Keywords: Nitrate, Drinking water, Remediation, Zeolite, chitosan

**P463 - 183: EVALUATION OF VIRULENCE GENES IN ENTEROCOCCUS SPECIES WITH
PROBIOTIC POTENTIALS**

Mahzad Khatibi¹, Naheed Mojgani²

1. Department of microbiology, karaj Branch, Islamic Azad University, karaj, IR Iran
2. Department, Razi vaccine and serum research institute, karaj, IR Iran

Background and Aim: Probiotics are live microorganisms, which when administered in adequate amounts confer a health benefit on the host. Currently, bacteria are used as probiotics, including lactic acid bacteria. Enterococci are ubiquitous bacteria present in the environment and in the gastrointestinal tract of healthy animals and humans. The aim of the present study was to determine the safety of Enterococcus species isolated from dairy products and breast milk samples.

Methods: A number of locally isolated Enterococcus species were isolated from different sources and identified to genus level by phenotypic characteristics and 16S rRNA sequencing. The selected bacteria were screened for their probiotic properties by testing their acid and bile resistance, antibacterial activity. The presence or absence of a number of virulence genes including hyl, esp, cylA, efaAfm was evaluated by PCR assay

Results: In this research, 8 Enterococcus species were isolated and identified. The isolates appeared resistant to acidic pH values and different bile salt concentrations. The isolates demonstrated significant antibacterial activity against a number of pathogens. To evaluate the safety of these isolates, the DNA of the selected isolates was subjected to primers targeting cytolysin (cylA), hyaluronidas (hly), enterococcal surface protein (esp) and cell wall adhesions genes (efaAfm), respectively. Based on our results, all the tested Enterococcus isolates lacked the genes hyl, esp and cylA genes, while all contained genes efaAfm, except for E.faecium TA00154 which lacked the respective gene.

Conclusion: Enterococcus strains selected as starter cultures or as probiotics should be evaluated for their safety and the absence of different virulence traits including virulence genes and antibiotic resistance.

Keywords: Probiotic, Enterococcus, virulence genes, 16srRNA gene sequencing

P464 - 197: MULTILAYERED ANTIMICROBIAL EDIBLE COATING AND ITS EFFECT ON LACTIC ACID BACTERIA ON RAINBOW TROUT (ONCORHYNCHUS MYKISS) FILLETS DURING REFRIGERATED STORAGE

Leila Tabatabaei moradi¹, Anusheh Sharifan², Kambiz Larijani³

1. Master of Science of college of Food Science and Technology, Science and Research Branch, Islamic Azad University, Tehran, IR Iran
2. Assistant professor of food microbiology, Science and Research Branch, Islamic Azad University, Tehran, IR Iran
3. Assistant professor of chemistry, Science and Research Branch, Islamic Azad University, Tehran, IR Iran

Background and Aim:essential oils are used as flavoring agents in various foods. Layer -by- layer (LBL) technique is a method where the material is dipped into a series of different solutions that contain oppositely charged polyelectrolytes.the aim of this study was to investigate the effectiveness of a multilayered edible coating with an antimicrobial compound (Lemon and Peppermint) in enhancing the quality and shelf-life of rainbow trout (*Oncorhynchus mykiss*) during refrigerated storage ($4 \pm 1^{\circ}\text{C}$) over a period of 16 days.

Methods:In this study, multilayered coating were used with two concentrations of Lemon (LEO) and Peppermint (PEO) essential oils (0.5 and 1%) . antibacterial effect of these treatments was evaluated by enumeration of bacteria in special culture media. The control and the coated fish samples were analysed periodically for pH, total viable count, psychrotrophic count, and Lactic acid bacteria.

Results:the results obtained in this study demonstrate that multilayered coating in combination with Lemon and Peppermint essential oils significantly can decrease the number of bacteria and delay the spoilage of the samples ($p<0.05$).

Conclusion:Multilayered edible coating with an antimicrobial compound can properly delay the growth of spoilage microorganisms and prolong the shelf life of meat products.

Keywords:layer-by-layer, Lactic acid bacteria, rainbow trout, essential oil

**P465 - 205: POLYMORPHISM OF COAGULASE GEN IN STAPHYLOCOCCOUS AREUES
ISOLATED FROM COW MILK AND CHEESE IN TABRIZ CITY**

Mohammadhossein Sadeghi Zali¹

1. Islamic Azad Uni,Urmia

Background and Aim: The aim of the present study was to analyse the coA gene on *Staphylococcus aureus* isolates collected from cow milks(19) , buffaloes milk(7) and cheese(14) in Tabriz, north-west of Iran

Methods: For this purpose, forty *S. aureus* isolates were examined by PCR-RFLP.

Results: Amplification of coA gene revealed a different amplicon with a sizes of approximately 600,700,760 and 850 bp in 6, 11, 11 and 12 isolates

Conclusion: AluI digestion of this amplicons demonstrated that the isolates having the same PCR band size were in the same PCR-RFLP patterns and there was not variation into isolates belonged to the same PCR amplicon.

Keywords: *Staphylococcus areues*, cow milk, cheese, coagulase gen, Polymorphism, PCR-RFLP

**P466 - 215: DETECTION OF ZOITES AND MICROSCOPIC TISSUE CYSTS OF
SARCOCYSTIS IN MEAT USING DIGESTION METHOD AND DOB SMEAR IN RASHT,
IRAN**

Fatemeh Zendedel¹, Mohammad Taghi Ahady², Masoud Fardin³

1. Department of Biology, Ardabil Branch, Islamic Azad University, Ardabil, Iran
2. Department of Biology, Ardabil Branch, Islamic Azad University, Ardabil, Iran
3. Department of Biology, Ardabil Branch, Islamic Azad University, Ardabil, Iran

Background and Aim: Sarcosystis is a zoonotic, heteroxenous and obligatory intracellular protozoan parasite which can infect humans and animals. This parasite may introduce macroscopic and microscopic tissue cysts in the meat of infected cattle. Humans acquire the infection by ingestion of cysts or eating raw and/or under-cooked infected beef. The aim of this study was to determine the prevalence of Sarcosystis infection in the meat of cattle in Rasht city (north of Iran).

Methods: In this descriptive and cross sectional study, one hundred random selected samples were examined by digestion method (using pepsin and HCl solution) and dob smear (preparing tissue smear and staining by Giemsa) for detecting Sarcosystis cysts and zoites. Finally, the data were analyzed using SPSS 23 software.

Results: From 100 examined beef samples, 42.9% of shoulder muscle and 43.2% of thigh muscle were diagnosed to be infected by microscopic cysts in digestion method, while these rates were 14.3% and 13.6% respectively in dob smear method. On the other hand, the old carcasses (69.8%) were more contaminated than the young carcasses (30.2%). There was no significant association between sex and infection rate.

Conclusion: We concluded that digestion method was more precise and confident than dob smear, for detecting of microscopic tissue cysts of Sarcocystis. According to high infection rate (43%) of cattle meat with microscopic tissue cysts of Sarcocystis, we recommend that people avoid consumption of raw and/or under-cooked beef.

Keywords: Sarcocystis, Digestion method, Dob smear, Zoites, Tissue cysts, Rasht

**P467 - 232: PSEUDOMONAS AERUGINOSA IN PUBLIC HOT SPRING POOLS OF
MESHGHINSHAHR**

Leyla Movassagh gharamaleki¹, Leila Movassagh gharamaleki², Gholamreza Zarrini³, Mehdi Ghiamirad⁴

1. Department of microbiology, faculty of basic science, Islamic Azad University Ahar Branch, Ahar, Iran.
2. 2-Department of Biology, Faculty of Natural Sciences, University of Tabriz, Tabriz- Iran.
3. Department of microbiology, faculty of basic science, Islamic Azad University Ahar Branch, Ahar, Iran.

Background and Aim: *Pseudomonas aeruginosa* is one of the organisms that causes infectious diseases such as skin infections and ear infections in swimmers in swimming public pools. The aim of this study was to evaluate the prevalence of *Pseudomonas aeruginosa* in public hot spring pools of Meshghinshahr.

Methods: In this study, 52 samples were taken from hot spring pools named Gheynargeh and Moeil in Meshghinshahr from Sep 2014 to Aug 2015. The physicochemical parameters including temperature, pH, EC, hardness, alkalinity, residual chlorine and also *Pseudomonas aeruginosa* were determined by standard methods for examination of water and wastewater. Membrane Filter Technique and Surface plate were used to test for bacterial agents' presence.

Results: The results of this study showed *Pseudomonas aeruginosa* in 53/58% of samples was more than the standard rate. The level of contamination mostly depended on seasonal changes, in which the highest level of contamination was observed in summer samples. None of the measured physico-chemical parameters did not comply with standards.

Conclusion: The results indicated that *P. aeruginosa* contamination level of hot spring pools in Meshghinshahr is higher than standards. There is a need to monitor water quality to increase swimmers' awareness of the risks. Presence of bacterial contamination is a reason for inefficiency of chlorination and treatment system.

Keywords: hot spring pool, microbial contamination, *Pseudomonas aeruginosa*, swimming pool, MeshghinShahr

**P468 - 242: RAPID MOLECULAR DETECTION OF LISTERIA MONOCYTOGENES IN IRAN
INDUSTRIAL SAUCE**

Atefeh Shahhosseiny¹, Peyman mahasti shotorbani², Afshin akhundzade basti³

1. Department of food industry, Faculty of food science and technology, science and research branch, Islamic azad university/Tehran, Iran
2. Department of food industry, Faculty of food science and technology, science and research branch, Islamic azad university/Tehran, Iran
3. Department of food industry, Tehran University/ Tehran, Iran

Background and Aim:For many reasons, today Food-borne diseases in the world are growing and every year cause morbidity and mortality a significant number of people. *Listeria monocytogenes* as a pathogen transmitted through food responsible for causing disease in humans. *Listeria monocytogenes* is an opportunistic pathogen and cause listeriosis. Contamination with *Listeria monocytogenes* are threat to health especially people with suppressed immune systems considered. The aim of this study is rapid molecular detection of *Listeria monocytogenes* in industrial sauce by PCR method.

Methods:25 Industrial sauces were collected from iran markets. DNA of sauce samples extracted by phenol-chloroform method. PCR test optimized and limit of detection (LOD) and specificity evaluated. PCR product was cloned by T/A cloning for positive control construction and sequencing.

Results:Amplicon with 226 bp size was observed in 2% agarose gel electrophoresis and confirmed by sequencing method. No PCR product observed by other microorganisms DNA in specificity test. After PCR testing on samples,4 were positive for *Listeria monocytogenes*

Conclusion:Molecular methods such as PCR have high sensitivity and specificity and suitable for detection of pathogen bacteria in foods. In this study, the use of PCR for detection of *Listeria monocytogenes* in industrial sauces, show that positive samples in this high consumer foods. This results confirmed pasteurization method of sauces. The results show PCR techniques is sensitive and effective molecular test for detection of pathogen microorganism in foods.

Keywords:Sauces, PCR, *Listeria monocytogenes*

**P469 - 243: RAPID MOLECULAR DETECTION OF CAMPYLOBACTER JEJUNI IN IRAN
INDUSTRIAL SAUCE**

Atefeh Shahhosseiny¹, Peyman mahasti shotorbani², Afshin akhundzade basti³

1. Department of food industry, Faculty of food science and technology, science and research branch, Islamic azad university/Tehran, Iran
2. Department of food industry, Faculty of food science and technology, science and research branch, Islamic azad university/Tehran, Iran
3. Department of food industry, Tehran University/ Tehran, Iran

Background and Aim:Consumption of foods contaminated with pathogens microorganisms can lead to food poisoning. Campylobacter causes gastrointestinal infections in humans. The purpose of this study is rapid PCR identification of Campylobacter jejuni in samples of industrial sauces based on molecular method.

Methods:25 industrial sauces were collected from Tehran markets. DNA samples extracted by phenol-chloroform standard method. PCR test optimized and limit of detection (LOD) and specificity evaluated. Amplicon was cloned by T/A cloning method by pTZ57R plasmid. Optimized test carry out on all of the samples.

Results:By optimized PCR test, amplicon 589 bp observed by electrophoresis method. The LOD of test was 100 copy/reaction and no PCR product observed by other microorganisms DNA. After PCR testing on 25 industrial sauce in Iran, None were positive for Campylobacter jejuni.

Conclusion:Molecular methods such as PCR have high sensitivity and specificity and suitable for detection of pathogen bacteria in foods. In this study, the use of PCR for detectin of Campylobacteria in industrial sauces, show that no positive samples in this high consumer foods. This results confirmed pasteurization method of sauces.

Keywords:Campylobacter jejuni , PCR, sauces, Molecular Detection

**P470 - 259: ANTIMICROBIAL ACTIVITY, ANTIBIOTIC SENSITIVITY AND VIRULENCE
FACTORS OF LOCALLY ISOLATED BACILLUS SPECIES INTENDED FOR USE AS
PROBIOTICS**

Nazanin Rezvanian¹, Naheed Mojgani²

1. Department of microbiology, karaj Branch, Islamic Azad University, karaj, IR Iran
2. Biotechnology Department, Razi Vaccine and Serum research Institute, Karaj- IR Iran

Background and Aim:probiotics are increasingly used for therapeutic and prophylactic purpose for treating diseases of the gastrointestinal tract as well as a dietary supplement recommended. Probiotics in Bacillus species, are known to directly and indirectly prevent pathogenic damage through antagonistic action or secretion. In this regard, Bacillus species virulence genes hbl, Nhe, cytK, cse, lipA constitute the main cause of their disease

Methods:In this study 11 Bacillus strains belonging to subtilis, megaterium and leichniformis isolated previously from different sources locally were selected and assessed for their virulence traits. The isolates were tested for their probiotic potential including their resistance to antibiotic, acid, bile, antimicrobial activity. Finally the virulence genes were determined by subjecting the genomic DNA of the selected isolates to a pair of primers including hbl, Nhe, cytK, cse, lipA. All results were analyzes statistically

Results:Among of the 11 selected Bacillus species few showed significant probiotic characteristics including resistance to acidic pH and high bile salt concentrations. Additionally all the Bacillus strains in study appeared sensitive to the tested antibiotics. The virulence gene-specific primers hbl, Nhe, cytK, cse, lipA used in study indicated 4 bacillus isolates to harbor virulence genes like lipA and cytK. LipA and CytK genes were positive in isolates which were also beta hemolytic. None of the other virulence genes including Ces gene, which encodes the toxin vomiting,Non-hemolytic enterotoxin (NHE), hemolysin enterotoxin (HBL) were present in the tested isolates

Conclusion:Bacillus isolates in this study were significantly probiotic properties and may be used as a probiotic in human products, livestock and poultry used in the future

Keywords:Probiotic,Bacillus, virulence genes, 16srRNA gene sequencing

**P471 - 263: TEST OF CHEMICAL TOXICITY OF A NEUROTOXIN, COLCHICINE, ON
SAVAGE WATER LIVING MICROORGANISM PARAMECIUM CAUDATUM**

Robabeh Mohammadi¹

1. Manizheh Karami

Background and Aim:: Chemical toxicity of savage water living microorganisms has been shown in literatures. But, no evidence indicates the toxicity of a microtubule element degrader, colchicine, in the *Paramecium caudatum*.

Methods: The organisms were isolated from savage water sources around the Shahed University main campus in Khalij-e-Fars highway and cultivated at the laboratory. After preparing the pure cultivation of the organisms 0.1 mL of the cultivation was added in the slides. The drug in a volume of 0.01 - 1 $\mu\text{g}/\mu\text{L}$ was infused into the cell drop, at a defined point of the field provided by 4X of the photomicroscopy. The microorganisms' movements were recorded as count per 60 sec considering the 5 sec interval times' points. All data were also recorded using the video- and photo-microscopy. The data further were analyzed using the compare of means program

Results: The *Paramecia* locomotors activities under the infusion of toxin were not significantly affected at the point of the drug infusion. The most effect (dispersal of the organisms) was observed at a relatively high doses of the drug (0.1 - 1 μg) at a significant level ($p < 0.05$).

Conclusion: Toxicity by chemical substances in the savage water living microorganisms may rarely be shown. The dispersal of the *P. caudatum* may provide a sign to show the chemical toxicity by materials with no effect on the cells' activities at the cellular and molecular levels.

Keywords: *Paramecium caudatum*, Savage water, Chemical toxicity, colchicine

**P472 - 355: RAPID MOLECULAR DETECTION OF LISTERIA MONOCYTOGENES, IN IRAN
INDUSTRIAL FRUIT JUICES BY PCR**

Newsha Samie zafarghandi¹, Nioosha Samiee zafarghandi², Houshang nikoopour³, Mohammad Hassan Shahhosseiny⁴

1. -
2. Department of food Science and Technology, Science and Research Branch, Islamic Azad University, Tehran/Iran
3. Department of food Science and Technology, Science and Research Branch, Islamic Azad University, Tehran/Iran
4. Department of Microbiology- Shahr-e-Qods Branch-Islamic Azad University- Tehran/Iran. Iranian Gene Fanavar Institute (IGF), Tehran/Iran

Background and Aim: In recent years the phenomenon of spontaneous abortion of the fetus, has attracted many researches and bacteria such as *Listeria monocytogenes* are important factors that if not detected, leading to recurrent pregnancy loss and will be increase antibiotic resistance. *Listeria monocytogenes* is a pathogen that is transmitted through food and communicate with many severe invasive infections in humans and animals. Prevalence of invasive listeriosis cases in one million people per year is 2-9 person and seldom occurs. But the most serious infections are transmitted through food that has a high mortality rate about 30%. The aim of this study is Molecular Detection of *Listeria monocytogenes* in industrial juices Iran by PCR.

Methods: 50 different of fruit juice samples were collected from the Tehran. PCR testing optimized by using of *hlyA* target genes and a standard strain. The limit of detection (LOD) and specificity tests were examined. DNA samples extracted by DNG-Plus modified method and PCR testing was performed on them.

Results: The product of *L. monocytogenes* (210 bp) was observed in agarose gel electrophoresis. The LOD was calculated 100 hundreds of DNA / Reaction. Also no product observed with genome of other organisms. In 50 samples were analyzed along with positive and negative controls, there was no positive samples observed.

Conclusion: Fortunately Industrial juices studied were pasteurized and processing correctly. And through the rapid, sensitive and accurate PCR method did not show any contamination of *Listeria monocytogenes*

Keywords: *Listeria monocytogenes*, fruit juice, PCR

P473 - 358: MOLECULAR DIAGNOSIS OF CAMPYLOBACTER JEJUNI IN TRADITIONAL ICE CREAM USING PCR METHOD

Hengameh Hamrahi¹, Anousheh Sharifan², Mohammad Hassan Shahhosseiny³

1. Department of Food Science and Technology, Faculty of Agriculture, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. Department of Food Science and Technology, Faculty of Agriculture, Science and Research Branch, Islamic Azad University, Tehran, Iran
3. Department of Microbiology- Shahr-e-Qods Branch-Islamic Azad University-Tehran/Iran. Iranian Gene Fanavar Institute (IGF), Tehran/Iran

Background and Aim: Ice cream is one of the favorite dairy products for people, especially in the warm season. Basic hygiene and storage conditions and distribution of these products can be a variety of microorganisms, including *Campylobacter jejuni*. Infected, source original this bacteria was been in duct digestive of animals that transferred from milk to human and creation poisoning. The aim of this study was rapid identification of *Campylobacter jejuni* by PCR method in traditional ice cream.

Methods: PCR test was optimized by standard strain *Campylobacter jejuni*. The limit of detection (LOD) was done by serial dilution in specified genome copy number DNA solution, and specificity test carry out by online and offline method. The optimized test was done on 50 samples of traditional ice cream.

Results: The amplicon with 589 bp size was observed in agarose gel electrophoresis method and confirmed by sequencing method. The LOD of test was calculated as 100 copy/reaction. No PCR product observed in any genome DNA tested. All of 50 samples were negative by PCR optimized test.

Conclusion: Traditional detection methods have a drawbacks include time consuming and low accuracy. For this reason, in recent years, molecular techniques specially polymerase chain reaction techniques substituted with conventional method. Fortunately in this study we hadnt any positive samples.

Keywords: PCR, *Campylobacter jejuni*, Diagnosis, Traditional ice cream

**P474 - 361: STUDY OF THE ANTIMICROBIAL ACTIVITY OF THE BACTERIOCIN
AGAINST SOME OF THE PATHOGENS**

Fatemeh Kheirollahi¹, Dr. Masoumeh Anvari²

1. M.S in Biology, Field microbiology, free university, Rasht, Iran. Email: kheirollahi.fatima@yahoo.com
2. Member of the faculty, biology group, free university, Rasht, Iran

Background and Aim: Bacteriocins are antimicrobial proteins which prevent the growth of sensitive strains. The purpose of this research is to produce antimicrobial products by using the lactic bacteria separated from low fat yogurt which prevent the pathogen bacteria.

Methods: This is a research study in which bacteriocin is produced by lactobacillus separated from two kinds of pasteurized yogurt of Gilan and then its influence on E.coli and staphylococcus aureus is studied by disc diffusion and gel diffusion methods against two species of gram positive and gram negative bacteria. Then the diameter of non – growth halo is measured (mm). The effect of different factors is studied by Taguchi method.

Results: Findings show that the greatest halo diameter and the highest rate of bacteriocin production occurred on the substrate number 7 on E.coli (17 mm). This diameter was observed in the following conditions: pH 5, inoculation level 20% , temperature 25oC, Glucose and yeast extract as the carbon and nitrogen resources. These resources had a meaningful impact on the production.

Conclusion: The early results of bacteriocin inhibitory effect were optimized by Taguchi software analysis. The best production condition was observed on the substrate number 7 and E.coli. The comparison between halo diameters made by Bacteriocin in two optimized MRS broth showed that Bacteriocin production in the optimized environment increased by 70%. This increase can prevent pathogen bacteria.

Keywords: Probiotic, Bacteriocin, optimization, Lactobacillus

**P475 - 372: MOLECULAR SURVEY, SEROTYPING AND ANTIBIOGRAM PATTERN IN
MARKETED LOCAL, INDUSTRIAL AND BREEDER POULTRY EGG IN TABRIZ CITY**

Soniya Daneshgohar¹, Afshin Javadi²

1. master student of Microbiology cellular and Molecular biology Dept. Rabe e –Rashidieh University, Tabriz, Iran
2. Associate Professor, food hygiene Bio-Technology Research center Azad University, Tabriz, Iran.

Background and Aim: Diseases with the original of foods are one of palms of public Hygiene in the world and salmonella serotypes are of the most important pathogens causing this type of infections. Present work has been done aiming to isolating and determining antibiotic sensitivity and also determining serum from local, industrial and breeder poultry eggs.

Methods: In this cross-sectional survey, 100 local eggs, 100 industrial and 100 breeder poultry eggs were gathered in Tabriz and assessed in the laboratory of food health department of Azad University of Tabriz. Isolation of salmonella from egg yolk was performed based on Iran standard method (ISM) and for definitive diagnosis of salmonella, Biochemical observations, serotyping, and (Polymerase chain reaction) (PCR) have been performed and were followed by antibiogram test.

Results: From a total of 300 analyzed eggs, just 3 out of local sample (3%) were determined as contaminated with salmonella Enteritidis. 100 percent of isolation were sensitive to ciprofloxacin, Gentamycin, Neomycin and trimethoprim Sulfamethoxazole and all isolations were resistant to at least 5 of 9 antibiotics under observation.

Conclusion: Based on results of this study, the rate of contamination of local eggs supplied and distributed in Tabriz is 3 %. Regarding the salmonella contamination in local eggs, it is deemed necessary to pay specific attention to storing cooling hygiene, but industrial and breeder poultry eggs were determined safe for domestic use.

Keywords: Salmonella, Serotyping, Antibiogram, PCR

**P476 - 378: THE INCIDENCE OF VIRULENCE FACTORS IN ENTEROCOCCUS FAECALIS
AND ENTEROCOCCUS FAECIUM ISOLATED FROM TRADITIONAL CHEESES IN NORTH-
WEST OF IRAN**

Ali Jahansepas¹, Mohammad Aghazadeh², Mohammad Ahangarzadeh Rezaee³, Alka Hasani⁴, Yaeghob Sharifi⁵, Jalal Mardaneh⁶

1. Department of Clinical Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran and Research Center of Infectious Diseases and Tropical Medicine, Tabriz University of Medical Sciences, Tabriz, Iran
2. Department of Clinical Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran
3. Department of Clinical Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran
4. Department of Clinical Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran and Research Center of Infectious Diseases and Tropical Medicine, Tabriz University of Medical Sciences, Tabriz, Iran
5. Department of Clinical Microbiology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran
6. Department of Microbiology, School of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran

Background and Aim: Enterococci can occur in foods, especially in those of animal origin such as meat, fermented sausages and cheeses. The aim of this research was to study the incidence of potential virulence factors in *E. faecalis* and *E. faecium* isolates obtained from traditional cheeses in North-west of Iran.

Methods: The presence of the virulence factors *ace* and *cpd* genes was evaluated by multiplex PCR in 48 *E. faecalis* and *E. faecium* strains isolated from traditional cheese samples.

Results: Among all isolates, The prevalence of *ace* and *cpd* genes was 87.50% and 93.75%, respectively. *E. faecalis* displayed more virulence determinants than *E. faecium*.

Conclusion: The results show that *E. faecalis* and *E. faecium* Isolated from Traditional Cheeses can harbor potential virulence traits. Therefore, further studies are necessary in order to understand the possible role played by potential virulence factors of dairy isolates in relation to their ecological habitat as well as the transferability of these virulence traits among strains in the cheese environment.

Keywords: *E. faecalis*, *E. faecium*, Traditional cheese, Virulence factors, North-west, Iran.

**P477 - 388: DETECTION OF BACILLUS COAGULANS IN PROBIOTIC PRODUCTS BY PCR
MOLECULAR METHOD**

Farima Motazedi¹, Houshang Nikoopour², Mohammad Hassan Shahhosseiny³

1. Research Department of food Technology ,National Nutrition and food Technology Research Institute , Faculty of Nutrition Sciences and food Technology ,Shahid Beheshti University of Medical Sciences ,Tehran,Iran
2. Research Department of food Technology ,National Nutrition and food Technology Research Institute , Faculty of Nutrition Sciences and food Technology ,Shahid Beheshti University of Medical Sciences ,Tehran,Iran
3. Department of Microbiology- Shahr-e-Qods Branch-Islamic Azad University-Tehran/Iran. Iranian Gene Fanavar Institute (IGF), Tehran/Iran

Background and Aim: Probiotics are microorganisms that if administered in adequate amounts they will have beneficial effects on the host's health. *Bacillus coagulans* is a spore probiotic bacteria which sometimes mistakenly called *Lactobacillus sporogenes*. *B. Coagulans* is gram positive, optional aerobic and anaerobic, catalase positive, oxidase negative and endospore forming bacteria. The aim of this study is molecular rapid detection of *B. Coagulans* in probiotic products and various samples.

Methods: PCR test was optimized by using standard *B. Coagulans* strain. Limit of detection (LOD) and specificity of this test were investigated by using related species DNA. samples of probiotic products that own *B. Coagulans* were collected from Iran market and various methods of DNA extraction were optimized of these products

Results: Amplicon 400 bp was amplified with PCR and observed by electrophoresis method. In specificity test none of them were positive by DNA of intended organisms. Best DNA extraction is boiling in addition DNG-Plus methods. *B. coagulans* species were identified in all samples used by PCR method.

Conclusion: According to the results of this study *B. Coagulans* was found in all samples, It can be concluded that the PCR method is reliable and accurate to identify these products that is own *B. Coagulans* probiotics

Keywords: *Bacillus Coagulans*, PCR, Detection, probiotics

**P478 - 390: ENRICHMENT, ISOLATION AND IDENTIFICATION OF INDIGENOUS
SACCHAROMYCES CEREVISIAE STRAINS AND THEIR QUALIFICATION AS BAKER'S
YEAST**

Pouya Mohamadi Nasab¹, Shaghayegh Nasr², Seyed Kazem Bidoki³

1. Department of Biology, Faculty of Sciences, Payame Noor University, Tehran, Iran
2. Microorganisms Bank, Iranian Biological Resource Center (IBRC), ACECR, Tehran, Iran Department of Microbial Biotechnology, Faculty of Basic Sciences and Advanced Technologies in Biology, University of Science and Culture, Tehran, Iran
3. Department of Biology, Faculty of Sciences, Payame Noor University, Tehran, Iran

Background and Aim: The budding yeast, *Saccharomyces cerevisiae*, is able to convert sugar into ethanol and CO₂ via fermentation. They have been used for thousands of years for the production of foods, bread and fermented beverages. In this study, we used conventional and molecular techniques to isolate and propagate most useful yeast species in bakery industry.

Methods: Isolation of native strains of *S. cerevisiae* was carried out from different environmental and industrial samples including local fruits, surface of different plants, vinegar, date, sugar cane molasses and malt extract during enrichment procedure of using liquid medium containing 8% ethanol, low pH (3.8) and 7 days incubation at 30 °C. The isolates were identified through determination of morphological, sporulation and biochemical characteristics. Species-specific primers used for distinguishing between *S. cerevisiae* and other members of *Saccharomyces sensu stricto* complex. CO₂ Production rate was evaluated using S.J.A fermentograph and leavening properties of each strain was studied by preparing standard dough.

Results: A total of 10 strain of *S. cerevisiae* were isolated and verified using both traditional and molecular methods. Two strains named S8 and SSL1 have the maximum CO₂ production level of 310 ml/2hours in the standard dough and strains S4 and S1 were able to leaven the dough in similar level of commercial baker's yeast (240 ml/2hours).

Conclusion: The research represents an efficient strategy to select and identify native strains of *S. cerevisiae* with desirable ability to use as leavening agent in bakery products.

Keywords: baker's yeast, *Saccharomyces cerevisiae*, traditional and molecular identification, CO₂ production, leavening agent

**P479 - 412: ASSESSMENT OF FECAL COLIFORM CONTAMINATION OF THE
WASTEWATER TREATMENT PLANT (WWTP) IN INDUSTRIAL FACTORIES OF
HAMADAN WITH MOST PROBABLE NUMBER TEST, IRAN IN 2016**

Somayeh Noroozi¹, Khatereh. Khanlarzadeh², Mahdi. Hashemi ³, A.Mirmohammadi⁴

1. MSc of Microbiology, Department of Microbiology, Environment reliable Laboratory , Hamadan , Iran
2. Ph.D.Physical chemistry , Department of chemistry, Environment reliable Laboratory , Hamadan , Iran .
3. Ph .D. chemistry , Department of chemistry, Environment reliable Laboratory , Hamadan , Iran
4. B.Sc of Environment health. En

Background and Aim:Today , sewage is one of the agents environmental contamination .therefore ought to beginning those to muster then to liquidate. Wastewater reuse in the area studied is an important issue to reuse. Of the factors to consider wastewater treatment for reuse is microbial contamination of the total coliform and fecal coliform . In this study microbial quality of Hamadan WWTP effluent has been reviewed for reuse

Methods:In this descriptive cross-sectional study sampling from 15 Hamadan WWTP was performed to determine microbial contamination of the total coliform and fecal coliform of effluent .the presence of total coliform (TC) and fecal coliform(FC) by the(Most probable number) MPN test. Sampling and sample transportation and sample analysis were done according to water and wastewater standard methods.

Results:46 and 26% of the samples presented total and fecal coliforms more than 1.1×10^3 , respectively. That is not recommended for agricultural irrigation according to the relevant standard.

Conclusion:Disinfection and continuously monitoring of effluent and improvement of Hamadan WWTP is strongly recommended.

Keywords:Hamadan; Wastewater Treatment Plant; Wastewater Reuse; agriculture

**P480 - 504: ASSESSMENT OF AFLATOXIN IN CULTURED RICE OF KHOZESTAN
PROVINCE**

Razie Ranjbar¹

1. Department of biology , Faculty of science , University of shahid chamran, Ahvaz, Iran

Background and Aim: All mycotoxins are low-molecular-weight natural products that are produced as secondary metabolites by filamentous fungi. Aflatoxins are mycotoxins which are produced by *Aspergillus* mainly *Aspergillus flavus* and *Aspergillus parasiticus* and their presence in food is very important since they have virulent characteristics such as carcinogenic, mutagenic and teratogenic features. AFs B1, B2, G1 and G2 occur the most frequently and can be found in a wide range of food and feedstuffs, especially cereals (wheat, barley, sorghum, rice and so on), dried fruits (pistachios and nuts) and spices. International Agency for Research on Cancer (IARC) of the World Health Organization (WHO) accepted that aflatoxin should be classified as a Group 1 carcinogen.

Methods: In this study, we investigated the rate of aflatoxin B1, B2, G1 and G2 in rice grain collected from farms in three regions of the rice field in Khuzestan. The samples were grinded and separately packed. Then, they were assessed during three stages of extraction, purification, and determination. The diagnosis was done using fluorescence detector, The rate was determined comparing the under curve level of each sample and the standards

Results: No Aflatoxins B2, G1, G2 were found in the samples (rate=0.0). Aflatoxin B1 was found in some samples; however, the rates were below the standards of Iran (5 ppb) and Europe (2- 4 ppb).

Conclusion: Due to the presence and increase of fungi producing aflatoxin in optimal environmental conditions (high temperature and moisture); it needs to attend storage conditions, establish a continuous monitoring program, and manage the occurrence of these contaminants.

Keywords: Aflatoxin, carcinogen, *Aspergillus*, rice, HPLC, Khuzestan

**P481 - 519: ANTIMICROBIAL PROPERTIES OF AQUEOUS AND ALCOHOLIC EXTRACTS
OF RED AND WHITE SUMAC (RHUS CORIARIA) ON SOME FOOD BORN BACTERIA**

Neda Saghaoghli¹, Afshin Javadi²

1. M.SC student, Microbiology, cellular and Molecular biology Dept. Rabe Rashid University, Tbriz, Iran
2. Associate professor, Food hygiene Bio-Technology Research center Azad University, Tabriz, Iran

Background and Aim: Sumac, in addition to antibacterial properties is widely used as seasoning meat products. This study has been performed aiming to study the anti-microbial effects of ethanol, watery and ethereal extracts of white and red sumac on 10 species of bacteria from food.

Methods: In this empirical study the watery, ethanol and ethereal extracts of white and red sumac have been provided through soaking of them. Revival of Resazurin color has been used to determine the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) through microplate method.

Results: results show that the watery, ethanol and ethereal extracts have inhibitory effects on bacteria. There is insignificant difference between inhibitory effect of red and white sumac. The most sensitive bacteria to ethanol and watery extracts are *Bacillus cereus*, *Bacillus subtilis*, *Staphylococcus Aureus*, *Clostridium Perfringens*, *Yersinia Enterocolitica* and *Shigella flexneri* with a MIC of 0.78, and sensitive bacteria to ethereal extracts of sumac are *Bacillus subtilis*, *Bacillus cereus*, *Clostridium Perfringens*, *Staphylococcus Aureus*, *Yersinia Enterocolitica* and *Shigella flexneri* with a MIC of 1.56. The most resistant bacteria to extracts is *Listeria Monocytogenes* with MIC of 6.25. It is notable that the extracts of white and red sumac have more effects on positive gram bacteria than negative gram bacteria. Also results on MBC have been cross matched with MIC results in white and red sumac.

Conclusion: The results obtained from this study suggest that applying red and white sumac can have anti-microbial effects. However, more studies are required to prove these effects.

Keywords: extract, sumac, MIC, MBC

**P482 - 552: MOLECULAR DETECTION OF CAMPYLOBACTER JEJUNI IN RAW MILK BY
PCR**

Hengameh Hamrahi¹, Anousheh Sharifan², Mohammad Hassan Shahhosseiny³

1. Department of Food Science and Technology, Faculty of Agriculture, Science and Research Branch, Islamic azad University, Tehran, Iran
2. Department of Food Science and Technology, Faculty of Agriculture, Science and Research Branch, Islamic azad University, Tehran, Iran
3. Department of Microbiology- Shahr-e-Qods Branch-Islamic Azad University-Tehran/Iran. Iranian Gene Fanavar Institute (IGF), Tehran/Iran

Background and Aim: Sickness and food poisoning were caused during failure to comply with food hygiene and preparation. *Campylobacter jejuni* is one of the rare bacterial in poisoning that contaminated mainly through raw milk. The aim of this study is Molecular detection of *Campylobacter jejuni* in raw milk by rapid PCR method.

Methods: PCR test for the detection of *C. jejuni* optimized by using of *mapA* target gene. The limit of detection (LOD) and specificity of optimized test were evaluated. 50 samples of raw milk collected from farms of Tehran and DNA was extracted and optimized test was performed on 50 samples of raw milk

Results: Optimized PCR product with 589 bp amplicon for *Campylobacter jejuni* observed on agarose gel electrophoresis. The limit of detection (LOD) of test was determined 100 Copy / reaction. All 50 samples of raw milk were examined. None of them were positive

Conclusion: Fortunately all raw milk samples examined for the presence of *Campylobacter jejuni* were negative by using of accurate, rapid and sensitive PCR method. The PCR method can be faster to achieve the desired result.

Keywords: PCR, *Campylobacter jejuni*, Detection, raw milk.

**P483 - 553: PREVALENCE OF LIVER FLUKE INFECTIONS IN SLAUGHTERED ANIMALS
IN JAVANRUD CITY, KERMANSHAH PROVINCE, IRAN**

Naser Nazari¹, Shokofeh Osmani²

1. Dept of parasitology & mycology, Medical school, Kermanshah university of medical sciences, kermanshah, Iran
2. Dept of parasitology & mycology, Medical school, Kermanshah university of medical sciences, kermanshah, Iran

Background and Aim: Liver fluke (*Fasciola hepatica* and *Dicrocoelium dendriticum*) is a widespread parasite of ruminants which can have significant economic impact on cattle production. This retrospective study has been done to evaluate contamination rate of slaughtered animals with fasciolosis and dicrocoeliosis at Javanrud city.

Methods: This study is a kind of descriptive study in which we have studied the infection conditions of the slaughtered animals in Javanrud city during 2010-2014. Information was collected using a questionnaire and all of the data were analyzed using SPSS-21. Results

Results: According to collected results from 30076 sheeps, 3102 goats and also from 4102 cows, (0.93%), (1.95%) and (0.56%) have been infected to dicrocoeliosis and (2.81%), (3%) and (6.49%) have been infected to fasciolosis.

Conclusion: This study shows that goats are more infected than sheeps and cows to dicrocoeliosis (1.95%). Cows are more infected than goats and sheeps to fasciolosis (6.49%). This study is representative of the necessity of more attention about the prevention and controlling of this disease in animals in order to decrease economical damages and possibility of transferring of this disease from animal to man.

Keywords: *Fasciola hepatica*, *Dicrocoelium dendriticum*, Javanrud, Kermanshah

**P484 - 602: A STUDY ON THE MICROBIAL QUALITY AND ANTIBIOTIC RESISTANCE OF
KARUN RIVER**

Sotoudeh Besharati¹, Hossein Motamedi², Roya Zallaghi³

1. Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Iran
2. Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Iran
3. Department of Soil Science, Faculty of Agriculture, Shahid Chamran University of Ahvaz, Iran

Background and Aim: Karun River is the most important river in Iran that provide the major drinking water for Khuzestan province. More than 40% of industrial, municipal and agricultural sewage are directly entered into this river. So antibiotic resistance bacteria are found in this river as a consequent of healthcare facilities wastewater entrance to this river. The purpose of this study was to determine the microbial quality and also antibiotic resistance patterns of isolated bacteria from this ecosystem.

Methods: Water samples were prepared from a station along Karun river during spring season. These samples were cultured on nutritive and differential media and bacterial isolation and enumeration was done. The isolates were identified through biochemical tests. The antibiotic susceptibility pattern of isolates was investigated against erythromycin, sulfamethoxazole, cefoxitin, ciprofloxacin, gentamicin, penicillin and cephalixin.

Results: As a result of this study members of Enterobacteriaceae family including *E. coli* and *Klebsiella* sp. and also *Pseudomonas aeruginosa* were isolated. The antibiogram results revealed that all isolates were resistant to penicillin and some of them had multidrug resistance to erythromycin, cefoxitin, sulfamethoxazole and cephalixin.

Conclusion: According to these results it can be concluded that antibiotic resistance in bacterial isolates from Karun river is a serious health problem especially regarding MDR strains that can cause failure in bacterial infection treatment.

Keywords: water quality, Antibiotic resistance, Karun

P485 - 613: MICROBIAL ANALYSIS OF IRANIAN SAFFRON

Ameneh Elikaei¹, fatemeh Shafaei², Soude Hormozi³

1. Microbiology Department, Faculty of Biological Science, Alzahra university
2. Microbiology Department, Khak Azma Negin Reaserch Laboratory Tehran, Iran
3. Microbiology Department, Khak Azma Negin Reaserch Laboratory Tehran, Iran

Background and Aim: Saffron is one of the most famous plant that produce in Iran and usually for export to other countries. But the lack of hygiene in different parts of process causes contamination increasing in saffron so the quality goes wrong. The aim of this study was to determine the microbial quality of Iranian saffron

Methods: 45 Packages of 15 different brands (grade 1 or 2) from Iranian saffron select accidentally and provide from the markets in Tehran and Mashhad. And their microbial quality determine according to Iranian standard protocols. ESIRI 2198 for Enterococcus, ESIRI 2946 for E.coli, ESIRI 9432 for spores of sulfate reduction Clostridiums, ESIRI 10899-2 for molds and yeasts.

Results: The results show 2 different brands of grade 2 have E.coli contaminations and one of them has spores of sulfate reducing clostridiums more than acceptable range.

Conclusion: Microbial analysis indicated that there are some contaminations in Saffron products that reduce this product's quality than most countries standard and this causes many exporting problems of this valuable products. The most contamination belongs to fecal coliforms. So determine the critical points in Saffron production and using some antimicrobial technics such as irradiation and pasteurization can reduce the microbial contamination.

Keywords:: Microbial analysis, Saffron, Iran

**P486 - 671: MOLECULAR DETECTION OF SALMONELLA ENTERICA SEROTYPE
INFANTIS STRAINS USING MLST**

Hedieh Rahmati¹, Reza Ranjbar²

1. 1- Microbiology Department, Islamic Azad University, Ahar, Iran
2. 2- Molecular Biology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran

Background and Aim: Salmonella serotypes are potential pathogens for human as well as many animals. Human poisoning is usually caused due to the consumption of raw foods such as meat and eggs. In this study, the isolates of Salmonella enterica serotypes Infantis were investigated via the method of Multi Locus Sequence Typing. MLST is one of the new molecular techniques of bacterial typing which is based on the investigation of allelic differences in the sequence of housekeeping genes. This technique is performed on the clinical samples of possible infected patients with salmonella hospitalized in some hospitals in Tehran. The samples were transferred in the laboratories with bacteriological technique and in order to identify the Salmonella serotypes, biochemical and serotypical tests were used.

Methods: Seven housekeeping genes were subjected to the PCR. Amplified PCR products were sequenced subsequently. For each gene the various sequences were allelic and alleles in seven positions would create one allelic profile which obviously defined the sequence type in each isolate.

Results: Based on the allelic type the sequence type allocated to the isolates were kept in the assigned sites and were compared with the sequence types which had been formerly registered in the MLST program.

Conclusion: The results based on MLST revealed that the determined sequence of typing in this research is a derivation of ST31 and the dominant sequence type was that of number 32 or ST32. Also, 80% of the Salmonella strains had the sequence type of 32.

Keywords: Salmonella infantis, Housekeeping, MLST

**P487 - 691: MICROBIAL FUEL CELL TECHNOLOGY, AS A NEW TECHNOLOGY IN
WASTEWATER TREATMENT AND ENERGY PRODUCTION**

Behzad Kanani¹, Alireza Sadeghi²

1. Urmia University
2. Varamin – Pishva branch, Islamic Azad University

Background and Aim: Recently, considering the high cost of energy, the environmental problems, and the difficulties faced at wastewater treatment facilities in foodstuff factories, use of microbial fuel cell (MFC) technology has been introduced as a very novel and suitable solution for simultaneous wastewater treatment and bioelectricity generation.

Methods: MFC is a technology in which electrogenic bacteria use organic matter as substrate to generate an electric current by producing electrons and transferring them between two electrodes. Simultaneously with the consumption of the materials in wastewater, its COD decreases.

Results: The factor that influences the efficiency of MFC systems the most is the substrate provided for the microorganisms. Therefore, wastewater with sources of carbon, nitrogen, various acids, and of complicated complexes and compounds was studied. Moreover, wastewater from most food plants, synthetic wastewater, and some types of industrial wastewater was studied and compared. The selected source of wastewater and the ion exchange capacities of wastewater from various sources are among the most important factors in achieving high efficiency in MFC systems. Furthermore, process conditions such as flow mode, temperature, pH, organic loading rate (OLR), and hydraulic retention time of wastewater, microorganisms selected for the microbial cells, etc. play important roles in MFC systems.

Conclusion: Results showed wastewater from beer manufacturing plants and wastewater containing cellulose compounds such as that of chocolate and molasses industries had the highest efficiencies in MFC systems. Wastewater of distilleries, dairy industry and pig abattoirs also had high efficiencies. This point will be discussed in detail.

Keywords: wastewater, bioelectricity, substrate, MFC

**P488 - 757: BACTERIOGIN PRODUCTION IN CURTOBACTERIUM FLACCUMFACIENS
STRAINS ISOLATED FROM IRAN**

Amal Fazliarab¹, Seyed Mohsen Taghavi², Ebrahim Osdaghi³

1. Department of Plant Protection, College of Agriculture, Shiraz University, Shiraz, Iran
2. Department of Plant Protection, College of Agriculture, Shiraz University, Shiraz, Iran
3. Department of Plant Protection, College of Agriculture, Shiraz University, Shiraz, Iran

Background and Aim: Bacteriocin typing, based on the production of or sensitivity to a certain bacteriocins, is useful to differentiate actinomycete strains. *Curtobacterium flaccumfaciens*, is the causal agent of common bean wilt, a new emerging plant disease in Iran. The objective of this study was to evaluate different strains of *C. flaccumfaciens* for production of or sensitivity to bacteriocins

Methods: Three representative strains of *C. flaccumfaciens* including yellow (20Y), red (50R), and orange (80O) variants were used in this study. Producer strain was inoculated on the surface of YPGA medium in three corners of an imaginary triangle. After 2 days, suspension of the indicator strains was sprayed on the surface of the YPGA plates, containing previously inoculated bacteriocin producer isolates. The plates were incubated at 25–27 °C for 3 days and the growth inhibition was quantified by measuring inhibition zone radius (IZR)

Results: Results show that, there is a significant differences among isolates 20Y, 50R and 80O in terms of their capacity to produce bacteriocin. Neither strain 50R nor 80O was as effective at inducing IZR as strain 20Y. In particular, strain 80O had the lowest level of bacteriocin production among the tested bacterial strains

Conclusion: Bacteriocin sensitivity patterns are useful to differentiate most phytopathogenic actinomycete strains. In this study, *C. flaccumfaciens* strains were differentiated based on the bacteriocin production versus the tested indicator strains. Further study for this subject such as correlation between the bacteriocin production capacity and the aggressiveness in pathogenic bacteria is required

Keywords: *Curtobacterium flaccumfaciens*, Bacterial wilt, Bacteriocin

P489 - 766: THE EFFECTS OF NISIN ,STORAGE TIME AND TEMPERATURE ON TOXIN PRODUCTION OF STAPHYLOCOCCUS AUREUS BY ELIZA METHOD.

Zohreh Mashak¹, Amir Rerza Saadati²

1. Department of Food Hygiene, Karaj Branch, Islamic Azad University, Karaj, Iran
2. Shahid Beheshti Medical University ,Tehran,Iran

Background and Aim:Today; for prevention of food-borne diseases and increase food shelf life is used natural preservatives such as Nisin. Nisin is a polycyclic antibacterial peptide that produce by *Lactococcus lactis* . It inhibits growth of gram-positive bacteria and has approved by world organizations such as WHO and FAO as generally recognized as safe. Staphylococcal food poisoning is a gastrointestinal illness, that outbreaks of it occurs by consumption of contaminated foods with toxins of it .So, the effect of Nisin (0,0.25 ,0.50 and 0.75) $\mu\text{g/ml}$ on toxin production of *S.aureus* ATCC 6539 at 25 and 35 °C,during 21days, has studied.

Methods:Four concentrations of nisin (0,0.25 ,0.50 and 0.75) $\mu\text{g/ml}$, two storage temperature(25 ,35°C) on growth and toxin production of *S. aureus*(ATCC 6539;with 106 cfu/ml inoculum size) during 21 days with Eliza method was experimented. The statistical analysis was done by analysis of variance SPSS version:22.

Results:Results shows nisin (0.5 $\mu\text{g/ml}$) delayed toxin production to second day in storage temperature(25 and 35°C) and combination of nisin (0.755 $\mu\text{g/ml}$) and both mentioned temperatures inhibit toxin production of *S. aureus* during 21 days.

Conclusion:So, there is possibility of using of nisin as a substitute food preservative instead of other chemicals in food industry.

Keywords:Nisin, *Staphylococcus aureus*, storage temperature

P490 - 776: STUDY OF OXYTETRACYCLINE ANTIBIOTIC RESIDUES IN RAW, PASTEURIZED AND STERILIZED COW MILK IN DAMGHAN CITY AND EFFECT OF THERMAL PROCESS ON LEVEL ANTIBIOTIC RESIDUE BY ELISA METHOD

Rezvan allah Pouya¹, ali fazlara², abolghasem rahbari³, seyed jalal taghavi⁴, javad seyed momeni⁵

1. Young Researchers and Elite Club, Damghan Branch, Islamic Azad University, Damghan, Iran
2. Department of Food Hygiene, Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz, Iran
3. Department of Agriculture College of food science, Islamic Azad university Damghan branch Damgha,iran
4. Department of Agriculture College of food science, Islamic Azad university Damghan branch Damgha,iran
5. Department of Agriculture College of food science, Islamic Azad university Damghan branch Damgha,iran

Background and Aim: Milk consumption estimations as milk being one of the most important food products for humans show that about 94% of the consumed milk in the world is in form of processed milk or milk products (dairy products). According to international standards the existence of antibiotics in milk is intolerable because it can cause allergic reactions and digestive problems. The purpose of this article is to study the level of remaining antibiotics in raw milk, Pasteurized milk and sterilized milk samples supplied in Damghan city.

Methods: 66 samples of milk which include raw, pasteurized and sterilized milk were used in this study.

Results: The results showed that out of the 66 samples 32 of them (48.48%) contained antibiotics and 34 of them (51.52%) had no remainder of oxytetracycline antibiotic. Among the contaminated milk the highest density of antibiotic existed in raw milk samples in higher than 2.5 nanogram in ml domain with 3.812 ng/ml. The lowest ranged between 0.3 and 0.625 ng/ml. The difference between amounts of antibiotics in the raw, pasteurized and sterilized milk showed no significant meaning ($P > 0.05$). Raw milk samples after sterilization were studied again for antibiotic residues. Results showed a significant difference between antibiotic concentrations before and after sterilization ($p < 0.05$).

Conclusion: Anyhow the results of this study show and emphasis the need of monitoring raw, pasteurize and sterilized milk at all time to preserve the health of milk and dairy products consumed by humans.

Keywords: Antibiotic residue, ELISA, oxytetracycline, pasteurized milk, raw milk, sterilized milk

**P491 - 778: DETECTION OF PATHOGENICITY GENES IN CURTOBACTERIUM
FLACCUMFACIENS, THE CAUSAL AGENT OF BACTERIAL WILT OF DRY BEANS**

Amal Fazliarab¹, Seyed Mohsen Taghavi², Ebrahim Osdaghi³

1. Department of Plant Protection, College of Agriculture, Shiraz University, Shiraz, Iran
2. Department of Plant Protection, College of Agriculture, Shiraz University, Shiraz, Iran
3. Department of Plant Protection, College of Agriculture, Shiraz University, Shiraz, Iran

Background and Aim: Plant pathogenic Actinomycetes, mainly the members of *Clavibacter michiganensis* are depend on several genes actively for their pathogenicity on the plant host. The pathogen mechanism of Cf the other species of Microbacteriaceae, has not been identified. In this study, in order to detect number of genes involved in bacterial virulence of Cf, the bacterial genome sequence near the bacterium, such as *Clavibacter michiganensis* subsp. *sepedonicus* (Cms) and *Clavibacter michiganensis* subsp. *michiganensis* (Cmm) were used as template

Methods: Representative strains of Cf namely 20Y, 50R, 80O, Tom50, P-990 were used in this study. Primers chpC-F/chpC-R, chpG-F/chpG-R, PFC3/PFC5, pCRcel-593/pCRcel-1860 were also used to trace some of the genes involved in pathogenicity

Results: Detection of chpC gene was done with used chpC-F/chpC-R primer. A 1150-bp fragment was amplified only in the Tom50, at the beginning of the isolates was not able to reproduce the mentioned gene. Using the primer pair chpG-F/chpG-R, a fragment of 400 bp on all isolates except Tom50 isolate were amplified. Detection of CD celA gene was done with PCRcel-593/PCRcel-1860 primer. Using the primer pair, a fragment of 1260 bp on 80O and P-990 were amplified. The other isolates were lacking this gene. PFC3/PFC5 primer pair using for CBD of celA gene. This primer pair, was amplified, 551 bp fragment in 20Y and 80O isolates

Conclusion: The use of the mentioned primers was provided an initial data on the presence of pathogenicity genes in the new emerging plant pathogen Cf. However, future studies are needed to better understand the pathogenicity mechanisms of Cf

Keywords: Common bean, Plant diseases, Actinomycetes

**P492 - 786: ANTIMICROBIAL EFFECTS KEFIR FERMENTATION AT DIFFERENT TIMES
E.COLI**

Farideh Sarabandy¹, Farokh Rokhbakhsh Zamein², Nadia Kazemipour³

1. graduate student of Microbiology, Islamic Azad University Kerman, Kerman, Tehran.
2. Assistant Professor, Faculty member, Islamic Azad University Kerman, Department of Microbiology, Kerman, Tehran.
3. Assistant Professor, Faculty member, Islamic Azad University Kerman, Department of Microbiology, Kerman, Tehran.

Background and Aim: kefir products such as sour milk, which originated in the north Caucasus. The nature of antimicrobial and antifungal effects are controversial and have not been precisely determined. Antimicrobial activity of probiotic kefir and some are complex. Because kefir extracts the bactericidal effect of organic acids and hydrogen peroxide and bacteriocin and alcohol during the fermentation process by microorganisms in kefir are produced. This study aimed to determine the antimicrobial effects of kefir on standard E.coli bacteria (ATCC 25922) was used.

Methods: In this study, antimicrobial effect on the bacteria E.coli kefir Standard (ATCC 25922) using microbiological culture media and MIC determined using the method of dilution and well diffusion method and Kinetic death in the presence of extracts kefir is fermented in 4 different times 24, 48, 72 and 96 h at 37 ° C for invitro were studied.

Results: The effect of antimicrobial in disk diffusion method kefir and kefir wells showed that the extract at 37 ° C with 96 hours of fermentation and concentration of 300-250 mg per ml most effective inhibition (MIC) on standard E.coli (ATCC 25922) was obtained.

Conclusion: kefir extracts inhibitory effects on E.coli bacteria is antibiotic resistance.

Keywords: antibacterial, buttermilk, kefir, fermented, E.coli.

P493 - 787: KEFIR ANTIMICROBIAL EFFECTS ON SHIGELLA FLEXNERI

Farideh Sarabandy¹, Farokh Rokhbakhsh Zamein², Nadia Kazemipour³

1. graduate student of Microbiology, Islamic Azad University Kerman, Kerman, Tehran.
2. Assistant Professor, Faculty member, Islamic Azad University Kerman, Department of Microbiology, Kerman, Tehran.
3. Assistant Professor, Faculty member, Islamic Azad University Kerman, Department of Microbiology, Kerman, Tehran.

Background and Aim: of milk kefir and kefir grains are fermented beverage that originated in the north Caucasus. Kefir grains are insoluble in water and common solvents, but are dipped in milk. Big, white and become swollen. Under the dual-acid fermentation alcohol create. In general, kefir grains with lactic acid bacteria such as streptococcus, lactobacilli mesophilic lactic acid, acetic acid bacteria and yeasts Fermentation of lactose and lactose Non-fermentation of lactose that therapeutic effects have been mentioned. This study was conducted to evaluate the antibacterial properties of kefir on Shyglafknsry.

Methods: In this study, the effect of kefir on standard Shigella flexneri bacteria (ATCC 12022) were evaluated. Antibacterial Activity of kefir extracts in 4 fermentation time 24, 48, 72 and 96 h at 37 ° C, with methods for invitro disc plate and in the pit and Kinetic death in vitro.

Results: In this study, antimicrobial effect of kefir at 37 ° C with 96 hours of fermentation and concentration of 250 mg per ml of the standard Shigella flexneri (ATCC 12022) is.

Conclusion: Dough has antimicrobial effect on some pathogenic bacteria such is Shigella flexneri.

Keywords: kefir, antibacterial, Shigella flexneri.

**P494 - 794: SPECIES IDENTIFICATION OF STAPHYLOCOCCI ISOLATED FROM
PASTRIES USING PARTIAL 16S RRNA SEQUENCING AND CONVENTIONAL METHODS**

Laleh Hoveyda¹, Soodabeh Rostami²

1. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran
2. Infectious Diseases and Tropical Medicine Research Center, Isfahan University of Medical Sciences, Isfahan, Iran

Background and Aim: Bacteria present in food could cause foodborne disease. Pastries are among the food items that can be potentially cause food poisoning and staphylococcal food poisoning is one of the most common food-borne diseases worldwide. The aim of this study was to isolation and identification of *Staphylococcus* spp. from pastries using partial 16S rRNA sequencing and conventional methods in Isfahan, Iran.

Methods: In the current cross sectional study 55 pastry samples were collected from different confectioneries located in various geographic regions of Isfahan from August 2015 to March 2016. The samples were processed within 12h of purchase in the laboratory of Infectious diseases and tropical medicine research center. The samples were cultured on Giolitti- Cantoni broth and Baird Parker agar media. Suspicious colonies of each sample were chosen and identified using conventional based on morphological and physiological characteristics of *Staphylococci* spp. Partial 16S rRNA sequencing was used for species identification of Coagulase-positive and Coagulase-negative *Staphylococci*.

Results: We detected *Staphylococci* spp. in 42 different samples. These identified isolates were belonged to 13 different species and included: *S. vitulinus*, *S. warneri*, *S. pasteurii*, *S. succinus*, *S. aureus*, *S. sciuri*, *S. saprophyticus*, *S. lugdunensis*, *S. epidermidis*, *S. gallinarum*, *S. carnosus*, *S. pulvereri*, *S. vitulinus*. About 10% of species were assessed positive for coagulase test.

Conclusion: In conclusion, 16S rRNA sequencing was an objective and accurate method for proper identification of *Staphylococci* species. Our results indicated that pastries could be considered an important route for *Staphylococcal* food poisoning and transmission of food born diseases.

Keywords: *Staphylococcus*, 16S ribosomal RNA, Foodborne diseases

P495 - 908: SALMONELLA AND FOOD HYGIENE A REVIEW

Salia Amini pooya¹, Reza shirazinia², abolfazl panahi mishkar³, said shahriari⁴

1. Student of zabol University of Medical Sciences, Zabol, Iran
2. student of Veterinary Medicine - Department of Basic Sciences, Faculty of Veterinary Medicine, University zabol,Iran
3. human ecology MSc student,kerman university of medical science,kerman,iran
4. veterinary medicine expert,Department of Basic Sciences, Faculty of Veterinary Medicine, University zabol,Iran,

Background and Aim:Salmonella is a desiasse caused by wide variety of salmonella species The chain of infection for foodborne salmonella goes from fecal material(either from humans or animals, particularly chickens) to water or food which, when consumed, leads to infection. Alternatively, it goes from faecal material to hands and then to food (during food preparation), which again leads to infection.the aim is to evaluation the salmonella and it's linkage with food hygiene.

Methods:This article is done based on information published in valid books,and internal and external journals

Results:one of important pathogens from this family is salmonella interitidis the most important source of infection is food and water and its way to make the infection is digestive system.Salmonella is a disease with universal prevalence and is an important food born disease the meat can be infected with this pathogen in the slaughter process and can be infected in the chain of transport to home or meat shop and therefore cause food poisoning.the best way to avoid this poisoning is to make the herds clean of this pathogen

Conclusion:the herds should be bought from valid sources and three consecutive tests should be done to make sure the cattle is clean about salmonella.Controlling of rodents is so important. Use antiseptic ways to make the herd places aseptic. The intensity of population should be in minimum valid range.Vaccination in cow,pig and poultry herds should be done.Stressing factors should be reduced as possible and the source of infection should be diagnosed and treated soon as possible.

Keywords:Salmonella;food hygiene;herds

**P496 - 965: EVALUATION OF ANTIBACTERIAL EFFECTS OF AQUEOUS EXTRACT OF
BARBERRY FRUITS ON METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS**

Mina Hassani¹, Abbas Yadegar ², Bahram Hassani³

1. Department of Food Science and Microbiology, Islamic Azad University, Quchan Branch, Quchan, Iran
2. Foodborne and Waterborne Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. Department of Food Science and Technology, Ferdowsi University of Mashhad, Khorasan, Iran.

Background and Aim:Antimicrobial properties of herbal extracts have been investigated through several studies which purpose them as alternative medicines to overcome the microbial drug resistance problem worldwide. In this study, the inhibitory effects of aqueous extract of barberry fruits on methicillin-resistant *Staphylococcus aureus* (MRSA) was investigated.

Methods:200 grams of barberry fruits were squeezed and added to a flask containing 500 mL of distilled water, and was placed in a water bath at 60±1°C for 2 h. Then the barberry extract was filtered and concentrated at 45°C using a vacuum rotary evaporator. Two-fold serial dilutions of the extracts were prepared in tubes with Mueller Hinton Broth as diluents. The antibacterial properties of the extract were assessed by Broth Dilution Method and Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC) of them were also determined.

Results:The aqueous extract of barberry fruits was able to inhibit and kill the MRSA strains at 6/25 mg/ml and 12/50 mg/ml concentrations as MIC and MBC values, respectively. The results of this study showed that the aqueous extract of barberry fruits has antibacterial activity against MRSA bacteria.

Conclusion:The present study supports the antibacterial properties of aqueous extract of barberry fruits and suggests them as an effective antimicrobial agent against drug resistant MRSA and also as antibacterial additives. However, a large-scale clinical trial is required to assess its therapeutic efficacy in vivo if they are to be used for medicinal purposes.

Keywords:Barberries vulgaris, Methicillin-Resistant *Staphylococcus aureus*, Aqueous extract, Antibacterial effects

P497 - 1028: FREQUENCY OF ASPERGILLUS FUMIGATUS , ASPERGILLUS FLAVUS AND AFLATOXIN LEVEL IN HONEYBEE AND PRODUCED HONEY IN SAQQUEZ AND BANEH, WEST OF IRAN IN 2014 -2015.

Hojjat Alizadeh mamaghani¹, Khalil Azizian², Foad Saedi³, Soda Amini⁴

1. Rooyana veterinary laboratory, Saqqez, Kurdistan, Iran
2. Medical Bacteriology, Tabriz University Faculty Of Medical Science
3. Islamic Azad University, Mahabad
4. veterinary laboratory Center, Saqqez, Kurdistan, Iran

Background and Aim: Identification and preventing of fungus growth in Honeybee is so important to increase of honey quality and public health. The hives have sufficient condition for *A. Aspergillus fumigatus* and *A. flavus* grows. These fungi are causing of decrease of honey production and also produced aflatoxin from these fungi is danger for human health. Saqqez and Baneh cities are major sources of honey production in Kurdistan province and west of Iran. Thus in this study *Aspergillus* and aflatoxin contamination were evaluated.

Methods: Samples are collected from 750 hives from 150 apiaries (75 apiaries from Saqqez and 75 apiaries from Baneh). Then samples were cultured on Sabouraud dextrose agar supplemented by chloramphenicol. Level of aflatoxin was evaluated by ELISA kit (neogen).

Results: 750 hives tested and 124 hives (16.53%) for *A. fumigatus* and *A. flavus* were positive. *A. fumigatus* (67.7%) was major isolate and followed by *A. flavus* (32.3%) that these samples were subclinical. Versus only 8 samples (1.06%) were clinically and Results of aflatoxin ELISA test showed that these eight samples have aflatoxin average concentration (45.2 µg/kg) more than maximum of acceptable range (4 µg/kg) in Europe.

Conclusion: Results of this study showed that only about one percent of samples were contaminated by aflatoxin and *aspergillus* contaminations were not so much. But with insurant support, contaminated hives have to identified and deleted. Also good processing and packaging of honey is very important to promotion of this product for exports and even introduce to world markets.

Keywords: *Aspergillus*, aflatoxin, honey, Saqqez, Iran

**P498 - 1044: EVALUATION OF BACTERIAL QUALITY AND ANTIBIOTIC RESISTANCE
PROFILES OF ISOLATED BACTERIAL FROM AVICULTURES WELL WATER IN SAQQEZ
CITY WEST OF IRAN IN 2014-2015**

Hojjat Alizadeh mamaghani¹, Khalil Azizian², Foad Saedi³, Mohamad hadi Kiani⁴, Soda Amini⁵

1. Rooyana veterinary laboratory, Saqqez, Kurdistan, Iran
2. Medical Bacteriology, Tabriz University Faculty Of Medical Science
3. Islamic Azad University, Mahabad
4. 4Young Researchers and Elites Club, Science and Research Branch, Islamic Azad University, Tehran, Iran
5. 5veterinary laboratory Center, Saqqez, Kurdistan, Iran

Background and Aim: Water is one of the major sources of microbial infection. Available microbial pathogens in water caused increase in human infection, decrease of meat quality and production output. Thus evaluation of water contamination in aviculture is so important. In this study contamination of avicultures well waters in Saqqez city that were activated evaluated about salmonella spp, streptococcus, MRSA, pseudomonas and E. coli O157 H7.

Methods: This is analytical study. In 2014-2015, we collected 200 water samples from 100 avicultures. Samples were transferred to Rooyana veterinary lab in sterile bottle and 10 ml thiosulfate sodium. For colony count, coliforms, TBC and MPN test performed respectively. All of tested bacteria cultured on specific culture medium and confirmed with phenotypic tests. In last AST performed with Padtenteb disc by diffusion method (According to CLSI Antibiotic resistance).

Results: From 200 samples tested in current study total bacteria were 184 that isolated and confirmed. All of S. aureus were resistance to penicillin, cloxaciline, amoxicillin, ampicillin, cephaprazone, cephoitin, tetracycline, oxytetracycline, chlortetracycline, doxycycline and thicoplanine. Only 15% of these isolates were susceptible to oxacilline. All of P. aureoginosa were resistant to colistin. Resistance to tetracycline, oxytetracycline, chlortetracycline, deoxycycline, amoxicyciline, and erythromycin in E. coli, salmonella were 100%.

Conclusion: According to prevalence and antibiotic resistance of isolated pathogen from aviculture water, identification of contamination sources, use of perfect and enough disinfectants and antibiotics in this stage of food chain are so necessary and can help to increase public health.

Keywords: Water, Microbial pollution, Aviculture well, Saqqez

**P499 - 1071: BACTERIAL CONTAMINATION OF SHAHRCHAY RIVERS IN URMIA WITH
THE INDICATOR OF E.COLI AND COLIFORMS**

Shabnam Jafari¹, Mahmoud Reza Zad²

1. faculty of science, Biolog department , Faculty of Science, islamic AZad university, urmia Branch, Iran
2. Faculty of Agricultural Sciences, microbiology department , islamic Azad university, urmia Branch, Iran

Background and Aim: Limited water resources and increase the potential for water pollution caused by human activities has led to types of contaminants to water quality control schemes been intensifying. On the other hand, the direct and indirect social and economic consequences resulting from the consumption of the contaminated water has doubled importance of this control. Fecal contamination of water and basic water sanitation is one of the most important problems that to prevent microbial gastrointestinal diseases and epidemic prevention, it is important to detect and should identify

Methods: months from Winter 93 to August 94 each month from 5 stations ranging from its origins to refinery was conducted. Water samples of microbial contamination, according to the indicators (total coliforms and E. coli) studied and analyzed with MPN method

Results: The results indicated that the bacteria contamination index in stations S1 (after the village of BARDEHSOOR) and S4 (entrance to the village Band) due to the influence of agricultural land, especially land around the river and the entrance of the village promenade clause increases in Band And microbial contamination of the Shahrchay river in June is more than in other months at all stations.

Conclusion: According to the results of this study, the contamination was higher in stations near the village but the quality of river water for agriculture and other users of public is in good condition and far a way from the critical situation.

Keywords:: Shahrchay River, microbial contamination, E. coli, coliforms

**P500 - 1137: SURVEY ON MICROBIAL POLLUTION OF SOY YOGURT IN IRAN FOR
DETERMINATION OF MICROBIOLOGICAL CHARACTERISTICS IN NATIONAL
STANDARD**

Maryam Ghobadi dana¹, Hoda nazarlotfi², Sevda Ameli³

1. microbiology research group standard institute of iran
2. Azad univercity of Arak
3. microbiology research group standard institute of iran

Background and Aim: Today, in the most countries, soy products are consumed as a source of protein. Soy yoghurt is a good alternative for consumers who do not have the ability to digest lactose. Determination of soy yoghurt characteristics in national standard is very important. The aim of this study was to survey on microbial pollution of soya yoghurt in Iran to determine the microbiological characteristics of soya yoghurt in national standard.

Methods: Several microbiological examinations were done on samples collected from market. The total counting of mesophilic microorganisms were done according to Iranian National standard (5272). The enumeration of the spore of clostridium were done according to Iranian National standard (9432). Detection of salmonella was done according to Iranian National standard (1810). Detection of Bacillus cereus was done according to Iranian National standard (2324). Enumeration of mold and yeast were done according to Iranian National standard (10899). Enumeration of coliform was done according to Iranian National standard (5486). Detection of E.Coli was done according to Iranian National standard (5234). Detection of staph.aureus was done according to Iranian National standard (6806).

Results: The results showed that, spore of clostridium, salmonella and staph. aureus were reported negative in all cases, 12% of samples have coliform and Escherichia coli pollution and 8% of samples have Bacillus cereus pollution. The enumeration of molds was $10^{-1.6} \times 10^6$ cfu/gr and total count of microorganisms was $2.8 \times 10^4 - 4 \times 10^8$ cfu/gr.

Conclusion: In study important to determination and control of critical control point of production line and determination of microbial characteristics in national standard for soy yogurt.

Keywords: soy yoghurt, microbiology, specification

**P501 - 1138: SURVEY ON MICROBIAL POLLUTION OF SOY DOUGH IN IRAN FOR
DETERMINATION OF MICROBIOLOGICAL CHARACTERISTICS IN NATIONAL
STANDARD**

Maryam Ghobadi dana¹, SevdA Ameli ², Hoda nazarlotfi³

1. microbiology research group standard institute of iran
2. microbiology research group standard institute of iran
3. Azad univercity of Arak

Background and Aim:Today, in the most countries, soy products are consumed as a source of protein .Soy doogh is a good alternative for consumers who do not have the ability to digest lactose. Determination of soy doogh characteristics in national standard is very important. The aim of this study was to survey on microbial pollution of soy doogh in Iran to determine the microbiological characteristics of soy doogh in national standard.

Methods:Several microbiological examinations were done on samples collected from market. The total counting of mesophilic microorganisms were done according to Iranian National standard (5272) The enumeration of the spore of clostridium were done according to Iranian National standard (9432) Detection of salmonella was done according to Iranian National standard (1810). Detection of Bacillus cereus was done according to Iranian National standard (2324). Enumeration of mold and yeast were done according to Iranian National standard (10899). Enumeration of coliform was done according to Iranian National standard(5486) Detection of E.Coli was done according to Iranian National standard (5234) Detection of staph.aureus (6806)

Results:The results showed that , salmonella and staph. aureus were reported negative in all cases, 8% of samples have coliform and Escherichia coli pollution. Bacillus cereus and spore of clostridium have less than 10 pollution in all cases. The enumeration of molds was $10-1.6 \times 10^6$ cfu/gr and total count of microorganisms was $2.8 \times 10^4 - 4 \times 10^8$ cfu/gr

Conclusion:In study important to determination and control of critical control point of production line and determination of microbial characteristics in national standard for soy doogh.

Keywords:soy doogh, microbiology,specification

**P502 - 1153: THE RELATIONSHIP BETWEEN MASTITIS FREQUENCY WITH TOTAL
COUNT ,SOMATIC CELL COUNT AND MILK PRODUCTION CITY ANDIMESHK**

Ali Khataminia¹, fatemeh boron², mohammad nemati³

1. PhD student Clinical Pathology of ahvaz shahid chamran university
2. PhD of Microbiology Ahvaz Jundishapour University of medical sciences
3. PhD student pharmacology Ahvaz Jundishapour University of medical sciences

Background and Aim: Milk in the diet of the importance of each household and Because of compounds such as protein, fat, lactose and minerals are essential for human life. But in the event of failure to comply with the hygienic rules of milk production, not just the body does not compensate for food shortages, it may even be irreparable damages and injuries

Methods: In this study for one year in 1392, based on information obtained from the veterinary clinic in the city of mastitis cases in the city were collected monthly. Moreover, the volume of milk production in different months was calculated through milk collection centers. At the same time milk production and SCC samples and the total count was measured

Results: According the survey of the incidence of mastitis was calculated as 3.5 percent. (12000 numbers of cows city and 366 cases of mastitis), the ratio of cases of mastitis in spring, 26% (96 cases), in the summer of 20 percent (76 cases), in the fall of 22 per cent (79) and in winter 32 percent (115 cases) were. The results showed that the highest incidence of mastitis in winter (January) and the lowest incidence occurred in the summer (August) was observed

Conclusion: The amount of milk produced and SCC , TC, were collected and analyzed. Spearman correlation coefficient showed the correlation between mastitis, Total Count, SCC, a direct connection is significant. (Spearman correlation coefficient 49/0 rs = and 05 / 0p <). Also a significant correlation between the percentage of cases of mastitis city milk production volume was observed

Keywords: mastitis - Total count ,Somatic cell count and Milk production

P503 - 1168: PREVALENCE RATE AND ANTIBIOTIC RESISTANT PATTERN OF E.COLI O157 ISOLATES FROM CONSUMED MINCED MEAT OF URMIA CITY (IRAN) DURING 2015

Mahmoud Abdollah pori hosseini¹, Seyed Mehdi Razavirohani²

1. Faculty of Sciences, Biology Department, Islamic Azad University, Urmia Branch, Urmia, Iran
2. Faculty of Veterinary, Food Hygiene and Quality Control Department, , Islamic Azad University, Urmia Branch, Urmia, Iran

Background and Aim: E.coli O157 is a member of enterohaemorrhagic E.coli(EHEC) group and causes important and dangerous diseases in humans such as hemolytic uremic syndrome and hemorrhagic colitis. The main source of transmission of E.coli O157 to meat is cow's feces, so sanitation in meat production and storage is very important. The contaminated minced meat may be used to manufacture hamburgers and expose consumers at risk.

Methods: In this study 100 samples of minced meat were taken randomly from dairy stores meat of Urmia city in 2015 year. First, samples were enriched in tryptic soy broth containing novobiocin. Enriched samples were streaked on Sorbitol-MacConkey agar. Colorless colonies in SMAC agar were selected for further testing. Streak on EMB agar, culture in lactose broth containing Durham tube and performance of IMViC tests were used for identification of E.coli. Finally, to confirm of E.coli O157, culture on O157 CHROMagar and agglutination with O157 specific antiserum was used. Antibigram was performed on isolates using disk diffusion method with some antibiotics.

Results: Out of 100 samples studied, E.coli O157 was isolated from 7 samples (7%). Isolates were susceptible to gentamicin, sulfamethoxazole-trimethoprim, chloramphenicol, ciprofloxacin antibiotics. In the case of ampicillin, 2 isolates sensitive (28/6%), 3 isolates intermediate (42/9%) and 2 isolates resistant (28/6 %) were. In the case of ceftriaxone, 5 isolates sensitive (71/4%) and 2 isolates intermediate (28/6%) were. In the case of tetracycline, 3 isolates sensitive (42/9%), 3 isolates intermediate (42/9%) and 1 isolate resistant (14/3%) were.

Conclusion: Considering sensitivity of isolates to Isolates were susceptible to gentamicin, sulfamethoxazole-trimethoprim, chloramphenicol, ciprofloxacin antibiotics, it is recommended the antibiotics used for clinical cases.

Keywords: consumed minced meat, E. coli O157, antibiogram, Urmia city (Iran)

P504 - 1172: MOLECULAR IDENTIFICATION VIRULENCE GENES (STX1, STX2,FLICH7, EAEA, HLY)OF E. COLI STEC PATHOVARS ISOLATED FROM UNSTERILE MILK BY MULTIPLEX PCR

Reyhaneh Aghamir mojtahed¹, gholamali moradli²

1. 1- Department of Microbiology, Faculty of Basic Sciences, Saveh Branch ,Islamic Azad University, Saveh, IR Iran.
2. Department of Microbiology, Assistant Professor, Medical faculty member, Saveh Branch ,Islamic Azad University, Saveh, IR Iran.

Background and Aim:E.-coli normal Flora of the intestinal tract of animals and humans. Most strain E.-coli can cause a variety of diseases of the intestinal and extraintestinal. (EHEC) Enterohemorrhagic Escherichia coli O157: H7 is an important verotoxin associated with Food and water borne infections. E. coli O157: H7can cause a syndrome of multiple diseases,syndrome,and thrombotic,thrombocytopenic, purpura in people. Disease caused by Enterohemorrhagic Escherichia coli grown is developed as is the third cause of diarrhea. (STEC) shiga toxin E. coli- associated strains of (EHEC) strains as the most common cause of diarrhea in developing countries will be introduced.

Methods:after collecting samples of human, biochemical and microbiological tests were conducted to identify the strains E. coli. In this study, using the following Multiplex PCR to detect molecular pathotypes EHEC possible.

Results:. A total of 60 samples, 3 samples (5 %) Gene flich7, 3 samples (5 %)Gene Stx2. The results obtained in this study, According to studies of other researchers around the world, it seems is a difference in the frequency of genes .one of these differences may be due the sample source, another difference that exists and can be geographical Location of samples

Conclusion:Most studies of pathotypes E. coli using Multiplex PCR followed over the world, have been including America and Europe. Even some of the results from one country to another, but there is very little difference between the amounts of research is done. in many studies to identify pathotypes E.-coli using Multiplex PCR has been realized that this could be the reason for the difference in results .

Keywords:: Escherichia coli, virulence Genes, Enterohemorrhagic Escherichia coli

**P505 - 1247: ANTIBACTERIAL ACTIVITY AND INHIBITORY EFFECT OF ZINC OXIDE
NANOPARTICLE ON ESCHERICHIA COLI BIOFILM FORMATION**

Maryam Abbasvali¹, Azizallah Ebrahimi ², Fatemeh shahriyari³

1. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
2. Department of Pathobiology, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
3. Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran

Background and Aim: Biofilm is a community of microbial cells attached to the surface. The presence of biofilms in food processing environments is a potential source of contamination that may lead to food spoilage and disease transmission. There is increased demand for improved antibacterial agents due to the growing concern regarding multidrug-resistant bacterial strains and biofilm associated infections. This study was conducted to evaluate the antibacterial activity of zinc oxide nanoparticles against an important foodborne pathogen, *Escherichia coli* (ATCC 35218) and its biofilm formation.

Methods: Microtitre plate-based antibacterial assay incorporating resazurin as an indicator of cell growth was used to determine the minimum inhibitory concentration (MIC) value of ZnO NPs against *E. coli*. Biofilm-formation assay was performed by using microtiter plates. The MIC was determined using different concentrations of ZnO NPs including 16, 8, 4, 2, 1, 0.5, 0.25, 0.125 and 0.0625 mg/ml. Different concentrations (0.0312- 8 mg/ml) of ZnO NPs were used to inhibit the *E. coli* biofilm formation.

Results: The MIC value of ZnO NPs against *E. coli* was 1 mg/ml. The antibacterial activity of ZnO NPs increased with increasing nanoparticle concentration. The percentage of biofilm formation inhibition was calculated. ZnO NPs inhibited *E. coli* biofilm production at 1×MIC (92.98%), 2×MIC (94.25%), 4×MIC (97.55%) and 8×MIC (98.10%) also showed inhibitory effect on biofilm formation at sub-MIC concentrations (1/2 MIC: 82.75%; 1/4 MIC: 40.41%; 1/8 MIC: 15.73% and 1/16 MIC: 5.17%).

Conclusion: These results suggest that ZnO NPs could potentially be used as an effective antibacterial agent to control the growth of *E. coli* and inhibit its biofilm formation.

Keywords: Antibacterial, biofilm, *Escherichia coli*, zinc oxide nanoparticle

**P506 - 1249: THE STUDY OF EFFECT AEROMONAS HYDROPHILA ON SWIM FIN
CORRSION AND NECROSIS IN CAPOETA DAMASCINA**

Laleh Yazdanpanah¹

1. Laleh Yazdanpanah

Background and Aim: Corssion and necrosis are caused by bacteria which are present in the water. Usually, when fish are subjected to temperature oscilliations then they get sick thus it is caused to be weakening their immune system and become susceptible to microbial infections. There are several Aeromonas species which can infect fish in aquaculture industries.

Methods: Some Capoeta damascina captured from rivers in Kerman province and were transferred to laboratory immediately. Then placed at several aquariums in rang variation of temperatures (0- 10, 10 - 20, 20 - 30 and to over 30 centigrade degree) respectively and 1 group control. After several days, infectious clinical signs were observed such as fin corrosions and the other signs.

Results: The results revealed that 80 percent of fish got sick at 20-30oC and above . Aeromonas hydrophila bacteria were isolated from their kidney and fin's erosions. The fish which were at 10-20oC and below 10oC were diseased 40% and 1%, respectively .In this experiment, total data were analyzed by using SPSS software.

Conclusion: Treatment differences were identifiedif disease susceptibility is attributed to poor water quality, then correction of the basic husbandry problem could result in a resolution of the bacterial disease outbreak. In addition, if the affected system is an indoor or closed system, good sanitation is essential to decrease the number of bacteria in the system.

Keywords: Aeromonas hydrophila , Corrsion and Necrosis- Capoeta damascina - Temperature Oscilliations

**P507 - 1250: ANTIMICROBIAL AND ANTI-BIOFILM FORMATION ACTIVITIES OF ZINC
OXIDE NANOPARTICLES ON STAPHYLOCOCCUS AUREUS**

Maryam Abbasvali¹, Azizallah Ebrahimi², Fatemeh shahriyari³

1. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
2. Department of Pathobiology, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
3. Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran

Background and Aim: The ability of bacteria to adhere to food-contact surfaces and to form biofilm has major implications in food industry where biofilms create a persistent source of contamination. Bacterial infections are still a major cause of morbidity and mortality. The growing concern regarding multidrug-resistant bacterial strains and biofilm-associated infections calls for the development of additional bactericidal means. In this study antimicrobial and anti-biofilm formation activities of zinc oxide nanoparticles were evaluated in vitro against an important foodborne pathogen, staphylococcus aureus (ATCC 6538).

Methods: Microtitre plate-based antibacterial assay incorporating resazurin as an indicator of cell growth was used to determine the minimum inhibitory concentration (MIC) value of ZnO-NPs against *S. aureus*. Biofilm-formation assay performed on the surfaces of polystyrene plates. Different concentrations (0.0312- 8 mg/ml) of ZnO NPs were used to inhibit the *S. aureus* biofilm formation.

Results: The MIC value for *S. aureus* was 0.5 mg/ml. ZnO NPs showed increasing inhibitory effects on the growth of *S. aureus* as the concentrations of ZnO NPs increased. The percentage of biofilm formation inhibition was calculated. ZnO NPs inhibited *S. aureus* biofilm production at 1×MIC (85.69%), 2×MIC (93.19%), 4×MIC (97.51%) and 8×MIC (98.15%) also showed inhibitory effect on biofilm formation at sub-MIC concentrations (1/2 MIC: 77.30%; 1/4 MIC: 68.59%; 1/8 MIC: 48.22%; 1/16 MIC: 20.32%).

Conclusion: This study revealed the efficacy of ZnO-NPs as a potential antibacterial agent for controlling the growth of *S. aureus* in both planktonic and biofilm form.

Keywords: Antimicrobial, Anti-biofilm, Staphylococcus aureus, zinc oxide nanoparticles

Fungi

P508 - 9: THE EPIDEMIOLOGY OF CANDIDA SPECIES RELATED TO VULVOVAGINAL CANDIDIASIS IN NEYSHABUR DURING 2013-2015

Mohammad Salehi¹, Abdolmajid Ghasemian², Seyyed Khalil Shokouhi Mostafavi³

1. 1Medical Diagnostic Laboratory of Neyshabour, Center of Medical, Pathological and Genetic 1Diagnostic Services, Iranian Academic Center for Education, Culture and Research (ACECR), Mashhad Branch, Mashhad, Iran
2. Department of Microbiology, Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran
3. 2Department of Microbiology, Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran

Background and Aim: *Candida* spp. as members of a genus, are polyphyletic group, containing closely related fungal species, such as *Candida albicans* (*C. albicans*), *C. tropicalis* and *C. parapsilosis*, and in addition, distantly related organisms of *C. glabrata* and *C. krusei*. The aim of this study was isolation of various *Candida* species from vulvovaginitis in Neyshabur, Northeast Iran from 2013 to 2015.

Methods: This descriptive-analytical survey was performed to identify *Candida* spp. causing vulvovaginitis during 2013-2015 in Neyshabur district Northeast Iran. A total of 451 vaginal samples were collected and 10 µl of each sample was cultured on CHROM agar plates and incubated at 37°C for 24-48h aerobically. *Candida* species were identified based on colony morphology, germ tube production and micro-morphology on corn meal agar including 1% Tween 80.

Results: The mean age was 34.7 ± 16.3 . *C. albicans* was the predominant species isolated. Moreover, age groups of 21-30 and 0-1 years were the most and the lowest infected individuals. Moreover, *Candida* spp had significantly higher rate in female than male patients. It was demonstrated that the prevalence of *C. albicans* was significantly declined from 2013-2014 to 2015. Furthermore, the prevalence of *C. tropicalis* was significantly higher in 2014 compared to 2013 and 2015. Moreover, all the species had the colony count of $>10^3$.

Conclusion: In this study, *C. albicans* was the most common species isolated from vulvovaginitis. The prevalence of *Candida* spp was significantly declined from 2013 to 2015. Moreover, the *Candida* spp counts were mostly higher than 10^3 cfu/ml.

Keywords: *Candida* species, vulvovaginitis, Iran

P509 - 23: EFFECT OF POLYSACCHARIDE ANTIGEN OF ASPERGILLUS NIGER CELL WALL ON SOME IMMUNOLOGICAL PARAMETER IN RABBITS

Frial Abd¹, Ghadeer Kadhim Abood ², Frial Jamael Abd ³, Nida'a Shihab Hamed⁴

1. Department of Biology , Faculty of Science , Babylon University , Babylon , Iraq
2. Department of Biology , Faculty of Science , Babylon University , Babylon , Iraq
3. Department of Biology , Faculty of Science , Babylon University , Babylon , Iraq

Background and Aim:The aim of this frequent experiment is to study the effect of polysaccharide antigen which had been isolated from *Aspergillus niger* walls of TB patients and soil specimens. The cellular response determined by using rabbit neutrophil Elastase Kit .The level of phagocytic increased in animals immunized with polysaccharide antigen which isolated from *A.niger* of TB patients .Cytokine IL-2 and IL-10 were determined in serum of immunized rabbit and control.Tcell were sensitized by using skin test

Methods:specimens collection fifty samples were collected twenty-five samples were collected from TB while the other half collected from soil of different sites. The sputum sample place in satirized and well closed plastic containers then transported to tab during 1hr to be cultured in petri dish .while the soil sample dilution method was used to isolate fungiAbout 0.5 ml of this solution was taken from each sample and cultured in to petri dish.Fungi identification Fungi had been identification taking a finger print from the edge of fungal colony.Preparation of *A.niger* Cell wall of polysaccharide antigen.The rabbit that immunized with were injected with 0.1 ml of Antigen in intradermal of skin

Results:The polysaccharide antigen isolated from soil and TB patients sputum were prepared to study its ability to activate the immunological response in lab animals .

Conclusion:polysaccharide antigen found in fungal hyphae was immunologically active and the glucose , galactose and mannose were the most common sugar in all fungal antigen

Keywords: *Aspergillus niger* , polysaccharide antigen, cell wall , TB , soil .

P510 - 58: ONYCHOMYCOSIS DUE TO FUSARIUM SPP. IN PATIENT WITH SQUAMOUS CELL CARCINOMA

Hojjatollah Shokri¹

1. Department of Pathobiology, Faculty of Veterinary Medicine, Amol University of Special Modern Technologies, Amol, Iran

Background and Aim: Fusarium species have been frequently reported as etiologic agents of opportunistic infections such as onychomycosis in humans.

Methods: The infection occurred in a man with finger squamous cell carcinoma. Nail specimen was examined by direct microscopy, culture and histopathology.

Results: Direct microscopic examination revealed the presence of irregular, narrow and septate hyphae in the nail specimens. In Sabouraud glucose agar, the colonies were developed in whitish pink color, flat and cottony, and reverse colourless to pink pigmentation. Microscopic observation of the colonies showed abundant production of large, sickle shaped, three or five-septate macroconidia. Conidiophores were polyblastic and produced abundant small and ovoid microconidia. It was identified as Fusarium spp. at genus level. Histologically, skin tissue showed hyperkeratosis with alternating columns of parakeratosis. Also, there was papillomatous and acanthosis of the epidermis with spongiosis, regenerative activity and slight atypical nuclei. Presence of fungal organisms near the nail bed epidermis was seen. Creamy-gray soft tissue demonstrated the squamous epithelium, predominantly consists of malignant cells with high N/C ratio, hyperchromatic nuclei showing atypical mitotic figures. Focal small nests of malignant cells were noted in dermis. The last diagnosis was included squamous cells carcinoma (microinvasive) coincided with onychomycosis caused by Fusarium spp. The antifungal treatment containing oral terbinafine, 100 mg daily given for two months, was used but with little improvement. Finally, after diagnosis of infected fingernail with squamous cells carcinoma, the infected finger was cut.

Conclusion: The predisposing factors such as cancer, which have result in development of infection and treatment failure.

Keywords: Onychomycosis, Fusarium, Squamous cell carcinoma

P511 - 59: THE DISTRIBUTION AND IDENTIFICATION OF MYCOFLORA FROM GENITAL SYSTEM OF HEALTHY SHEEP

Hojjatollah Shokri¹, Mohsen Yadollahi²

1. Department of Pathobiology, Faculty of Veterinary Medicine, Amol University of Special Modern Technologies, Amol, Iran
2. Department of Pathobiology, Faculty of Veterinary Medicine, Amol University of Special Modern Technologies, Amol, Iran

Background and Aim: Fungal elements are commensal organisms found in the skin, genital and gastrointestinal tracts, and other mucosal sites in mammals. The purpose of this study was to identify the fungal flora of genital tract of healthy female sheep.

Methods: The samples were taken from vagina, cervix, uterine body and uterine horns of 84 sheep using sterilized cotton swabs. They were cultured onto Sabouraud glucose agar containing chloramphenicol (0.005%) and incubated at 30°C for 7-10 days.

Results: A total of 313 fungal colonies were obtained from genital tract. Mixed filamentous fungi (moulds) and yeasts were determined. Fungal isolates belonged to 15 genera: *Candida* (27.2%; representing significant difference with other fungal species, $p < 0.05$), *Trichosporon* (16.7%), sterile hyphae (14.2%), *Penicillium* (8.3%), *Geotrichum* (7.1%), *Alternaria* (7.1%), *Cladosporium* (6.5%), *Aspergillus* (3.7%), *Fusarium* (3.4%), *Rhodotorula* (1.9%), *Dematiaceous fungi* (1.5%), *Mucor* (1.5%), *Rhizopus* (0.3%), *Trichothecium* (0.3%) and *Ulocladium* (0.3%). Among different *Candida* species, *C. tropicalis* and *C. krusei* were the most common yeast species. The mean number of fungi found in the vagina (36.7%) was significantly higher than the results obtained from other parts ($P < 0.05$). The most common fungi isolated from vagina, cervix and uterine horns were associated with *Candida* species, while *Trichosporon* species were the most frequent fungi in uterine horns.

Conclusion: The results showed that *Penicillium* and *Candida* species, particularly *C. tropicalis* and *C. krusei*, were the most common components of the genital mycoflora of healthy female sheep and the number of fungi varied among different parts of genital system.

Keywords: Sheep, Genital tract, Female, Fungal flora, *Candida*, *Candida tropicalis*

**P512 - 60: THE ANTIFUNGAL ACTIVITY OF IRANIAN PROPOLIS AGAINST AZOLE-
RESISTANT CANDIDA ALBICANS STRAINS ISOLATED FROM HIV+ PATIENTS WITH
OROPHARYNGEAL CANDIDIASIS**

Hojjatollah Shokri¹, Alireza Khosravi²

1. Department of Pathobiology, Faculty of Veterinary Medicine, Amol University of Special Modern Technologies, Amol, Iran
2. Mycology Research Center, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran

Background and Aim: Propolis is an antimicrobial agent and its compositions can vary depending on the area where it is collected. The aim of this study was to determine the in vitro activity of Iranian propolis sample against some azole-resistant *Candida albicans* strains isolated from HIV+ patients with oropharyngeal candidiasis (OPC).

Methods: The chemical composition of propolis sample was determined by high-resolution gas chromatography coupled to mass spectrometry (GC-MS). The propolis extract was prepared in a 25% (w/v) concentration with 100° ethyl alcohol. The minimum inhibitory concentrations (MICs) and minimum fungicidal concentrations (MFCs) of propolis on the growth of *C. albicans* isolates were determined by the broth microdilution method.

Results: Polyphenols such as phenolic acid (89.8%) and caffeic acid (2.2%) were the most predominant acid components in propolis sample. All resistant isolates of *C. albicans* were susceptible to this bee product and the inhibitory values ranged from 2 to 20 mg/ml. Among the isolates, 41.2% did not show the growth at concentration of 8 mg/ml against propolis sample. The concentration of 1 mg/ml of propolis sample was fungicidal for all resistant isolates as well.

Conclusion: Because of increased antifungal resistance, propolis may be used in the treatment of oral cavity diseases such as OPC in HIV+ patients.

Keywords: Propolis, Oropharyngeal candidiasis, *Candida albicans*, azole-resistance

**P513 - 82: INVESTIGATION AND IDENTIFICATION SKIN FUNGAL INFECTION OF
SALMONIDS FISH OF FARMS ARDABIL PROVINCE**

Mirsajjad Eslamkhah¹, Mirsajjad Eslamkhah taghizad², Mirmasoud eslamkhah taghizad³, hamid faghani
langroudi⁴, Nastaran Ghafeli⁵

1. -
2. M.sc student in Genetics, Islamic Azad university , tabriz Branch
3. M.s in Aquatic ecology, Islamic Azad university , Tonekabon Branch
4. Phd in aquaculture, Islamic Azad university , Tonekabon Branch
5. M.sc student in Genetics, Islamic Azad university , tabriz Branch

Background and Aim: Nowadays, developing of the aquaculture industry the fungal diseases and fungal infections are known as the main cause of marine loss especially farmed fish and consequently damage this industry. Pisciculture of two species of Salmon trimmings developing in farms are Rainbow trout and Salmon of Caspian sea (*salmo trutta caspius*) which is highly important species and native as well immigrates to Caspian Sea and is of special nutritional and economic value. Rain bow trout are native to North American.

Methods: The research is a field- experimental study and laboratory tests. In autumn, 1394, skin of 100 fish kinds with the average weight of (1500-200 gr) were sampled and the sample were cultured in Sabro dextrose agar, glucose peptone medium in vitro temperature, as well as some conventional Mycology method in a macroscopic manner the water temperature and PH was also measured

Results: oomycete identification is mainly dependent on microscopic and sporulation features. The accurate identification of a species is generally possible by studying sexual reproduction structures. Characteristics of second cyst Including shape, nature and traits of cell wall of saproligna oogonium have been successfully identified which is considered as one of the other main identifying features

Conclusion: In this research conducted in pisciculture farm of Ardabil province with heat value ranging from 4 to 18 centigrade with 8-5.7pH, the fungus was identified to belong to the saprolinga family and saprolinga marazitica has the most frequency among the family with thick hi-fi and globose cyst germinating directly

Keywords: Fungal infections, skin Fungai , salmon, culture farms

**P514 - 92: INVESTIGATION OF ANTIFUNGAL EFFECT OF PLANT EXTRACTS ON
CANDIDA ALBICANS**

Fatemeh Beigpour¹, Azar Sabokbar², Somayeh Talebi³

1. Ms.C of Microbiology, Department of Microbiology, Islamic Azad University, Karaj Branch, Karaj, Iran
2. Associated proffessor of Microbiology, Islamic Azad University, Karaj Branch, Karaj, Iran
3. Ph.D Student of Microbiology, Department of Biology, Islamic Azad University, Science and Research Branch, Tehran, Iran

Background and Aim: Candidiasis of the most common and most widespread human fungal disease, which in recent years has increased much compactness commonly used antifungal agents are not only limited number also many of them are toxic and expensive. This study was done with investigation of the antifungal effect distillates *F. parviflora*, thyme and fenugreek plants in order to achieve effective against the fungus *Candida albicans*.

Methods: In this work, the extract of *F. parviflora*, thyme and fenugreek plants prepared from company which produced these extracts and claimed that these had antifungal effect. First Sabouraud dextrose agar medium was prepared and then suspension of yeast was prepared at OD was read 530 nm. The agar diffusion method was performed, after culture of fungus in SDA medium, well established by using the Panchr, at first beverages were poured into the well with purified state and were incubated for 18 hours at 37 °C on the basis of create and lack of inhibition zone were studied. Next stages extracts of plant 2,4,8,10 times was concentrated and agar diffusion method was performed again. The experiment was repeated 5 times.

Results: Distillate in question were used in pure form but did not show any growth inhibition zone and beverages, two, four, eight and 10 who were concentrated in all cases no growth inhibition zone was observed.

Conclusion: The results showed that the sweat Fenugreek, *Fumaria parviflora* and thyme plants, were not antifungal effect to fungus *Candida albicans*.

Keywords: Antifungal effect, Plant extracts, *Candida albicans*

**P515 - 141: ELUCIDATION OF RISK GROUP , RADIOLOGICAL SIGNS, TREATMENT OF
PRIMARY PULMONARY COCCIDIOIDOMYCOSIS AND SURVEY ABOUT
COCCIDIOIDOMA**

Sayed alireza Mirsane¹, Shima Shafagh², Nasrin Oraei³, Sayed Mojtaba Mirsane⁴

1. Surgical Technologist, Kashan University of Medical Sciences, Kashan,I.R.IRAN
2. General Surgery Specialist, Medical School, Kashan University of Medical Science,Kashan,I.R.IRAN
3. Khansar education office,Esfahan, ,I.R.IRAN
4. Khansar education office,Esfahan, ,I.R.IRAN

Background and Aim:our aim was elucidation of risk group , radiological signs, treatment of Primary pulmonary coccidioidomycosis and survey about coccidioidoma

Methods:We did a systematic review of 27 studies identified by searching Google scholar,PubMed, SID and Elsevier.

Results:Studies showed persons in older age groups and Caucasian or Hispanic persons are risk groups members of primary pulmonary coccidioidomycosis and these indicated risks groups should be propounded in designing coccidioidomycosis supervision and prevention program. also results showed treatment included antifungal therapy with amphotericin B and diuresis to decrease noncardiogenic pulmonary edema and radiological signs of primary pulmonary coccidioidomycosis is miliary pulmonary disease and this disease is a part of the multisystem organ failure seen in fungemic patients also these supported coccidioidoma is a benign localized remaining granulomatous lesion or scar that can remain in the lung's tissues following primary pulmonary coccidioidomycosis in other words residual granulomatous nodules in the lungs in coccidioidomycosis disease and it resembles tuberculosis nodules

Conclusion:We concluded radiological signs of primary pulmonary coccidioidomycosis is miliary pulmonary disease and risk groups included persons that are in older age groups and also in Caucasian or Hispanic persons likewise treatment included antifungal therapy with amphotericin B and diuresis to reduction of noncardiogenic pulmonary edema.One of the lung's tissues complications is coccidioidoma and it is a benign localized remaining granulomatous lesion or scar following primary pulmonary coccidioidomycosis

Keywords:Primary pulmonary coccidioidomycosis, Risk group , Radiological signs, treatment , coccidioidoma

**P516 - 305: BIOREMEDIATION OF CRUDE OIL AND PYRENE BY HALOTOLERANT
FUNGUS EMBELLISIA PHRAGMOSPORA ISOLATED FROM SALINE SOIL**

Kian Jenab¹, Hamid Moghimi², Javad Hamed³

1. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran
2. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran
3. Department of Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran

Background and Aim: Nowadays, investigating halophilic and halotolerant fungi enzymes has confirmed their significant potential in biodegradation of crude oil hydrocarbons. The aim of the current study is biodegradation of crude oil by halotolerant fungal strain, *Embellisia phragmospora*.

Methods: The fungal strains were isolated on Czapek Dox agar (CDA), potato dextrose agar (PDB) and malt extract agar (MEA) containing 10% NaCl. Crude oil and pyrene removal on minimal salt medium (MSM) by *E. phragmospora* was assessed in different salinity. Furthermore, crude oil biodegradation on PDB were analyzed in diverse salinity.

Results: Nine strains which were able to grow on PDA in salinity, ranging from 0 to 17% were selected. Isolate S66 was selected as a superior strain because it could remove 58.9, 59.1 and 17.1% in salinity of 0, 2.5 and 5%, respectively on MSM containing 1% crude oil during 14-day period. Isolate S59 was identified as *Embellisia phragmospora* by morphological and molecular approaches. It could biodegrade 77, 83.4 and 77.4% of petroleum in salinity of 0, 2.5 and 5%, respectively on PDB containing 1% crude oil during 7 days. Pyrene removal by *E. phragmospora* was 82.4, 88.3 and 95.2% in salinity of 0, 2.5 and 5%, respectively on MSM containing 100 ppm pyrene for 14 days.

Conclusion: According to our results *E. phragmospora* can be introduced for bioremediation of crude oil hydrocarbons in saline and non-saline contaminated regions. It has potential for biodegradation and the case of growth using petroleum hydrocarbons as the sole or supplementary carbon source in the presence of different salt concentrations.

Keywords: Crude oil, Bioremediation, *Embellisia phragmospora*, Pyrene, saline environment

**P517 - 312: SEROPREVALENCE OF LISTERIA MONOCYTOGENES IN WOMEN WITH
RECURRENT SPONTANEOUS ABORTION**

Elaheh Tajedini¹, Somayeh Talebi², Jalil Vandyousefi³

1. Ph.D Student of Microbiology, Department of Microbiology, Islamic Azad University, Isfahan Branch, Isfahan, Iran
2. Ph.D Student of Microbiology, Department of Biology, Islamic Azad University, Science and Research Branch, Tehran, Iran
3. Professor of Microbiology, Department of Microbiology, Islamic Azad University, Karaj Branch, Karaj, Iran

Background and Aim: Spontaneous abortion and miscarriage are terms that are synonymous. It is the termination of pregnancy between 20 weeks gestation or the delivery of a foetus weighing less than 500 g. Bacterial infections were reported as major causes. This was supported by the isolation of *Staphylococcus aureus*, *Streptococcus agalactiae*, *Escherichia coli*, *Bacillus* spp and *Listeria monocytogenes* from aborted placenta bits by Mirdamadi and in some cases of spontaneous abortion. The severity of Spontaneous abortion was seen in the high mortality and morbidity recorded in neonatal deaths as well as pregnant mothers, as observed by Seale. *L. monocytogenes* is a gram positive coccobacilli. This study was performed to determine the prevalence of IgM antibodies in serum samples from women with recurrent spontaneous abortion.

Methods: IgM antibody titers against *L. monocytogenes* in samples of women serums in three of age with recurrent spontaneous abortion were referred to the hospital in Karaj Kamali, was measured by ELISA.

Results: 21 serum samples were positive for IgM antibody. 1 sample number with the highest antibody titer of 1/800 and 8 sample number with the lowest titer of 1/80.

Conclusion: Based on the high prevalence of *L. monocytogenes* infection in our community, especially in pregnant women, also according to this study, the pregnant women with recurrent abortions, mostly aged 20 to 30 years more of IgM antibody titer in their serum.

Keywords: *Listeria*, spontaneous abortion, ELISA

P518 - 328: EVALUATION OF ANTIFUNGAL ACTIVITY OF NYSTATIN AGAINST VARIOUS CANDIDA ISOLATES

Samira Salari¹

1. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran

Background and Aim: Candidiasis is the most common form of yeast infection. During the past decade, the incidence of systemic candidiasis has consistently increased. *Candida albicans*, together with other *Candida* species such as *C. glabrata*, *C. tropicalis*, *C. parapsilosis*, *C. krusei*, *C. lusitaniae*, and *C. guilliermondii*, are known as the main hospital-acquired (nosocomial) pathogens. Aim of the study was to evaluate the antifungal properties of nystatin against various *Candida* isolates.

Methods: In this study, a total of 96 *Candida* isolates were tested, including the following species: *C. albicans* (42), *C. glabrata* (16), *C. tropicalis* (11), *C. krusei* (9), *C. parapsilosis* (9), *C. lusitaniae* (7), and *C. guilliermondii* (2). The in vitro antifungal activity of nystatin was evaluated against *Candida* isolates by using a broth microdilution method according to CLSI

Results: The MIC and MFC values of nystatin ranged from 0.25 to 16 µg/ml and 0.5 to 64 µg/ml, respectively.

Conclusion: Our findings show that *C. albicans* isolates is the most susceptible to nystatin than other *Candida* isolates.

Keywords: Antifungal susceptibility, nystatin, *Candida*, broth microdilution method.

**P519 - 384: CAUSAL AGENTS IDENTIFICATION OF THOMSON NAVEL ORANGE FRUITS
DECAY IN CONVENTIONAL AND STANDARD STORAGES IN EAST OF MAZANDARAN**

Seyyed vahid Alavi¹, Faezeh Falaki²

1. Plant Protection Research Department, Mazandaran Agricultural and Natural Resources Research and Education Center, AREEO, Sari, Iran.
2. Plant Pests and diseases laboratory of Mazandaran gardener's cooperatives consortium, Sari, Iran.

Background and Aim: Mazandaran province is one of the major poles of agriculture and the main citrus planting areas in Iran. The study was performed during the 2012-2014 storage periods of Thomson navel orange fruits (*Citrus sinensis* (L.) Osbeck).

Methods: Samples were collected from the rotten fruits in conventional and standard storages in the east of Mazandaran (Sari, Neka and Quaemshahr). Tecto (Thiabendazole) was used as the fungicide treatment for orange fruits in all of the storages. Pieces of the each sample were cultured in PDA medium and incubated for 5-7 days in 25 °C. The fungal colonies were isolated and purified. Pathogenicity test was done by the fungal isolates inoculation on the healthy fruits and the same agents isolated.

Results: The fungal isolates were identified as *Penicillium digitatum* (Pers.) Sacc. and *Geotrichum candidum* link. With 65 and 35 percents frequency, respectively.

Conclusion: The fungal isolates were identified as *Penicillium digitatum* (Pers.) Sacc. and *Geotrichum candidum* link. With 65 and 35 percents frequency, respectively.

Keywords: Thomson navel orange, Mazandaran, *Penicillium digitatum*, *Geotrichum candidum*.

**P520 - 435: ISOLATION AND ENUMERATION OF GEOTRICUM CANDIDUM IN
UNPASTEURIZED DAIRY PRODUCTS MARKETING IN TABRIZ BY PCR**

Elnaz Homeyni¹, Afshin Javadi²

1. M.sc Student in microbiology, Rab-Rashid University, Tabriz, Iran
2. Associate Professor of food hygiene department, Bio-Technology Research center, Tabriz branch, Islamic Azad University, Tabriz, Iran.

Background and Aim: Geotricum candidom is dimorphism yeast that causes contamination and spoilage in milk and dairy product. Due to the importance of unpasteurized dairy products and contamination of these nutrients and lack of previous molecular studies in this field we decided to study unpasteurized dairy products which supplies in Tabriz in term of yeast Geotricum candidom contamination.

Methods: In this study, 150 samples of unpasteurized dairy products from unpasteurized distribution centers of the Tabriz were randomly assigned and microbial experiments was performed. Geotricum candidom isolation of unpasteurized dairy products was performed by using of Iran standard method and for confirmation of Geotricum candidom genetic, PCR molecular method by genetics Keith of the suspected samples were used.

Results: 10 butter samples, 10 buttermilk samples and 8 whey sample of total 150 analyzed unpasteurized dairy products samples were CandidomGeotricum infected.

Conclusion: The study showed that 18.66% of sample of Tabriz city's unpasteurized dairy products were contaminated to Yeast GeotricumCandidom. The results of the survey will help us in terms of causing disease and control ofunpasteurizeddairy products supplied in the manufacturing and unpasteurized centers and monitoring organizations.

Keywords: Geotrichum candidum, Dairy Product, Unpasturized, PCR

**P521 - 518: THE STUDY OF PREVALENCE OF (OTOMYCOSIS) IN PATIENTS REFERRING
TO THE REFERENCE LABORATORY OF MYCOLOGY OF KASHAN DURING THE YEARS
1390 TO 1394.**

Mahdis Anvari¹, mohammad ali asadi²

1. Student Research Committee
2. Student Research Committee

Background and Aim:Otomycosis is an external ear canal infection caused by various fungi. This disease is prevalent in tropical regions or regions that have warm and humid climates. Since the weather of kashan township is like previously mentioned, this fungi and other microbes can get transported from area to area by strong winds and may enter the nose, mouth or ear and cause the disease. Hence, this research was done.

Methods:This retrospective descriptive study was conducted in patients with a history of itching, burning, pain, discharge of pus from the ear. A mycology reference laboratory has been using sterile swab to remove samples from the external auditory canal. The samples were later used for smear and culture.

Results:In this study, from Farvardin 1390 to Esfand 1394, a total of 66 patients were diagnosed with Otomycosis. Within the 66 patients, 53 of them were female patients (80%) and 13 of them were male patients (20%). From all the infected ears, 32 cases were infected in their right ear, 31 cases were infected in their left ear and 3 cases had infections in both their right and left ears. In all patients, there was no trouble with the hearing screen.

Conclusion:According to the achieved data, the number of patients being diagnosed with the disease is relatively high in the township. Therefore, this research was done to recognize the causes of the disease and to realize the effects of improved health education to reduce the number of effected people

Keywords:Otomycosis, Aspergillus Niger, Candida

**P522 - 530: EVALUATION OF SATUREJA RECHINGERI ESSENTIAL OILS ON GROWTH
AND AFLATOXIN B1 PRODUCTION BY ASPERGILLUS FLAVUS PICC-AF39**

Roghieh Zergani najad¹, Eskandar Moghimipour², Abdulghani Ameri³

1. Microbiology Department, Yasouj Branch, Islamic Azad University, Yasouj, IR Iran
2. Medicinal Plant Research Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, IR Iran
3. Pharmaceutical Sciences Research Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, IR Iran.

Background and Aim: Contamination of agricultural products by aflatoxins, toxic secondary metabolites of fungi, is a worldwide human and livestock health. Aflatoxins produced by some *Aspergillus* sp. generate the most concern because of their potent toxicity, carcinogenicity [1,2]. In this study was to examine essential oil of *Satureja rechingeri* as antifungal agents against of *Aspergillus flavus* PICC-AF39 (toxigenic aflatoxin B1). Antifungal activities of the oil were studied with special reference to the inhibition of *Aspergillus flavus* growth and aflatoxin production.

Methods: Antifungal activity assay was performed using the disk diffusion method. The minimum inhibitory concentration (MIC) and minimum fungicidal concentration (MFC) was determined essential. [3]

Results: minimum inhibitory concentration and mortality, 50 and 250 ppm and inhibition zone diameter for a concentration of 20 ml oil in a concentration of 10⁶ spores of the fungus *Aspergillus flavus*, 75 mm was reported. The results, in this study showed that the essential oil of *S. rechingeri* had strong antifungal activity against pathogen fungi tested. So, the essential oil of *S. rechingeri* could be used for management of this pathogen as a potential source.

Conclusion: Thanks to the lady doctor Hndaly and School of Pharmacy Jundishapur for all their hard work and companies Khorramabad Khrman Thank you.

Keywords: Keywords: *Satureja rechingeri*, Essential oil, Antifungal, Aflatoxin

**P523 - 542: CULTURE MEDIA SELECTION FOR CHITIN-GLUCAN COMPLEX PRODUCTION
BY GANODERMA LUCIDUM**

Akram Moradi Tanha¹, Zahra-Beigom Mokhtari-Hosseini², Ashrafalsadat Hatamian-Zarmi³, Bahman Ebrahimi-Hosseinzadeh⁴

1. Department of Life science Engineering, Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran
2. Department of Chemical Engineering, Faculty of Petroleum and Petrochemical Engineering, Hakim Sabzevari University, Sabzevar
3. Department of Life science Engineering, Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran
4. Department of Life science Engineering, Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran

Background and Aim: Chitin-glucan complex (CGC) is a natural co-polymer of most fungi and yeast cell wall. It is a biocompatible and biodegradable biopolymer that has demonstrated to combine antioxidant, antibacterial and anti-inflammatory properties. In this research we studied production of Chitin-glucan complex (CGC), an exopolysaccharide, by a pharmaceutical fungus, *Ganoderma lucidum*.

Methods: At first, *G. lucidum* was cultured in commonly used medium YPG (Yeast Peptone Glucose) in 28°C, 180 rpm for 14 days. Produced CGC was extracted and confirmed using FTIR. Then, to determine the appropriate medium for maximum production of CGC by *G. lucidum*, the fungus was cultured in abovementioned environmental conditions on ten different mediums. CGC was extracted and measured in each medium.

Results: The results showed that the medium containing peptone (1g / L) and PDB (24g / L) has the highest CGC production. The CGC content in this medium was 42% (g CGC / g biomass) in which showed 37.6 % increase in comparison to the YPG medium with 4.4 % CGC content. We concluded the new combination of medium that introduced here is more productive than the other fungi media and can be used in similar studies.

Conclusion: Review of other studies showed that the amount of CGC content in *G. lucidum* is about two times more than other studied fungi. Therefore we propose *G. lucidum* as an appropriate source for CGC production.

Keywords: *Ganoderma lucidum*, Exopolysaccharide, Chitin-glucan complex (CGC)

P524 - 758: COMPARISON OF IN-VITRO ANTIFUNGAL ACTIVITY OF OLIVE LEAF EXTRACT, BERBERIS VULGARIS AND BLACKBERRY ON STANDARD STRAIN OF CANDIDA ALBICANS PTCC 5027

Maryam Abolhasannezhad¹

1. bums.ac.ir

Background and Aim: The incidence of severe infections caused by yeast particularly species of candida has increased during the past decade. *C. albicans* is the most common yeast on the mucosal membranes of humans. Candidiasis can appear under bad conditions and has become one of the main causes of morbidity and mortality worldwide among immunocompromised individuals. In this study we investigated antifungal effect of Olive leaf extract, Berberis vulgaris and Blackberry on candida albicans.

Methods: To evaluate the antifungal activity of olive leaf, berberis vulgaris and blackberry, standard strain of candida albicans ptcc 5027 was used. Minimum inhibitory concentration (MIC) and Minimal fungicidal concentration (MFC) were assessed by microdilution broth.

Results: The results showed that MICS for Olive leaf extract and Berberis vulgaris respectively was 12/5% and 25%, and the MFCS was 50%. There was no significant effect for Blackberry.

Conclusion: In this study Olive leaf and Berberis vulgaris showed an effective antifungal activity against candida albicans ptcc 5027 but no antifungal activity was found for Blackberry

Keywords: Antifungal effects, Candida albicans, Olive leaf, Berberis vulgaris, Blackberry.

**P525 - 762: EVALUATION AND COMPARISON THE EXPRESSION OF THE ENZYME
GLUCOSE OXIDASE RECOMBINANT EXPRESSION IN YEAST SYSTEMS PICHIA
PASTORIS**

Fakhry Belyad¹, Jamshid Raheb², Ali asghar Karkhanei³

1. National Institute of Genetic Engineering and Biotechnology
2. National Institute of Genetic Engineering and Biotechnology
3. National Institute of Genetic Engineering and Biotechnology

Background and Aim: Glucose oxidase (GOD; β -D-glucose: oxygen 1-oxidoreductase, EC 1.1.3.4), a glycoprotein, catalyzes the oxidation of β -D-glucose to D-glucono- δ -lactone and hydrogen peroxide. Thus, the enzyme is widely used in the fields of food engineering, biotechnology, and medicine like as a source of hydrogen peroxidase in food preservation, as a means for gluconic acid production, and tested as the basis for glucose sensors and glucose detection kits

Methods: DNA Isolation and Cloning of the GOD Gene from *Aspergillus niger* Construction of the Expression Plasmid Transformation of *P. pastoris* Screening of High-Level Expression Transformants Optimization of Expression Conditions in Shake Flask Enzyme Assay and SDS-PAGE Analysis Purification of Recombinant GOD and Protein Concentration Measurement

Results: Recombinant glucose oxidase from *Aspergillus niger* expressed in *Pichia pastoris* by fed-batch fermentation was purified and assessed with 1.26 purification fold to homogeneity using Q-Sepharose F.F. chromatography. The enzyme was determined by SDS-PAGE, which showed a dimeric form of 150 kDa. The purified rGOD was proved to be a glycoprotein. Characteristics demonstrated that the highest activity was in pH 6:0 at 50°C and was stable at a broad pH range from 5:0 to 7:0 at 50°C. The optimum substrate for this enzyme was D-glucose

Conclusion: Characteristics demonstrated that the highest activity was in pH 6:0 at 50°C and was stable at a broad pH range from 5:0 to 7:0 at 50°C. The optimum substrate for this enzyme was D-glucose

Keywords: Glucose oxidase . *Aspergillus niger* . Overexpression . *Pichia pastoris* . Properties

**P526 - 901: NECROTIZING FUNGAL OTITIS EXTERNA IN A DIABETIC
IMMUNOCOMPROMISED PATIENT**

Nahid Gholinejad¹, Tahereh Shokohi², Hassan Asghari³, Seyed Reza Aghili⁴, Zahra seifi⁵, Mostafa roudbari⁶, Fatemeh nourollahi⁷

1. Student Research Committee, Faculty of Medicine, Mazandaran University of Medical Sciences , Sari. Iran
2. Department parasitology and Mycology, Faculty of Medicine and Invasive Fungi Research Center, ,Mazandaran University of Medical Sciences, Sari, Iran.
3. Specialist in Infectious Diseases & Tropical Medicine, Zare Hospital, Sari, Iran.
4. Department parasitology and Mycology, Faculty of Medicine and Invasive Fungi Research Center, ,Mazandaran University of Medical Sciences, Sari, Iran.
5. Student Research Committee, Faculty of Medicine, Mazandaran University of Medical Sciences , Sari. Iran
6. Specialist in Infectious Diseases & Tropical Medicine, Zare Hospital, Sari, Iran.
7. Specialist in Infectious Diseases & Tropical Medicine, Zare Hospital, Sari, Iran.

Background and Aim:A recent increased incidence of fungal otitis may be due to use of systemic broad-spectrum antibiotics and increased use of topical fluoroquinolone antibiotics. In immunocompromised patients, the fungal otitis externa is potentially life-threatening infection and can spread to the surrounding tissues. Here, we describe this rare entity of necrotizing fungal otitis externa in a diabetic immunocompromised patient.

Methods:A 55-year-old man with a history of squamous cell carcinoma and type II diabetes was diagnosed with necrotizing external otitis characterized by acute ear pain, deafness and a foreign-body sensation. The specimen was obtained from the right ear and stained with calcoflour white for direct microscopy.

Results:Culture of the purulent exudates was performed on sabouraud dextrose agar (SDA) plates and fungal colonies were grown after 5 days at 30 °C. *Aspergillus fumigates* identified using morphological characterization. In bacteriological culture media, *Citrobacter* species and *E. coli* were isolated as well. Combination therapy with Meropenem, Voriconazole, surgical debridement were used and the patient's signs improved.

Conclusion:This report highlights the rare necrotizing fungal otitis externa in a diabetic immunocompromised and thereby it turns the physicians' attention towards the possibility of coexistence of fungal and bacterial infections. Thus, it is important that both organisms should be considered as etiologic agents in protocols for treatment of otitis externa.

Keywords:otitis externa, polymicrobial, immunocompromised, fungal, Diabetes

**P527 - 920: A SURVEY OF THE EFFECT OF CAMPHOR ON INT1 AND EFG1 GENES
EXPRESSION OF CANDIDA ALBICANS IN THREE TIME POINTS OF TREATMENT, 24
HOURS, 48 HOURS AND 72 HOURS VIA REAL-TIME PCR**

Reza Ghaffaripour¹, Masoumeh Rajabi Bazl², Mohammad Hossein Yadegari³

1. M.Sc in Medical Mycology, Department of Medical Mycology, Faculty of Medicine, Tarbiat Modares University, Tehran, Iran.
2. P.hD, Associate Professor of Clinical Biochemistry, Department of Clinical Biochemistry, Faculty of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
3. P.hD, Associate Professor of Medical Mycology, Department of Medical Mycology, Faculty of Medicine, Tarbiat Modares University, Tehran, Iran.

Background and Aim: *Candida albicans* is a virulent opportunistic yeast that its growth gets out of control leading to a pathogenic form in immunocompromised population. Ingredients of medicinal plants like Camphor, can suppress the virulence genes through their antifungal properties. INT1 and EFG1 genes are implicated in inducing filamentous growth, adhesion and virulence of *C. albicans*. This study focuses on the evaluation of Camphor effects on INT1 and EFG1 genes expression via Real Time PCR.

Methods: Serial dilution of Camphor in concentrations 512 to 1 mg/ml be prepared and cocultured with 1.5×10^3 cells/ml of *Candida albicans* for 48 hours in 350C then the MIC_{50/90} and MFC was determined. The cells was treated to MIC₅₀ concentration of Camphor for 24, 48 and 72 hours. RNA from cells was extracted before and after treatment, back translated into cDNA and finally Real Time PCR was carried out.

Results: The results revealed that the MIC₅₀ of Camphor is 16 mg/ml, MIC₉₀ is 32 mg/ml and MFC is 64 mg/ml and qPCR showed that Camphor can inhibit the expression of INT1 and EFG1 genes in all treatments. However, the highest level of gene suppression was found in cells that were treated for 48 hours.

Conclusion: Recently, advancement has been seen in herbalism due to the increased drug resistance and side effects of drugs. The Results of this study show that use of Camphor that is found in medicinal plants, can significantly reduce the expression of virulence genes in fungi such as INT1 and EFG1.

Keywords: *Candida albicans*, EFG1, INT1, Camphor, Virulence factors

**P528 - 971: THE EFFECT OF ETHANOL EXTRACT DERACOCEPHALUM KOTSCHYI OF
THE LEVEL OF SERUM PROTEINS IN MICE INFECTED WITH CANDIDA ALBICANS**

Razieh Zareiyan jahromi¹, mahboobeh madani²

1. islamic azad university of falavarjan
2. islamic azad university of falavarjan

Background and Aim: Deracocephalum kotschy Boiss, is a wild-growing flowering plant, belonging to the family lamiaceae including aromatic and medicinal plant in Iran. The purpose of this study was to evaluate the effect of the ethanol extract Deracocephalum kotschy of blood serum proteins in mice infected with candida albicans.

Methods: in this study, 93 female mice of the strain NMRI were selected and divided to 9 groups, including control, normal saline, candida, candida and extract, and extract alone. Treatment groups with extract received ethanolic extract with dosages of 50, 100, 200 Mg/Kg every other day for 20 days through intraperitoneally injection. Candida, candida and extract groups infection candida albicans only once in the sixth day of received intraperitoneal injection. The results obtained with a comprehensive statistical analysis of variance and duncan at level $p < 0/001$ were analyzed.

Results: the results showed that albumin level in the two groups 100 and 200 Mg/Kg treatment doses compared to placebo and control group significantly decreased ($p < 0/001$).

Conclusion: the results showed that reduce of albumin sentetic is one of the sign Symptoms of liver cell function changes.

Keywords: Deracocephalum kotschy, candida albicans, mice, Blood proteins

P529 - 1068: REPETITIVE SEQUENCES BASED ON GENOTYPING OF CANDIDA ALBICANS ISOLATES OBTAINED FROM IRANIAN PATIENTS WITH HUMAN IMMUNODEFICIENCY VIRUS

Ramak Yahyaraeyat¹, Iradj Ashrafi tamai², Taghi Zahraei Salehi³

1. Assistant professor, departement of microbiology, faculty of veterinary medicine, university of Tehran
2. Ph.D. Of microbiology, departement of microbiology, faculty of veterinary medicine, university of Tehran
3. Professor, departement of microbiology, faculty of veterinary medicine, university of Tehran

Background and Aim: Candida species have commonly been considered harmless commensals, and are isolated from the vagina, mouth and gastrointestinal tracts. Candidiasis infection caused by Candida albicans has been known as a major problem in patients with immune disorders. The objective of this study was to genotype the C. albicans isolates obtained from oral cavity of patients with positive human immunodeficiency virus (HIV+) with or/and without oropharyngeal candidiasis (OPC).

Methods: A total of 100 C. albicans isolates from Iranian HIV+patients were genotyped using specific PCR primers of the 25S rDNA and RPS genes.

Results: The frequencies of genotypes A, B and C which were achieved using 25S rDNA , were 66, 24 and 10 percent, respectively. In addition, genotypes D and E were not found in this study. Each C. albicans genotype was further classified into four subtypes (types 2, 3, 2/3 and 3/4) by PCR amplification targeting RPS sequence.

Conclusion: In general, genotype A3 constituted the majority of understudy clinical isolates obtained from oral cavity of Iranian HIV+ patients.

Keywords: Candida albicans, Candidiasis, Genotyping, HIV+, RPS sequence

P530 - 1198: ETHNOMEDICINAL PLANTS: SCREENING OF IN VITRO ANTIFUNGAL EFFECT OF PISTACIA KHINJUKS ESSENTIAL OIL (COMBINED WITH THE DOMINANCE γ -TERPINENE) WITH AGAR DISK DIFFUSION METHOD ON CANDIDA ALBICANS.

majid hajialiani¹, hossein yazdani², akram zangeneh³, mohammad mahdi zangeneh⁴, hossin zhaleh⁵, rohalah moradi⁶, reza tahvilian⁷

1. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran
2. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran
3. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran
4. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran
5. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran
6. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran
7. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran

Background and Aim: *Candida albicans* is a fast growing fungus that cause the candidiasis infection in humans. The aim of the current study was to determine chemical composition of *P. khinjuk* essential oil and evaluate its antifungal activity against common pathogen (*C. albicans*) with broth macro-dilution and agar disk

Methods: Agar disk diffusion method was performed as screen test. Macrobrot h dilution method was accomplished to determination of MIC value. *C. albicans* was chosen to survey. Serial dilutions were prepared from essential oil of the aerial parts in 1 (1g/ml), 1/2 (0.5g/ml), 1/4 (0.25g/ml), 1/8 (0.125 g/ml), 1/16 (0.062 g/ml), 1/32 (0.031 g/ml), 1/64 (0.015 g/ml), 1/128 (0.007 g/ml), 1/256 (0.003 g/ml), 1/512 (0.002 g/ml), 1/1024 (0.001 g/ml) ratios in DMSO. Amphotericin B was used as positive control for this fungus. DMSO was used as negative control

Results: According to results of GC-MS analysis, γ -terpinene (81.14%) (w/w) was the most abundant component of the essential oil. In agar disk diffusion method, in positive control, 1, 1/2, 1/4, 1/8, 1/16, 1/32, 1/64, 1/128, 1/256, 1/512, and 1/1024 dilutions, inhibitory zones were seen 16, 50, 36, 22, 13, 13, 12, 11, 10, 9, 8, and 8 mm in diameters for *C. albicans*. 1/256 dilution was realized for both MIC and MFC about this fungus

Conclusion: Based on the results, *P. khinjuk* has a fair antifungal effect on tested fungus as representatives of pathogenic fungus. Thus, *P. khinjuk* can be used in the treatment of candidiasis infection in humans

Keywords: *Pistacia khinjuk*, essential oil, antifungus effect

**P531 - 1246: CHARACTERIZATION OF FUNGI ISOLATED FROM THE SUNFLOWER
(HELIANTHUS ANNUS L.) RHIZOSPHERE IN WEST AZARBAYJAN**

Seyed Majid Safari¹, Kiomars Rouhrazi²

1. Department of Agriculture, Malekan branch, Islamic Azad University, Malekan, Iran
2. Department of Agriculture, Malekan branch, Islamic Azad University, Malekan, Iran

Background and Aim: The fungi coexist with other organisms due to many biotic and abiotic factors in the environment which are favorable to the occupation of a common habitat. The term rhizosphere is defined as the soil volume adjacent to the roots and influenced by them and represents an area of intense microbial activity, in which the organic nutrients coming from the roots favour the development of microorganisms.

Methods: Isolates were recovered from soil by a serial dilution method. The fungi were isolated according to Warcup. the growth of the colonies was accompanied up to 72 h. Fragments of the individual colonies were transferred separately to the same medium containing 50 mg L-1 of chloranphenicol. The strains were identified after growth on Czapek Agar and Potato Dextrose Agar medium, by observing its macroscopic characteristics (colour, texture appearance and diameter of the colonies) and microscopic (microstructures). In PCR reactions, the ITS genes of isolates were sequenced and compared with other sequences in NCBI with blastn program.

Results: From the control soil (T0) used to grow sunflower and from the sunflower rhizosphere cultivated in field and in greenhouse, 6 species were isolated. From the control soil (T0) based on morphological and genotypic properties, 6 species of filamentous fungi were identified as *Fusarium proliferatum* F. solani, *F. nygamai* F. oxysporum, *Trichoderma harzianum* and *T. virens*.

Conclusion: Filamentous fungi able to hydrolyse inulin have been isolated from the rhizosphere of plants whose roots contain this polysaccharide. In this study 6 species of filamentous fungi were identified from rhizosphere of sunflower.

Keywords: Fungi, ITS gene, *Fusarium* sp., *Trichoderma* sp. Rhizosphere

**P532 - 1248: IN VITRO ACTIVITIES OF FLUCONAZOLE AND AMPHOTERICIN B ALONE
AND IN COMBINATION AGAINST CANDIDA ALBICANS**

Fatemeh Khezrian¹, Fahimeh Alizadeh²

1. Department of Microbiology, Yasooj Branch, Islamic Azad University, Yasooj, Iran.
2. Department of Microbiology, Yasooj Branch, Islamic Azad University, Yasooj, Iran.

Background and Aim: Candidiasis represents a serious threat, in an expanding population of immune- and medically compromised patients. However, the number of antifungal drugs is limited for the treatment of candidiasis. Combination therapy is one of the most frequently used techniques to alleviate this problem. In this paper, we were aimed to evaluate the combined antifungal effects of amphotericin B with fluconazole against *C. albicans*.

Methods: Ten clinical isolates of *C. albicans* were identified from the immunocompromised patients in Yasooj and *C. albicans* ATCC 10231 as a reference quality-control strain was employed. Antifungal susceptibilities to fluconazole and amphotericin B alone and in combination were performed using the CLSI standard reference method (M27-A3) for broth microdilution antifungal susceptibility testing of yeasts.

Results: The combination of amphotericin B with fluconazole resulted in synergic activity with eight of the 10 *Candida* isolates studied, with fractional inhibitory concentration index (FICI) <0.5.

Conclusion: Taken together, the results of antifungal susceptibility assay demonstrated that the synergistic antifungal effects of fluconazole combined with amphotericin B. These results suggest that the combination of fluconazole with amphotericin B would be worth exploring in the treatment of candidiasis.

Keywords: *Candida albicans*; fluconazole; amphotericin B

Immunology

P533 - 453: PRODUCTION OF NANOPARTICLE CONTAINING ENTEROTOXIGENIC ESCHERICHIA COLI MAJOR PILIN SUBUNIT RECOMBINANT PROTEIN, CFAB, FROM COLONIZATION FACTOR ANTIGEN I (CFA/I) FIMBRIAE, AND ITS IMMUNOLOGICAL EVALUATION AFTER ORAL ADMINISTRATION IN MICE MODEL

Samaneh Hoseinpour¹, Jafar Salimian², Ali Ahmadi³, GHolamreza Olad⁴

1. Master of Microbial Biotechnology, Department of Biology, Damghan Branch, Islamic Azad University, Damghan, Iran
2. Associate Professor, Chemical Injuries Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran
3. Associate Professor, Applied Microbiology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran
4. Associate Professor, Applied Biotechnology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran

Background and Aim: Enterotoxigenic *Escherichia coli* (ETEC) is the most common cause of bacterial diarrhea in the world, particularly diarrhea in children in developing countries and Travelers to this areas. Research shows major subunit of colonization factor I (CfaB), due to its prevalence in most strains of enterotoxigenic *E. coli* bacteria, antibodies, property adjuvant for vaccines is considered as one of the candidates. Also according to the flow and bacterial pathogenesis, production of mucosal vaccine is very important. Therefore, the design of mucosal vaccine by using nanoparticle, the antigen protection against degradation and also controlled release of antigens on mucosal surfaces, will cause induction of mucosal immune system response against colonization factor

Methods: In this study, expression of gene CfaB, was used clone *E. coli* BL21DE3 containing pET28a-CfaB vector. purification of recombinant protein CfaB was done After induction of gene expression. Then, produce the chitosan nanoparticle containing recombinant protein and The mice Balb /c were administrated orally four times. immunogenicity after evaluated IgA and IgG titers in serum and IgA titers in fecal of immunized and control against CfaB was determined by ELISA

Results: The results showed that recombinant protein CfaB was observed after expression and purification, the weight of 20 kDa band on gel. The size of nanoparticle containing the recombinant protein was estimated 300 nm. After immunization, the results of ELISA showed that serum IgG and IgA titers and the titer of stool IgA, were 3200/1 and 16/1, 8/1, respectively

Conclusion: It seems that oral administration of nanoparticles containing recombinant protein CfaB of enterotoxigenic *E. coli* as a vaccine candidate can induce systemic and mucosal immune responses against colonization factor in mice

Keywords: Enterotoxigenic *Escherichia Coli*, recombinant protein of major subunit colonization factor I (CfaB), Chitosan nanoparticle, mucosal vaccine, evaluate the immunogenicity

**P534 - 632: PRODUCING AND EVALUATION QUANTITY AND QUALITY OF
POLYCLONAL ANTIBODY AGAINST EXOTOXIN A PSEUDOMONAS AERUGINOSA IN
RABBITS**

Shabnam Saeidvafa¹, Asghar Tanomand²

1. Department of Microbiology, Islamic Azad University Maragheh Branch, Maragheh, Iran
2. Department of Microbiology, Maragheh University Of Medical sciences, Iran

Background and Aim: Exotoxin A is one of the pathogenic factors of *P.aeruginosa*. Moreover, antibody against exotoxin A *P.aeruginosa* can be employed in immunotherapy in burn patients. Production and investigation of quantity and quality of polyclonal antibody against exotoxin A of *pseudomonas aeruginosa* in rabbits was done in this study.

Methods: In order to supply and study polyclonal antibody, 40 micrograms nontoxic exotoxin A was mixed with the same volume of adjuvant and was subcutaneously injected to a rabbit. The injection was administered on the days 0-14-28 and 42. After a week of each injection, blood sample of the rabbit was collected and serum was obtained through centrifuge. quantity and quality of antibody production were evaluated through double diffusion, agglutination, and ELISA methods.

Results: In double diffusion method, after pouring the immune rabbit's serum with different dilutions in the wells and incubating it under wet conditions for 24 hours, the lines of sediment was considered. Based on the obtained results, a sediment line was established between 1/2 and 1/4 dilutions with a dense antigen, which showed the reaction of antibody and antigen in those dilutions. In agglutination test, according to the observations, there were agglutinated particles in 0, 1/2, 1/4, and 1/8 dilutions and the result was positive. Further, agglutination was not perceived after 1/16 dilutions. In addition to this, when considering through ELISA method, a remarkable production of antibody was observed.

Conclusion: In this study, administration of immune reaction in rabbits to produce polyclonal antibody with high titer was done, which was of acceptable quantity and quality.

Keywords: Freund's adjuvant, ELISA, Polyclonal antibody, Agglutination, Double diffusion

**P535 - 777: THE EFFECT OF AQUEOUS EXTRACT OF ELAEAGNUS ANGUSTIFOLIA ON
SERUM TNF LEVEL IN MICE WERE RECEIVED BRUCELLA ABORTUS LPS**

Ali Pandooneh¹, sadraei H,² kaka GH,³ mofid M,⁴ Esmaeili D,⁵

1. Baqiyatallah MedSci Uni
2. department of anatomy, Baqiyatallah (a.s.) Medical Sciences University, Tehran, Iran.
3. department of anatomy, Baqiyatallah (a.s.) Medical Sciences University, Tehran, Iran
4. department of anatomy, Baqiyatallah (a.s.) Medical Sciences University, Tehran, Iran.
5. department of microbiology, Baqiyatallah (a.s.) Medical Sciences University, Tehran

Background and Aim: one of the cells that make TNF is Th1 lymphocyte. This cytokine plays an important role in inflammatory disease (1). Conversely, recent studies have found that *Elaeagnus angustifolia* fruit extract has anti-inflammatory effects (2). We decided to study the effect of *Elaeagnus angustifolia* on serum TNF level of mice that were received *Brucella abortus* LPS.

Methods: Souri mice were evaluated through the injection of different doses (10, 20, 30 and 40 mg/kg) of extract to the peritoneum in four days. In the fourth day of each mouse was injected peritoneally with 100 microgram *Brucella abortus* LPS. Blood was collected from heart in the next day and serum was separated and stored at -80°C until assay. Serum TNF levels were measured by Elisa kit.

Results: the research data showed a significant increase in serum TNF level in all treatment groups compared to control except in mice that received 10 mg/kg of extract.

Conclusion: due to the inhibitory effect of IL-6 on Th1 lymphocytes (3) as well as the decreasing effect of *Elaeagnus angustifolia* fruit extract on IL-6 (4), serum TNF (as a Th1 lymphocyte cytokine) in P2 to P4 groups (received 20, 30 and 40 mg/kg of extract respectively) were increased significantly.

Keywords: IL-6, TNF, Th1 lymphocyte, inflammation

P536 - 779: DEVELOPMENT OF ANTI- ETEC IGY ANTIBODY IN QUAIL

Khalil Ghuryani khervi¹, Gholamreza Nikbakht², kaveh veisi³, yoones attari⁴, khalil alalo⁵

1. 1. Department of Microbiology and immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
2. . Department of Microbiology and immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
3. . Department of Microbiology and immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
4. . Department of Microbiology and immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
5. . Department of Microbiology and immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran

Background and Aim:Enterotoxigenic Escherichia Coli (ETEC) is diarrhea causing microbe in humans and animals. Generated data using Egg yolk antibodies (IgY) strengthens the efforts on developing an alternative therapy instead of antibiotics in controlling and preventing ETEC infections. Egg yolk contains high amounts of IgY per egg and is considered to be a more hygienic and economical source of antibodies, than those from mammalian sera.

Methods:In this study we used heat inactivated ETEC (strain k510) to immunize quails. They were injected intramuscularly three times with 2 weeks intervals. Eggs were collected within 45 days and purified by water dilution-ammonium sulfate precipitation method and the activity was determined by enzyme-linked immunosorbent assay (ELISA). On the other hand to confirm the specificities and characteristics of the desired antibody, western blot analysis was performed.

Results:On the basis of statistical analysis, it was found that in the quail eggs there is an acceptable level of antibodies against ETEC. It was also found that the highest titer was in the fifth week after the first injection

Conclusion:This study indicated that high amounts of IgY antibody can be developed in quail following whole germ immunization and injection is not necessary for efficient immunization of the quail

Keywords:IgY-Quail-ETEC -ELISA

**P537 - 800: THE EFFECTS OF CYTHOLETHAL DISTENDING TOXIN- ENCODING
SALMONELLA ENTERICA ON EXPRESSION OF TLR2, TLR4 AND TLR5 IN HT-29 CELLS**

Leila Ganji¹, Masoud Aleboyeh ², Mohammad Hassan Shirazi^{1,3}, Mohammad Raze Zali ⁴

1. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
2. 2 Foodborne and Waterborne Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Science, Tehran, Iran.
3. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
4. 2 Foodborne and Waterborne Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Science, Tehran, Iran.

Background and Aim:Interaction of *Salmonella enterica* with the intestine could induce immune receptors of the epithelial cells that promote inflammatory response in this tissue. In this study, changes in mRNA expression levels of toll like receptors (TLRs), i.e. TLR4, TLR2 and TLR5, by Cytholethal distending toxin positive and negative strains of *S. enteritica* were examined in HT-29 cell line.

Methods:Three of each cdt+ and cdt- strains were randomly selected for bacterial genus and their interaction with differentiated HT-29 cell line was characterized. Expression of TLR2, TLR4 and TLR5 mRNA levels was examined at two time scales (4 and 24 h post infection) by quantitative real- time PCR.

Results:The levels of TLR2 induced by CDT positive *S. enterica* strains were significantly higher than those induced by CDT negative strains. CDT positive *S. enterica* induced more than two-fold increase of TLR4 in compare to the CDT negative strains. Also all CDT negative *S. enterica* strains didn't change the expression of TLR5 in HT-29 cells.

Conclusion:This study shows that CDT positive *S. enterica* strains are able to induce TLR 2 and TLR4 more efficiency than CDT negative strains. Indeed CDT has no effect on expression of TLR5. This data suggest that CDT has a role in modulating the intestinal epithelial responses to induce inflammation

Keywords:Cytholethal distending toxin, *Salmonella enterica*, Toll like receptors

P538 - 802: FMD FORMULATION IN MONTANIDE ISA-201 VG : ROBUST TH1 PATTERN

Fatemeh sadat Sarkeshik zadeh moghadas¹, Akbar Khorasani ², Mehdi Mahdavi ³

1. Department of Microbiology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, IR Iran.
2. FMD Department, Razi Vaccine & Serum Research Institute of Iran, Karaj, Iran
3. Department of Immunology, Pasteur Institute of Iran, Tehran, Ira

Background and Aim:Foot-and-mouth disease virus, a member of genus Aphthovirus and the family Picornaviridae. The virus causing disease in cloven hoofed animals that are highly contagious and cause economic loss to society. Currently available FMD vaccines are mainly based on inactivated viral antigens formulated in alum. The aim of this study was to evaluate the immunogenicity of FMD vaccine formulated in Montanide ISA-201 VG with alum based one.

Methods:FMD virus is produced in BHK-21 cell cultures. In-activated virus is used in formulation of vaccine in alum and Montanide ISA-201 VG . Experimental mice were immunized two time subcutaneously, with two week interval with vaccine formulations. Ten days after last immunization, IL-4 and IFN- γ cytokines, total antibodies and IgG subtypes were determined with ELISA method.

Results:Results show that immunization with both formulations of vaccines induced strong Th1 pattern and also Th2 immune platform in the experimental groups.

Conclusion:Based on this study results, Montanide ISA-201 VG can be used an adjuvant for FMD virus. How ever more study like challenge in animal model is needed to present the new formulation as a candidate vaccine.

Keywords:FMD , vaccine , adjuvant , Montanide

**P539 - 824: SELECTION OF ANTI-HUMAN PD-1 SINGLE-CHAIN VARIABLE FRAGMENT
ANTIBODY FROM A HUMAN PHAGE LIBRARY**

Sepideh Safaie¹, Zahra Sharifzadeh², Salman Bagheri³, fahimeh nemati⁴, Farhad Riazirad⁵, Elmira safaie⁶

1. Department of Biotechnology, Faculty of Advanced Sciences & Technology , Pharmaceutical Sciences Branch, Islamic Azad University , Tehran-Iran(IAUPS)
2. Hybridoma laboratory, Immunology department , pasteur Institute of Iran
3. Department of Immunology, Faculty of Medicine , Tabriz University of Medical Sciences , Tabriz, Iran.
4. Department of Biotechnology, Faculty of Advanced Sciences & Technology , Pharmaceutical Sciences Branch, Islamic Azad University , Tehran-Iran(IAUPS)
5. Hybridoma laboratory, Immunology department , pasteur Institute of Iran
6. Department of Immunology, Faculty of Medicine , Tabriz University of Medical Sciences , Tabriz, Iran.

Background and Aim: Non-small-cell lung cancer (NSCLC) is one of the most common causes of cancer death in the world. Programmed death 1 (PD-1) is an immune checkpoint receptor expressed on activated T cells. Expression of the inhibitory co-receptor PD-1 on tumor-infiltrating lymphocytes in NSCLC tumors, as well as the expression of the PD-1 ligand (PD-L1) on NSCLC tumor cells, are strong negative prognostic markers for disease-specific death in the NSCLC patients. PD-1 pathway blockade with scFV offers a novel approach to restoring T cell-mediated anti-tumor immunity, with the potential for application across a broad population of patients with NSCLC.

Methods: Human scFV libraries Tomlinson I+J were amplified and biopanning process was performed on this phage library to isolate scFvs against a PD-1 receptor. The relative binding affinity of phage clones to PD-1 were determined using polyclonal and monoclonal scFV-phage ELISA and screening of clones were done by soluble ELISA. Double strand phagemid DNAs were extracted from each positive clone and sequenced with LMB3 and pHEN primers.

Results: After five rounds of Biopanning, hundred phage clones from outputs two, three and four were randomly selected and tested for PD-1 binding by monoclonal phage ELISA. Twenty one clones were identified that specifically bound to PD-1 but not to BSA control protein.

Conclusion: These results shown that specifically blocking PD-1 immunosuppression can potentially prevent T-cell downregulation and promote immune responses against cancer.

Keywords: PD-1, scFV, phage display, NSCLC

**P540 - 838: IL-35 IS A NEW ANTI-INFLAMMATORY CYTOKINE IN THE DEVELOPMENT
OF SEPSIS**

Nazanin Chatrabnous¹, farzaneh ghassabi², mohammad sadegh razeghi³, Tayebbeh Hashempoor⁴

1. 1. Department of Immunology, Medical School, Kerman University of Medical Sciences, Kerman, Iran
2. 2. Department of Bacteriology & Virology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran.
3. Department of Immunology, Medical School, Kerman University of Medical Sciences, Kerman, Iran
4. Professor Alborzi Clinical Microbiology Research Center, Nemazee Hospital, Shiraz University of Medical Sciences, Shiraz, Iran

Background and Aim:Sepsis, recognized as a deadly immunological disorder, is one of the major causes of morbidity and mortality in intensive care units globally. Interleukin-35 (IL-35) is a new anti-inflammatory/immunosuppressive cytokine involved in sepsis. Until later studies, IL-35 concentration in serum samples from adult or child patients with sepsis was significantly higher compared with that from healthy controls. The aim of this mini review is to determine IL-35 and its structural and functional characteristics as well as its role in the development of sepsis in different studies.

Methods:Search terms “IL-35”, “anti- inflammatory” and “Sepsis” were used in PubMed, Science Direct, Scopus and Google Scholar. We find 5 studies in the world about IL-35 and its structural and functional characteristics as well as its role in the development of sepsis and were included in this mini review.

Results:All of studies belonged to 2012-2016. In human models, serum level of IL-35 significantly increased and is a credible biomarker to predict mortality and MODS morbidity in septic ARDS patients. In murine models suggested, IL-35 inhibits acute inflammatory response via the suppression of vascular EC activation, which implies a therapeutic potential for IL-35 in sepsis and cardiovascular diseases.

Conclusion:Sepsis is associated with enhanced release of IL-35 and likely facilitates bacterial dissemination. IL-35 plays a major role in the immunopathogenesis of sepsis. Therefor IL-35 as the new categorization system of anti-inflammatory cytokines are important for the design of new strategies of immune therapies.

Keywords:Interleukin-35, Sepsis. Anti-inflammatory cytokines

P541 - 916: IMPACT OF HSA-MIR-590-5P, HSA-MIR-520F, HSA-MIR-338-5P, HAS-MIR942 TO JURKAT CELL SIGNALING PHATWAYS UNDER INDUCTION WITH IL-2

Maryam Mapar¹, Seyed mehdi Sadat ², Najmeh Ranji ³, Mehrdad Hashemi ⁴

1. Department of new science, Islamic Azad University, Tehran Medical Branch, Tehran,Iran
2. Department of Hepatitis and AIDS, Pasteur Institute of Iran. Tehran, Iran
3. Department of Genetics, College of Science, Islamic Azad University, Rasht Branch, Rasht, Iran
4. Department of new science, Islamic Azad University, Tehran Medical Branch, Tehran,Iran

Background and Aim:MicroRNAs, which encode small non-coding RNAs of approximately 22 nucleotides.IL-2 is one of the factors influencing the proliferation of immune cells. Many studies have been done on the effect of IL-2 to cell proliferation but the role of miRNAs on these cells is not obvious.In current study, the effect of miRNAs to cell signaling phatways under induction with IL-2 were investigated.

Methods:hsa-miR-590-5p hsa-miR-520f,hsa-miR-338-5p,has-mir942 and miR-neg is synthesized in the form of freeze-dried powder.These transfection of miRNAs were performed to Jurkat cells using Lipofectamine 2000 reagent.Putative targets of up/ down regulated miRNAs were predicted using Targetscan and miRWalk software. Cell viability was measured using XTT assay.

Results:After transfection which operate in different conditions and concentration ,the miRNAs investigated with the fluorescence microscope 72 hours after treatment with miRNA ,then XTT assay performed on Jurkat cells transfected,we found that rate of transfection in Jurkat cell are low and a large number of cells have lost. miRNA decreasing effect due to the low transfected gene targets Jurkat cell signaling pathway was not examine by Real-time PCR.

Conclusion:The impact of micro-RNA hsa-miR-590-5p, hsa-miR-520f, hsa-miR-338-5p, has-mir942 and miR-neg on Jurkat cells was also evaluated after transfection, no significant difference was observed between the treatment and control cells.This could be due to the fact that these miRNA are synthetic and transfected them with no factor such as plasmid transfer,maybe the concentration of transfected miRNA into the cell was not sufficient or Maybe during the transfection structure of miRNA was destroyed and could not posed their affection.

Keywords:Jurkat, miR-20a, miR-17, XTT, Il-2

P542 - 958: INCREASED SYNTHESIS OF IL-8 BY MONONUCLEAR CELLS OF NON-SECRETOR INDIVIDUALS WITH A BLOOD GROUP A AFTER CULTIVATION AND STIMULATION WITH ANTIGENS EXTRACTED FROM PSEUDOMONAS AERUGINOSA

Soheila Farshidfar¹, Kambiz Bagheri², Majid Baseri Salehi³

1. Department of Microbiology, Kazerun Branch, Islamic Azad University, Kazerun, Iran.
2. Department of Immunology, Faculty of Medicine, Kazerun Branch, Islamic Azad University, Kazerun, Iran.
3. Department of Microbiology, Kazerun Branch, Islamic Azad University, Kazerun, Iran.

Background and Aim: So far, several studies have been conducted on the association between different blood types or secretor status and susceptibility to various diseases. The aim of this study is to evaluate the amount of IL-8 production under the influence of *Pseudomonas aeruginosa* stimulation in secretor and non-secretor individuals.

Methods: After dividing the participants with blood group A into two groups of secretor and non-secretor, mononuclear cells of each individual were separated. Then the bacterial extract of *P. aeruginosa* (ATCC: 27853, PTCC: 1430) was prepared, and added to the mononuclear cell culture and after incubation the levels of IL-8 in the cultured groups by the ELISA assay.

Results: out of 204 participants the frequency of non-secretor was 25% and for secretors 70.1%. 4.9% were also weakly secretors and excluded. The results show that IL-8 produced after bacterial stimulation was significantly more than IL-8 of the plasma and control in both secretor and non-secretor. On the other hand, the production of these inflammatory cytokine in non-secretor group was higher which probably suggests a different and stronger response of leukocytes against the inflammatory stimulation in non-secretor subjects

Conclusion: The common feature of most infectious and inflammatory complications, as well as autoimmune diseases, is the production of high amount of inflammatory cytokines, so it is likely that a reason behind high prevalence of such diseases in non-secretor people is the production of higher amount of certain inflammatory cytokines by their leukocytes. Although more research is needed to confirm this finding.

Keywords: Blood Group, Non-Secretor status, Secretor status, Interleukin-8, Mononuclear Cells, *Pseudomonas aeruginosa*

**P543 - 972: THE EFFECT OF ETHANOL EXTRACT DRACOCEPHALUM KOTSCHYI BOISS.
ON CELLULAR DEFENSE IN MICE INFECTED BY CANDIDA ALBICANS INVIVO**

Razieh Zareiyan jahromi¹, mahboobeh madani²

1. islamic azad university of falavarjan
2. islamic azad university of falavarjan

Background and Aim: *Dracocephalum kotschyi* boiss of the family lamiaceae which is rich in aromatic components and valuable for its pharmaceutical

Methods:: in this study, 93 female mice of the strain NMRI were selected and divided to 9 groups, including control, normal saline , candida, candida and extract, and extract alone. Treatment groups with extract received ethanolic extract with dosages of 50, 100, 200 Mg/Kg every other day for 20 days through intraperitoneally injection. Candida , candida and extract groups infection candida albicans only once in the sixth day of received intraperitoneal injection. The results obtained with a comprehensive statistical analysis of variance and duncan at level $p < 0/001$ were analyzed.

Results: study blood parameters showed that the average lymphocytes , monocytes and neutrophils significant increase in candida compared to other groups ($p < 0/001$).

Conclusion:: the results of this study suggest ethanolic extract *Dracocephalum kotschyi* can be used as an effective cellular immune system stimulant.

Keywords: *Dracocephalum kotschyi*, candida albicans , cellular defense , lymphocytes , monocytes

P544 - 989: POLYMORPHISMS OF INTERLEUKIN IMPACT ON HEPATITIS

Mahrokh Motevalli¹, Dr.Jamshid Mehrzad²

1. Neyshabur Branch, Islamic Azad University, Neyshabur, Iran
2. Department of Biochemistry, Neyshabur Branch, Islamic Azad University, Neyshabur, Iran

Background and Aim:Infection with hepatitis viruses B, C range of responses that stimulate innate and adaptive immunity genetic studies on multiple carriers have found that human leukocyte antigen genes and the genes of various cytokines, such as: (IL - 4 , IL - 1, IL - 10, IL - 18, IL - 12, IL - 28, ...) with HBV and HCV susceptibility to or severity of illness associated with its durability.

Methods:Blood and serum from patients and healthy people was prepared . questionnaire was prepared . And to check polymorphism of PCR-RFLP method and ARMS-PCR method is used. Blood and serum from patients and healthy people was prepared . questionnaire was prepared . And to check polymorphism of PCR-RFLP method and ARMS-PCR method is used.

Results:The impact of non-coding region of the gene polymorphism P40 subunit protein 12 in chronic hepatitis C, it seems that unusual amounts of cytokines in hepatitis C infection as the disease progresses, the presence of the virus in host and associated chronic disease. And also seems to IL-10 polymorphisms associated with HBV infection, but patients who have moderate to high IL-10 haplotype produce a greater ability to produce anti-HBe are.

Conclusion:Since interleukins diverse needs further investigation. But according to studies on hepatitis have a significant impact and be used as a biomarker of them

Keywords:Polymorphism-IL-hepatitis

P545 - 990: THE PHYLOGENIC STUDY OF HIV IN KHORASAN RAZAVI

Faeze Fakour¹, Mojghani H.R², Rezaee S.A.R³

1. MSc student of microbiology ,Islamic Azad University ,Neyshabur ,Iran
2. Virology Dept. Health College, Tehran University of Medical Sciences
3. Immunology Research Center, Inflammation and Inflammatory Diseases Division, Medical School, Mashhad University of Medical Sciences

Background and Aim: HIV is a virus with very high genetic diversity due to rapid replication and low fidelity characteristic of reverse transcriptase. This virus has several subtypes with different distribution. Determination of the virus subtypes can be helpful for vaccine design, drug resistance outbreak and epidemiological study. This study aimed to do a molecular epidemiology and genotyping of HIV-1 in patient referred to Ghaem hospitals, Mashhad, Iran.

Methods: Fourteen HIV positive patients selected and the p17 region of gag in addition of c2-v5 of env gene were amplified with PCR. The results of PCR product have sequenced and then clustered by phylogenetic analysis.

Results: The results of phylogenetic analysis obtained from 14 samples of p17 regions in gag and c2-v5 in env genes showed that all of the patients were CRF35-AD. The results of both phylogenetic trees confirmed each other.

Conclusion: First study by Naderi and his colleagues on 12 HIV-1 seropositive IDUs in 2005, showed the presence of subtype A in Iran. They proposed the transmission source in connection with African countries including Uganda and Kenya but the present study consistent with the studies were carried out after 2007 that reported CRF35-AD as the predominant circulating subtypes. Low levels of education and poor housing increase the risk of transmission.

Keywords: HIV-1, subtype, Iran, phylogeny, CRF35-AD

**P546 - 994: DEVELOPMENT OF ANTI-BOVINE IGG IMMUNOGLOBULIN Y (IGYS) IN
QUAIL**

Yoones Attari roodi¹, Kave Veisi², Reyhaneh Ghorbanpoor³, Khalil Ghouriani⁴, Gholamreza Nikbakht⁵

1. Department of Microbiology and immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
2. Department of Microbiology and immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
3. Department of Microbiology and immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
4. Department of Microbiology and immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
5. Department of Microbiology and immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran

Background and Aim: IgY is the functional equivalent of mammalian IgG, the major serum antibody found in mammals, but it is structurally different, and has been found to exhibit several important differences when compared to mammalian antibodies, including its physico-chemical properties and immunological capabilities. Recently, considerable research has focused on the use of IgY as an alternative to mammalian antibodies for several applications, including for various immunodiagnostic and immunotherapeutic applications. Quail is a small bird with great benefits such as minimal requirements of feed and breeding space, high resistance against diseases and is therefore economical. Consequently, it is a viable alternative for chickens in production of IgY for medical and research purposes.

Methods: Sixteen weeks old quail were obtained from a local breeding unit. Birds immunized with bovine IgG and booster doses were given 2 and 6 weeks after first injection. Eggs were collected weekly after first immunization for 12 weeks. Yolk IgY was isolated using precipitation method of water dilution combined with chloroform. ELISA were used for determining the quantifying the titer of IgY in egg yolks.

Results: Reactive egg yolk samples were used for ELISA checkerboard titration. According to the checkerboard titration, the best concentrations were found. ELISA showed acceptable amount of anti-bovine IgG in most weeks after immunization and the peak value was in the 5th week.

Conclusion: Our results suggest that anti-bovine IgG IgY produced in quails could be recruited as a specific probe for detection of bovine IgG-specific proteins.

Keywords: IgY-Bovine-IgG-Quail

P547 - 1050: THE EFFECT OF GENE POLYMORPHISMS TUMOR NECROSIS FACTOR (TNF) PRODUCTION OF ACUTE PHASE PROTEINS IN THE LIVER IN PATIENTS WITH HEPATITIS B

Soheila Jahan tigh¹, Jamshid Mehrzad²

1. MSC-Student of Microbiology-,Islamic Azad University-,Neyshabur-,IRAN
2. Sincerely, Dr.Jamshid Mehrzad Department of Biochemistry, Neyshabur Branch, Islamic Azad University, Neyshabur, Iran

Background and Aim:Chronic infection with hepatitis B virus is a multifactorial disease that is associated with serious clinical complications. Host genetics, especially genetic factors in the pathogenesis of hepatitis B, is crucial. Tumor necrosis factor (TNF) α plays an important role in the inflammatory response and the pathogenesis of hepatitis. The aim of this study was to evaluate the association between single nucleotide polymorphism gene region 308- TNF- α production of acute phase proteins in patients with HBV, respectively.

Methods:Genomic DNA from peripheral blood samples of 70 patients with chronic hepatitis B infection and 70 healthy subjects in this case-control study is extracted. And their DNA is analyzed by ARMS-PCR method. TNF- α serum levels measured by ELISA. CRP and serum amyloid A and haptoglobin is measured by Nephelometry.

Results:Similar studies carried out significant differences between healthy subjects and patients with different single nucleotide polymorphisms observed gene.

Conclusion:Similar studies carried out in single nucleotide polymorphism TNF- α gene can be used as a factor in susceptibility to chronic hepatitis B. Take into account the need to examine the association between polymorphisms in the gene for the production of acute phase proteins. Perform new study demands.

Keywords:Single nucleotide polymorphisms (TNF- α), the production of acute phase proteins, hepatitis B

P548 - 1120: CORRELATION BETWEEN EXPRESSION OF GINGIVAL TLR5 AS THE MOST IMPORTANT RECEPTOR FOR BACTERIAL FIMBRIA AND RANKL IN TISSUES AND PERIODONTAL DISEASES

Ali Saeedi¹, Ali Saeedi-Boroujeni², Mandana Sattari³, Sarira Shahnavaz⁴

1. -
2. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN
3. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN
4. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN

Background and Aim:Periodontal diseases are the most common chronic infections in human. Inflammatory responses play an important role in periodontal disease. TLRs play a key role in induction of inflammatory responses by periodontal cells. In addition to TLR4, LPS of *Porphyromonas gingivalis* and its fimbria can stimulate can stimulate TLR5, so the aim of this study was to evaluate the gingival gene expression of TLR5 and also RANKL as the most important factor in bone resorption, in periodontal diseases.

Methods:Gingival samples were collected from 20 individuals with clinically healthy gingival; 25 patients with moderate to severe chronic periodontitis; and 25 patients with generalized aggressive periodontitis. After homogenizing tissue samples, RNA extraction and cDNA synthesis were done. Then, Real-time PCR technique was used for evaluating gene expression.

Results:There were only significant differences between the expression of TLR5 ($P=0.021$) and RANKL ($P=0.021$) between aggressive and chronic periodontitis. The expression of both genes were higher in aggressive than chronic periodontitis.

Conclusion:It is concluded that probably TLR5 may cooperate with disease progression by inducing the expression of RANKL and other inflammatory mediators.

Keywords:TLR5, RANKL, Periodontal disease

**P549 - 1122: COMPARISON OF HEALTHY AND CHRONIC PERIODONTITIS REGARDING
GINGIVAL EXPRESSION OF HSP70**

Anahita Fooladzadeh¹, Mandana Sattari², Sarira Shahnava³

1. Dept. Pharmacology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN
2. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN
3. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN

Background and Aim:Periodontal diseases are amongst polymicrobial infections that cause the degeneration of bones and lead to loss of teeth. Observations show that prokaryotic and eukaryotic HSP are very similar in peptide sequence. These observations support the theory that HSP is a strong candidate of molecular mimicry and can be considered as a dangerous auto antigen. The pathogenicity of HSP60 molecule and its role in the development of the disease is proved, but there has not been sufficient information about the role and performance of HSP70 in periodontal disease. However, the role of this molecule in development of some diseases has been proven. Hence, defining the expressiveness of HSP70 to help identification of immunopathogenesis of Chronic periodontitis are the priorities of this research.

Methods:Samples of gum tissue of 20 clinically healthy gingival people, and 25 people suffering from moderate to severe chronic periodontitis, are collected. After extracting RNA and synthesizing of cDNA of each sample, the expressiveness of HSP70 was studied by using the Real-time PCR technique.

Results:This research showed that expressiveness of HSP70 in chronic periodontitis does not have a significant difference with healthy ones. Though the expressiveness of HSP70 in chronic periodontitis samples was higher than the healthy ones, but this difference was not significantly important.

Conclusion:The findings show that in pathogenesis of periodontal diseases, the expressiveness of HSP70 is not significant, and they may not be considered as danger signals or DAMPs, because their expressiveness is not significantly different to the healthy group.

Keywords:Periodontal disease, Heat shock protein, HSP70, Danger signal

P550 - 1123: CORRELATION BETWEEN CXCR4 AND TLR2 AND CHRONIC PERIODONTITIS

Sarira Shahnava¹, Mandana Sattari², Aram Mohammadi³

1. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN
2. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN
3. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN

Background and Aim: Periodontal diseases are among the most prevalent infections in humans; they are characterized by the classic hallmarks, including erythema and edema. A wide variety of cytokines, chemokines and their receptors are synthesized by gingival fibroblasts, epithelial cells, endothelial cells and inflammatory cells. Chemokine Receptor 4 (CXCR4) is involved in the trafficking of leukocytes into and out of extravascular tissues. CXCR4 may serve a homeostatic role to prevent excessive Toll Like Receptor 2 (TLR2)-induced inflammation or, alternatively, CXCR4 may be exploited by *Porphyromonas gingivalis* for suppressing TLR2-mediated innate immunity. However, the interaction of *P. gingivalis* with CXCR4 impairs antimicrobial host defense and it may be one mechanisms of immune evasion. So the aim of this study was to evaluate the relationship between expression of CXCR4 and TLR2 with chronic periodontitis.

Methods: For this purpose, gingival tissue samples were collected from 20 individuals with clinically healthy gingiva and 25 patients with moderate to severe chronic periodontitis. After homogenizing the gingival tissues, RNA was extracted by RNA isolation kit. After synthesis of cDNA, expression of CXCR4 and TLR2 was evaluated by Real-time PCR.

Results: Higher expression of CXCR4 and TLR2 was found in chronic periodontitis in comparison with healthy cases ($P < 0.05$).

Conclusion: Higher expression of CXCR4 and TLR2 may be related to cross-talk with *P. gingivalis* fimbria, which leads to decrease host immune response. *P. gingivalis* in chronic periodontitis is important and also *P. gingivalis* may be the main pathogen in chronic periodontitis.

Keywords: CXCR4, TLR2, Chronic periodontitis

**P551 - 1124: CORRELATION BETWEEN THE LEVEL OF SOLUBLE CD14 AS A RECEPTOR
FOR BACTERIAL LPS AND NEUTROPHIL DEATH**

Shideh Mehrmofakham¹, Mandana Sattari², Hassan Darbandi³

1. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN
2. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN
3. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN

Background and Aim: Periodontopathic bacteria can cause the death of immunity cells such as neutrophils and mononeuclear cells and this effect is related to LPS. It has also been cleared that the saliva of patients with periodontal disease considerably caused the death of neutrophils. So the main objective of this study was to identify the relationship between the concentration of sCD14 in saliva and existence of apoptosis of neutrophils of blood by the saliva of patients with periodontitis whom refer to dental school of Shahid Beheshti university of Medical Sciences.

Methods: Samples of saliva of three groups including healthy, patients with gingivitis, Patients with periodontitis (each group containing 30 samples) had been collected. After isolation of the neutrophils from the blood and treated them with the saliva samples, Gimsa staining was done in order to determine the percentage of apoptosis neutrophils. The concentration of sCD14 of saliva samples was measured by ELISA.

Results: There was a significant difference ($P \approx 0.001$) regarding the concentration of sCD14 between 3 groups (moderate to severe chronic periodontitis; gingivitis and healthy gingiva) There was also significant difference between the healthy and gingivitis groups; and healthy and periodontitis groups. There was also a positive correlation between the concentrations of sCD14 and apoptosis of neutrophils.

Conclusion: It is concluded that increased level of sCD14 in the saliva of the patients with periodontal disease can be related to stimulation of the immune system by LPS of gram negative periodontopathic bacteria.

Keywords: CD14, Neutrophil, Apoptosis, Periodontal disease, LPS

P552 - 1128: MOESIN, A NOVEL MOLECULE, IN RECOGNIZING LPS AND PERIODONTITIS

Shaghayegh Pezeshki¹, Mandana Sattari², Hediye Ghalikhani³, Sarira Shahnava⁴

1. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN
2. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN
3. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN
4. Dept. Immunology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran-IRAN

Background and Aim: Periodontal diseases are primarily initiated by periodontopathic bacteria, especially *Porphyromonas gingivalis*. In addition to bacteria, immune responses against bacteria especially by stimulating TLRs has an important role in disease progression. Moesin is considered as a new co-receptor for TLR4. Since there is not enough information about the role of moesin in periodontal disease, the aim of this study was to evaluate moesin expression and chronic and aggressive periodontitis.

Methods: For each patient group, 25 samples (25 samples for aggressive and 25 samples for chronic periodontitis) and for healthy group 20 samples were collected (totally 75 gingival samples). After extracting the RNA, cDNA prepared from all of samples and for determining of the quality of the cDNA, PCR amplification was performed. Then Beta actin and Moesin gene expression was investigated by Real-time PCR technique.

Results: There was a significant lower expression of moesin in patient groups (chronic and aggressive periodontitis) compared to and control group ($P \approx 0.025$). In the case of aggressive periodontitis, there was significant lower expression of moesin, compared to control group. Despite of higher expression of moesin chronic periodontitis compared to aggressive periodontitis, but it was not significant.

Conclusion: It is concluded that recognition of periopathogens by moesin does not have an important role. Since *P. gingivalis* the most important periodontopathic bacteria, can stimulate both TLR2 and TLR4, it seems that in pathogenesis of periodontal diseases, recognition of pathogen might be done by TLR2 which leads to synthesis of proinflammatory cytokines.

Keywords: Moesin, TLR4, Periodontal disease

**P553 - 1129: STUDY OF SOME HEMATOLOGICAL AND BIOCHEMICAL PARAMETERS IN
VACCINATED CHICKEN WITH COMBINED INACTIVATED NEWCASTLE-INFLUENZA
VACCINE**

Mahdi Ezdiyadi¹, Ali Akbar Abolfathi ²

1. MSc Student, Department of Biochemistry, Ahar Branch, Islamic Azad University, Ahar, Iran
2. Department of Biological Science, Ahar Branch, Islamic Azad University, Ahar, Iran

Background and Aim: In this study we investigated the immune responses of vaccinated chickens with inactive twofold oily Newcastle – poultry influenza vaccine through muscular and subcutaneous injection.

Methods: We although studied the possible variation in the amount of biochemical factors of serum. We evaluated the amount of serum anti body and Hemato- biochemical factors on the 7th, 14th, 21th and 28th days after injection.

Results: Results show that there is not meaningful differences in the amounts of biochemical parameters like Albumin, glucose, total protein, triglyceride, cholesterol, and enzymes like ALT, AST, ALP and minerals like sodium and potassium and hematocrit – hemoglobin values between vaccinated and non-vaccinated chickens. Vaccinated chickens with antigens show meaningful differences in Newcastle and influenza antibody titer against the groups with adjuvant.

Conclusion: Results confirm that muscular and subcutaneous injection of twofold vaccine show similar efficacy of variation in biochemical – hematology factors. Although Newcastle and influenza titer are similar in both methods. To develop a proper immune response for inactive vaccines, adding a suitable adjuvant is necessary

Keywords: Poultry influenza virus, Newcastle virus, biochemical factors

**P554 - 1256: EVALUATION OF RABBIT HUMORAL IMMUNE RESPONSES AFTER
ADMINISTRATION OF FRACTIONATED AND CRUDE SNAKE VENOM**

Shiva Kashkool koluee¹, majid tebianian²

1. Active Pharmaceutical Ingredient Research Center, pharmaceutical Sciences Branch, Islamic Azad University, Tehran-Iran
2. Razi Vaccine and Serum Research Institute. Karaj, Iran

Background and Aim: snakebite is considered to be a top medical emergency worldwide. *Naja naja oxiana* (NNO) with neurotoxic effects is one of the important venomous species in Iran. Current snakebite treatment is antivenom therapy that deals with hyperimmunization of horses with crude snake venom, antivenom is produced and extracted from serum to use for venom neutralization therapy. But use of crude venom to obtain antivenom cause some unsought and interfering antibody responses that lead to diminish antivenom potency and proficiency because of diversity of proteins that constitute crude venom. In this study we compared 2 most immunogenic fractions of NNO venom and compared their humoral immune responses with crude venom by hyperimmunization of 2 groups of 1.5kg Dutch female rabbits with both forms respectively.

Methods: NNO venom was chromatographed and two most immunogenic fractions were collected. Fractions and crude venom with appropriate formulation plus proper adjuvant injected subcutaneously 10 days intervals into 2 groups of rabbits respectively. Serums were collected 10 days after each shot. ELISA was performed according to Theakston et al by some changes using fraction and crude venom as coating antigens. A standard curve between log antisera and log optical density (OD) at 450 nm was plotted.

Results: optical densities that were read and analysed by SPSS analysis, represented the significant resemblance in antibody levels between two hyperimmunized groups.

Conclusion: The established ELISA results show the importance of the purified fractionated parts as immunogens for raising therapeutic antisera and as diagnostic components for in vitro determination of the potency of the therapeutic antisera.

Keywords: *Naja naja oxiana*, antivenom, crude venom, fraction, ELISA, Hyperimmunization

Medicinal Plants

P555 - 28: ANTIMICROBIAL ACTIVITY OF PHOENIX DACTYLIFERA ON ISOLATED VIBRIO SPP. FROM SHRIMP AQUACULTURE IN BUSHEHR PROVINCE, IRAN

Somaye Baseri¹, Nima Bahador², Maryam Mirbakhsh³

1. Master in Microbiology, Bushehr University of Medical Sciences, Iran
2. Department of Microbiology, Shiraz Branch, Islamic Azad University, Shiraz, Iran
3. Iran Shrimp Research Center

Background and Aim: Vibriosis is one of the most prevalent bacterial fish diseases worldwide. Use of antimicrobial agents in aquacultures may could alter the dynamics of bacterial communities and induce antibiotic resistance.

Methods: In the present study totally 315 water, sediment and shrimp (*Litopenaeus vannamei*) samples were collected from three aquaculture in Delvar, Helle and Mond in Bushehr province during May–August 2014. The samples were cultivated on TCBS agar medium and incubated at 37°C for 24 hrs. Then the pure isolates were identified using ApiKit 20E and Molecular methods. Furthermore, effect of methanol, acetone and aqueous extract of *Phoenix dactylifera* leaves were evaluated on the isolates using well diffusion agar technique and MIC of the herbal plant for each organism were calculated.

Results: The results of PCR obtained from this study indicated that out of 252 isolates the species were belonging to *V. corallilyticus* strain ATCC BAA-450 (48.41%), *V. alginolyticus* strain 167 (11.11%), *V. alginolyticus* strain CIFRIV-TSB1 (7.54%), *V. harveyi* (3.57%), *V. hepatarius* strain CIBAAG5 (3.57%) and others (25.75%) were belong to *Aeromonas* species. Among the three solvents, all extracts of *Phoenix dactylifera* pro showed Minimum inhibitory zone of inhibition against isolate except *V. harveyi*. The Minimum inhibitory concentration (MIC) of aqueous extract against these pathogens was calculated as 0.0043 ± 0.0013 gr/ml.

Conclusion: Consequently it could be concluded that *Phoenix dactylifera* could be use for remedy of vibriosis in shrimp aquacultures.

Keywords: Antibacterial activity, Shrimp aquaculture, Vibriosis, *Phoenix dactylifera*

**P556 - 35: DEVELOPMENT OF A SYMBIOTIC IRANIAN WHITE CHEESE ADDED WITH
BIFIDOBACTERIUM BIFIDUM AND ALLIUM AMPELOPRASUM**

Mina Razavi¹, Tooraj Mehdizadeh²

1. Department of Biology, Urmia Branch, Islamic Azad university, Urmia, Iran
2. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Urmia University, Urmia, Iran

Background and Aim: In recent years there has been a significant increase in research on the functional foods in human nutrition. Probiotics and prebiotics play an important role in this regard. Prebiotics are non-digestible complex carbohydrates that their fermentation in the colon, yield energy and short chain fatty acids, and selectively promote the growth of probiotic bacteria in the gastro-intestinal tract. A. ampeloprasum contains about 12% of fructan, that is a proved prebiotic compounds. The aims of this study was to evaluate efficiency of this plant in synbiotic Iranian white cheese to increase growth and sustainability of Bifidobacterium bifidum and development a new dairy product.

Methods: Cheeses prepared from five different formulas (1% fresh plant, 2% fresh plant, 1% dry plant, 2% fresh plant and without plant) plus B. bifidum were assessed during 45 days of storage at 4°C. Samples were tested for pH, microbial count, as well as sensory evaluation.

Results: The results indicated that the samples containing 1% fresh and dry plant have the most flavor and texture score. As well as, the Iranian white cheese enriched with leek proved to be an efficient carrier for B. bifidum.

Conclusion: It can be concluded that Leek and B. bifidum can be successfully used for production of a synbiotic cheese.

Keywords: Bifidobacterium bifidum, Allium ampeloprasum, Prebiotic, Probiotic, Iranian white cheese

P557 - 73: THE EFFECTS OF MENTHA SPICATA L., CUMINUM CYMINUM L. AND MENTHA LONGIFOLIA L. ESSENTIAL OILS INDIVIDUALLY AND COMBINED WITH SODIUM BENZOATE AGAINST ESCHERICHIA COLI O157:H7

Maryam Ekhtelat¹, Zeinab Bahrani², Amir Siahpoosh³, Abdolghani Ameri⁴

1. Medicinal Plants and Natural Products Research Center, School of Pharmacy, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
2. Medicinal Plants and Natural Products Research Center, School of Pharmacy, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
3. Medicinal Plants and Natural Products Research Center, School of Pharmacy, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
4. Department of Drug and Food Control, School of Pharmacy, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Background and Aim: Many people are used medicinal plants due to natural, low risks and complications, and low costs as compared with the synthetic drugs. Incidence of drug resistance against chemical antimicrobial drugs has led the use of medicinal plants for treatment of infections in recent years. The aim of this study was to examine possible antibacterial effects of the essential oils individually and combined with Sodium Benzoate against Escherichia coli O157:H7.

Methods: In this study, the essential oils were obtained from the Barij Esans Company and analyzed by GC/MS. Disc diffusion and broth microdilution assays were used for in vitro antimicrobial screening in triplicate. The collected data was analyzed by the SPSS software using ANOVA.

Results: Statistical analysis showed significant difference between different antibacterial effects of essential oils individually and combined with sodium benzoate. In comparing the individual effects of these factors, antibacterial effect of sodium benzoate was highest and then Mentha longifolia, Cuminum cyminum and Mentha spicata essential oils indicated antibacterial activity respectively. These results are relatively consistent with the disc diffusion test. The effects of sodium benzoate combined with Mentha longifolia and Mentha spicata essential oils showed significant differences with sodium benzoate effect individually ($P < 0.05$).

Conclusion: The results indicated that these essential oils have a good antibacterial activity and combined with sodium benzoate could reduce the use of sodium benzoate as a chemical preservative in food, cosmetic and drug products, which can decrease the possible side effects of it.

Keywords: Antibacterial effect, Essential oil, Sodium benzoate, Escherichia coli O157:H7

بر روی گونه (CITRUS AURANTIUM L) بررسی فعالیت ضد باکتریایی عصاره های مختلف گل بهار نارنج: 81 - P558
های میکروبی در شرایط آزمایشگاهی

Mohammad Ahanjan¹

1. Mazandaran Uni of Med Sci

Background and Aim: تجاری و از مهم ترین فعالیت های Citrus aurantium L از خانواده مرکبات با نام علمی نارنج: ترکیبات فرار و هیدروکربن مونوترپن می بسیاری از فلاون ها صنعتی و کشاورزی جهان است مرکبات منبع غنی از فلاونوئیدها و ایران بهار نارنج به عنوان یک گیاه بهار نارنج دارای خاصیت آنتی اکسیدانی و ضد میکروبی می باشد. در طب سنتی باشند اسانس است آرامبخش و تقویت کننده خواب شناخته شده

Methods: اسفیورد از باغات مرکبات استان مازندران (بخش مرکزی ساری، دهستان Citrus aurantium L گل های Mazandaran province (The central part of Sari, Esfivard shorab rural district, , Kord Kheyl_ Galeh Kola Sofla) (شوراب، روستای کردخیل_گله کلا سفلی تهیه شد. با حلال های آبی، متانلی و استونی به روش پرکولاسیون عصاره گیری (MIC و Disc diffusion آزمایش تعیین شده و خشک گردید. از عصاره های تغلیظ شده غلظتهای مختلف جهت استفاده در سوسپانسیون میکروبی تهیه گردید مولر هینتون براث استریل اشیریشیاکلیبیسورت لیوفلیزه تهیه شد و در محیط باکتری های کلیسیلا و

Results: ضد میکروبی عصاره استونی بهتر از به روش میکرودایلوشن خاصیت Klebsiella مطالعه نشان داد بر روی باکتری نتایج: و در مورد چاهک نیز به همین منوال است و بیشترین میانگین قطر هاله عدم MIC آن mg/ml 100 عصاره های آبی و متانلی بوده و آن MBC. فعالیت عصاره متانلی بهتر بود Escherichia coli بوده است. بر روی باکتری 11.33 mm رشد با احتساب 3 تکرار ، بوده است mm و میانگین قطر هاله 12 mg/m 150

Conclusion: اثرات آنتی باکتریال در غلظتهای بالای متانلی و استونی این موضوع نسبتا بیشتر بوده از گیاه بهار نارنج در مجموع: خود نشان دادند.

Keywords: activity Antibacterial , , extract Citrus aurantium L (عصاره بهار نارنج) ساری، ضد باکتریال

**P559 - 93: GREEN TEA EXTRACT INHIBITS BIOFILM FORMATION BY CANDIDA
ALBICANS (IN VITRO STUDY)**

Parisa Raei¹

1. MSc Graduated Student, Department and Food Science and Technology, University of Tabriz, Tabriz Iran

Background and Aim: Candidiasis is one of the most incident and important opportunistic fungal infections which caused by Candida yeast species like *C. albicans*, *C. glabrata* and *C. krusei*. The purpose of the present study is to evaluate the antifungal and anti-biofilm property of green tea extracts against Candida species and its effect on their biofilm formation.

Methods: green tea ethanolic extract as potential mouth washer was used to evaluate its effect against fungi agar dilution method and biofilm was evaluated by crystal violet staining method.

Results: MIC of green tea extract for evaluated strains were 40, 40, 20 mg/ml for *C. krusei*, *C. albicans*, *C. glabrata* respectively. Green tea extract successfully inhibited biofilm formation by *C. krusei* and *C. albicans* and *C. glabrata*

Conclusion: Findings of the present study indicates that green tea extract have a good antifungal and antibiofilm formation by fungi against *C. albicans* and *C. Krusei* and *C. glabrata* Concentrations between 40 mg/ml till 5 mg/ml had the highest antibiofilm and antifungal effect. using herbal extract such as green tea can be a new era for antimicrobial therapy after developing antibiotic resistance in microbes.

Keywords: green tea extract, biofilm, *C. albicans*, *C. Krusei*, antifungal

**P560 - 99: ESSENTIAL OIL OF TRACHYSPERMUM AMMI LINK EFFECTIVE
ANTIBACTERIAL AGENT AGAINST ISOLATED AND STANDARD BACTERIA**

Sahar Omidpanah¹, Manayi Azadeh², Hadjiakhondi Abbas³

1. Medicinal Plants Research Center, Faculty of Pharmacy, Tehran University of Medical Sciences, Tehran, Iran.
2. Medicinal Plants Research Center, Faculty of Pharmacy, Tehran University of Medical Sciences, Tehran, Iran.
3. 1-Medicinal Plants Research Center, Faculty of Pharmacy, Tehran University of Medical Sciences, Tehran, Iran. 2-Department of Pharmacognosy, Faculty of Pharmacy, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: *Trachyspermum ammi*, According to traditional medicine, the seeds are hot, pungent, stomachic, appetizer, aphrodisiac, carminative, laxative and diuretic.

Methods: The fruit of the plant were subjected to extract oil using Clevenger type apparatus in the present study. The residue of the fruit treated with hydrochloric acid to hydrolyzed glycosidally bound compounds and again hydrodistilled to obtain volatile compounds. The components of obtained oils were identified using GC-MS by comparison of retention indices with those reported in the literatures. Antibacterial activity of the oils and pure thymol were examined against *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, and *Enterococcus faecalis* as well as two isolated bacteria from diseased hen, *Salmonella typhimurium* and *E. coli* using disk diffusion and microdilution methods.

Results: The fruit of the plant yielded 3.5 and 2.4 mL oils before and after acid treatment, respectively. Thirteen and twenty four compounds were identified in the oil before and after acid hydrolysis. Thymol, para-cymene, and gamma-terpinene were the major components of the both oils. All the tested bacteria sufficiently suppressed by the oils with inhibition zone (IZD) diameters ranging 26.6-50.3 mm with minimum inhibitory concentration (MIC) of $<0.02 \mu\text{L/mL}$ for all strains. Thymol inhibited growth of the bacteria with concentration of 100 mg/mL.

Conclusion: The results of the present study revealed that the fruit of *T. ammi* may serve for production of supplements or therapeutic antibacterial agents for poultry industries

Keywords: *Trachyspermum ammi*, antibacterial, poultry disease, acid hydrolysis

**P561 - 100: ANTIBACTERIAL ACTIVITY OF SOME MEDICINAL PLANTS AGAINST
ISOLATED ESCHERICHIA COLI FROM DISEASED LAYING HENS**

Sahar Omidpanah¹, Manayi Azadeh², Hadjiakhondi Abbas³

1. Medicinal Plants Research Center, Faculty of Pharmacy, Tehran University of Medical Sciences, Tehran, Iran.
2. Medicinal Plants Research Center, Faculty of Pharmacy, Tehran University of Medical Sciences, Tehran, Iran.
3. 1-Medicinal Plants Research Center, Faculty of Pharmacy, Tehran University of Medical Sciences, Tehran, Iran. 2-Department of Pharmacognosy, Faculty of Pharmacy, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: The phenomenon of antibiotic resistance exhibited by the pathogenic microorganisms have led to the need for screening of several medicinal plants for their potential antimicrobial activity.

Methods: In the present study, inhibitory activity of aqueous and ethanol 90 % extracts of *Zataria multiflora*, *Thymus vulgaris*, *Mentha pulegium*, *Mentha piperita*, *Ocimum basilicum*, *Cassia senna*, and *Carthamus tinctorius* on the growth of *Escherichia coli* isolated from diseased chickens were tested in vitro using disk diffusion method. Inhibition zone diameters of bacterium were calculated in the presence of the plants extract.

Results: All the ethanol 90 % extracts with concentration of 0.2-1.0 mg/mL effectively inhibited the growth of the bacterium, while aqueous extracts showed no activity against *E. coli*. Inhibition zone diameters (IZD) of the bacterium treated with different concentrations of ethanol 90 % extracts of the plants ranging 14.6-41.0 mm. *Zataria multiflora* and *M. pulegium* with concentration of 1.0 mg/mL exhibited highest antibacterial activity compared with other plants with IZDs of 41.0 and 39.0 mm, respectively. According to the results, the order of inhibitory effect of plants extract with concentration of 1.0 mg/mL against *E. coli* was *Z. multiflora* > *M. pulegium* > *T. vulgaris* > *M. piperita* > *C. angustifolia* > *C. tinctorius* > *O. basilicum*.

Conclusion: Our findings revealed that the tested plants could be considered as suitable source of phytochemicals for prevention of *E. coli* growth. The extracts of the examined plants are suitable supplementary alternative for control of *E. coli* in laying hens.

Keywords: antibacterial, *E. coli*, *Z. multiflora*, *M. pulegium*

**P562 - 113: THE STUDY EFFECTS ANTIMICROBIAL OF FOENICULUM VULGARE MILL
AND ACHILLES MILLE FOLIUM PLANT ON BACTERIAL PATHOGENS CAUSING
URINARY TRACT INFECTIONS AND NOSOCOMIAL INFECTION**

Hassan Mahmoudi¹, Mohammad Yousef Alikhani ², Hossein vazini³, Kolsoom shirzadi karamolah⁴,
Nayere Zare Fahim⁵

1. Microbiology Department, Hamadan University of Medical Sciences, Hamadan, Iran
2. Microbiology Department, Hamadan University of Medical Sciences, Hamadan, Iran
3. Nursing Department, Basic Sciences faculty, Hamedan Branch, Islamic Azad University, Hamedan, Iran
4. M. Sc Microbiology, Boroujerd Branch, Islamic Azad University, Boroujerd Branch, Iran
5. B. Sc Laboratory Science, Medical Sciences, Hamadan, Iran

Background and Aim: Urinary tract infections due to prevalence global and having of complications such as, kidney stones, miscarriage, urinary tract disorders, hypertension, uremia, and increase the costs economic on countries, is particularly important. As well as increasing antibiotics resistance and drug side effect. The reasons for the replacement herbal medicines and natural antimicrobial substances have more fight infections.

Methods: In this study, twenty strains from verity sample hospitals obtained. Therefore Foeniculum vulgare mill and Achilles mille folium plants of the growing season and dried in darken collected. Then aqueous and alcoholic extracts of plants by soaking method distillation with water were prepared. The concentration of 0.25, 0.50, 1, 2, µg/ml was prepared. Then for determined antimicrobial effects were used disk and agar diffusion method and MIC (minimum inhibitory concentration) were investigated. Data analysis using (x2) was done (P<0.001).

Results: The results of this study showed that alcoholic and aqueous extraction plants have to antibacterial effect on these bacteria Staphylococcus aureus and E.coli, Staphylococcus saprophyticus. That with the increase in the concentration of antibacterial effect increased. In this study, Achilles mille folium plant did not affect inhibitory of Pseudomonas aeruginosa.

Conclusion: The finding of this study and another studies in this field showed that, alcoholic and aqueous extracts Achilles mille folium and Foeniculum vulgare mill plants can be of has an its inhibitory effect on pathogenic bacteria. However, they are offered as a composition of antibacterial needs rather Study.

Keywords: Urinary tract infection, Minimum inhibitory concentration, Disk diffusion method

**P563 - 126: A REVIEW OF HERBAL REMEDIES LEISHMANIASIS IN IRAN: SYSTEMATIC
REVIEW**

Ahmad Mahmoodi kouhi¹, Yasin Mehdipoor²

1. BS. Student of medical laboratory, faculty of para medicine, Dezful University of Medical Sciences, Dezful, Dezful, Iran
2. B.S student of Medical Laboratory, Paramedical faculty, Dezful University of Medical Sciences , Dezful, Dezful, Iran

Background and Aim:: Drugs, treatments for leishmaniasis are often faced with complications and limitations, and also increasing parasite resistance to chemical treatments has attracted the attention of researchers in herbal medicines. The purpose of this study was to review the treatment plant studies have been done to control leishmaniasis in Iran.

Methods:this systematic review was done by searching in databases such as: Google, Google Scholar, IRCT, Magiran, Iranmedex, SID, PubMed, ScienceDirect. Articles were published from 1997 to 2015 by keywords like Leishmaniasis, Kalaaza, Salak(Persian), Treatment plant , Iran , Herb in both Persian and English.

Results:review 70 articles showed that purified extract of vulgaris , artemether , yarrow , thyme , cream HH1125, lavender , honey , Honey , Cassia , ointment R10, black alum , Vinca , wormwood and walnut leaves reduces the diameter of the Cutaneous leishmaniasis and Prevent the progression of it. also, Vulgaris , artemether , Mymvzayy Flora , onions , cassia , asafetida , cotton boll , foot mountain , medlar , oleander , marigold Reduce the Leishmania promastigotes. wormwood and walnut leaf causing immobility of parasite and about Henna and garlic and Flora conflicting results were obtained .

Conclusion:The results of the review show that there are a lot of plants that have anti- Leishmania effect in Iran, and are effective in wound healing Cutaneous leishmaniasis. Given that most research has been done on the experimental model, it is recommended that more research be done on humans.

Keywords:: Leishmaniasis , treatment plant , Iran

**P564 - 154: THE ROLE OF PEGANUM HARMALA ETHANOLIC EXTRACT AND TYPE II
TOXIN ANTITOXIN SYSTEM IN BIOFILM FORMATION**

Bitā Aalipour¹, Sara Malekshahian², Sobhan Ghafourian³

1. Clinical Microbiology Research Center, Ilam university of Medical Sciences, Ilam, Iran
2. Clinical Microbiology Research Center, Ilam university of Medical Sciences, Ilam, Iran
3. Clinical Microbiology Research Center, Ilam university of Medical Sciences, Ilam, Iran

Background and Aim:Note, the biofilm formation known as a major worldwide concern. Toxin antitoxin system is a regulatory system that antitoxin inhibits the toxin. We aimed to determine the role of TA loci in biofilm formation in *K. pneumoniae* clinical and environmental isolates; also inhibition of biofilm formation by *Peganum harmala*.

Methods:40 *K. pneumoniae* clinical and environmental isolates were subjected for PCR to determine the frequency of *mazEF*, *relEB*, and *mqsRA* TA loci. Biofilm formation assay subjected for all isolates. Then, *P. harmala* was tested against positive biofilm formation strains.

Results:Our results demonstrated that *relBE* TA loci were dominant TA loci; whereas *mqsRA* TA loci were negative in all isolates. The most environmental isolates showed weak and no biofilm formation while strong and moderate biofilm formation observed in clinical isolates. Biofilm formations by *K. pneumoniae* in 9 ug/ml concentration were inhibited by *P. harmala*.

Conclusion:Our data suggested TA loci could control biofilm formation in *K. pneumoniae*. Also, *Peganum harmala* was introduced as an anti biofilm formation drug. It is recommended for future analysis to do in vivo study and also protein quantity of TA loci to show the importance of TA loci in non biofilm formation strains.

Keywords:*Klebsiella pneumoniae*; Biofilm formation; *Peganum harmala*

**P565 - 169: SANITIZING AND ANTIBIOFILM PROPERTIES OF ZATARIAMULTIFLORA
ESSENTIAL OIL AGAINST STAPHYLOCOCCUS AUREUS**

Maryam Shirdel¹, Hossein Tajik², Mehran Moradi³

1. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine Urmia University, Urmia, Iran
2. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine Urmia University, Urmia, Iran
3. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine Urmia University, Urmia, Iran

Background and Aim:essential oils are known as a new and promising natural sanitizing agent. The aim of this study was to determine sanitizing and antibiofilm activity of different concentrations of Zatariamultiflora essential oil (ZEO) on planktonic and biofilm forms of *S. aureus*.

Methods:Minimal inhibitory concentrations (MIC) of ZEO was determined using a broth micro-dilution assay, then, the sanitizing activity of MIC, 2MIC and 4MIC concentrations of ZEO were explained as the reduction of bacteria at room temperature after 15 min contact time. The antibiofilm activity of the same concentrations were also evaluated on one day old biofilm of *S. aureus* according to microtitertest.

Results:The MIC value was 1250 µg mL⁻¹.All tested concentrations were reduced 100% of primary inoculated bacteria during 15 min contact time. Moreover, ZEO at MIC concentration represented a strong ability on biofilm and reduced 92% of biofilm, but the activity was decreased as ZEO concentrations increased which reduction were 88 and 78% for 2MIC and 4MIC, respectively.

Conclusion:The findings of the present study well demonstrated ZEO as good sanitizing solution for use at sanitation in food plant.

Keywords:Essential oil, Biofilm, Sanitation,*S. aureus*

P566 - 180: EVALUATION OF ANTIFUNGAL ACTIVITY OF ASTRAGALUS HAMOSUS

Asie Shojaii¹, Nahid Rahimi Fard², Mahbobeh shamsiPoor³

1. Research Institute for Islamic and Complementary Medicine, Iran University of Medical Sciences, Tehran, Iran
2. Food and Drug Laboratory Research center (FDLRC), Food and Drug Control Laboratories (FDCLs), Ministry of Health (MOH), Pharmaceutical sciences branch, Islamic Azad university, Tehran, Iran
3. Pharmaceutical Sciences Branch, Islamic Azad university, Tehran, Iran

Background and Aim: Due to multiple drug resistance against antimicrobial drugs, investigations to discovering new antibacterial compounds from natural sources have been designated. This study was carried out to evaluate the antifungal activity of the extract and fractions of the pods of *Astragalus hamosus*

Methods: Fruits of *A. hamosus* was purchased from herbal market in Tehran and authenticated by an herbalist. Fruits were extracted by methanol using maceration method. Total methanolic extract was fractionated by liquid-liquid fractionation method using hexane, chloroform, and water. The antifungal activity of the extract and fractions was studied against *Candida albicans*, *Aspergillus niger*, *Aspergillus fumigatus* and *Aspergillus flavus* using cup plate, disk diffusion, MIC and MFC microplate methods

Results: Total extract and fractions of *A. hamosus*, showed significant antifungal activity against tested microorganism. Total methanolic extract showed the best antifungal activity with MIC 3.12 and MFC 6.25 µg/ml against *Candida albicans* and *Aspergillus fumigatus*.

Conclusion: The findings showed that *Astragalus hamosus* possessed antifungal activity. There are some flavonoids isolated from *A. hamosus* which may responsible for the antimicrobial activity. More studies are necessary to determine the active constituent of *A. hamosus*.

Keywords: *Astragalus hamosus*, antifungal, MIC, MFC

P567 - 193: THE ANTIBACTERIAL EFFECT OF ETHANOLIC EXTRACT OF SAFFRON ON GROUP A BETA-HEMOLYTIC STREPTOCOCCUS (A GRAM-POSITIVE BACTERIA)

Hanieh Asadallahi¹, Fetemeh Anifat², Leila Abouahi³

1. shahid Ahmadi-Roushan student research center, Baharestan 1 education office- Baharestan, Tehran, Iran
2. shahid Ahmadi-Roushan student research center, Baharestan 1 education office- Baharestan, Tehran, Iran
3. shahid Ahmadi-Roushan student research center, Baharestan 1 education office- Baharestan, Tehran, Iran

Background and Aim: Beta-hemolytic streptococcus is a gram-positive bacteria that causes human diseases, including pharyngitis, otitis media, pneumonia, sinusitis, and tonsillitis. Saffron is a medicinal herb which in traditional medicine has used for different diseases such as depressant, infections, blood pressure and etc. In the current study, the antibacterial effect of ethanolic extract of saffron on beta-hemolytic streptococcus was investigated.

Methods: After preparation of the extract, the minimum inhibitory concentration and minimal bactericidal concentration (MIC / MBC) were determined. In disc diffusion method, the mean diameter of growth inhibition zones on agar media were determined by preparing discs from different concentrations (400, 600 and 800 ppm). In order to compare the antibacterial effect of saffron extract with antibiotics, antibiogram kits for penicillin, amoxicillin and vancomycin were used as a positive control groups.

Results: The results revealed that certain concentrations of the saffron extract showed significant antibacterial effect on the strains. Extracts with 400, 600 and 800 ppm concentration showed defined growth inhibitory effect and 600 and 800 ppm concentration showed both inhibitory and bacteriocidal effects on the bacteria. The results of used antibiogram kits indicated that the effect of extract on beta-hemolytic streptococcus was similar to the effects of penicillin, amoxicillin and vancomycin antibiotics.

Conclusion: Findings from this study showed that saffron extract inhibits the growth of Gram-positive bacteria beta-hemolytic streptococci. This plant can be considered as a medicinal plant used for treating infections caused by beta-hemolytic streptococcus.

Keywords: Beta-hemolytic streptococcus; Ethanolic extract of saffron

**P568 - 210: THE VIEW OF TRADITIONAL PERSIAN MEDICINE ABOUT MICROBE AND
ANTIMIROBIAL AGENTS**

Roja Rahimi¹

1. Tehran University of Medical Sciences

Background and Aim:Traditional Persian medicine (TPM) is a temperament-based medicine and pay to manage diseases with holistic view. In TPM literatures, it has not been implied directly to microbe or bacteria. The aim of the present paper is to discuss about the view of TPM about infections and the methods of treatment.

Methods:For this purpose, the TPM literatures have been searched to find any subjects related to concept of infection as well as its treatment strategy.

Results:Increase in body moisture has been mentioned as a predisposing factor for infection. Thus, natural remedies which can dry moisture called Mojaffif (Arabic term means desiccative agent) in TPM have been considered for prevention or treatment of infections. Natural remedies with dry temperament including cold and dry or hot and dry temperament have desiccant activity. Medicinal plants with cold and dry temperament have an astringent taste and phytochemically contain tannins as their major chemical constituents. Antimicrobial properties of tannins have been evaluated and confirmed by different studies. medicinal plants with hot and dry temperament have bitter, pungent or salty taste. in TPM it is believed that the most desiccant properties is belong to bitter taste. So, the medicinal plants with bitter and astringent flavor can produce the best antimicrobial properties. From the medicinal plants with this characteristics it could be named from Terminalia chebula fruit, fruit from Quercus species, and the peel of Punica granatum.

Conclusion:Survey of TPM literatures can be useful in discovering new ways to prevent and treat infections.

Keywords:infection; antimicrobe; traditional Persian medicine; astringent; bitter; temperament

**P569 - 218: EFFLUX PUMP INHIBITORS DERIVED FROM PLANTS: A PROMISING
APPROACH TO INTERFERE EFFLUX-MEDIATED DRUG RESISTANCE IN BACTERIA**

Seyede Nargess Sadati Lamardi¹

1. Assistant professor of Pharmacognosy, Department of traditional pharmacy, School of traditional medicine, Tehran University of Medical Sciences

Background and Aim: Inherent resistance of bacteria mediated by efflux pumps play an important role in the improvement of resistances. Bacteria have developed these membrane transport proteins in order to extrude xenobiotics out of the cell. One possible approach to overcome this resistance is the co-administration of so called 'efflux pump inhibitors' (EPI) derived from plant source together with an antibiotic (AB).

Methods: The aim of this study is to present newly discovered efflux pump inhibitors with plant based origin against bacterial strains of concern using electronic databases such as Pubmed, Scopus and Google Scholar up to 2016.

Results: Some EPI with plant origin have been patented in the last years: a tetrandrine-based EPI which restores the activity of fluoroquinolones in *E. coli*, liquiritin as EPI against fluoroquinolone resistance in *E. coli*, phenylpropanoids as lead compounds as EPI against mycobacteria and also geraniol served as basis for a new EPI against *Enterobacter aerogenes*. The co-administration of EPI allows the reduction of required AB, therefore increasing the efficacy while preserving the same effect, reduction of side effects and resistances are developed in a slower or fewer manner. These inhibitors have also the possibility to reactivate ineffective antibiotics again for therapy.

Conclusion: Plants are promising sources for new efflux pump inhibitors due to the enormous compound variety, low toxicity and high tolerability. At this time, no EPI from natural sources is in the clinical services that can act effectively in synergy with antibiotics; however, extensive research is on-going to identify these useful chemicals.

Keywords: Antibiotic, Bacterial resistance, Efflux pump inhibitors, Phytochemicals, Plant

P570 - 219: NATURAL MEDICINE, AN OLD BUT NEW APPROACH TO ANTIMICROBIAL RESISTANCE

Mahdi Vazirian¹

1. Department of Pharmacognosy, Faculty of Pharmacy, Tehran University of Medical Sciences

Background and Aim:Antimicrobial resistance endangers the existence of human being, while ensures the survival of microorganisms. In recent years, antimicrobial agents have faced the resistance challenge and a massive search for new antibiotics has emerged. Since ancient times, natural medicines (i.e. crude natural sources or their unpurified extracts) have been the main choice of humans to fight diseases. Nowadays, they seem an opportunity in combating microorganisms by their multi-component nature, which bring us desirable features. The present review discusses the potential role of natural medicines in facing antimicrobial resistance by illustrating some of the unique features of them in recent studies.

Methods:Recent literature about with the keywords of antimicrobial resistance, herbal, natural and complementary medicine were found in authentic databases (i.e. Sciencedirect, Elsevier, Scopus and Pubmed).

Results:Different components of natural medicines may contribute in distinct mechanisms of action, including inhibition of enzymes, disabling the efflux pumping systems of microorganism, attacking the microorganism's cell wall and inhibiting quorum sensing. On the other hand, different components, with direct and indirect antimicrobial activity, may lead to pharmacodynamic or pharmacokinetic synergism, which can potentiate the antimicrobial effect of other components of the natural source, or conventional antibiotics. Natural medicines, can also fight pathogens indirectly by strengthening the self-healing capacities of the host which can fight the microorganisms. Besides, natural medicines with antimicrobial effect can reserve new approved antibiotics for severe cases, saving them from microorganism resistance.

Conclusion:Natural medicines can be considered as an effective, while inexpensive source to front antimicrobial resistance.

Keywords:Natural Medicine, Antimicrobial resistance, Multi-component, Synergism

**P571 - 227: ANTIMICROBIAL ACTIVITY OF LEAF EXTRACT OF A NATIVE PLANT FROM
SOUTHWEST OF MARIVAN**

Morteza Yazdani¹, Fereshteh Jookar Kashi²

1. Natural Essential Oil Research Institute, University Of Kashan, Kashan, I.R. Iran
2. Department of Biotechnology, Faculty of Chemistry, University of Kashan, Kashan, I.R. Iran

Background and Aim: *Tragopogon dubius* is a species of salsify native to southern and central Europe and western Asia and found as far north and west as northern France.

Methods: We collected this plant in april 2016 from southwest of marivan. Extraction methanolic was performed with a Soxhlet apparatus. The extract was concentrated using a rotary evaporator. To evaluate the antimicrobial activities extract of leaves were examined against a set of twelve microorganisms. The methanolic leaves extracts of *Tragopogon dubius* investigated for antimicrobial activity by agar well diffusion method. The dried plant extract was dissolved in DMSO (30 mg/ml) and filtered by 0.45 ml Millipore filters for sterilization. Suspension of bacteria (100 μ l of 108 CFU/ml) spread on müller-hinton agar (MHA) medium The discs (6 mm in diameter) impregnated with 10 μ l of the extract solution (300 μ g/disc) +DMSO (as negative control) and Gentamicin and rifampin (as positive controls) were placed on the inoculated agar (24 h at 37 °C). The diameters of inhibition zones were used as a measure of antimicrobial activity and each assay was repeated twice.

Results: The leaves extract of *Tragopogon dubius* showed activity against *Staphylococcus epidermidis*, *Candida albicans* and *pseudomonas aeruginosa*. Extract with inhibition zone diameter of 17,14 and 12 mm for *Staphylococcus epidermidis* (ethyl acetate fraction), *pseudomonas aeruginosa* (water fraction) and *Candida albicans* (hexan fraction), exhibited the best results respectively.

Conclusion: Results of present study indicated that *Tragopogon dubius* leaf extract had moderate antimicrobial activity.

Keywords: *Tragopogon dubius*, antimicrobial activities, MIC, Microorganism, Plant extract

P572 - 233: ANTIBACTERIAL ACTIVITIES OF ROSEMARY (ROSMARINUS OFFICINALIS) AND ITS INTERACTION IN COMBINATION WITH CONVENTIONAL ANTIMICROBIAL, AGAINST GRAM POSITIVE AND NEGATIVE BACTERIA

Elnaz Afshari¹, Elnaz Afshari^{*2}, Ziba kolouei³

1. -
2. *Young Researchers & Elite Club, Pharmaceutical Sciences Branch, Islamic Azad University (IAUPS), Tehran, Iran
3. Department of Food Sciences & Technology, Faculty of Advanced Sciences & Technology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, Iran (IAUPS)

Background and Aim: Rosemary is member of the Lamiaceae family that is known as a valuable medicinal herb. The essential oil of Rosemary has been studied as several studies antioxidant activity, anti inflammatory, toxicity insecticidal, anti fungal. Due to the advent of multidrug resistance, alternatives to conventional antimicrobial therapy are needed. This aims of current study were evaluate the antibacterial activities of *R. officinalis* and investigate the in vitro pharmacological interactions essential oil (considered valuable as natural therapeutic treatment) and conventional antimicrobial (ciprofloxacin) when used in combination.

Methods: To evaluate the antibacterial activities of *R. officinalis* essential oils, disk diffusion testing and minimum inhibitory concentration (MIC) was performed.

Results: The results indicated that *Rosmarinus* extract was a stronger inhibitory effect on the bacteria. The combination of the essential oil of *R. officinalis* with ciprofloxacin against gram-positive bacteria gave an antagonistic profile while *R. officinalis*/ciprofloxacin against gram-negative bacteria displayed a favorable synergistic pattern.

Conclusion: Rosemary essential oil can be used as a natural antibacterial agent for treatment of several infectious disease caused by bacteria which have antibiotic resistance and an essential oil with known antimicrobial activity will produce beneficial or harmful effects when combined with conventional antimicrobials depends on the ratio in which the two components exist.

Keywords: Rosemary, Essential oil, Antibacterial Activities, Ciprofloxacin, Iran.

**P573 - 248: ANTIBACTERIAL ACTIVITY OF LAVANDULA ANGUSTIFALIE ALCHOLI AND
WATER EXTRACT ON PATHOGENIC BACTERIA**

Mojtaba Najafi farid¹, mehdi ghyamirad², changhiz lotfi ³

1. Department of Biology, Faculty of Microbiology, Islamic Azad University of Ahar, Iran.
2. Department of Biology, Faculty of Microbiology, Islamic Azad University of Ahar, Iran.
3. Department of Biology, Faculty of Microbiology, Islamic Azad University of Ahar, Iran.

Background and Aim: As a result of the indiscriminate use of antimicrobial drugs, microorganisms resistant have been developed in front of to many antibiotics and there is a need for the development of natural antimicrobial drugs. One way is to use herbs. This study was done due to the rapid increase in antibiotic resistance, side effects of chemistry drugs and with goal of the comparative study of antibacterial effects of methanolie and water extract of *Lavandula angustifalie* on some of pathogenic bacteria.

Methods: In this study the scientific name *Lavandula angustifalie* for plant *Lavandula* firest alcoholic extract and water of plant *Lavandula* were taken and effect of the concentration of 100, 50, 25, 12.5, ... , 0.81, 0.40 mg/ml of the extract was investigated. All test done procedares difilon by the well and set the *B.subtilis*, *S.mutans*, *L.monocytogenes*, *R.enterocolitica* and *S.enteritidis*.

Results: Results showed that the alcholi and water extract of plants *Lavandula angustifalie* significantly inhibited on each of the five bacteria tested and much higher concentration of alcholi and water extrace increase of inhibition zone more powerful. Also both extracts were more effective on gram-pasitive bacteria. As rue alcholic and water extract the greatest impact on *Bacillus subtilis* and the least effects on *S.enteritidis* bacteria and severity of inhibition and cytotoxicity alcholi extract of plant *Lavandula angustifalie* of extract more water.

Conclusion: The alcoholic and water extract *Lavandula angustifalie* has a significant inhibitory effect on the groth of pathogenic bacteria. The inhibitory effects on Gram-positive bacteria are more than Gram-negative bacteria.

Keywords: *Lavandula angustifalie*, Pathogenic bacteria, Antibacteria effect.

P574 - 253: ANTIMICROBIAL ACTIVITY OF A NATIVE PLANT EXTRACT FROM SOUTH WEST OF MARIVAN

Morteza Yazdani¹, Fereshteh Jookar Kashi²

1. Natural Essential Oil Research Institute, University Of Kashan, Kashan, I.R. Iran.
2. Department of Biotechnology, Faculty of Chemistry, University of Kashan, Kashan, I.R. Iran

Background and Aim: *Tragopogon dubius* is a species of salsify native to southern and central Europe and western Asia and found as far north and west as northern France.

Methods: We collected this plant in april 2016 from south west of marivan. Extraction methanolic was performed with a Soxhlet apparatus. The extract was concentrated using a rotary evaporator. The antimicrobial activity of the extract was examined against a set of twelve microorganisms. The extract of *Tragopogon dubius* investigated for antimicrobial activity by agar well diffusion method. The dried plant extract was dissolved in DMSO (30 mg/ml) and filtered by 0.45 µm millipore filters for sterilization. The suspension of bacteria (100 µl of 10⁸ CFU/ml) were spread on miller-Hilton agar (MHA) medium. The discs (6 mm in diameter) impregnated with 10 µl of the extract solution (300 µg/disc) +DMSO (as negative control) and Gentamicin and rifampin (as positive controls) were placed on the inoculated agar (24 h at 37 °C). The diameters of inhibition zones were used as a measure of antimicrobial activity and each assay was repeated twice.

Results: The extract of *Tragopogon dubius* showed activity against *Staphylococcus epidermidis*, *Candida albicans* and *pseudomonas aeruginosa*. The extract with inhibition zone diameter of 17,14 and 12 mm for *Staphylococcus epidermidis*, *pseudomonas aeruginosa* and *Candida albicans* , exhibited the best results respectively.

Conclusion: Results of present study indicated that *Tragopogon dubius* extract had moderate antimicrobial activity.

Keywords: *Tragopogon dubius*, Antimicrobial activity, Microorganism, Plant extract

P575 - 260: ANTIMICROBIAL ACTIVITIES OF ESSENTIAL OIL OF SOME PHLOMIS SPECIES

Marjan Nikan¹, Soodabeh Saeidnia², Azadeh Manayi³, Sara Saadatmand⁴

1. Medicinal Plants Research Center, Tehran University of Medical Sciences, Tehran, Iran
2. Medicinal Plants Research Center, Tehran University of Medical Sciences, Tehran, Iran
3. Medicinal Plants Research Center, Tehran University of Medical Sciences, Tehran, Iran
4. Department of Biology, Islamic Azad University, Science and Research Branch, Tehran, Iran.

Background and Aim: The essential oils of four *Phlomis* species (*Phlomis olivieri*, *Phlomis bruguieri*, *Phlomis rigida* and *Phlomis kurdica*), collected from Kordestan province of Iran during the flowering stage.

Methods: All these plants were obtained by hydrodistillation and analyzed by gas chromatography/mass spectrometry (GC-MS).

Results: Totally, 21 compounds in the oil of *P. olivieri*, (representing 87%), 18 compounds in the oil of *P. bruguieri*, (representing 81.3%), 17 compounds in the oil of *P. rigida*, (representing 93.6%) and 26 compounds in the oil of *P. kurdica* (representing 92.1%) were identified. Germacrene D, trans-caryophyllene and caryophyllene oxide were identified as the major components. The antimicrobial activities of the oils were tested against a gram-positive and two gram-negative bacteria and a pathogenic fungus. The essential oils displayed varied antibacterial and antifungal activities against the studied pathogens.

Conclusion: The essential oil of *P. rigida* was found to be the most active oil against *Staphylococcus aureus* in the test system (MIC value 6 mg/ml). The essential oils of *P. kurdica* and *P. olivieri* showed moderate antifungal activity (MICs: 20 and 25 mg/ml, respectively) against *Candida albicans*.

Keywords: *Phlomis*, Germacrene D, Trans-Caryophyllene, *Staphylococcus aureus*

**P576 - 269: USING BOILED BEET FOR IMPROVING THE YOLK QUALITY AND
PREVENTION OF MAREK DISEASE OUTBREAK IN LAYER**

Abdolreza Nabinejad¹

1. Isfahan Res center of Agriculture

Background and Aim:Laying hens normally start laying after 16 weeks of age ,One of The most important phase for layer is starting egg and in this condition some problem were affect them included prolepses, cage fractures and Marek beside of the infections, Marek disease (MD) is a neoplasia caused by a herpes virus and affect the lymphoblast for metastasis to the visceral organs such as liver, ovary and spleen, in the other hand yolk quality act is an important factor for marketing and egg trading.

Methods:In current report the effects of root of boiled beet (Red Beta vulgaris) were studied on the egg quality and outbreak of Marek disease in layer, The boiled beet is a herbal plant which is full of antioxidant of betaine that act as anti tumor and has a good red color could be used as natural dye

Results:The treatment group were 30 layers with the age of 15 weeks which reared up to 55 weeks and used 0.1 percent red beta vulgaris roots in diet, the control groups were 30 layers of 15 weeks old without using Red Beta vulgaris. During the study the egg production percent, egg quality and MD outbreak were analyzed in two groups .

Conclusion:Regarding to the results the laying percent, egg quality and MD outbreak were improved in treated group.

Keywords:Layer, Red Beta vulgaris, yolk, Marek, Improvement

صعتر و اکلیل کوهی ریحان، فعالیت ضد باکتریایی عصاره متانولی چهار گیاه لاوند، 311 - P577

Narges Beigizadeh¹, Ashraf kariminik²

1. Department of Microbiology, Faculty of science, kerman Branch, Islamic Azad University, Kerman, Iran
2. Department of Microbiology, Faculty of science, kerman Branch, Islamic Azad University, Kerman, Iran

Background and Aim: با وجود آورده اند جانبی و مقاومتی که میکرواورگانیزم های بیماریزا در مقابل آنتی بیوتیک-ها اثرات: اهمیت و اهمیت کاربرد گیاهان دارویی فزونی یافته است

Methods: بررسی قرار گرفت. عصاره ضد باکتریایی عصاره متانولی گیاهان لاوند، ریحان، صعتر و اکلیل کوهی مورد اثرات: تهیه غلظت های متفاوت اثر ضدباکتریایی هر یک به روش چاهک بر متانولی این گیاهان به روش ماسراسیون تهیه و پس از از مرکز پژوهش های تهیه شده Escherichia coli ATCC 25922 و Staphylococcus aureus ATCC 25923 باکتری-های بازدارندگی از رشد عصاره-ها تعیین گردید علمی و صنعتی مورد بررسی قرار گرفت و حداقل غلظت کشندگی و

Results: استافیلوکوک ۱۰، ۵ و ۵ غلظت بازدارندگی از رشد عصاره-های لاوند، صعتر و اکلیل کوهی نسبت به باکتری حداقل: بود. عصاره متانولی ریحان بر mg/ml باکتری استافیلوکوک اورپوس ۱۰، ۱۰ و ۵ بود و حداقل غلظت کشندگی آنها نسبت به mg/ml عصاره های صعتر و اکلیل کوهی نسبت به باکتری باکتری استافیلوکوک اورپوس بی تاثیر بود. حداقل غلظت بازدارندگی از رشد متانولی ریحان بود. عصاره mg/ml و حداقل غلظت کشندگی نسبت به باکتری اشرشیا کلی ۱۰ و ۲۰ بود mg/ml اشرشیا کلی ۱۰ و ۵ و لاوند بر باکتری اشرشیا کلی بی تاثیر بودند

Conclusion: اثر قابل توجه ضدباکتریایی صعتر و اکلیل کوهی مشاهده شد که جایگزین ترکیبات شیمیایی با خاصیت ضد میکروبی در صنعت غذا ایفا کند

Keywords: فعالیت ضد باکتریایی، لاوند ریحان صعتر اکلیل کوهی

**P578 - 327: INHIBITORY EFFECT OF SALVIA RHYTIDEA BENTH. (LAMIACEAE)
EXTRACT AGAINST VARIOUS CANDIDA ISOLATES**

Samira Salari¹

1. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran

Background and Aim:Salvia species have long been described in traditional medicine for various indications. Owing to the widespread use of this genus by ethnic populations, especially for various infections ranging from skin disease to gastrointestinal disorders, we were encouraged to determine whether Salvia rhytidea could be effective against fungal infections. Given the increased incidence of candidiasis in the past decade, limits on the use of antifungal drugs, emergence of azole-resistant Candida species, and increased incidence of treatment failures, it is necessary to identify a novel agent with antifungal properties. Aim of the study was to evaluate the antifungal properties of S. rhytidea against various Candida isolates.

Methods:In this study, at first rosmarinic acid content of plant extract was determined. A total of 96 Candida isolates were tested, including the following species: C. albicans (42), C. glabrata (16), C. tropicalis (11), C. krusei (9), C. parapsilosis (9), C. lusitaniae (7), and C. guilliermondii (2). The in vitro antifungal activity of methanolic extracts of S. rhytidea Benth. was evaluated against Candida isolates by using a broth microdilution method, according to CLSI.

Results:Phytochemical screening results showed that the methanolic extract of S. rhytidea Benth was rich in flavonoids and tannins. The MIC and MFC values of S. rhytidea Benth ranged from 3.125 to >100 ?g/ml and 6.25 to >100 ?g/ml, respectively. The growth inhibition value displayed that C. tropicalis, C. krusei and C. albicans isolates were most susceptible to S. rhytidea.

Conclusion:Findings show that S. rhytidea possess an antifungal effect against Candida isolates.

Keywords:Antifungal susceptibility, Salvia rhytidea, Candida, broth microdilution method

**P579 - 351: THE ANTI-DERMATOPHYTE AND ANTI-ELASTASE ACTIVITY OF ZATARIA
MULTIFLORA ESSENTIAL OILS**

Elahe mahdizade¹, Rezvan Heidarytabar², Mohaddese Mahboubi³

1. Department of Microbiology, Medicinal Plant, Research Center of Barij Essence, Kashan, Iran
2. Department of Microbiology, Medicinal Plant, Research Center of Barij Essence, Kashan, Iran
3. Department of Microbiology, Medicinal Plant, Research Center of Barij Essence, Kashan, Iran

Background and Aim: Treatment of dermatophytes disease by natural essential oils instead of chemical drugs is one of the important issues in recent researches. In Iranian Traditional Medicine, Zataria multiflora is famous as strong antiseptic plant for treatment of many infectious diseases.

Methods: In this study, the anti-fungal activity of three samples of Zataria multiflora essential oils were evaluated against *Trichophyton rubrum* PTCC 5143, *Trichophyton mentagrophytes* PTCC 5054, *Microsporum canis* PTCC 5069, *Microsporum gypseum* PTCC 5070 and *Trichophyton schoenleinii* PTCC 5221 by microbroth dilution and inhibition of mycelia growth methods. The chemical compositions of essential oils were determined by GC and GC-MS. Furthermore, the potency of essential oils against the elastase enzyme was determined by porcine pancreatic elastase and dermatophyte's elastase in vitro condition.

Results: Carvacrol (1.5-34.4%), thymol (25.8-41.2%), carvacrol methyl ether (1.9-28.3%) and p-cymene (2.3-8.3%) were the main components of *Z. multiflora* essential oils. The anti-fungal evaluation showed, 100 ppm of essential oils inhibited 6-41.4% of dermatophytes mycelium growth and had the MIC and MFC values of 0.03-0.25 µl/ml. These essential oils were also inhibited elastase production dose dependently in dermatophytes and against pure porcine elastase.

Conclusion: *Z. multiflora* essential oil can be proposed as natural antifungal agents for treatment of dermatophytes infections in further pre-clinical and clinical studies.

Keywords: Zataria multiflora, Anti-dermatophyte activity, elastase activity

**P580 - 422: ANTIBACTERIAL ACTIVITIES OF PLARGONIUM GRAVEOLENS IN
COMBINATION WITH CONVENTIONAL ANTIMICROBIAL, AGAINST GRAM POSITIVE
AND NEGATIVE BACTERIA**

Ziba Koluei¹, Ziba Kolouei², Elnaz Afshari³

1. -
2. Department of Food Sciences & Technology, Faculty of Advanced Sciences & Technology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, Iran (IAUPS).
3. *Young Researchers & Elite Club, Pharmaceutical Sciences Branch, Islamic Azad University (IAUPS), Tehran, Iran

Background and Aim: Urinary tract infections (UTIs) are amongst the most common infections causing individuals to seek medical care. Ciprofloxacin is the most frequently prescribed fluoroquinolone for UTIs because of its availability in oral and intravenous formulations. However, the resistance of uropathogens (such as *Klebsiella pneumoniae*, *Proteus mirabilis* and *Staphylococcus aureus*) to ciprofloxacin has increased markedly since its introduction for UTI treatment. Nowadays the combination therapy also overcomes the problem of multi-drug resistance. The essential oil of *Plargonium graveolens* commonly known as geranium essential oil and also used as a fragrance in creams, lotions, soaps and has been shown to be inhibitory against a number of bacterial and yeast pathogens associated with food-borne illness. The objective of the present study was that of verifying a possible synergistic antibacterial effect between *P. graveolens* essential oil and Norfloxacin antibiotic.

Methods: The determination of minimum inhibitory concentration (MIC) of individual combining agents' *P. graveolens* essential oil and ciprofloxacin was determined by the agar dilution method (ADM).

Results: The results obtained highlighted the occurrence of a pronounced synergism between *P. graveolens* essential oil and Norfloxacin in the treatment of infections caused by some bacterial species is likely to reduce the minimum effective dose of Norfloxacin thus minimizing the side effects of the antibiotic.

Conclusion: The combination of Norfloxacin with *P. graveolens* essential oil may be applied for the treatment of UTIs, which have hitherto been treated by using only synthetic drugs.

Keywords: *Plargonium graveolens*, Essential oil, Antibacterial Activities, Norfloxacin, Iran.

**P581 - 423: ANTIMICROBIAL EFFECTS OF ETHANOL EXTRACTS OF PLANTS STALKS
CENTAUREA CYANUS AND FLOWERS CENTAUREA CYANUS ON A NUMBER OF GRAM
POSITIVE AND NEGATIVE BACTERIA IN VITRO**

Mansoor Khaledi¹, mohamad rahimi mediseh², abolfazl gholipour³

1. M.Sc. of Microbiology. Students Research Committee, sharekord University of Medical Sciences, sharekord, Iran
2. PHD by research Medicinal Plants, Medical Plants Research Center, Shahrekord University of Medical Sciences, Sharhekord, Iran
3. Assistant Professor of Microbiology, Department of Microbiology and Immunology, sharekord University, of Medical Sciences, sharekord, Iran

Background and Aim: Despite the discovery of numerous antibiotics, drug resistance still remains as a major problem. Therefore, it is important to introduce and replace new sources of drug such as medicinal plants with antimicrobial properties. This study was designed to determine the antimicrobial efficacy of the alcoholic extracts of stalks *Centaurea cyanus* and Flowers *Centaurea cyanus* against different kinds of bacterial viz. *Escherichia coli*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*.

Methods: hydro alcoholic extract of two medicinal plants collected from The scope of Chaharmahal va Bakhtiari; Extraction produced by soaking method then The MIC values and MBC of the *Centaurea cyanus* and Flowers *Centaurea* extracts against the bacterial strains(*Escherichia coli* ATCC 25922 , *Pseudomonas aeruginosa* ATCC 27853 , *Staphylococcus aureus* ATCC 25923) were determined by a micro broth dilution method based on instructions CLSI

Results: The MIC value for the hydro alcoholic extract of stalks *Centaurea cyanus* was 200 µg/mL for *E. coli* and 350 µg/mL for *S. aureus* and 150 µg/mL for *Pseudomonas aeruginosa*. The MIC value of the ethanol extract of Flowers *Centaurea cyanus* was 100 µg/mL for *E. coli* and 200 µg/mL for *Pseudomonas aeruginosa* and 400 µg/mL for *S. aureus*.

Conclusion: According to antibacterial effects of alcoholic extracts, The best inhibitory effect on *Pseudomonas aeruginosa* for stalks *Centaurea cyanus* and The best inhibitory effect on *E. coli* for Flowers *Centaurea cyanus* and The two plants have a limited impact on *Staphylococcus aureus*.

Keywords: Antimicrobial effects, *Centaurea cyanus*, gram positive, gram negative

P582 - 426: ANTI LEISHMANIA EFFECT OF NANO CURCUMIN: IN VITRO ANALYSIS

Abazar Razavinia¹, Majid Sadeghizadeh ², Mehdi Mahdavi³

1. Department of Genetics, School of Biological Sciences, Tarbiat Modares University, Tehran, Iran
2. Department of Genetics, School of Biological Sciences, Tarbiat Modares University, Tehran, Iran
3. Department of Immunology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim:Leishmania major is intracellular protozoan parasite that able to survive and replicate in the hostile phagolysosomal environment of infected macrophages. They cause leishmaniasis, a representing a paradigm of neglected diseases that are mainly embedded in impoverished populations. At present there is not a fully effective and non-toxic drug for Leishmania infection. In this study the anti-proliferative effect of dendrosomal curcumin has been studied against Leishmania Major Strain proliferation in the in vitro condition

Methods:Leishmania major promastigote forms were cultured in RPMI 1640 medium enriched with 10 % FBS and incubated at 26°C. For anti Leishmania effect study, the parasite was cultured in 96 well plates with different concentration of nano-curcumin, curcumin or without treatment. Also amphotericin B was used as positive control. Culture continued for 24, 48, and 72hrs the anti Leishmania effect was evaluated via MTT assay.

Results:Treatment with nano- curcumin and also amphotericin B suppress parasite proliferation in a dose dependent manner. However anti Leishmania effect of nano-curcumin was not at high level.

Conclusion:Nano-curcumin shows anti Leishmania effect at in vitro analysis. Because of immunomodulatory effect of nano-curcumin may be nano-curcumin shows better anti Leishmania effect at the in- vivo condition.

Keywords:dendrosomal curcumin, nano-curcumin , Leishmania major ,

P583 - 451: ANTIBACTERIAL EFFECT OF FRACTIONS OF POLAR AND SEMI-POLAR, NONPOLAR WORMWOOD EXTRACT THE BACTERIA STAPHYLOCOCCUS AUREUS, ESCHERICHIA COLI, PSEUDOMONAS AERUGINOSA

Changiz Ahmadizadeh¹, Mojtaba Babaei Daylari², Rozita Tamjidifar³, Farid Zarei⁴

1. Assistant Professor, Department of Microbiology, Islamic Azad University of Ahar
2. Master of Science Microbiology
3. Master of Science Microbiology
4. Genetics Expert

Background and Aim: The scientific name of this plant is *Artemisia absinthium* and The family Asteraceae A (Asteraceae) and the family of steroids and local aromatic plants, especially in the northern and eastern Iran And in England with wood worm shape (Worm Wood) and famous names in Iran is Khargush, Gandvash, Marwe, Afsantin. According to again approach to drugs and herbal, medicinal properties of plants is important. Afsantin is a herb that is used to treat certain diseases.

Methods: Wormwood plant in March 2016 from around Astara collected and prepared. Then dried at room temperature and away from sunlight. Next, twigs and leaves dry, powder form was by electric mill and pure extract obtained by maceration method. Fractions of methanol, chloroform and hexane was prepared by pure extract. In order to investigate the antimicrobial activity against strains listed for MIC determination method by dilution plate and the pit were stored in clean containers and cool place

Results: MIC (Minimum Inhibitor Concentration) extracts and fractions prepared on the microbial Specie in the pit of 0.39 to 100 mg/ml and in micro plate in the methanol extract, *Staphylococcus aureus* 6.25% mg/ml, the bacterium *Escherichia coli* 50% mg/ml and *Pseudomonas aeruginosa* were 50% sensitive, In the Chloroform extract, three *Staphylococcus aureus*, *Escherichia coli* and *Pseudomonas aeruginosa* 12.5% mg/ml are sensitive and ether extract also three *Staphylococcus aureus*, *Escherichia coli* and *Pseudomonas aeruginosa* 25% mg/ml are sensitive

Conclusion: The results show that the extract of wormwood plant's antimicrobial effect against Species listed. the methanol extract and chloroform extract, have the highest antimicrobial effect on *Staphylococcus aureus*

Keywords: Worm Wood, plant extracts, *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*

**P584 - 454: ANTIMICROBIAL ACTIVITY OF THE PLANT EXTRACT FROM
ZYGOPHYLLACEAE FAMILY FROM SOUTHWEST OF MARIVAN**

Morteza Yazdani¹, Fereshteh Jookar Kashi²

1. Natural Essential Oil Research Institute, University Of Kashan, Kashan, I.R. Iran
2. Department of Biotechnology, Faculty of Chemistry, University of Kashan, Kashan, I.R. Iran

Background and Aim: *Tribulus terrestris* is an annual plant in the Zygophyllaceae family widely distributed around the world. *Tribulus terrestris* grows as a summer annual in colder climates.

Methods: This plant was collected in September 2015 from southwest of marivan. Extractions methanolic were performed with a Soxhlet apparatus. The extract was concentrated using a rotary evaporator. The antimicrobial activity of the extract was examined against a set of twelve microorganisms (9 bacteria and 3 fungi). The extract of *Tribulus terrestris* was investigated for antimicrobial activity by agar well diffusion method. The dried plant extract was dissolved in DMSO (30 mg/ml) and filtered by 0.45 µm millipore filter for sterilization. The suspension of bacteria (100 µl of 10⁸ CFU/ml) were spread on miller-Hilton agar (MHA) medium. The discs (6 mm in diameter) impregnated with 10 µl of the extract solution (300 µg/disc)•DMSO (as negative control) and Gentamicin and rifampin (as positive controls) were placed on the inoculated agar (24 h at 37 °C). The diameters of inhibition zones were used as a measure of antimicrobial activity and each assay was repeated twice.

Results: The methanolic extract of *Tribulus terrestris* showed activity against *pseudomonas aeruginosa* (ATCC 27853). The inhibition zone diameter for this bacteria was 24 mm. The extract had no effect against the rest of the microorganisms.

Conclusion: Results of present study indicated that extract of *Tribulus terrestris* had high antimicrobial activity against *pseudomonas aeruginosa* (ATCC 27853).

Keywords: *Tribulus terrestris*, Antimicrobial activity, Microorganism, Plant extract

**P585 - 467: EVALUATION OF ANTIBACTERIAL ACTIVITY OF ESSENTIAL OIL OF
ZIZIPHORA CLINOPODIOIDES AND ACHILLEA WILHELMSII ON ANTIBIOTIC-
RESISTANT STRAINS OF STAPHYLOCOCCUS AUREUS**

Abolfazl Jafari sales¹, Haedeh Mobaiyen², Reza Fathi³

1. Young Researchers and Elite Club, Ahar Branch, Islamic Azad University, Ahar, Iran
2. Department of Microbiology, College of Medicine, Tabriz Branch, Islamic Azad University, Tabriz, Iran
3. Medical physiology and post doctorate follow at endocrinology at marmara university

Background and Aim: Infections caused by antibiotic-resistant strains of *Staphylococcus aureus* are mainly hospital-based prevalence is increasing in many countries; Hence efforts taken to find new compounds as an alternative to antibiotics. This study is done to evaluate the antimicrobial effects of Essential Oil of *Ziziphora clinopodioides* and *Achillea wilhelmsii* on against resistant clinical strains of *Staphylococcus aureus*.

Methods: After collecting plants and validate its scientific name by botanists of Agricultural Organization and after drying in shade, Essential Oil of *Ziziphora clinopodioides* and *Achillea wilhelmsii*, extracted with steam distillation method by Clevenger and antimicrobial effects of Essential Oil by well diffusion on above mentioned bacteria were interpreted. Amount of Essential Oil were injected to gas chromatography linked to mass spectrometry (GC / Ms), and the amount and type compounds of the Essential Oils were identified.

Results: The results showed that the extracted essence Essential Oil from the *Ziziphora clinopodioides* and *Achillea wilhelmsii* has bactericidal effect. In the obtained results by GC/Ms chromatography, in *Ziziphora clinopodioides* and *Achillea wilhelmsii* Essential Oils, 22 and 18 compounds, were identified respectively.

Conclusion: The results of this study show that can be taken *Ziziphora clinopodioides* and *Achillea wilhelmsii* in herbals groups with antibacterial properties and after evaluating their effects in vivo condition and to identify the active ingredients, as an alternative to synthetic drugs that commonly used to treat infections are used.

Keywords: Antibacterial effects, Essential Oil , *Staphylococcus aureus*

**P586 - 488: ANTIBACTERIAL ACTIVITY OF LEAVES HYDROALCOHOLIC EXTRACT OF
CHAEROPHYLLUM MACROPODUM(APIACEAE)**

Hossein Nazari¹, Farahnaz Bineshian², Neda Bakhshandeh³, Mohammadreza Freidounian⁴

1. Department of Biochemistry, Faculty of Medicine, Seman University of Medical Sciences, Semnan, Iran.
2. Department of Mycology, Faculty of Medicine, Semnan University of Medical Sciences, Semnan, Iran.
3. Department of Biochemistry, Faculty of Medicine, Seman University of Medical Sciences, Semnan, Iran.
4. Semnan Technical College, Semnan, Iran

Background and Aim:The genus *Chaerophyllum*, belonging to Apiaceae family is widely distributed in E. Asia and grows in moist shady places, grassy places. *Chaerophyllum macropodum* have been used in food, spice and also as medicine. The purpose of this study was to investigate of anti bacterial activities of hydroalcoholic extract from leaves of *Chaerophyllum macropodum*.

Methods:The *Chaerophyllum macropodum* Leaves were extracted using Ethyl acetate: methanol: distilled water (6:3:1) by Soxhlet system. The hydroalcoholic extraction of *Chaerophyllum macropodum* was evaluated for their antioxidant capacities using in vitro methods, including 1-diphenyl-2-picrylhydrazyl radical scavenging, β -Carotene bleaching test and reducing power assay. Total free phenolics and total flavonoids content as well as antibacterial activity were also examined.

Results:This study revealed a moderate antioxidant capacity in the leaves of *Chaerophyllum macropodum* as compared to the control groups. The minimum inhibitory concentration values at 24 and 48 hours were 400 $\mu\text{g}/\mu\text{L}$ for *Escherichia coli* and 300 $\mu\text{g}/\mu\text{L}$ for *Staphylococcus aureus*.

Conclusion:The leaves hydroalcoholic extract of *Chaerophyllum macropodum* showed antibacterial activity and it could be used as natural antibacterial in food.

Keywords:*Chaerophyllum macropodum*; antibacterial activity; Hydro alcoholic extract ; Apiaceae

P587 - 490: ANTIMICROBIAL EFFECTS OF AQUEOUS AND METHANOL EXTRACTS OF ORANGE PEEL AND ITS EFFECT ON THE SHELF-LIFE OF FLAVORED MILK

Maryam Razmjoo¹, pejvak khaki², meisam asadpour³, sajad dostdari⁴

1. Razi Vaccine & Serum Research Institute
2. Razi Vaccine & Serum Research Institute
3. Razi Vaccine & Serum Research Institute
4. Razi Vaccine & Serum Research Institute

Background and Aim: Dairy products such as milk are needed for a better life but because of being highly perishable, increasing their shelf life using natural preservatives such as plant extracts is necessary. One of the most popular milk products that has recently received attention is flavored milks. Among the flavors are fruit and their extracts which increase the shelf life of milk and because of having antimicrobial agents.

Methods: In this study the effect of extracts was investigated by using disk diffusion method and minimum inhibitory concentration (MIC) on *Escherichia coli* and *Candida albicans* and then its impact on physicochemical, sensory and microbial properties of the milk.

Results: The growth diameter of disk diffusion method in Aqueous and methanol extracts was 7/11 and 50 mm for *Escherichia coli* and *Candida albicans*, respectively and MIC in the aqueous and methanol extract, for *Escherichia coli* and *Candida albicans*, was 0/015, 0/002, 0/03, 0/004 g/ml respectively.

Conclusion: The results of disk diffusion method and minimum inhibitory concentration (MIC) showed that aqueous extracts were more effective than methanol extracts in addition its effect on fungus was more than *Escherichia coli*. Furthermore the result of this investigation was the same as Kivanc & Akgul, Kirbaslari and et al and Ashok kumar and et al's results.

Keywords: orange peel, Essential oils, antimicrobial activity, milk

**P588 - 549: STUDY OF ANTIBACTERIAL ACTIVITY OF ETHYLACETAT TOTAL EXTRACT
AND ITS ALKALOID FRACTION FROM FLOWERING AERIAL PARTS OF GLAUCIUM
VITELLINUM BOISS. ET BUHSE AGAINST CLINICAL ESCHERICHIA COLI STRAINS
ISOLATED FROM UTI**

Shohreh Tavaf langeroudi¹, mojdeh Hakemi Vala², fatemeh Baghery Bejestany³

1. Department of microbiology, faculty of pharmacy, Islamic Azad university Tehran-Iran
2. Department of microbiology, medical school, Shahid Beheshti university of medical sciences Tehran-Iran
3. Department of microbiology, faculty of pharmacy, Islamic Azad university Tehran-Iran

Background and Aim: *G. vitellinum* which is a member of tribe Opium poppy of Papaveraceae family, In previous studies the antimicrobial effect of whole ethylacetat total extract and alkaloids extracts of aerial and flowering section of *Glaucium vitellinum* against clinical and standard staphylococcus spp. and salmonella strains was evaluated. In this study we decided to evaluate the antimicrobial effect of whole ethylacetat total extract and alkaloids extracts of aerial and flowering section of *Glaucium vitellinum* against clinical *Escherichia coli* spp. strains isolated from patients of Sina and Emam hospital of Tehran.

Methods: After scientific identification, its flowering and aerial sections were washed and dried, powdered and extracted by methanol as solvent by maceration method and using percolation method. Its alkaloid part that includes all available alkaloids in this plant was separated from whole extract and its antibacterial effect against *Escherichia coli* isolates from urine of patients of Sina and Imam Hospitals of Tehran evaluated and MIC determination by microdilution method based on CLSI protocol.

Results: The detected average of MIC of whole ethylacetat total extract was 152.81 ± 66.80 mg/mL while MIC of alkaloids extracts of aerial and flowering section of *Glaucium vitellinum* against the same bacteria in the studied patients was 134.40 ± 68.99 mg/mL.

Conclusion: Based on the interesting results which were detected in this study further in vitro and in vivo investigation is recommended.

Keywords: *Glaucium vitellinum*, ethylacetat total extract, alkaloid fraction, *Escherichia coli*

P589 - 559: ANTIBACTERIAL AND ANTIFUNGAL PROPERTIES OF THYME

Masoume Hadavand¹, hojat es-haghi²

1. Food and Drug Department of Shahid Beheshti University of Medical Sciences
2. Food and Drug Department of Shahid Beheshti University of Medical Sciences

Background and Aim: plant products, like the essential oils are renewable in nature and safe for human health. there are extracts and essential oils from different medicinal plants that are widely use for antibacterial and fungicidal properties.

Methods: Thyme essential oil is applied as 5, 8 and 12% concentrations in methanol at 1.2 ml per 1 g of dry fabric using the padding method. This equipment applying the thyme oil uniformly on the fabric surface. The reference samples were treated with methanol only. After padding, tested samples of fabrics were dried at ambient temperature. The protected and unprotected samples of linene-cotton blended fabric and linen fabric were exposed to the mixture of the mould fungi like *A. niger*, *Ch. globosum* and bacterial species like *S. aureus* ATCC 6538 as Gram positive bacteria and *Pseudomonas aeruginosa* £ock 0885, *E. coli* ATCC 10536 as Gram negative ones in specific medium. Then are incubated for a specified time.

Results:: the sample protected with thyme essential oil (8%) no moulds growth and inhibition zone around the sample were seen. the reference sample complete destroyed by moulds activity. Linene-cotton blended fabric protected with thyme essential oil at both 8% and 12% showed strong effect against both Gram positive and Gram negative bacteria.

Conclusion: Thyme essential oil during cultivation showed very high antibacterial and antifungal activity.

Keywords: thyme oil, antibacterial, antifungal

**P590 - 583: ANTIMICROBIAL ACTIVITY OF SALVIA GLOTINOSA L. METHANOL
EXTRACT FROM GILAN-MASAL**

Maryam Iravani¹, Roya Mahinpour², Zohreh Zahraie³, Zeinab Toluei⁴

1. . Department of Biotechnology, Faculty of Chemistry, University of Kashan, Kashan, Iran
2. . Department of Biotechnology, Faculty of Chemistry, University of Kashan, Kashan, Iran
3. . Department of Biotechnology, Faculty of Chemistry, University of Kashan, Kashan, Iran
4. Department of Biotechnology, Faculty of Chemistry, University of Kashan, Kashan, Iran

Background and Aim: Drug resistance rate of pathogenic bacteria is increasing, with regards to excessive consumption of chemical drugs. Therefore the need to find new compounds is necessary. The aim of this study was investigation of the antibacterial activity of methanol extract of *Salvia glotinos*a against some of common standard bacteria.

Methods: In this study, antibacterial activity of methanol extract of *Salvia glotinos*a plant on bacteria such as; *Pseudomonas aeruginos*, *Bacillus subtilis*, *Escherichia coli*, *Staphylococcus aureus*, *Klebsiella pneumonia*, *Staphylococcus epidermidis*, *Proteus vulgaris*, *Salmonella paratyphi-A* serotype was performed by agar diffusion technique and micro-well dilution assay method.

Results: Our results indicated that methanol extract of *Salvia glotinos*a was active against gram positive bacteria *B. subtilis* and *S. aureus*. The MIC results showed that methanol extract of *Salvia glotinos*a was more active against *B. subtilis* with MIC value 500 µg/ml as compared with *S. aureus* with MIC value 1000 µg/ml. In this study, the methanol extract of *Salvia glotinos*a had not antimicrobial activity against *Pseudomonas aeruginos*, *Escherichia coli*, *Klebsiella pneumonia*, *Staphylococcus epidermidis*, *Salmonella paratyphi-A* serotype and *Proteus vulgaris*.

Conclusion: Results indicated that methanol extracts of *Salvia glotinos*a has antibacterial effect against *B. subtilis* and *S. aureus*. The application of *Salvia glotinos*a herb after more extensive pharmacological studies, for treatment recommended

Keywords: *Salvia glotinos*a, Antimicrobial activity, Agar diffusion method, Micro-well dilution assay method

**P591 - 594: ANTIBACTERIAL ACTIVITY OF 4 METHANOL EXTRACTS OF LAVANDULA
STOECHAS, OCIMUM BASILICAM, THYMUS VULGARIS AND ROSMARINUS
OFFICINALIS**

Narges Beigizadeh¹, Ashraf kariminik²

1. Department of Microbiology, Faculty of science, kerman Branch, Islamic Azad University, Kerman, Iran
2. Department of Microbiology, Faculty of science, kerman Branch, Islamic Azad University, Kerman, Iran

Background and Aim:: Because of the side effects and the resistance that pathogenic microorganisms build against the antibiotics, there has been an increasing awareness about the importance and usage of medicinal plants. So that today, herbal medicines play a major role in treatment.

Methods: This study describes the anti-bacterial activity of methanol extract of *Lavandula stoechas*, *Ocimum basilicam*, *Thymus vulgaris* and *Rosmarinus officinalis* against bacteria include *Staphylococcus aureus* (ATCC 25923), *Escherichia coli* (ATCC 25922). For this purpose extraction were done by maceration method and tested by agar well diffusion method. The MIC & MBC of the extracts were determined

Results: The MIC value of 3 plant extract *Lavandula stoechas*, *Thymus vulgaris* and *Rosmarinus officinalis* extracts against *S. aureus* was 10, 5 and 5 mg/ml. The MBC value of them against *S. aureus* was 10, 10 and 5 mg/ml. *Ocimum basilicam* methanol extract had no effect on *S. aureus*. The MIC value of 2 plant extracts, *Thymus vulgaris* and *Rosmarinus officinalis* against *E. coli* was 10 and 5 mg/ml. The MBC value of both against *E. coli* was 10 and 20 mg/ml. *Ocimum basilicam* and *Lavandula stoechas* methanol extracts had no activity on *S. aureus*.

Conclusion: The results reveals significantly higher broad-spectrum in vitro antibacterial activity of the *Thymus vulgaris* & *Rosmarinus officinalis* methanol extracts and they may be represent a potential alternative to chemical antimicrobial in food industry

Keywords: Antibacterial activity, *Lavandula stoechas*, *Ocimum basilicam*, *Thymus vulgaris*, *Rosmarinus officinalis*, , Methanol extract

P592 - 620: ANTIOXIDANT AND ANTIBACTERIAL PROPERTIES OF SAFFRON LEAVES

Ali Rismanbaf¹, Ali Ebrahimi Pure², Sepideh Noori³

1. Department of Pharmaceutics, Faculty of Pharmacy, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran – Iran (IAUPS)
2. Department of Food Sciences & Technology, Faculty of Advanced Sciences & Technology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran-Iran (IAUPS)
3. Department of Pharmaceutics, Faculty of Pharmacy, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran – Iran (IAUPS)

Background and Aim: Saffron has been used as a flavoring agent in foods since about 3000 years ago. This expensive food ingredient is obtained from *Crocus Sativus* L. (A genus from Iridaceae family with purple flowers). After discharging saffron stigmas, the flowers' leaves are usually thrown useless. In this study we have evaluated the antioxidant and antibacterial properties of ethanol and aqueous extracts of saffron flower leaves.

Methods: Maceration method was used to prepare extracts; ratio of solvent to dry herbal material was 2:1. Folin-Ciocalteu assay was applied to evaluate total phenolic contents of samples; Free radical scavenging activity was evaluated using 2,2-diphenyl-1-picrylhydrazyl. Disk diffusion method was performed to measure inhibitory activity against testing bacteria.

Results: Total phenolic compounds of aqueous and ethanol extracts were measured 339 and 56 ppm gAE (gallic acid equivalent) respectively. Antioxidant evaluation indicated high free-radical inhibition capacity of extracts. 0.02% of aqueous extract could inhibit DPPH by 99%. No antibacterial activity observed from either of extracts on tested bacteria.

Conclusion: Considering the high antioxidant activity and phenolic content, saffron flower leaves can be a potential and cheap source of phenolics.

Keywords: Saffron, Antioxidant, antibacterial, DPPH

**P593 - 653: EVALUATION OF ANTIBACTERIAL ACTIVITY AND ANTI BIOFILM
FORMATION OF METHANOL EXTRACT OF RUMEX ALVEOLLATUS LEAVES AGAINST
STAPHYLOCOCCUS AUREUS AND PSEUDOMONAS AERUGINOSA**

Neda Korkorian¹, Maryam Mohammadi-Sichani²

1. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran.
2. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran.

Background and Aim: Microorganisms form biomass as biofilm in response to many factors, in order to adapt to hostile extracellular environments and biocides. Using different herbal compounds are of those strategies to deal with biofilm. This study aimed to evaluate the effect of different concentrations of methanol extract of leaves of *Rumex alveollatus* on the *Pseudomonas aeruginosa* and *Staphylococcus aureus* biofilm formation.

Methods: This study was performed by standard strains of *Pseudomonas aeruginosa* (ATCC: 1310) and *Staphylococcus aureus* (ATCC: 25923). The methanol extract of leaves of *Rumex alveollatus* were prepared by Soxhlet apparatus. Antibacterial activities of extracts were evaluated well diffusion method. Also minimum inhibitory concentration (MIC) and minimal bactericidal concentration (MBC) were assessed by microdilution method. The data were analyzed using the SPSS statistical software version 17. P-values <0.05 were considered as statistically significant.

Results: Inhibitory zone of methanol extract of leaves (500 mg/ml) on *Pseudomonas aeruginosa* and *Staphylococcus aureus* were 22.83±0.78 mm and 10.66±1.25 mm, respectively. MIC and MBC results for methanol extracts leaves were 125 mg/ml and 250 mg/ml for *Pseudomonas aeruginosa* and *Staphylococcus aureus*, respectively. Biofilm inhibitory effects of methanol extract of leaves for *Pseudomonas aeruginosa* and *Staphylococcus aureus* were observed 62.5 mg/ml.

Conclusion: *Rumex alveollatus* methanol extract applied as antimicrobial agents against testing bacteria particularly in biofilm forms.

Keywords: Methanolic extracts, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Rumex alveollatus*, Biofilm formation.

**P594 - 678: ANTIBACTERIAL ACTIVITY OF EXTRACT AND PURE COMPOUNDS OF
LEUTEAE AVICENNIA MOZAFF.**

Mahsa Sabernavaei¹, Nargeuss yassa², Mohsen Amin³

1. Department of Pharmacognosy, Faculty of Pharmacy, Tehran University of Medical Sciences, Tehran, Iran.
2. Department of Pharmacognosy, Faculty of Pharmacy, Tehran University of Medical Sciences, Tehran, Iran.
3. Department of Drug and Food control, Faculty of Pharmacy, Tehran University of Medical Sciences, Tehran, Iran.

Background and Aim: Medicinal plants are potential of antimicrobial compounds. The present study deals with the antibacterial activity of total extract, fractions and pure compounds of *Leutea avicennia* Mozaff. (Apiaceae).

Methods: Aerial parts of the plant were collected from Kaboudarahang mountainside (Hamadan, Iran) in June 2012. Antibacterial activity of the extracts and compound was evaluated against various Gram-positive and Gram-negative bacteria using disk diffusion technique. Blank paper disks were loaded with 40 micro of the solvent and then dried up. The impregnated disks were placed on Mueller-Hinton agar inoculated with bacterial suspension equal to 0.5 McFarland. The extract inhibited the growth Gram-positive and Gram-negative bacteria

Results: The most significant effect was seen against *S. aureus*, which are important nosocomial pathogens. MIC of the methanol extract was determined against Gram-positive bacteria (10.84 mg/ml), Gram-negative (22.50 mg/ml).

Conclusion: These findings demonstrate that *L. avicennia* and some of its isolated compounds have interesting antimicrobial activity.

Keywords: *Leutea avicennia*, antibacterial activity, Minimum inhibitory concentration

**P595 - 708: THE ANTIBACTERIAL EFFECTS ON PATHOGENIC BACTERIA METHANOL
EXTRACT OF LEMON GRASS**

Nader Nezamdoost shadbad¹, Behboud Jafari², changiz zhamadizadeh³, jalal abdolalizadeh⁴

1. Young Researches and Elite Club, Ahar Branch, Islamic Azad University, Ahar, Iran
2. Department of Microbiology, Ahar Branch, Islamic Azad University, Ahar, Iran
3. Department of Microbiology, Ahar Branch, Islamic Azad University, Ahar, Iran
4. Immunology Lab, Drug Applied Research Center Tabriz University of Medical Sciences-Tabriz-Iran

Background and Aim: Purposes: In recent years, Use of natural substances rather than synthetic chemical drugs Side effects, The emphasis is on prevention and control of infections. Increasing use of medicinal plants in the treatment, This branch of complementary medicine, has found a special place in the treatment of diseases. The present study was microbial determine the effect of ethanol extract of Lemon grass on standard pathogenic bacteria were studied. Including Staphylococcus aureus, Pseudomonas aeruginosa, Escherichia coli and Enterococcus faecalis is.

Methods: Methods : In this study, the bacteria as Lyophilized of microbial collection Biotechnology Research Institute of Tehran University were prepared and ethanol extract of lemon grass with the Minimum Inhibitory Concentration (Minimum Inhibitory Concentration; MIC) and minimum bactericidal concentration (Minimum Bactericidal Concentration; MBC) using the dilution method was evaluated. Data analyzed using SPSS 17 software was used.

Results: Findings: The results showed that ethanol extract of Lemon grass Rubber greatest impact on gram-positive bacteria were Staphylococcus aureus and Enterococcus faecalis. As for the effect on gram-negative bacterium Escherichia coli, Pseudomonas aeruginosa higher concentrations are needed.

Conclusion: Conclusion: According to the results obtained can be hoped that using ethanol extract of Lemon grass can be used to inhibit some resistant bacteria such as Enterococcus faecalis.

Keywords: Keywords: Anti-Bacterial; Pathogenic Bacteria; Lemon Grass; Plant Extracts

**P596 - 747: EVALUATION OF GROWTH INHIBITORY EFFECT OF MICROEMULSION
PRODUCED FROM AQUEOUS EXTRACT OF HYPERICUM ON GRAM-NEGATIVE
CLINICAL STRAINS**

Maryam Sadrnia¹, Mohammad Arjomandzadegan², Ghasem Habibi³

1. Department of Biology, Payame Noor University, Iran
2. Infectious Diseases Research Center (IDRC), Arak University of Medical Sciences, Arak, Iran
3. Infectious Diseases Research Center (IDRC), Arak University of Medical Sciences, Arak, Iran

Background and Aim:Hypericum perforatum L has good anti-microbial effects. The aim of this study was to investigate the antimicrobial properties of aqueous extract and microemulsion obtained from the plant on the clinical strains of gram-negative microorganisms.

Methods:Methods: The clinical strains were as *Morganella morganii*, *Klebsiella pneumoniae*, *Salmonella paratyphi*, *Salmonella*, *Pseudomonas aeruginosa*, *Proteus*, *Citrobacter*, *Shigella*, *Serratia* and *Escherichia coli*. Hypericum extract was prepared by water in boiling temperature and microemulsion with help of two types of emulsifiers. Antibacterial properties of the two materials were performed by determining the inhibition zone in disk diffusion method and the measurement of minimum inhibitory concentrations (MIC) by the microplate dilution and a ELISA reader device.

Results:Results: *Salmonella typhi* have the highest zone of inhibition around 42 mm at a concentration of 8 mg / ml for extract and 30 mm in 0.1mg/ml Microemulsion but *Pseudomonas* have not any zone. The MIC with microplate for *Salmonella* have greatest effect amount of 0.01563 mg / ml for *Shigella* concentration of 0.00625 mg / ml respectively. MIC for *E. coli* and *Proteus* extract 0.5 mg / ml and the microemulsion 0.025 mg / ml for both bacteria.

Conclusion:Conclusion: Hypericum extract was a good antibacterial effect on gram negative clinical strains. Microemulsion was confirmed that in lower concentrations has the antibacterial effect.

Keywords:Hypericum, Aqueous extract, Microemulsion, Disk diffusion, Microplate dilution.

P597 - 759: ANTIBACTERIAL ACTIVITY OF CURCUMA LONGA EXTRACT AGAINST STAPHYLOCOCCUS AUREUS ISOLATED FROM DIFFERENT INFECTIONS

Mohammad Mehdi Attarpour Yazdi¹

1. Department of Microbiology, Faculty of Medicine, Shahed University, Tehran, Iran

Background and Aim:Background and Aim: Staphylococcus aureus is an important pathogen and produce different infections. Increasing of antibiotic usage for Staphylococcus aureus infections, created antibiotic resistance. Medical herbs with anti microbial activity have always been important role in traditional medicine. The aims of this study was to determine the antibacterial activity of methanol extract of Curcuma longa rhizome against Staphylococcus aureus isolated from different infections and to compare with effects of selected antibiotics in vitro.

Methods:Methods: First, a sample of methanol extract of dried roots of Curcuma longa by maceration method was prepared and then its antibacterial activity against 136 strain of Staphylococcus aureus isolates obtained from 500 samples of different infections was tested for the determination of MIC (minimum inhibitory concentration) using well diffusion and agar serial dilution assays. Also the antibacterial activity of penicillin, oxacillin, vancomycin, was tested by the disk diffusion method.

Results:Results: Statistical methods were used to analyze the data. The results demonstrated that the Curcuma longa methanol extract had been effective against 77.9% of Staphylococcus aureus. The MIC of the extract was about 2.5 mg/ml. while that was often resistant to selected antibiotics (96.2% and 50% resistant to penicillin and oxacillin respectively). There was significant difference between the effects of plant and antibiotics on Staphylococcus aureus. ($P < 0.05$)

Conclusion:Conclusion: This study demonstrates that a methanol extract of Curcuma longa is effective on Staphylococcus aureus isolated from different infections and its effect is even better than often selective antibiotics. Further investigations will be necessary.

Keywords: Keywords: Staphylococcus aureus, different infections, Curcuma longa, Antibiotic resistance

**P598 - 760: ANTIBACTERIAL ACTIVITY OF PUNICA GRANATUM PEEL EXTRACTS
AGAINST ESCHERICHIA COLI ISOLATED FROM URINARY TRACT INFECTIONS**

Mohammad Mehdi Attarpour Yazdi¹

1. Department of Microbiology, Faculty of Medicine, Shahed University, Tehran, Iran

Background and Aim:Background: Escherichia coli (E.coli) is an important pathogen in the Urinary Tract Infection (UTI). Increasing of antibiotic usage for E.coli infections, created antibiotic resistance. Medical herbs with anti-microbial activity have always been important role in traditional medicine. The purpose of this study was to determine the antibacterial activity of aqueous, methanolic and ethanolic extracts of Punica granatum peel against E.coli isolated from UTI in vitro.

Methods:Methods: This research is a descriptive analytic study. First, samples of aqueous, methanolic and ethanolic of Punica granatum peel were prepare by maceration method. Then its antibacterial activity against 158 isolates of E.coli from 200 samples of UTI was evaluated by well diffusion and then agar serial dilution method. Also, the MIC (Minimum Inhibitory Concentration) of extract was determined.

Results:Results: The diagrams, T- test were used to compare the results. The results demonstrated that the aqueous, methanolic and ethanolic extracts of Punica granatum peel show an average inhibitory zone diameter of 22.5, 21, and 23 respectively. The ethanolic extract shows best result having ZOI greater than that of the selective antibiotics. Ethanolic extract of Punica granatum has lowest MIC of 1.45 µg/mg showing that it is most effective as compared to MICs of other extract. There was significant difference between the effects of the plant and antibiotics on E.coli ($P<0.001$).

Conclusion: Conclusion: This study demonstrates that an ethanolic extract of Punica granatum peel have excellent antibacterial activity against E.coli isolated from UTI and its effect is even better than selective antibiotic. Further investigations will be necessary.

Keywords:Key words: UTI, Escherichia coli, punica granatum, Antibacterial Activity

**P599 - 771: THE SURVEY OF ANTIBACTERIAL EFFECT OF HYPERICUM PERFORATUM
L. EXTRACT POLAR, SEMI-POLAR AND NON-POLAR FRACTIONS ON
STAPHYLOCOCCUS AUREUS, BACILLUS CEREUS ESCHERICHIA COLI AND
PSEUDOMONAS AERUGINOSA BACTERIA**

Changiz Ahmadizadeh¹, Mojtaba Babaei Daylari², Rozita Tamjidifar³

1. Assistant Professor, Department of Microbiology, Islamic Azad University of Ahar
2. Master of Science Microbiology
3. Master of Science Microbiology

Background and Aim:Increasing drug resistance among bacteria has caused more attention to finding ways to prevent the development of resistance and appropriate drugs with toxic effects and fewer side effects and for this purpose are Medicinal herbs are paid special attention with. The aim of this study was to evaluate the effect of antibacterial fractions of polar and semi-polar, nonpolar Hypericum perforatum extract on Staphylococcus aureus, Bacillus cereus, Escherichia coli, Pseudomonas aeruginosa, respectively

Methods:In this study of Hypericum perforatum extract was used. The extracts of methanol, chloroform and ether were prepared and the effect of different concentrations of the extracts of Hypericum perforatum was investigated. All experiments with the release of the wells and determine the MIC and MBC on standard strains of Staphylococcus aureus, Bacillus cereus, Escherichia coli, Pseudomonas aeruginosa was performed

Results:The extract of methanol, chloroform and petroleum Hypericum perforatum had the greatest impact on gram-positive bacteria Bacillus cereus. As for the effect on gram-negative bacteria Escherichia coli and Pseudomonas aeruginosa higher concentrations are needed

Conclusion:Methanol and chloroform extracts of Hypericum on the bacteria Bacillus cereus, Staphylococcus aureus and Pseudomonas aeruginosa was shown to be effective. In the E. coli bacteria was resistant to all three fractions tested

Keywords:Hypericum Perforatum L., Bacillus cereus, Herbal extracts, Escherichia coli

P600 - 810: ANTIBACTERIAL EFFECT OF SILVER NANOPARTICLES USING EXTRACT OF OLIVE LEAF

Somayeh Shirkhani¹

1. Faculty of medicine, Lorestan university of medical sciences, Khorramabad, Iran

Background and Aim:olive (*Olea europaea*) is an evergreen tree that grows in Mediterranean region. So, the aim of this study was to evaluate the antibacterial effect of silver nanoparticles using olive leaf extract.

Methods:parameters affecting the formation of nanoparticles such as temperature, exposure time to extract, pH, concentration of silver nitrate and extract were investigated and optimized. Antibacterial test had done by Broth Micro Dilution and Disk Diffusion methods and Minimum Inhibitory Concentration (MIC) and Minimum bactericidal concentration (MBC) after 24 and 48 h determined and compared to control of antibiotic. Plant antibacterial activity was carried out on bacteria *Staphylococcus aureus*, *Listeria monocytogenes*, *Pseudomonas aeruginosa*, *Escherichia coli* and MRSA.

Results:Optimum conditions for the synthesis of silver nanoparticles are as follows: Ag concentration 1mM, extract concentration, 8% w/v; pH=7, time, 4 h and temperature, 45°C. Synthesized silver nanoparticles were characterized using UV-Visible absorption spectroscopy. Fourier-transform infrared spectroscopy, X-ray diffraction, dynamic light scattering (DLS), and scanning electron microscopy (SEM). SEM and DLS analysis showed that the synthesized AgNPs were predominantly spherical in shape with an average size of 90 nm. Strong antibacterial effects observed on bacteria standard *Staphylococcus aureus* and determined MIC= 0.16 (μg / ml) and MBC= 0.63(μg / ml). The effect on MRSA-resistant *staphylococcus* and *E. coli* was weaker. *Pseudomonas aeruginosa* was resistant.

Conclusion: The antibacterial properties of silver nanoparticles using extract of olive leaf can be used in the food industry, pharmaceuticals, cosmetics and health.

Keywords:Silver nanoparticles, Olive leaf extract, Antibacterial.

**P601 - 857: ANTIBACTERIAL ACTIVITY OF ISOLATED BACTERIAL ENDOPHYTES OF
SUPERNATANT CULTURE BROTH AND CHLOROFORM INACTIVATED BACTERIAL
COLONIES FROM ACHILLEA MILLEFOLIUM ON SOME FIELD ISOLATES OF
BACTERIAL PATHOGENS**

Masoumeh Amidi¹, Azizollah Ebrahimi²

1. MSc student of bacteriology graduating in School of Veterinary Science, Shahrekord University, Shahrekord, Iran
2. 2 Department of Pathology, Microbiology School of Veterinary Science, Shahrekord University, Shahrekord, Iran

Background and Aim:Background:Endophytic organisms associated with plants are varied and complex. Endophytic microbes occupy a relatively privileged niche within plant and usually contribute to plant health. Some groups of endophytic microorganisms have been believed to be mutualists that protect plants against biotic stresses.In this study, we focused on the isolation of bacterial endophytes from two medicinal plants Achillea millefolium screening them for activities against some field isolates of animal bacterial pathogens.

Methods:Materials and Methods: Random samples from asymptomatic leaves and branches of two medicinal plants namely: Achillea millefolium were collected. For isolation of endophytic bacteria, the disinfected portions of the plants were distributed onto the isolation media.To examine endophytic bacterial contents, the bioassays were conducted using growing colonies in PA and YEA inactivating them by chloroform. Staphylococcus aureus and Streptococcus agalactiae were isolated from mastitis cow's milk in our previous works

Results: Results: A total of 15 phenotypically distinguishable bacterial endophytes were isolated in pure form from one medicinal plant. In part of endophytes of supernatant culture broth and chloroform inactivated colonies of all 15 isolated endophytes the 3 most effective herb was branche on some Staphylococcus aureus.

Conclusion:Conclusions: Endophytic microorganisms reside in A. millefolium are a very promising source for production of bioactive compounds at least against some field isolates of veterinary pathogenic bacteria.

Keywords:Keywords: Endophytes, antibacterial activity, chloroform inactivated bacterial

**P602 - 890: THE EFFECT OF POMEGRANATE, CASTOR AND GARLIC EXTRACTS ON
CLINICAL MULTI-DRUG RESISTANT E. COLI ISOLATES**

Somaye Kermani jamkarani¹, Farhad Qasemi Ostad², Jamile Sadat Havaeji³, Zeinab Vesali Jamshid⁴,
Saeed Shams⁵

1. Department of Microbiology, Qom University of medical sciences. Qom, Iran
2. Ms. student of Bacteriology. Iran university , Tehran , Iran
3. . Bs.c clinical laboratory science. Cellular and Molecular Research Center, Qom University of Medical Sciences, Qom, Iran
4. . Bs.c clinical laboratory science. Cellular and Molecular Research Center, Qom University of Medical Sciences, Qom, Iran
5. Department of Microbiology, Qom University of medical sciences. Qom, Iran

Background and Aim:Antibiotic resistance is a health problem and has been discussed as a particular concern for hospitals and community .This in vitro study sought to evaluate the effectiveness of plant extracts (pomegranate, castor and garlic extracts) on clinical multi-drug resistant Escherichia coli isolates.

Methods:Different clinical samples including faeces, wound, sputum, urine, cerebrospinal fluid (CSF), tracheal, blood etc. Sent to microbiology laboratory. Isolation and identification of bacteria was carried out using conventional microbiological tests. Antibacterial activity was tested on Escherichia coli using a micro dilution method.The resistant E. coli strains (17) were isolated from isolated bacterial total. Three plant extracts were prepared (200 mg/ml).samples separately were treated with each dilution of extract.incubate for one day in 37 c and the next day all samples should culture on a general media (nutrient agar). Last step is observation the culture results.

Results:Castor extract showed strong broad-spectrum activity against multi-drug resistant Escherichia coli isolates. (47%), with the minimum inhibitory concentrations (MIC) ranging from 12.5 to 100 mg/ml. garlic extracts showed inhibitory activity against 29% of samples with the(MIC) ranging from 6.25 to 100 mg/ml and5.8% (one sample) response to pomegranate fruit peel. This sample belonged to a 5 months baby.

Conclusion:Our study suggest that pomegranate, castor, garlic extracts could be exploited as a potential source of natural antimicrobial. Future studies are needed to evaluate antimicrobial mechanisms of extracts and to study in vivo

Keywords:multi-drug resistant E. coli isolates, pomegranate, castor, garlic

**P603 - 921: COMPARISON OF ANTIMICROBIAL ACTIVITY OF FENNEL ESSENTIAL OIL
AGAINST STAPHYLOCOCCUS AUREUS WITH SOME ANTIBACTERIAL DRUGS**

Mahsa Shokri¹, Ali Kazemi², Mahdi Ebrahimi³

1. Department of Microbiology, Islamic Azad University, Varamin-Pishva Branch ,Varamin, Iran
2. Department of Nursing, Islamic Azad University, Varamin-Pishva Branch ,Varamin, Iran
3. Department of Biochemistry, Islamic Azad University, Varamin-Pishva Branch ,Varamin, Iran

Background and Aim: The excessive use of antibiotics could result in the generation of drug-resistant bacteria. Essential oils produced by plants have been traditionally used for treatment of different infections. Some essential oils are known to possess antimicrobial activity, which has been evaluated mainly in liquid medium. In this study, antimicrobial activity of fennel essential was investigated against *Staphylococcus aureus* in comparison with vancomycin, ciprofloxacin, ceftriaxone and co-trimoxazole drugs and *Escherichia coli* was used as a control strain. The fennel essential oil were obtained using hydrodistillation method.

Methods: The antimicrobial activity was evaluated using disc diffusion and microbroth dilution methods.

Results: The results showed a significant activity against *S. aureus* with inhibitory concentration values in the range of 11-13 mm and 32-64 μ l/ml for fennel essential oil whereas, inhibitory concentration values in disk diffusion method in the range of 21-24 mm, 23-28 mm, 15-30 mm, 17-31 mm and 9-28 mm were obtained for vancomycin, cephalixin, ciprofloxacin, ceftriaxone and co-trimoxazole , respectively. Minimum inhibitory concentration were obtained 0.5, 2,4,4 and 32 μ l/ml for mentioned drugs, respectively.

Conclusion: With regard to results, fennel essential oil has the potent antimicrobial activity against *Staphylococcus aureus*. Further studies are required to evaluate the practical values of therapeutic applications and other administrations. The use of essential oils with antibacterial effect is recommended with or without antibacterial drugs.

Keywords: fennel, *Staphylococcus aureus*, antibacterial drugs

**P604 - 928: SURVEY OF ANTIBACTERIAL PROPERTIES OF GINGER EXTRACT ON
ISOLATED BACTERIA FROM PATIENTS WITH URINARY TRACT INFECTIONS**

Mehdi Simaei¹, Parvaneh Bideh²

1. Department of Microbiology, Faculty of science, Islamic Azad University, Lahijan Branch, Lahijan, Iran
2. Laboratory of Karaj Hospital, Karaj, Iran

Background and Aim: Urinary infection is a common disease with dangerous effects in human and *E. coli* is the agent of acute urinary tract infection in more than 80% of cases. Different studies reported antibiotic resistance increase in strains agent of infection. Choosing an appropriate antibiotic is hard due to acquisition of antibiotic resistance genes and changes in bacterial sensitivity pattern against antibiotics. Also, finding antimicrobial components with natural origin is essential due to side effects of antibiotics. Ginger is a medicinal plant with medical records.

Methods: Due to its medical effects, *Zingiber officinalis* (ginger) rhizome was provided and powdered after drying in oven with 40 °C. Ginger powder was extracted using Soxhlet method by ethanol and methanol. The solution was evaporated in an incubator with temperature 40 °C and serial dilutions were prepared from each extract with 10% D-methyl sulfoxide solution. 4 patients suffered from *E. coli* infection were chosen from Karaj hospitals to do antimicrobial indexes, including antibiogram disk, disk diffusion, MIC and MBC determination.

Results: According to obtained results some patients infected to *E. coli* were resistance against gram negative specific antibiotics. This despite the fact that methanol and ethanol extract in all methods had inhibitory effect and inhibitory effect in disc diffusion of methanol extract and sink diffusion of ethanol extract were more than other so that no bacteria had grown.

Conclusion: Based on the results, more extract concentration causes the more inhibitory effect. MIC and MBC for both ethanol and methanol extracts were 40%.

Keywords: *E. coli*, Ginger, Urinary infection, extract

P605 - 929: EXPRESSION OF RECOMBINANT α -LUFFIN IN ESCHERIACHIA COLI

Shaghayegh Namvar¹, Fatemeh Davami², Hoda Jahandar³, Leila Nematollahi⁴, Farzaneh Barkhordari⁵

1. Department of Biotechnology; Pharmaceutical Sciences Branch; Islamic Azad University; Tehran – Iran (IAUPS)
2. Biotechnology Research Center; Pasteur Institute of Iran
3. Department of Biotechnology , Faculty of Advanced Sciences & Technology , Pharmaceutical Sciences Branch, Islamic Azad University ,Tehran – Iran (IAUPS)
4. Biotechnology Research Center; Pasteur Institute of Iran
5. Biotechnology Research Center; Pasteur Institute of Iran

Background and Aim: Around 80% of world's population use herbal medicines for treatment of diseases. Vinca alkaloids and Taxanes are some examples of plant-based cytotoxic agents. Apoptosis inducing property is one of the most important mechanisms of these components. *Luffa cylindrica* is a sub-tropical plant and belongs to Cucurbitaceae family. It has long been used as a medicinal herb to treat respiratory complaints and skin diseases. α -Luffin is a ribosome-inactivating protein (RIP) in *Luffa cylindrica* seeds. α -Luffin has cytotoxicity and apoptosis inducing properties that makes it an antitumor agent for developing immunotoxins. Limited plant resources are one of the main problems in the use of native toxins. Therefore, generating toxins by recombinant techniques may be the best way to produce therapeutic proteins in a large scale.

Methods: In this study the recombinant α -luffin was expressed in *Escheriachia coli* as a host. For this purpose first the α -luffin gene was synthesized based on available documents. The gene and vector of interest was co-transformed into *E.coli* competent cells through the heat shock method. Protein expression was induced with rhamnose in Luria-Bertani medium. Expression was evaluated at different intervals (0, 4, 6, 8, 24 hours) post induction. Expression of recombinant α -luffin was confirmed by SDS-PAGE analysis and western blotting.

Results: The enzymatic digestion and colony PCR showed that the cloning was performed successfully in vivo. The SDS-PAGE and western blot analysis confirmed that recombinant α -luffin was produced in *E.coli* host in the LB medium.

Conclusion: This study suggests that *E.coli* can be an appropriate host for α -luffin expression.

Keywords: α -luffin , *Luffa cylindrica*, *Escheriachia coli*

P606 - 940: EVALUATION ANTIFUNGAL EFFECT OF SALVIA RHYTIDEA AGAINST C. GLABRATA ISOLATES

Samira Salari¹

1. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran

Background and Aim: *Candida* spp cause life-threatening infections in immunocompromised patients, leading to an increase in mortality rate. *C. glabrata* has been considered a relatively nonpathogenic saprophyte of the normal flora of healthy individuals, rarely causing serious infection in humans. Due to limits on the use of an antifungal drug and emergence of azole resistance isolates and increased incidence of treatment failures, finding novel agent with antifungal properties is necessary. The aim of the present study was to assess the anti-fungal activity of methanolic extract of *salvia rhytidea* against *C. glabrata*.

Methods: In this study antifungal effect of methanolic extract of *salvia rhytidea* against 16 *C. glabrata* isolates obtained from patients with different forms of candidiasis were evaluated using Clinical and Laboratory Standard Institute (CLSI) guidelines.

Results: The antifungal activity of *salvia rhytidea* against *C. glabrata* exhibited MIC of 6.25 µg/mL for one *C. glabrata* isolate. Three isolates showed MIC 50 µg/mL. As well as, the MIC of *salvia rhytidea* on 2 and 10 *C. glabrata* isolates were 100 and >100 µg/mL, respectively.

Conclusion: Our Results showed that methanolic extract of *salvia rhytidea* was effective against *C. glabrata* but various concentrations of it showed varying degree of antifungal activity.

Keywords: Antifungal Activity, *salvia rhytidea*, *C. glabrata*

**P607 - 950: EVALUATION OF ANTIFUNGAL PROPERTY OF METHANOLIC EXTRACT OF
SALVIA RHYTIDEA AGAINST C. TROPICALIS ISOLATES**

Samira Salari¹

1. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran

Background and Aim: *Candida* spp cause life-threatening infections in immunocompromised patients such as cancer patients, organ transplant patients, and patients receiving immunosuppressive therapy in general, PLWH, and undergoing major surgeries, leading to an increase in mortality rate. Human fungal pathogen, *C. tropicalis* is an opportunistic organism capable of causing mucosal and systemic infections. *Salvia* is the largest genus of the Lamiaceae family and includes approximately 900 species globally, 58 of which can be found in Iran. This plant is popularly known as *Salvia* or sage (“maryam-goli” in the Persian language). Regard to limits on the use of an antifungal drugs and emergence of azole resistance isolates and increased incidence of treatment failures, finding novel agent with antifungal properties is very important. The purpose of the present study was to assess the antifungal property of methanolic extract of *S. rhytidea* against *C. tropicalis* isolates.

Methods: Here, antifungal property of *S. rhytidea* against 11 *C. tropicalis* isolates which obtained from patients with candidiasis were evaluated using CLSI guidelines.

Results: The antifungal activity of *S. rhytidea* against *C. tropicalis* exhibited MIC of 6.25 and 12.50 µg/mL for four and three *C. tropicalis* isolates, respectively. Only one isolate showed MIC 25 µg/mL and three of them exhibited >100 µg/ml for MIC.

Conclusion: Our Results showed that methanolic extract of *S. rhytidea* was effective against *C. tropicalis* but various concentrations of it showed varying degree of antifungal activity.

Keywords: Antifungal property , Methanolic Extract of *Salvia rhytidea*, *C. tropicalis*

P608 - 954: CHEMICAL COMPOSITION AND IN VITRO ANTIBACTERIAL EFFECT OF ESSENTIAL OIL OF PISTACIA KHINJUK (COMBINED WITH THE DOMINANCE Γ -TERPINENE) ON PSEUDOMONAS AERUGINOSA.

reza tahvilian¹, rohalah moradi², hossein zhale³, mohammad mahdi zangeneh⁴, akram zangeneh⁵, hossein yazdani⁶, majid hajialiani⁷

1. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran
2. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran
3. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran
4. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran and Microbiology section, Pathobiology & Basic sciences department, Veterinary faculty, Razi University, Kermanshah, Iran
5. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran and Microbiology section, Pathobiology & Basic sciences department, Veterinary faculty, Razi University, Kermanshah, Iran
6. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran
7. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran

Background and Aim: Pistacia khinjuk is a native plant in Iran, which this plant has been used as an indigestion, tonic, toothache, anti-inflammatory, antipyretic and astringent in Iran. The aim of the current study was to determine chemical composition of P. khinjuk essential oil and evaluate its antibacterial activity against common pathogen (*Pseudomonas aeruginosa*)

Methods: Agar well diffusion and disk diffusion methods were performed as screen tests. Macrobrotth dilution method was accomplished to determination of MIC value. *P. aeruginosa* was chosen to survey. Serial dilutions were prepared from essential oil of the aerial parts in 1/16, 1/32, 1/64, 1/128, 1/256, and 1/512 ratios in DMSO. Gentamicin was used as positive control for this bacteria. DMSO was used as negative control, too

Results: According to results of GC-MS analysis, γ -terpinene (81.14%) (w/w) was the most abundant component of the essential oil. In agar well diffusion method, in 1/16, 1/32, 1/64, and 1/128 dilutions, inhibitory zones were seen 10, 10, 9, and 8 mm in diameters for *P. aeruginosa*. In disk diffusion, in 1/16, 1/32, 1/64, and 1/128 dilutions, there were 14, 10, 10, and 8 mm halos for *P. aeruginosa*. Gentamicin was used as positive control for *P. aeruginosa* (34 mm halo). 1/64 dilution was realized for both MIC and MBC about this bacteria

Conclusion: *P. khinjuk* has a good antimicrobial effect on above bacteria as representatives of pathogenic bacteria. In addition, perhaps disk diffusion is more reliable method than agar well diffusion for antimicrobial screening test in this plant

Keywords: Pistacia khinjuk, essential oil, antibacterial effect

**P609 - 956: ETHNOMEDICINAL PLANTS: SCREENING OF IN VITRO ANTIBACTERIAL
ACTIVITY OF ESSENTIAL OIL OF PISTACIA KHINJUK (COMBINED WITH THE
DOMINANCE Γ -TERPINENE) ON BACILLUS SUBTILIS.**

reza tahvilian¹, rohalah moradi², hossein zhale³, mohammad mahdi zangeneh⁴, akram zangeneh⁵, hossein yazdani⁶, majid hajialiani⁷

1. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran
2. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran
3. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran
4. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran and Microbiology section, Pathobiology & Basic sciences department, Veterinary faculty, Razi University, Kermanshah, Iran
5. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran and Microbiology section, Pathobiology & Basic sciences department, Veterinary faculty, Razi University, Kermanshah, Iran
6. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran
7. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran

Background and Aim: Pistacia khinjuk is an endemic and resistance species in dry and sub-dry forests in mountainous regions of Western Iran. The aim of the current study was to determine chemical composition of P. khinjuk essential oil and evaluate its antibacterial activity against common pathogen (*Bacillus subtilis*)

Methods: Agar well diffusion and disk diffusion methods were performed as screen tests. Macrobrotth dilution method was accomplished to determination of MIC value. *B. subtilis* was chosen to survey. Serial dilutions were prepared from essential oil of the aerial parts in 1/16, 1/32, 1/64, 1/128, 1/256, and 1/512 ratios in DMSO. Cephalixin was used as positive control for this bacteria. DMSO was used as negative control, too

Results: According to results of GC-MS analysis, γ -terpinene (81.14%) (w/w) was the most abundant component of the essential oil. In agar well diffusion method, in 1/16, 1/32, 1/64, and 1/128 dilutions, inhibitory zones were seen 12, 10, 9, and 8 mm in diameters for *B. subtilis*. In disk diffusion, in 1/16, 1/32, 1/64, and 1/128 dilutions, there were 18, 12, 10, and 8 mm halos for *B. subtilis*. Cephalixin was used as positive control for *B. subtilis* (32 mm halo). 1/32 dilution was realized for both MIC and MBC about this bacteria

Conclusion: Based on the results, *P. khinjuk* has a fair antibacterial effect on tested bacteria as representatives of pathogenic bacteria. It sounds disk diffusion is more reliable method than agar well diffusion for antimicrobial screening test in this plant

Keywords: Pistacia khinjuk, essential oil, antibacterial activity

**P610 - 964: COMPARISON OF QUANTITATIVE DIAGNOSTIC KIT AND GAS
CHROMATOGRAPHY TECHNIQUE FOR DETERMINATION OF METHANOL AT TRACE
LEVELS IN HERBACEOUS DISTILLATES**

Maliheh Rahati noveir¹, Ali Rafizadeh²

1. Islamic Azad University, Rasht Branch, Faculty of Agriculture, Rasht, Iran
2. Islamic Azad University, Rasht Branch, Faculty of Science, Dep. of Chemistry, Rasht, Iran

Background and Aim: Methanol is one of the popular organic solvents and finds extensive applications in industries and household uses. It is rapidly and well absorbed by inhalation, and by oral and topical exposure. Also methanol occurs naturally in different herbal distillates and formed when various plants are physically prepared for consumption.

Methods: The objective of this study was comparison of determination efficiency of the trace levels of methanol in herbaceous distillates by using quantitative diagnostic kit and gas chromatography-mass spectrometry (GC-MS) technique. In this study were taken 40 samples of various herbaceous distillates of Iran markets selected as representative types, by their production and origin.

Results: It was confirmed that methanol was present in all studied samples. The range of trace methanol in the studied samples was 23-300 ppm. There weren't any significant difference between GC and quantitative diagnostic kit results for determination of methanol levels.

Conclusion: The GC-MS procedure was found to be very tedious but the diagnostic kit, was found to be much simpler (easy application with no need to professional and expensive equipment) for the quantification of methanol and also the obtained results were shown, the kit sensitivity and accuracy were suitable (like GC) for exact measuring of herbal distillates methanol content.

Keywords: methanol, gas chromatography, diagnostic kit, herbaceous distillates

**P611 - 975: PREVALENCE OF POSITIVE SAMPLES OF TUBERCULOSIS IN PATIENTS
REFERRED TO BOOALI HOSPITAL IN ZAHEDAN IN 2011**

Hadi Hosseini¹, iman hormozi², najmeh shakib³

1. Young Researchers and Elite Club, zahedan Branch, Islamic Azad university, zahedan, Iran.
2. Young Researchers and Elite Club, zahedan Branch, Islamic Azad university, zahedan, Iran.
3. Young Researchers and Elite Club, zahedan Branch, Islamic Azad university, zahedan, Iran.

Background and Aim: Because of all seven of the past century in one case leading to death, has been recognized as the major cause of death worldwide. In developing countries the rate of death from the disease is higher in comparison with other bacterial diseases. TB is the second leading cause of fatal infectious disease after AIDS

Methods: Epidemiological information is recorded by referring to data of the people who visit this center were collected. After 3 innings of sputum smear test, if positive sputum smear-positive pulmonary TB sputum smears were negative, and if 3 times after 2 weeks of treatment with antibiotics, if not treated with them and clinical and radiological evidence of TB, your doctor as pulmonary tuberculosis (smear negative) consider positive and necessary review after testing positive culture and culture as positive pulmonary tuberculosis (positive culture) is considered. Data obtained using statistical software (v17) SPSS software and statistical tests EPI6 k1 and comparison of the percentages obtained in the significant level of $p < 0.05$ were analyzed.

Results: According to the findings of this study in 2011, 180 patients with pulmonary tuberculosis were referred to this center. 4020 samples were taken and tested 180 samples of which 373 samples were smear positive and smear negative (positive culture), respectively. The sex distribution among 62 patients (36%) were male and 118 (64%) are female.

Conclusion: The results of this study show that the incidence of TB is higher than smear negative pulmonary tuberculosis. And its prevalence in females than in males (less than 2 times).

Keywords: zahedan, tb, booali, 2011

P612 - 985: COMPARATIVE STUDY OF THE ANTIMICROBIAL EFFECTS OF AQUEOUS AND ORGANIC EXTRACTS OF NETTLE ON MEMBERS OF THE GENUS KLEBSIELLA, AND THEIR COMPARISON WITH COMMONLY USED ANTIBIOTICS

Fatemeh Azizi alidoust¹, Masoumeh Anvari², Somayeh Ataei Jaliseh³

1. Department of Biology, Rasht Branch, Islamic Azad University, Rasht, Iran
2. Department of Biology, Rasht Branch, Islamic Azad University, Rasht, Iran
3. Department of Biology, Rasht Branch, Islamic Azad University, Rasht, Iran

Background and Aim:the problems in the treatment of infections caused by resistant strains of micro-organisms, on one hand, and increasing resistance of bacteria to antibiotics and their side effects, on the other hand, have made us to look closer at natural herbs, because they are natural and have no harmful side effects. This study is to investigate the antimicrobial activity of aqueous and organic (ethanol) extracts of nettle against Klebsiella.

Methods:the problems in the treatment of infections caused by resistant strains of micro-organisms, on one hand, and increasing resistance of bacteria to antibiotics and their side effects, on the other hand, have made us to look closer at natural herbs, because they are natural and have no harmful side effects. This study is to investigate the antimicrobial activity of aqueous and organic (ethanol) extracts of nettle against Klebsiella.

Results:The results indicated that the minimal inhibitory concentration of aqueous and organic extracts of nettle against *Klebsiella pneumoniae* were 0.39 and 1.5 micrograms per ml, respectively. The maximum diameter of the inhibition produced by alcoholic extract of nettle was 11 mm and that of aqueous extract of nettle was 10 mm.

Conclusion:The results of this study demonstrated an increase in *Klebsiella pneumoniae* resistance against antibiotics such as Gentamycin, Tetracycline, Ampicillin and Cefixime; maybe this is due to irregular usage of antibiotics, Therefore, identification and purification of antimicrobial agents of mentioned extracts is recommended.

Keywords:Antibacterial effects, herbs, Minimum inhibitory concentration.

**P613 - 1011: ANTIMICROBIAL ACTIVITIES OF ISOLATED BACTERIAL ENDOPHYTES
FROM PETROSELINUM CRISPUM ON SOME FIELD ISOLATES OF VETERINARY
BACTERIAL PATHOGENS**

Masoumeh Amidi¹, Azizollah Ebrahimi²

1. MSc student of bacteriology graduating in School of Veterinary Science, Shahrekord University, Shahrekord, Iran.
2. Department of Pathology, Microbiology School of Veterinary Science, Shahrekord University, Shahrekord, Iran

Background and Aim:Background: Bacterial endophytes are ubiquitous colonizers of the inner plant tissues where they do not normally cause any substantial morphological changes and disease symptoms. Endophytic bacteria are harmless that reside within the plant hosts and known to boost the growth and development of host plants probably by secreting growth hormones..In this study, we focused on the isolation of bacterial endophytes from one medicinal plant *Petroselinum crispum* screening them for activities against some field isolates of animal bacterial pathogens.

Methods:Methods: Random samples from asymptomatic leave and branche of one medicinal plant namely: *Petroselinum crispum* were collected. For isolation of endophytic bacteria, the disinfected portions of the plant were distributed onto the isolation media.To examine endophytic bacterial contents, the bioassays were conducted using growing colonies in PA and YEA inactivating them by chloroform. To test antibacterial activity of endophytic bacterial culture broth, filter-sterilized supernatants were poured in cylinders on each bacterial plate. Isolates of *Escherichia coli* were isolated from dead poultry referred to veterinary clinic of Shahrekord university by regional poultry farms

Results:Results: A total of 20 phenotypically distinguishable bacterial endophytes were isolated in pure form one medicinal plant. In part of supernatant culture broth of all 20 isolated endophytes the 5 most effective herb was leaves and branches *P.crispum* on some *Escherichia coli*.

Conclusion:Conclusions: Endophytic in *P.crispum* Investigation proceeds in order to classify the microorganisms and exploit the potential of the substance produced to inhibit these pathogenic bacteria.

Keywords:Keywords: *P.crispum*, Endophytes, supernatant culture broth, Shahrekord, Iran.

**P614 - 1046: EVALUATION EFFECT OF DANDELION EXTRACT ON SOME NEGATIVE
AND POSITIVE GRAM BACTERIA**

Mona Shahpari¹, mohsen mohammadi²

1. Active Pharmaceutical Ingredient Research Center, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran-Iran (IAUPS)
2. Department of pharmaceutical biotechnology, university of Tehran, Tehran-Iran

Background and Aim: Bacterial strain disease represents an important cause of morbidity and mortality worldwide. The antimicrobial activity of plant extracts was considered as an appropriate method for curing infection caused by bacteria. In this study we evaluate effect of extract of dandelion on some negative and positive gram bacteria.

Methods: some negative or positive gram bacteria obtained from a standard laboratory for microbial testing, including *Lactobacillus subtilis*, *Enterococcus faecalis*, *Listeria*, *E. coli* and *Staphylococcus aureus*. Extract was used and its composition was determined by SPME-GC-MS technique. Maximum Inhibitory concentration (MIC) and minimum bacteriocidal concentration (MBC) was used in this evaluation.

Results: our finding showed that extract of dandelion can inhibit growth of *L. subtilis*, *E. faecalis* and *Listeria* and MIC values for them were 0.7, 11.25 and 2.81, respectively. Also indicated that extract of dandelion not any growth inhibitory effect against *E. coli* and *S. aureus*.

Conclusion: our results indicated that dandelion extract can inhibit growth of some bacterial strain. Therefore using plant extract can be useful method for curing bacterial infection.

Keywords: plant extract, dandelion, MIC, MBC

**P615 - 1047: STUDY ON ANTIBACTERIAL ACTIVITY OF ESSENTIAL OIL OF
CINNAMOMUM ZEYLANICUM ON ESCHERICHIA COLI O157:H7.**

mohammad mahdi zangeneh¹, lida haghazari², akram zangeneh³

1. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran and Microbiology section, Pathobiology & Basic sciences department, Veterinary faculty, Razi University, Kermanshah, Iran .
2. Faculty of medical, Kermanshah University of Medical Sciences, Kermanshah, Iran
3. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran and Microbiology section, Pathobiology & Basic sciences department, Veterinary faculty, Razi University, Kermanshah, Iran.

Background and Aim: In modern countries today, herbal medicines are known to help in the treatment of different diseases such as bacterial infections. To study the effect of *Cinnamomum zeylanicum* on *Escherichia coli* O157:H7.

Methods: Agar well diffusion and disk diffusion methods were performed as screen tests. Macrobrotth dilution method was accomplished to determination of MIC value. *E. coli* was chosen to survey. Serial dilutions were prepared from essential oil of the aerial parts in 1/16(0.062 g/ml), 1/32(0.031 g/ml), 1/64(0.015 g/ml), 1/128(0.007 g/ml), 1/256(0.003 g/ml), and 1/512(0.002 g/ml) ratios in DMSO. Kanamycin was used as positive control for this bacteria. DMSO was used as negative control, too.

Results: In agar well diffusion method, in 1/16, 1/32, 1/64, 1/128, 1/256, and 1/512 dilutions, inhibitory zones were seen 37, 23, 18, 14, 16, and 11 mm in diameters for *E. coli*. In disk diffusion, in 1/16, 1/32, 1/64, 1/128, 1/256, and 1/512 dilutions, there were 54, 38, 19, 19, 13, and 10 mm halos for *E. coli*. Kanamycin was used as positive control for *E. coli* (28 mm halo). 1/256 dilution was realized for both MIC and MBC about this bacteria.

Conclusion: Our data express essential oil of *C. zeylanicum* have great potential as antimicrobial compounds against *E. coli*. Thus, *C. zeylanicum* can be used in the treatment of infectious diseases caused by resistant microbes.

Keywords: *Cinnamomum zeylanicum*, essential oil, antibacterial activity.

**P616 - 1051: INVESTIGATION EFFECT OF SATUREJA KHUZESTANICA AGAINST SOME
GRAM NEGATIVE AND POSITIVE BACTERIA**

Mona Shahpari¹, mohsen mohammadi²

1. Active Pharmaceutical Ingredient Research Center, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran-Iran (IAUPS)
2. Department of pharmaceutical biotechnology, university of Tehran, Tehran-Iran

Background and Aim: Use of herbs is the most ancient approach to healing known. Many investigations have demonstrated that antimicrobial activity of the constituents of some higher plants which can give benefit treatments for microbial bacteria. In present study we examine inhibitory growth effect of *S.khuzestanica* extract on some negative/positive gram bacteria.

Methods: Root extraction of *satureja khuzestanica* was utilized and SPME-GC-MS technique was used to identify root's plant composition. The strain of *S.aureus*, *E-coli*, *Pseudomonas aeruginosa*, *Micrococcus luteus* faecalis were used for microbial testing of the extraction result. Eventually minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) values was used in this investigation.

Results: The finding indicated that *S.khuzestanica* extract had growth inhibitory effect against tested bacteria, except *E.fecalis*. MIC value for *S.aureus*, *E-coli*, *P.aeruginosa* and *M.luteus* were 25, 25, 12.5 and 6.25, respectively.

Conclusion: The results of our study showed that plant extracts can be an effective approach for curing infection caused by bacteria.

Keywords: Plant extract, *satureja khuzestanica*, MIC, MBC

**P617 - 1053: ETHNOMEDICINAL PLANTS: THE ANTIBACTERIAL ACTIVITY OF
ESSENTIAL OIL OF CORIANDRUM SATIVUM ON STAPHYLOCOCCUS AUREUS.**

akram zangeneh¹, lida haghazari², mohammad mahdi zangeneh³

1. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran and Microbiology section, Pathobiology & Basic sciences department, Veterinary faculty, Razi University, Kermanshah, Iran.
2. Faculty of medical, Kermanshah University of Medical Sciences, Kermanshah, Iran
3. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran and Microbiology section, Pathobiology & Basic sciences department, Veterinary faculty, Razi University, Kermanshah, Iran.

Background and Aim: There are some evidences on antibacterial effects of this plant in the world but to our knowledge, there is no study on antibacterial effects of *Coriandrum sativum* essential oil of the native plant in west of Iran. Therefore, the aim of this study was determination of antibacterial activity of this plant growing in Kermanshah.

Methods: Agar well diffusion and disk diffusion methods were performed as screen tests. Macrobroth dilution method was accomplished to determination of MIC value. *Staphylococcus aureus* was chosen to survey. Serial dilutions were prepared from essential oil of the aerial parts in 1/16, 1/32, 1/64, 1/128, 1/256, and 1/512 ratios in DMSO. Cephalixin was used as positive control for this bacteria. DMSO was used as negative control, too.

Results: In agar well diffusion method, in 1/16, 1/32, and 1/64 dilutions, inhibitory zones were seen 13, 11, and 8 mm in diameters for *S. aureus*. In disk diffusion, in 1/16, 1/32, 1/64, 1/128, 1/256, and 1/512 dilutions, there were 26, 21, 11, 10, 10, and 10 mm halos for this bacteria. Cephalixin was used as positive control for *S. aureus* (24 mm halo). MIC and MBC values for this examined bacteria were the same and equal to 1/256 dilution.

Conclusion: The results of the present study support the traditional use of this essential oil in the treatment of bacterial infections. This study also provide an important basis for the use of this plant used to control infectious diseases caused by *S. aureus*.

Keywords: *Coriandrum sativum*, essential oil, antibacterial activity.

**P618 - 1056: MEDICINAL PLANTS: ANTIBACTERIAL ACTIVITY OF ESSENTIAL OIL OF
ROSMARINUS OFFICINALIS AGAINST PSEUDOMONAS AERUGINOSA BACTERIA.**

Mohammad mahdi Zangeneh¹, lida haghazari², akram zangeneh³

1. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran and Microbiology section, Pathobiology & Basic sciences department, Veterinary faculty, Razi University, Kermanshah, Iran
2. Faculty of medical, Kermanshah University of Medical Sciences, Kermanshah, Iran
3. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran and Microbiology section, Pathobiology & Basic sciences department, Veterinary faculty, Razi University, Kermanshah, Iran

Background and Aim: The use of and search for drugs and dietary supplements derived from plants have accelerated in recent years. The aim of the current study was to determine chemical composition of *Rosmarinus officinalis* essential oil and evaluate its antibacterial activity against common pathogen (*Pseudomonas aeruginosa*) with broth macro-dilution and agar well and disk diffusion methods.

Methods: Agar well diffusion and disk diffusion methods were performed as screen tests. Macrobrot dilution method was accomplished to determination of MIC value. *P. aeruginosa* was chosen to survey. Serial dilutions were prepared from essential oil of the aerial parts in 1/16, 1/32, 1/64, 1/128, 1/256, and 1/512 ratios in DMSO. Kanamycin was used as positive control for this bacteria. DMSO was used as negative control, too.

Results: In agar well diffusion method, in 1/16, 1/32, 1/64, 1/128, and 1/256 dilutions, inhibitory zones were seen 13, 12, 11, 10, and 9 mm in diameters for *P. aeruginosa*. In disk diffusion, in 1/16, 1/32, 1/64, 1/128, 1/256, and 1/512 dilutions, there were 25, 22, 16, 11, 10, and 10 mm halos for *P. aeruginosa*. Kanamycin was used as positive control for *P. aeruginosa* (26 mm halo). 1/64 and 1/32 dilutions were realized for MIC and MBC, respectively about this bacteria.

Conclusion: The results of the present study support the traditional use of this essential oil in the treatment of bacterial infections. In addition, perhaps disk diffusion is more reliable method than agar well diffusion for antimicrobial screening test in this plant.

Keywords: *Rosmarinus officinalis*, essential oil, antibacterial activity.

**P619 - 1057: THE STUDY OF PASTEURIZATION DIFFERENT TEMPERATURES OF DILL
DISTILLATE**

Mehri Pourhosseini¹

1. MSc in Food Microbiology, Islamic Azad University of Varamin-Pishva branch, Varamin, Iran

Background and Aim: *Anethum graveolens* is an annual herb in the celery family Apiaceae. *Anethum graveolens* grows up to 40–60 cm, with slender hollow stems and alternate, finely divided, softly delicate leaves 10–20 cm long. The flowers are white to yellow, in small umbels 2–9 cm diameter. The seeds are 4–5 mm long and 1 mm thick. the fernlike leaves of dill are aromatic and are used to flavor many foods fish dishes and soups, as well as pickles.

Methods: We collected this plant in August 2016 from southwest of Kashan. The distillation plant was poured in and with a certain amount of water, the cooking was done. The resulting distillate was making the transfer Pastor devices and pasteurization effect of different temperatures (64 to 85 Celsius degree) were evaluated on the growth of microorganisms in distillation. Tests for coliform, total count of bacteria, mold and yeast, *Enterobacter Cocos*, *Pseudomonas aeruginosa* and sulfite reducing clostridium was done for dill distillate

Results: All of microorganisms growth in their plates At 64, 67, 70 and 73 degrees. microorganisms were not observed at a temperature of 76 degree also quality and taste of the product was retained. microorganisms were not observed at 85 degrees, but organoleptic properties of dill distillate were decline.

Conclusion: The best temperature for sure pasteurization is 76 degree. Because in this temperature addition to preventing microbial growth, product organoleptic characteristics were maintained. The product was accordance with iran national Standards.

Keywords: *Anethum graveolens*, pasteurization, Plant distillate, microorganisms

P620 - 1058: SCREENING OF A IRANIAN MEDICINAL PLANT (ESSENTIAL OIL OF TRACHYSpermum AMMI) FOR ITS ANTIBACTERIAL ACTIVITY ON BACILLUS SUBTILIS.

akram zangeneh¹, lida haghazari², mohammad mahdi zangeneh³

1. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran and Microbiology section, Pathobiology & Basic sciences department, Veterinary faculty, Razi University, Kermanshah, Iran
2. Faculty of medical, Kermanshah University of Medical Sciences, Kermanshah, Iran
3. Research pharmaceutical center, School of pharmacy, Kermanshah University of Medical Sciences, Kermanshah, Iran and Microbiology section, Pathobiology & Basic sciences department, Veterinary faculty, Razi University, Kermanshah, Iran

Background and Aim: Many of the plants used to treat appointed diseases, because they have showed antibacterial activity. In this study, we decided to evaluate antibacterial activity of essential oil of *Trachyspermum ammi* against *Bacillus subtilis*.

Methods: Agar well diffusion and disk diffusion methods were performed as screen tests. Macrobroth dilution method was accomplished to determination of MIC value. *B. subtilis* was chosen to survey. Serial dilutions were prepared from essential oil of the aerial parts in 1/16 (0.062 g/ml), 1/32 (0.031 g/ml), 1/64 (0.015 g/ml), 1/128 (0.007 g/ml), 1/256 (0.003 g/ml), 1/512 (0.002 g/ml) ratios in DMSO. Cephalexin was used as positive control for this bacteria. DMSO was used as negative control, too.

Results: In agar well diffusion method, in 1/16, 1/32, 1/64, 1/128, and 1/256 dilutions, inhibitory zones were seen 24, 21, 11, 10, and 10 mm in diameters for *B. subtilis*. In disk diffusion, in 1/16, 1/32, 1/64, 1/128, 1/256, and 1/512 dilutions, there were 34, 28, 16, 15, and 11 mm halos for this bacteria. Cephalexin was used as positive control for *B. subtilis* (15 mm halo). 1/256 and 1/32 dilutions were realized for MIC and MBC, respectively about this bacteria.

Conclusion: Our data express essential oil of *T. ammi* have great potential as antimicrobial compounds against *B. subtilis*. Thus, *T. ammi* can be used in the treatment of infectious diseases caused by resistant microbes.

Keywords: *Trachyspermum ammi*, essential oil, antibacterial effect.

**P621 - 1061: THE STUDY OF PASTEURIZATION DIFFERENT TEMPERATURES OF
CHICORY DISTILLATE**

Mehri Pourhosseini¹

1. MSc in Food Microbiology, Islamic Azad University of Varamin-Pishva branch, Varamin, Iran

Background and Aim: Chicory (*Cichorium intybus* L.) belongs to the family Asteraceae and it is a small aromatic biennial or perennial herb. The whole plant contains a number of medicinally important compounds such as inulin, esculin, volatile compounds (monoterpenes and sesquiterpenes), coumarins, flavonoids and vitamins. Dandelion roots are thick and its length is 25 to 30 cm and In some countries, after drying and roasting instead of coffee consumed.

Methods: We collected this plant in May 2016 from southwest of Kashan and after drying, was used in August. The distillation plant was poured in and with a certain amount of water, the cooking was done. The resulting distillate was making the transfer Pastor devices and pasteurization effect of different temperatures (60 to 85 Celsius degree) were evaluated on the growth of microorganisms in distillate. Tests for coliform, total count of bacteria, mold and yeast, *Enterobacter Cocos*, *Pseudomonas aeruginosa* and sulfite reducing clostridium was done for Chicory distillate.

Results: All of microorganisms growth in their plates At 60, 63, 66, 69, 72 and 75 degrees. microorganisms were not observed at a temperature of 78 degree also quality and taste of the product was retained. Plate microorganism was observed at 85 degree but but organoleptic properties of Chicory distillate were decline.

Conclusion: The best temperature for sure pasteurization, the temperature is 78 degree. Because the temperature in addition to the growth of microorganisms, product organoleptic characteristics were maintained. The product was accordance with iran national Standards.

Keywords: *Cichorium intybus*, pasteurization, Plant distillate, microorganisms

P622 - 1117: ANTIMICROBIAL EFFECTS OF VERBASCUM SP. EXTRACT

Bitah Bahonar¹, ensieh salehghamari²

1. 1Department Plant Science, School of Biological Science, Kharazmi University, Karaj, Iran.
2. 2Department of Cellular and Molecular Science, School of Biological Science, Kharazmi

Background and Aim: Many plant species among the flora of Iran play an important role in traditional and conventional medicine. Verbascum genus has been used for the treatment of different diseases including asthma, spasmodic cough, migraine and earache [1-2] and it is also used in folkloric medicine. In recent years, multiple drug/chemical resistance in both human and plant pathogenic microorganisms has developed due to indiscriminate use of commercial antimicrobial drugs/chemicals commonly applied in the treatment of infectious diseases [3]. This situation has prompted scientists to search for new antimicrobial substances from various sources, including medicinal plants.

Methods: The ethanol extracts of different parts of a species of Verbascum from north of Khorasan, including root, stem, leaf and flower were investigated for in-vitro antimicrobial properties. Some pathogenic test strains were used in this study including methicillin resistant *Staphylococcus aureus* ATCC 33591, *Klebsiella pneumoniae* ATCC 10031, *Escherichia coli* ATCC 29998, *Pseudomonas aeruginosa* ATCC 9027, *Salmonella Typhi*, *Aspergillus niger* ATCC 16404 and *Candida albicans* ATCC 10231. Well diffusion agar method was used for antimicrobial assay and 100 µl from each of the extracts at concentration of 500 µg/ml were applied in each well

Results: The results indicated that the ethanol extracts of Verbascum sp. flower has an interesting inhibitory effect on the growth of *A. niger*. However, the other extracts did not show any antibacterial activity against all other strains tested

Conclusion: Thus, the results suggest that Verbascum sp. flower extract possesses compounds with antimicrobial properties that might be utilized for developing new drugs.

Keywords: Antimicrobial, verbascum, Extract

**P623 - 1134: COMPARISON OF THE ANTIBACTERIAL EFFECT OF ROSA DAMASCENA
AND ALOEVERA EXTRACTS ON E.COLI**

Reza Besharati¹, Neda Bakhshabadi², Sepideh gholami³, Maryam Besharati⁴

1. North khorasan university of medical science, Bojnurd, Iran
2. Islamic Azad University, Quchan Branch, Quchan, Iran.
3. North khorasan university of medical science, Bojnurd, Iran
4. PhD student of microbial biotechnology, Tehran university, Tehran, Iran

Background and Aim: Herbal essences and extracts have vast applications in medical field and food industry. They also have antimicrobial effect on broad spectrum of microorganisms. In this research the effect of ethanol extracts of Rosa Damascena and Aloe vera on E.coli bacteria has been studied.

Methods: Distillation was done with soaking method ; after providing mentioned extracts, Agar diffusion was used to determine antimicrobial effect of Ethanol extracts of Rosa Damascena and Aloe vera on E.coli bacteria. Minimum restraining concentration (MIC) was measured by subinoculation method.

Results: Results showed ethanol extracts of Rosa Damascena has more antibacterial effect on E.coli bacteria in comparison with ethanol extracts of Aloe vera. Zone diameter and minimum restraining concentration for ethanol extract of Rosa Damascena are 14 mm and MIC=25 Mg/ml respectively . Zone diameter and minimum restraining concentration for ethanol extract of Aloe vera are 7mm and MIC = 50Mg/ml respectively.

Conclusion: Extract of Rosa Damascena has more antibacterial effects in comparison with extracts of Aloe vera. Also, admixture of ethanol extracts of Rosa Damascena and Aloe vera leads to decrease of antibacterial effect of this extract.

Keywords: Extract, Rosa damascena, Aloe vera gel, Anti-bacterial, E.coli.

**P624 - 1151: ANTIMICROBIAL EFFECTS RED LENTILS ON SOME BACTERIA CAUSING
WOUND INFECTIONS**

Ali Khataminia¹, mohammad nemati², Fatemeh boron³

1. PhD student Clinical Pathology of ahvaz shahid chamran university
2. PhD student pharmacology Ahvaz Jundishapour University of medical sciences.
3. PhD of Microbiology Ahvaz Jundishapour University of medical sciences

Background and Aim:The use of medicinal plants for fewer side effects than chemical drugs of interest to the world's scientific community.

Methods:In this study, we extract from red lentils methanol, ethanol and aqueous dilutions of 25, 50, 75 and 100 percent prepared using the method Laboratory Filtration was sterile. susceptibility testing of *S. aureus*, *P. aeruginosa* and *E. coli* with different concentrations compared with the control extract in sterile saline and using disk diffusion method (Kirby-bauer) was performed.

Results:Red lentils extract inhibited the growth of all three bacteria, and bacterial growth inhibition zone size was measured by disk method. The size of inhibition of bacteria varied between 6-13 mm. The results showed that certain concentration of the extract has an inhibitory effect on the growth of all three bacteria *Staphylococcus aureus*, *Pseudomonas aeruginosa* and *E. coli*. Halo's biggest concentration of 75% versus control samples (normal saline) was created.

Conclusion:Red lentils in the future due to the effects of the bacterial wound, with the standard as a viable alternative to antimicrobial drugs used .

Keywords:Red lentils - Medicinal plants - Wound healing - Antimicrobial

**P625 - 1165: PHYTOCHEMICAL EVALUATION OF METHANOLIC EXTRACT OF LEAVES
OF STEVIA REBAUDIANA BERTONI FROM GUILAN**

Shahab Ojani¹, Ali Samkhaniani², Sanaz Nikoumanesh³, Fatemeh Safari⁴, Leila Safari⁵

1. Young Researchers and Elite Club, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran.
2. Master of Cellular and Molecular Biology, Department of Biology, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran.
3. Master of Cellular and Molecular Biology, Department of Biology, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran.
4. Master of Microbiology, Department of Biology, Ayatollah Amoli Branch, Islamic Azad University, Amol, Iran.
5. Master of Microbiology, Department of Biology, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran.

Background and Aim:Plants are the richest resource of drugs of traditional systems of medicine, modern medicines, food supplements, pharmaceutical intermediates and chemical entities for synthetic drugs. To study the phytochemicals present in *Stevia rebaudiana* Bertoni collected from the Guilan, Iran.

Methods:The leaves were collected and extract prepared from methanol by microwave assisted extraction (MAE) method. In this study reveals that the phytochemicals analysis of eight different chemical compounds (alkaloids, flavonoids, coumarins, saponins, tannins, terpenoids, cardiac glycosides and proteins) were tested in methanolic extracts by using standard methods. Whereas, In vitro antibacterial activity of the methanolic extract of leaves of *Stevia rebaudiana* Bertoni against *Staphylococcus aureus* (PTCC 1113) and *Escherichia coli* (PTCC 1399) determined by the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) assay.

Results:The results of the phytochemical screening of methanolic extract of leaves of *Stevia rebaudiana* Bertoni were flavonoids, coumarins, saponins, cardiac glycosides, tannins, terpenoids and alkaloids presented. The methanolic extract of leaves of *Stevia rebaudiana* Bertoni showed significant antibacterial activity against both Gram positive and Gram negative bacteria.

Conclusion:The result showed methanolic extract of leaves of *Stevia rebaudiana* Bertoni can be used instead of chemical drugs to treat bacterial infections.

Keywords:*Stevia rebaudiana* Bertoni - Phytochemicals analysis – Terpenoids – MIC - MAE.

**P626 - 1187: COMBINATION EFFECT OF CINAMON AND CLOVE EXTRACTS AGAINST
EXTENDED EXPECTRUM BETALACTAMASE PRODUCING ESCHERICHIA COLI**

Khatereh Kafshdouzan¹, A. Jebelli Javan², M. Salimi Bejestani³, B. Malek Pour⁴

1. Semnan Uni
2. Semnan Uni
3. Semnan Uni
4. Semnan Uni

Background and Aim: The extended-spectrum beta-lactamase (ESBL) -producing *Escherichia coli* isolates cause many serious infections, especially colibacillisi and urinary tract infections in human and animals. As respects that bacterial resistance to antimicrobial is a global prob-lem; discovery of newer antibacterial agents is always necessary. In this study the effect of cinnamon and clove extract on ESBL-producing *E. coli* isolates was evaluated, individually and in combination, using microdilution broth method.

Methods: Evaluation was carried out on 50 *E. coli* isolated from cloac of apparently healthy broilers and 50 *E. coli* isolated from viscera of broilers suspected to colibacillosis in Semnan, Iran. Combined disk method according to CLSI(Clinical and Laboratory Standards Institute)2014guidelines by MAST® D67C5 set was carried out for detection of ESBL production. The minimal inhibitory concentration (MIC) of the alcoholic extract of Cinnamon and Clove against the ESBL-producing *E. coli* isolates, were determined using the microdilution method

Results:The results of this study showed that in disk diffusion method 32% of strains produced ESBLs (n=17cloacal, n=15 visceral group). The minimum inhibitory concentration (MIC) of cinnamon and clove extract against the mentioned bacteria were from 400 to 1600 ppm and 800 to 3200 ppm, respectively. Combination of cinnamon and clove extract showed a range of synergistic effect against all ESBL-producing *E. coli* isolates

Conclusion:Cinnamon and clove extracts showed to be effective against ESBL-producing *E. coli* isolates growth, especially when are used in a combination status, and their potential application in pharmaceutical systems may be suggested

Keywords:*Escherichia coli*; ESBL, Cinnamon extract ,Clove extract; colibacillosis

**P627 - 1215: ANTIMICROBIAL ACTIVITY OF ALCOHOLIC EXTRACT FROM
BLACKBERRY GROWN IN SHIRAZ (IRAN)**

Maryam Homayoon¹, Yahya Tahamtan²

1. Microbiology Department, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. Microbiology Department, Razi Vaccine and Serum Research Institute, Shiraz, Iran

Background and Aim:Antimicrobial agents provide valuable adjunctive therapy for prevention and control of infective diseases. Limitations in their prolonged use have stimulated the research for new natural occurring agents with more specific activity and fewer adverse effects. Here we sought to determine the anti-bacterial properties of alcoholic blackberry extract in vitro against some Gram negative bacteria including Pasteurella, Salmonella, E. coli K12 and E. coli O157.

Methods:The compounds of the blackberry were extracted by distillation method. Distillation may be a partial separation that increases the concentration of selected components of the mixture. The antibacterial test was carried out by bacterial broth dilution method. By using different concentrations of the alcoholic extract, minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) were determined.

Results:The alcoholic extract show strong antibacterial activity against all the test bacterial strains. Extract with 20 mg concentration showed defined growth inhibitory effect and 30 mg concentration showed both inhibitory and bactericidal effects on Salmonella, E. coli K12 and E. coli O157.

Conclusion:This study showed that certain concentrations of alcoholic blackberry extract exhibit antimicrobial properties against important enteric pathogens. Extract of blackberry may be suitable for the preparation of medicinal products. We recommended that it can be used as prevention against infective disease specially diarrhea and dysentery.

Keywords:Blackberry Extract, Infective Bacteria, Antibacterial Effect

**P628 - 1218: ANTIMICROBIAL ACTIVITY OF METHANOL EXTRACT OF SALVIA
LIMBATA C. A. MEY FROM KASHAN-GHAZAAN**

Maryam Iravani¹, Roya Mahinpour², Zohreh Zahraie³, Zeinab Toluei⁴

1. Department of Biotechnology, Faculty of Chemistry, University of Kashan, Kashan, Iran
2. Department of Biotechnology, Faculty of Chemistry, University of Kashan, Kashan, Iran
3. Department of Biotechnology, Faculty of Chemistry, University of Kashan, Kashan, Iran
4. Department of Biotechnology, Faculty of Chemistry, University of Kashan, Kashan, Iran

Background and Aim: The various species of salvia L. genuse are known in folk medicine for therapeutic purpose in Iran. In the present study aerial parts of salvia limbata plant collected from kashan, then antimicrobial activity of methanol extract was evaluated against some of standard bacteria and yeast (candida albicans).

Methods: Antibacterial activity of methanol extract of Salvia limbata plant (MIC and MBC) was tested against ten bacteria species and yeast such as; Pseudomonas aeruginos, Bacillus subtilis, Escherichia coli, Staphylococcus aureus, Klebsiella pneumonia, Shigella dysenteriae, Staphylococcus epidermidis, Proteus vulgaris, Salmonella paratyphi-A serotype and candida albicans using the agar diffusion technique and micro-well dilution assay method.

Results: In our study the methanol extract of Salvia limbata showed antimicrobial activity against the gram positive bacteria B. subtilis and S. aureus. The MIC and MBC results showed that methanol extract of Salvia limbata was more active against B. subtilis with MIC value 125 µg/ml and MBC value 500 µg/ml as compared with S. aureus with MIC value 250 µg/ml and MBC >2000 µg/ml. In this study the methanol extract of Salvia limbata had not antimicrobial activity against the other tested microorganisms.

Conclusion: The results showed that methanol extracts of Salvia limbata has antibacterial effect against B. subtilis and S. aureus. Therefore this extract could be suitable for using in traditional herbal medicines. More experiments need to understand pharmacological activities of these salvia species for therapeutic purpose.

Keywords:: Salvia limbata, Antimicrobial activity, Agar diffusion method, Micro-well dilution assay method

**P629 - 1221: INHIBITORY EFFECT OF SCROPHULARIA STRIATA ON AFLATOXINS B1
AND B2 PRODUCTION BY ASPERGILLUS FLAVUS**

Leila Moradi¹, Zohreh Jafari², Mohsen Farzaneh³

1. MSc. student, Department of Microbiology, Islamic Azad University, Arak Branch, Arak.Iran
2. Assistant professor, Department of Microbiology, Islamic Azad University, Arak Branch, Arak.Iran
3. Assistant professor, Medicinal Plants and Drugs Research Institute, Shahid Beheshti University, Tehran, GC. Evin, Iran

Background and Aim: Aflatoxins (AFs) are toxic, carcinogenic, mutagenic, teratogenic and immunosuppressive by products of *Aspergillus flavus* that contaminate a wide range of crops such as maize, peanut, and cotton. Natural sources such as plants extracts can reduce AFs-content from food

Methods: In this study, the aerial part of *Scrophularia striata* Boiss was collected from Elam province, Iran, and dried at room temperature. The ability of various plant extracts (n-hexane, ethyl acetate, methanol and aqueous extracts) was investigated to inhibit aflatoxins B1 and B2 production by *A. flavus* contents in the liquid culture at four concentrations (250 - 500- 1000 and 2000 mg.L⁻¹). The AFs contents were determined by use of HPTLC, fluorescence mode at excitation and emission wavelengths of 365 and 435 nm, respectively.

Results: The methanol and aqueous extracts could completely inhibit AFB1 and AFB2 biosynthesis at minimum concentrations 2000 and 1000 mg.L⁻¹ respectively. However, ethyl acetate extract caused to inhibit 100% of AFB2 at 2000 mg.L⁻¹

Conclusion: It has been demonstrated that *S. striata* have some pharmacological effects such as analgesic, anti-microbial, and nitric oxide suppressive properties. Finally *S. striata* introduce as a new strong botanical source to inhibit both AFB1 and AFB2 biosynthesis from *A. flavus* in food products.

Keywords: *Scrophularia striata*, *Aspergillus flavus*, Aflatoxins inhibition

**P630 - 1224: IN VITRO ANTIBACTERIAL EFFECTS OF THE GARLIC CRUDE EXTRACT
AGAINST ISOLATES OF PSEUDOMONAS AERUGINOSA.**

AKRAM JAFARPOUR¹, Alireza Khodavandi², Sirous Naeimi³

1. Department of Microbiology, Kazerun Branch, Islamic Azad University, Kazerun, Iran
2. Department of Microbiology, Shiraz Branch, Islamic Azad University, Shiraz, Iran
3. Department of Microbiology, Kazerun Branch, Islamic Azad University, Kazerun, Iran

Background and Aim: Today with raised use of antibiotics and prevalence of resistant bacterial strains, there is need for antibacterial drugs that have fewer side effects than antibiotics. Garlic is a medical plant which had many uses in traditional medicine. The aim of this study was to evaluate the crude garlic extract on the isolates of *Pseudomonas aeruginosa*.

Methods: Antibacterial effects garlic crude extract against 40 isolates of *Pseudomonas aeruginosa* were measured using disk diffusion agar and microdilution broth techniques.

Results: In this study, the most efficacy of garlic crude extract was at concentration of 30-40 mg/ml against *Pseudomonas aeruginosa*. Minimum inhibitory concentration of the extract on the growth of this bacteria showed range from 4 mg/ml to 15 mg/ml. Also Minimum Bacteriocidal Concentration of extract showed range from 6 to 30 mg/ml respectively.

Conclusion: It was found that garlic crude extract can inhibit growth of *Pseudomonas aeruginosa*. The hope is that, replacement of the chemical anti-bacterial drugs by this plant extract, can reduce many harmful side effects of synthetic antibiotics.

Keywords: *Pseudomonas aeruginosa*, crude garlic extract, minimum Inhibitory Concentration

**P631 - 1227: GENE EXPRESSION ANALYSIS OF THE EFECCT OF GARLIC- CRUDE
EXTRACT AGAINST PSEUDOMONAS AERUGINOSA BIOFILM FORMATION**

AKRAM JAFARPOUR¹, Alireza Khodavandi², Sirous Naeimi³

1. Department of Microbiology, Kazerun Branch, Islamic Azad University, Kazerun, Iran
2. Department of Microbiology, Shiraz Branch, Islamic Azad University, Shiraz, Iran
3. Department of Microbiology, Kazerun Branch, Islamic Azad University, Kazerun, Iran

Background and Aim: Pseudomonas aeruginosa is one of the most important bacteria causing biofilm. Pel A gene is a structural gene, that plays a role in the early stages of biofilm formation. The aim of this study was to evaluate the effect of garlic crude extract on the Pel A gene expression in biofilm formation of Pseudomonas aeruginosa ATCC 27853.

Methods: In vitro of Pseudomonas aeruginosa ATCC 27853 was used for biofilm formation. Pel A gene expression as well as Pro Gene expression (Housekeeping gene) Pseudomonas aeruginosa ATCC 27853, were evaluated in the states of MIC 1 and MIC ½ compared to untreated control.

Results: Garlic crude extract in both the desired concentration is cause significant decrease Pel A gene expression. Although the concentration of MIC 1 reduction were more effective in the expression of this gene. Pro gene expression was relatively fixed compared to untreated control in both the concentration of the Pseudomonas aeruginosa ATCC 27853.

Conclusion: The analysis of molecular mechanism of the possible effects of other effective genes involved in biofilm formation will be evaluated using other techniques gene expression, such as Quantitative Real-Time PCR.

Keywords: Pseudomonas aeruginosa, Gene expression.

**P632 - 1228: GENE EXPRESSION ANALYSIS THE EFFECT OF SHALLOT CRUDE EXTRACT
AGAINST CANDIDA ALBICANS HYPHAE FORMATION.**

Negin Sherafati¹, Alireza Khodavandi², Sirous Naeimi³

1. Department of Microbiology, Kazerun Branch, Islamic Azad University, Kazerun, Iran
2. Department of Microbiology, Shiraz Branch, Islamic Azad University, Shiraz, Iran
3. Department of Microbiology, Kazerun Branch, Islamic Azad University, Kazerun, Iran

Background and Aim:One of the main factors for virulence of fungus such as *Candida albicans* the ability to change its morphology from yeast to hyphae. Shallot has been proven to possess some antimicrobial properties against some of bacteria, viruses and fungi. SAP1 is one of the virulence factors of *Candida albicans* ,There is some correlation between expression of SAP1 and hyphae formation. Indeed the aim of this study was to evaluate the SAP1 Gene expression analysis the effect of shallot crude extract against *Candida albicans* hyphae formation.

Methods:*Candida albicans* ATCC 14053 was evaluated in the states of 2 ,1, 1/2 and 1/4 MIC compared to untreated control. SAP1 gene expression was performed by semi-quantitative RT-PCR and Beta-Actin gene was used as an housekeeping gene.

Results:The findings results showed the shallot could inhibit the growth and suppress hyphae formation in *Candida albicans* with increasing MIC concentrations of shallot crude extract.(MIC>1).

Conclusion:The results of this study indicates that SAP1 could be one of the possible targets of shallot to inhibit hyphae formation in *Candida albicans*. Additionally, further more extensive studies are necessary to gene expression of other genes involved in the hyphae formation.

Keywords:*Candida albicans*, Hyphae formation, Shallot crude extract

**P633 - 1229: IN VITRO ANTI FUNGAL EFFECTS OF SHALLOT CRUDE EXTRACT
AGAINST ISOLATES OF CANDIDA ALBICANS .**

Negin Sherafati¹, Alireza Khodavandi², Sirous Naeimi³

1. Department of Microbiology, Kazerun Branch, Islamic Azad University, Kazerun, Iran
2. Department of Microbiology, Shiraz Branch, Islamic Azad University, Shiraz, Iran
3. Department of Microbiology, Kazerun Branch, Islamic Azad University, Kazerun, Iran

Background and Aim: Recently, the incidence of systemic candidiasis which is caused by *Candida albicans* has increased. In the last decade, Shallot has been reported to display antifungal activity. An antifungal effect of shallot was reported previously for growth inhibition of *Candida albicans*. The aim of this study was to evaluate the Shallot crude extract on the isolates of *Candida albicans*.

Methods: In this experimental, shallot crude extract were effected against 30 isolates of *Candida albicans* by the laboratory standard methods for disk diffusion agar and microdilution broth testing. Subsequently, the minimum inhibitory concentration (MIC_{50,90}) was calculated of the extract. As a reference strain, we used *Candida albicans* ATCC 14053.

Results: The results of testing multiple concentrations showed that, most efficacy of shallot crude extract was at concentration range from 25-35 mg/ml against isolates of *Candida albicans*. However, Minimum inhibitory concentration of the extract on the growth of this fungal showed range from 0/23–4/68 µg/ml .

Conclusion: According to the study, using of shallot crude extract is suitable for prevention and treatment of fungal infection due to *Candida albicans*.

Keywords: *Candida albicans*, Shallot crude extract

**P634 - 1240: THE ANTIMICROBIAL ACTIVITY OF MALVA SYLVESTRIS EXTRACT
AGAINST UROPATHOGENIC ISOLATES OF ESCHERICHIA COLI**

Elaheh Zadeh Hosseingholi¹, Ghader Molavi²

1. Department of Cellular and Molecular Biology, Faculty of Sciences, Azarbaijan Shahid Madani University, Tabriz, Iran
2. Department of Molecular Medicine, Faculty of Advanced Medical Science, Tabriz University of Medical Sciences, Tabriz, Iran

Background and Aim: Urinary tract infection (UTI) is the second most common type of infection found in human body. Annually UTIs result in spending more than 6 billion dollars on medical costs worldwide. The most important cause of community and hospital acquired UTIs is *Escherichia coli*. Because of increasing antibiotic resistance among this uropathogen, the aim of this study was to find alternative antimicrobial agents from plant extracts. So the antibacterial activities of *Malva sylvestris* extract against uropathogenic *E. coli* isolates were investigated.

Methods: A total 30 *E. coli* isolates were collected from midstream urine specimens of patients examined for urinary tract infection in Emam Hossein Hospital, Hashtroud, Iran. Different extracts were prepared with n-hexane, dichloromethane and methanol. The susceptibility of bacterial isolates to extracts was tested by Standard Disk-Diffusion Method and Minimum Inhibitory Concentrations (MIC) in accordance to Clinical and Laboratory Standards Institute guidelines. The concentrations of extracts tested were 400, 600, 800, 1000, 1200 µg/ml.

Results: The results indicated that the methanolic extracts exhibit high antimicrobial effects. So that about 83% of the isolates having an MIC of ≤ 1.2 mg/ml. About 36% of the isolates having an MIC of ≤ 0.8 mg/ml. Only a third of isolates had MIC of ≤ 0.6 mg/ml. Concentration of 0.4 mg/ml had no effect on the isolates.

Conclusion: These MIC results suggest that this plant can be used as a natural treatment agent against UTIs caused by *E. coli*.

Keywords: *Malva sylvestris*, antimicrobial, MIC, *Escherichia coli*, Urinary tract infection

Microbial infections in Surgical, metabolic and Burns Wounds

**P635 - 11: PREVALENCE OF ESBLs AND BLACTX-M-I, BLASHV AND BLATEM GENES
AMONG UROPATHOGENIC ESCHERICHIA COLI ISOLATES**

Mohammad Salehi¹, Farshad Nojoomi², Abdolmajid Ghasemian³

1. Medical Diagnostic Laboratory of Neyshabour, Center of Medical, Pathological and Genetic Diagnostic Services, Iranian Academic Center for Education, Culture and Research (ACECR), Mashhad Branch, Mashhad, Iran
2. Department of Microbiology, Faculty of Medical Sciences, AJA University, Tehran, Iran
3. Department of Microbiology, Faculty of Medical Sciences, AJA University, Tehran, Iran

Background and Aim: The prevalence of ESBLs; especially the predominant beta-lactamase blaCTX-M1 has increased worldwide. This study was conducted to determine the ESBL production and prevalence of blaCTX-M1, blaSHV and blaTEM genes among UPEC isolates from 3 military hospitals of Tehran during 2015-2016.

Methods: One-hundred and eleven isolates were adopted for study during the years 2015-2016. The antibiotic susceptibility testing was conducted according to CLSI guidelines. The combine disk was used for phenotypic ESBL production. The ceftazidime MIC was conducted with the micro-broth dilution test. The cloxacilin containing MH agar was used to detect the AmpC-lactamase. The PCR assay was used to detect the blaCTX-M-I, blaSHV and blaTEM genes.

Results: In the broth microdilution method, 103 (92.7%) isolates showed MIC $\geq$ 1, and also in the combined disk method, 89 (80.1% of all) were ESBL positive. On the other hand, among 91 ceftazidime resistant isolates, 86 (77.4% of all) were ESBL positive. The difference between the 2 methods for ESBL confirmation was not significant. The result of MIC was similar to the disk diffusion method in the detection of phenotypic ESBL production. Among ESBL producer isolates, the prevalence of blaCTX-M-I, blaSHV and blaTEM was 77.4% (n=86), 47.4% (n=53) and 2.4% (n=2) respectively. These genes were amplified in a wide range MIC of ceftazidime.

Conclusion: The prevalence of MDR UPEC and ESBL positive isolates was high in military hospitals. The majority of UPEC isolates amplified blaCTX-M-I and blaSHV type β -lactamases. One-third of isolates were positive in presence of both these genes.

Keywords: Uropathogenic E. coli, ESBL β -lactamase, military hospitals

**P636 - 202: DRUG RESISTANCE AND STATUS OF INFECTION OF ACINETOBACTER
BAUMANNII IN BURN INTENSIVE CARE**

Maryam Roham¹, Mostafa dahmardehei², mahnoush momeni³

1. assistant professor of infectious diseases, burn research center,iran university of medical science, tehran , iran
2. assistant professor of plastic surgery, burn research center,iran university of medical science, tehran , iran
3. assistant professor of general surgery , burn research center,iran university of medical science, tehran , iran

Background and Aim:To provide epidemiological data of the distribution characteristics and drug resistance of infection of *Acinetobacter baumannii* isolated from burn patients for guiding rational use of antibiotics in clinic.

Methods:A total of 550 specimens of wound secretion, blood, venous catheter attachment, sputum and urine were collected from 505 burn patients hospitalized in our burn ICU in one year and bacterial culture was performed. Pathogens were identified and drug sensitivity analyzer. Drug resistance of all the obtained AB to 9 antibiotics commonly used in clinic, was tested with K-B paper disk diffusion method. Patients with *Acinetobacter baumannii* infection were ascertained.

Results:A total of 250 strains of pathogens were isolated, among which 19.25% were Gram positive cocci, 78.75% Gram negative bacilli, and 2% fungi. A total of 122 strains of AB were isolated, ranking the first place among all the detected pathogens, with 68.95% from wound secretion, 13.40% from blood, 16.37% from venous catheter, and 1.28% from sputum. The AB strains were found sensitive to polymyxin and with relatively moderate drug resistance rate to aminoglycosids, while the drug resistance rates were over 90.0% to the other antibiotics. AB culture of wound secretion was positive in 67 patients.

Conclusion:AB in our burn ICU has a high detection rate and extensive drug resistance in above-mentioned 1 year. AB was mainly colonized in patients with extensive burns with a high mortality rate.

Keywords:*Acinetobacter baumannii* , burn, intensive care

**P637 - 407: MANIPULATION OF MESENCHYMAL STEM CELLS WITH ENZYBIOTICS TO
ENHANCE ANTIBACTERIAL ACTIVITY IN WOUND HEALING**

Pardis Saeedi¹, Abbas Ali Imani Fooladi², Rahele Halabian³

1. Applied Microbiology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran
2. Applied Microbiology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran
3. Applied Microbiology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran

Background and Aim: Many efforts are proceeding to develop novel bioengineered wound healing tools. Either natural or genetically modified mesenchymal stem cells (MSCs) are very interesting for regenerative medicine due to their broad range of differentiation capabilities and powerful tissue protective and reparative mechanisms. Wound healing by MSCs involves a coordinated interplay among cells, growth factors, extracellular proteins and antibacterial peptides along with anti-inflammatory, immunomodulative, and tissue reparative activities. The beneficial effects of exogenous MSCs on degenerative and infectious diseases have been tested in several animal models and many ongoing clinical trials.

Methods:-

Results: This field is expanding to improve the remarkable abilities of MSCs by variety of methods. On the other hand, with the global increasing prevalence of antibiotic resistant bacteria, “enzybiotics” such as lysins (bacteriophage endolysins) substitute a novel alternative antibacterial against infectious disease. Lysins, phage-encoded peptidoglycan hydrolases, cause rapid lysis and death of Gram-positive bacterial cell, specifically treatment of wounds containing MDR *Staphylococcus aureus* (MRSA/VRSA). LysK, a lysin from staphylococcal phage K described to kill nine species of *Staphylococcus* MRSA and VRSA.

Conclusion: Here we hypothesized that if MSCs can over express LysK, then topical transplantation of LysK-MSC on cutaneous wounds will accelerate the wound closure and attenuate local inflammation as well as cell proliferation, angiogenesis and increased collagen synthesis.

Keywords: Mesenchymal stem cells; Cellular therapy; Tissue regeneration; wound infection; enzybiotics; Phage Lysin

**P638 - 662: EVALUATING THE EFFECTS OF INACTIVE IMMUNIZATION WITH
POLYCLONAL EXOTOXIN A ANTIBODY OF PSEUDOMONAS AERUGINOSA IN BURNED
MOUSE MODEL**

Shabnam Saeidvafa¹, Asghar Tanomand²

1. Department of Microbiology, Islamic Azad University Maragheh Branch, Maragheh, Iran
2. Department of Microbiology, Maragheh University Of Medical sciences, Iran

Background and Aim: Due to high resistance in *Pseudomonas Aeruginosa* medication of hospital-acquired infections, especially prescription of antibiotics, often fails. This study aims to probe into the effects of inactive immunization with polyclonal exotoxin A antibody of *P.aeruginosa* on infections in burned mouse model.

Methods: In order to study the effectiveness of polyclonal exotoxin A antibody provided in rabbits, 18 mice were categorized into three groups. In the prevention group, before causing burn, polyclonal exotoxin A antibody was injected intraperitoneally into each mouse and then burn was caused. Then, 2×LD50 *P.aeruginosa* PAO1 level was inseminated in the burned spot and fatality rate of the mice was considered. In the treatment group, first burn was caused. Next, 2×LD50 *P.aeruginosa* PAO1 level was inseminated. After that, polyclonal exotoxin A antibody was injected intraperitoneally at different intervals. Like other groups, in the control group also burn was caused and then 2×LD50 *P.aeruginosa* PAO1 level was inseminated in the burned spot; however, the only difference here was that no treatment or prevention measure was taken.

Results: According to the obtained results, in the prevention group 50% of the mice were protected against 2×LD50 injections with polyclonal exotoxin A antibody. In the treatment group also, based on the statistics obtained, 25% of the mice after administering 2×LD50 survived because of polyclonal exotoxin A antibody. Based on the observations, all the mice of the control group perished.

Conclusion: Results of the present study showed that polyclonal exotoxin A antibody of *P.aeruginosa* can have a protective effect against infections resulting from burn wounds.

Keywords: *Pseudomonas aeruginosa*, Burn, Polyclonal antibody, Exotoxin A, Immunization, Lethal dose

**P639 - 753: INTESTINAL INFECTIONS IN CHILDREN REFERRED TO ABUZAR HOSPITAL
IN AHVAZ**

Ali Khorasanizadeh¹, askar rogani²

1. Laboratory sciences group, paramedical faculty, JundiShapur University of medical science , Ahvaz, Iran
2. Laboratory sciences group, paramedical faculty, JundiShapur University of medical science , Ahvaz, Iran

Background and Aim: Intestinal bacteria within a few days after birth, are based on normal gastrointestinal and since then, the major part of the normal flora are aerobic .E. Coli is ringleader of the bacteria. Bacteria Intestinal in water or milk indicating contamination through sewage or other contaminated sources said bacterial infection of Shigellosis- Salmonellosis. Intestinal infection, a bacterial infection of the respiratory infection is most common in poor countries and a significant cause of morbidity and mortality in developing children.

Methods: Samples of stool culture primarily on the selenit f are applied. Within 24 hours of the sf on the SS agar (Salmonella shigella agar), Hekton enteric passage into the environment causing further growth of Salmonella and shiglla than other Enterobacteriaceae can be. Typical children do on EMB agar or Macconkey (the differential), killed given these environments allow organisms non- fermentative the lactose- quickly be identified. Per colony lactose negative in by biochemical tests and serologic measures is located.

Results: The purpose of this study bacterial in children's hospital in Ahvaz Abuzar Hospital. Stool culture results in this study, 500 Patients Were studied, of which 21 samples positive salmonella typhi 3 cases(14.2%)-Shigella flexennei 5 cases (23.8%)- Shigella sonnei 5 cases(23.8%)- a total enteropathogenic 8 (38.09)

Conclusion: Enteropathogenic E.coli is generally in children because children can be attributed.

Keywords: Shigella, salmonella, Intestinal infections

**P640 - 827: DETERMINATION OF TEM GENE IN ESCHERICHIA COLI STRAINS
PRODUCING EXTENDED-SPECTRUM BETA-LACTAMASE ISOLATED FROM URINARY
TRACT INFECTIONS IN ESLAMABADGHARB CITY**

Mitra Chalabzardi¹

1. MSc in Microbiology, Faculty of Sciences, Faculty of Sciences, ILAM University, ILAM, Iran

Background and Aim: One of mechanisms of resistance to the beta-lactam antibiotics B-lactamase enzymes produced. TEM first EBSL detect which is widely spread in the family enterobacteriaceae more than 90 percent resistance E. coli strains are the resistant to beta-lactam drugs.[1] The aim of this study was to evaluate the frequency of TEM gene in E. coli strains isolated from urinary tract infections in Eslamabad Gharb City

Methods: a total of 116 strains of E. coli in urinary tract infections hospital (Imam Khomeini) Eslamabad Gharb city collection and were confirmed by biochemical testing. Phenotypic identification of the B-lactamase producing strains was performed using disk diffusion method according to CLSI of 11 antibiotics were determined. the antibiotic resistance of the isolated strains was to antibiotics include antibiotics: Ciprofloxacin 15.92%, Trykvmtaksazvl 83/30%, imipenem 26.6%, amikacin 46.39%, Amoxicillin 10.64%, Cephalotin 53.9%, Ceftriaxone 49%, Cefotaxime 33.63%, Cefazolin 21.72%, Ceftazidime 74.09%, Cephalexin 38.91%, was applied. The finally testing combined disk detect ESBL producing strains and of strains to antibiotic CAZ and CTX by microbroth dilution method. The presence of TEM gene in bacteria was studied using PCR approach

Results: The results of antibiogram showed that the highest amount of resistance is for Trykvmtaksazvl 83/30% and the least amount of resistance is Amoxicillin 10.64%. Phenotyping evaluation showed that hantayj from 116 strains of E. coli 42 strains (36.20%) were beta-lactamase producers. PCR results showed that 17 strains (40.47%) lactamase positive strains producing enzymes TEM.

Conclusion: Due to high risk factor of the betalactamase producing organisms in nosocomial infections further studies is prevent their spread and protocol based on the antibiogram pattern of the strains is highly recommended.

Keywords: TEM, Escherichia coli, EBSL, Eslamabad Gharb

**P641 - 829: EFFECT ANTIBACTERIAL OF METHANOL AND ASETON EXTRACT LICHENS
PROTOPARMELIOPSIS MURALIS, PHYSCONIA DISTORTA ON SOME PATHOGENIC
BACTERIA ISOLATED INFECTIONS HOSPITAL MOSTFA KHOMINI IN ILAM CITY**

Mitra Chalabzardi¹

1. MSc in Microbiology, Faculty of Sciences, Faculty of Sciences, ILAM University, ILAM, Iran,

Background and Aim: Lichens have metabolites have manifold biological activity: antiviral, antibiotic, antitumor, allergenic, plant growth inhibitory, antiherbivore, ecological roles and enzyme inhibitory. the use of lichens in the treating of diseases such as gout, seizures, convulsions, bacterial infections was customary the traditional medicine.[1,2] The purpose of this study antimicrobial effect of methanol extract 2 lichen species *Protoparmeliopsis muralis*, *Physconia distorta* on some pathogenic bacteria isolated infections Hospital Mostfa Khomini in Ilam city

Methods: Lichens collected from different parts of Ilam province methanol extract which were prepared using the soxhlet device extracts 8 different concentrations: 20, 50, 100, 200, 400, 800, 1000 and 1250 mg/ml on Bacteria (*E. coli*, *P. aeruginosa*, *B. cereus*, *S. epidermidis*, *Enterococcus fecalis*) agar diffusion method and disk diffusion effect. MIC and MBC determined for them and Ampicillin and Clindamicin as a positive control were compared and of dimethyl sulfoxide (DMSO) 10% was used as a negative control.

Results: The results showed of bacteria *Enterococcus fecalis* highest sensitivity and *Bacillus cereus* least sensitive ratio *Protoparmeliopsis muralis*, and *E. coli* Most sensitive and *S. epidermidis* lowest sensitivity ratio lichen *Physconia distorta*. amount MIC and MBC for *Protoparmeliopsis muralis*, respectively 200 mg/ml ? 400 mg/ml and MIC and MBC for *Physconia distorta*, respectively 100 mg/ml ? 800 mg/ml. Extract *Protoparmeliopsis muralis* was not effective against *E. coli*. Extract *Physconia distorta* was not effective against *P. aeruginosa*.

Conclusion: Extract the lichens Can be used as antibacterial as products used in the treatment infections Caused by bacteria

Keywords: Antibacterial, *Protoparmeliopsis muralis*, *Physconia distorta*, lichen

P642 - 831: THE PREVALENCE OF CTXM1 –CTX15 GENES IN ESCHERICHIA COLI STRAINS PRODUCING EXTENDED-SPECTRUM BETA-LACTAMASE ISOLATED FROM URINARY TRACT INFECTIONS INHOSPITAL IMAM KHOMEINI ESLAMABADGHARB CITY

Mitra Chalabzardi¹

1. MSc in Microbiology, Faculty of Sciences, Faculty of Sciences, ILAM University, ILAM, Iran,

Background and Aim: now a critical concern for the development for therapies against bacterial infection, the emergence of ESBL producing bacteria, particularly E.coli .multidrug- resistant ctx M- ctx 15 producing E.coli strains disseminate worldwide ctx by plasmid encoded and family enterobacteriaceae is expression [1] The aim of this study was to evaluate the frequency of CTX M- CTX 15 genes in E. coli strains isolated from urinary tract infections in Eslamabad Gharb City.

Methods: a total of 116 strains of E.coli in urinary tract infections hospital (Imam Khomeini) Eslamabad Gharb city collection and were confirmed by biochemical testing. Phenotypic identification of the B-lactamase producing strains was performed using disk diffusion method according to CLSI of 11 antibiotics were determined. the antibiotic resistance of the isolated strains was to antibiotics include antibiotics: Ciprofloxacin 15.92%, Trykvmtaksazvl 83/30%, imipenem 26.6%, amikacin 46.39%, Amoxicillin 10.64%, Cephalotin 53.9%, Ceftriaxone 49%, Cefotaxime 33.63%, Cefazolin 21.72%, Ceftazidime 74.09%, Cephalixin 38.91%, was applied. The finally testing combined disk detect ESBL producing strains and of strains to antibiotic CAZ and CTX by microbroth dilution method. The presence of CTXM1 –CTX15 genes in bacteria was studied using PCR approach

Results: The results of antibiogram showed that the highest amount of resistance is for Trykvmtaksazvl 83/30% and the least amount of resistance is Amoxicillin 10.64%. Phenotyping evaluation showed that hantayj from 116 strains of E. coli 42 strains (36.20%) were beta-lactamase producers. PCR results showed that 22 strains (52.38%) 14 strains (33.33%) lactamase positive strains producing enzymes CTXM1 –CTX15 genes respect

Conclusion: Frequency of Escherichia coli producing ESBL was 42% in city of Eslamabad Gharb and CTXM1 gene in ESBL producing E.coli isolated is the high frequency gene in Eslamabad Gharb City

Keywords: CTXM1, CTX 15, Escherichia coli, EBSL, Eslamabad Gharb

**P643 - 883: COMPARISON OF THE PREVALENCE OF COAGULASE-NEGATIVE
STAPHYLOCOCCI INFECTIONS IN MALE AND FEMALE PATIENTS ADMITTED TO
HOSPITAL CHALUS**

Qasem Sharifiyan totkaleh¹, esmaeil ghorbanalinezhad²

1. first author
2. Author

Background and Aim:Background: Coagulase Negative Staphylococci In The Living Body Are Open To All Members. Non-Pathogenic Or Low Pathogenic Factors And Died As Secondary Pollutants Are Considered. Over Two Decades, The Emergence Of Coagulase Negative Staphylococci As Opportunistic Pathogens, Especially In Immunocompromised Individuals And Patients With Implants Passes. Rising Incidence Of Nosocomial Infections Caused By These Bacteria And Raises Them To The Level Of Species. The Aim Of This Study Is To Identify Strains Of Coagulase Negative Staphylococci Isolated From Clinical Samples Using Culture And Biochemical Was 100.

Methods:Materials And Methods: A Total Of 100 Samples Of Coagulase Staphylococcus Various Clinical Samples, Including Urine, Skin, Wound Male And Female Patients Referred To The Ayatollah Taleghani Hospital Chalos Was Isolated. Phenotype Methods Include Mannitol Salt Agar And Cultured In Blood Agar And Dnase And Biochemical Tests Include Testing Oxidase And Catalase Using Bacitracin And Furazolidone And Novobiocin Discs Were Evaluated.

Results:Results: In This Study 35 Isolates Of Staphylococcus Coagulase Were Able To Isolate And Identify Ways Phenotype Of Our Desired Location. The Rate Of Infection Was Observed In The Urinary Tract Ladies And Men's Skin.

Conclusion:Discussion: Due To The Presence Of The Bacteria In The Urinary Tract Of Women As A Natural Flora Of Other Diseases Or Contamination When It Is Required That Women Hospitalized Special Attention To Hygiene Factors In This Area Hospitals With Patient Education To Help Control Nosocomial Infections.

Keywords:Staphylococcus, coagulase negative , common

P644 - 1130: DETECTION OF GENES ENCODING FNBP AND CLFA ADHESIONS AMONG STAPHYLOCOCCUSAUREUS ISOLATED FROM CLINICAL SAMPLE OF PATIENTS

Elmira Shafaei¹, Sahar Honarmand Jahromy², Niloofar Noorbakhsh³

1. Department of microbiology, Islamic Azad university, Varamin- Pishva branch, Iran
2. Department of microbiology, Islamic Azad university, Varamin- Pishva branch, Iran
3. Department of microbiology, Islamic Azad university, Varamin- Pishva branch, Iran

Background and Aim: Staphylococcus aureus has several virulence factors such as adhesion molecules, surface proteins, enzymes and toxins that are involved in the pathogenesis of bacteria. Bacteria-specific adhesion factors This includes proteins that covalently bind to the cell wall peptidoglycan of the bacterial cell and contains, collagen-binding protein (Cna) binding protein fibrinogen (ClfA), fibronectin-binding protein (FnBP) attached protein elastin binding only (EbpS)

Methods: In study of 74,572 clinical samples such as blood, urine, sputum and other clinical samples of patients hospitalized in various parts of Tehran Milad Hospital were collected and 180 strains were identified by diagnosing tests, such as Gram stain, Novobiocin disc, growing mannitol salt agar, catalase and coagulase. MRSA isolates were determined by Cefoxitin disc diffusion method. The prevalence of fnbA, fnbB & clf genes by multiplex PCR

Results: The results showed that from 180 Staphylococcus aureus fnbA gene was 159 (88%). fnbA gene in S. aureus clinical skin chip 23 (96%), respiratory 11 (92%), urine 86 (86%), blood 9 (81%), wound 19 (86%) fnbB gene (26%), urine 30 (63%), chip Skin 5 (21%), ulcers 5 (23%), respiratory sample 3 (25%), 2 (18%) blood and 2 (18%) from ulcer. fnbA gene in MRSA strains was 30 (32%) and in MSSA strains was 17 (20%). clf gene 36 (20%), urine samples 21 (58%), chip Skin 1 (4%), wound 1 (4%), respiratory 3 (25%), blood 4 (36%)

Conclusion: fnbA & fnbB was 42 (23%), fnbA & Clf 32 (18%), fnbB & Clf 9 (5%)

Keywords: Staphylococcus aureus, . FnA, FnbB and Clf adhesions, Multiplex PCR

Microbial Metabolite and Therapy

P645 - 256: EFFECTS OF EXTRACELLULAR LECTINS OF BACILLUS SUBTILIS ON BLOOD CANCER CELL LINE

Reyhaneh Mohamadnejad¹, Reyhaneh Mohammadnejad^{1,2}, Elham Moazamian³, Ali Asghar amiri⁴

1. -
2. MS.c student, Department of microbiology, College of Sciences, Science and Research branch, Islamic Azad University, Fars, Iran
3. Assistant professor, Department of microbiology, College of Sciences, agriculture and modern technologies, Shiraz Branch, Islamic Azad university, Shiraz, Iran
4. Assistant professor, Department of chemistry, College of Sciences, agriculture and modern technologies, Shiraz Branch, Islamic Azad university, Shiraz, Iran

Background and Aim: Lectins are well-known class of multivalent carbohydrate- binding proteins of non-immune origin that binds to specific carbohydrates . The aim of the study was to evaluate effect of extracellular lectins of *Bacillus subtilis* on the growth of blood cancer cell line in in vitro condition.

Methods: In order to purify lectins from the culture media of the specimens, sample were collected from different sites in soil texture, solar exposure and rainfall; and also from animal feces by serial dilution technique. Bacterial isolates were primarily identified by colony morphology and biochemical tests. Bacterial samples were cultured in liquid culture media supplemented by carbohydrates. Lectin proteins were obtained from liquid culture medium after precipitation by ammonium sulfate at 70% saturation and subsequent heat treatment at 70°C for 30 minutes to eliminate thermostable proteins. The activity of lectins was examined by visually observing the agglutination of %2 rabbit red blood cells. The Positive samples were chosen and their cytotoxic effect on red.

Results: In this study, 66 isolates were identified as *Bacillus subtilis* based on colony morphology and biochemical tests. The MTT assay results showed that the most samples containing lectin, not only did not inhibit the growth of cancerous cells but also have proliferative effect on them; although three of all showed cytotoxic effect and one sample (20a) demonstrated high toxic effect on KG1 cell line by a 80% cytotoxic effect.

Conclusion: Bacterial lectin proteins have anti- cancer activity and they can be used in medicine treatment.

Keywords: Lectins, *Bacillus subtilis*, blood cancer cell line, Cytotoxicity

**P646 - 370: EFFECT OF BACILLUS THURINGIENSIS TOXIN ON TRICHOMONAS
VAGINALIS IN VITRO CONDITION**

Negin Roghani¹, Elham moazamian², mohammad matini³

1. 1M.S.c student, Department of Microbiology, College of Science, Science and Research branch, Islamic Azad University, Fars, Iran negin12345@chmail.ir
2. *2Assistant Professor, Department of Microbiology, College of Science, Agriculture and modern technology, Shiraz Branch, Islamic Azad University, Shiraz, Iran elhammoazamian@gmail.com
3. 3Assistant Professor of Parasitology Department of Medical Parasitology and Mycology School of Medicine Hamadan University of Medical Sciences, Hamadan, Iran matini.mohammad@yahoo.com

Background and Aim: *Bacillus thuringiensis* is a gram-positive, spore-forming bacterium characterized by parasporal crystalline protein inclusions. Few *B. thuringiensis* strains produce insecticidal parasporal inclusions. Most strains isolated from natural environments are not known to have biological activity. In this study, the anti-trichomonal effects of *B. thuringiensis* parasporal inclusion proteins against the parasitic protozoa *Trichomonas vaginalis* were examined.

Methods: 80 isolates of *B. thuringiensis* used in this study. To prepare sporulated cultures, the strains were grown on nutrient agar, pH 7.6, at 37 ° C for 4 days. The *B. thuringiensis* parasporal inclusion proteins were prepared by alkali-solubilization and treatment with proteinase K. The strain of *T. vaginalis* were taken from medical sciences of Hamadan University. The *B. thuringiensis* parasporal inclusion proteins were examined with *T. vaginalis* growth inhibition test. After 24 and 48 h, the number of surviving parasites was counted using a hemocytometer. The counts were repeated three times, and the mean viability was determined.

Results: Four strains (E8, Jbn3, Fa2, g7_18) showed growth inhibition in 48 h. The normal parasites were actively rotating or showed movement of the anterior flagella. The cytoplasm of the normal parasites was clear and contained transparent granules. In the parasites killed by E8 and Fa2 parasporal inclusion proteins, the movement of the anterior flagella and undulating membrane became slower.

Conclusion: The results show that *B. thuringiensis* is biologically active against protozoa and suggests that screening *B. thuringiensis* parasporal inclusion proteins is essential for the further study of their biological activity against other protozoan parasites.

Keywords: *B. thuringiensis*, *T. vaginalis*, Parasporal, Anti trichomonal

**P647 - 500: USING PEPTIDE PHAGE LIBRARY FOR ISOLATION OF PEPTIDES
TARGETING ACINETOBACTER BAUMANNII**

Nazanin Irani¹, Fatemeh Rahimi Jamnani², Fatemeh Samiee³, Tallieh Moghadam⁴, Seyed Davar Siadat⁵,
Farzam Vaziri⁶, Mostafa Ghanei⁷, Mehdi Davari⁸, Morteza Masoumi⁹, Fatemeh Sakhaee¹⁰

1. M.Sc of Microbiology, Department of Microbiology, Islamic Azad University, North Tehran Branch, Tehran, Iran
2. Ph.D of Pharmaceutical Biotechnolog, Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran and Innovation Center, Pasteur Institute of Iran, Tehran, Iran
3. M.Sc of Microbial Biotechnology, Department of Biology, Islamic Azad University, Pharmaceutical Sciences Branch, Tehran, Iran and Innovation Center, Pasteur Institute of Iran, Tehran, Iran
4. M.Sc of Microbiology, Department of Microbiology, Islamic Azad University, Science and Research Branch, Tehran, Iran
5. Professor of Medical Microbiology, Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran and Innovation Center, Pasteur Institute of Iran, Tehran, Iran
6. Ph.D of Medical Microbiology, Department of Mycobacteriology and Pulmonary Research, Pasteur institute of Iran, Tehran, Iran and Innovation Center, Pasteur Institute of Iran, Tehran, Iran
7. Pulmonologist, Research Center of Chemical Injuries, Baghiatallah Medical Science University, Tehran, Iran and Innovation Center, Pasteur Institute of Iran, Tehran, Iran
8. M.Sc of Microbiology, Department Mycobacteriology of and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran and Innovation Center, Pasteur Institute of Iran, Tehran, Iran
9. M.Sc of microbiology, Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran and Innovation Center, Pasteur Institute of Iran, Tehran, Iran
10. M.Sc of Genetic, Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: *Acinetobacter baumannii* is one the most common causes of health care associated infections with a growing rate of resistance to traditional antibiotic therapies. In current decades, anti-microbial peptides due to their therapeutic effects on multi-drug resistant (MDR) strains of various bacteria have been attractive. The purpose of this study is detecting a panel of peptides with anti-bacterial effects against *A.baumannii*.

Methods: After applying six rounds of biopanning with peptide phage library on MDR strains of *A.baumannii*, a pool of enriched peptides against *A.baumannii* was isolated. Fifty colonies of the final biopanning round were selected, their single-stranded DNA were extracted and sequenced. The amino acids sequences were evaluated by Gene Runner program and then by Blastp. Peptides with different sequences were synthesized and then enzyme-linked immunosorbent (ELISA) assay was performed for each synthesized peptide on *A.baumannii* and controls (empty well and irrelevant bacteria).

Results: We found the panning process is possible on live bacteria. In this way, a panel of phages identifying *A.baumannii* was isolated. DNA sequenceing results showed that the selected phages carried on the peptides with correct sequences. Data obtained from ELISA revealed that the significant binding intensities of synthesized peptides to *A.baumannii* compared with controls.

Conclusion: Anti-microbial peptides are gaining importance as probes for detection and therapeutic purposes and thereby offer excellent templates for future drug design.



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Keywords: *Acinetobacter baumannii*, Anti-microbial peptide, Phage display, Panning.

**P648 - 573: USING PEPTIDE PHAGE LIBRARY FOR ISOLATION OF PEPTIDES
TARGETING KLEBSIELLA PNEUMONIAE**

Tallieh Moqaddam¹, Tallieh Moqaddam², Fatemeh Rahimi Jamnani³, Fatemeh Samiee⁴, Nazanin Irani⁵,
Mostafa Ghanei⁶, Seyed Davar Siadat⁷, Farzam Vaziri⁸, Fereshteh Shahcheraghi⁹, Morteza Ghazanfari¹⁰,
Akbar Oqalaei¹¹

1. -
2. M.Sc of Microbiology, Department of Microbiology, Islamic Azad University, Science and Research branch, Tehran, Iran
3. Ph.D of Pharmaceutical Biotechnology, Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran and Innovation center, Pasteur Institute of Iran, Tehran, Iran
4. M.Sc of Microbial Biotechnology, Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran and Innovation center, Pasteur Institute of Iran, Tehran, Iran
5. M.Sc of Microbiology, Department of Microbiology, Islamic Azad University, North of Tehran Branch, Tehean, Iran
6. Pulmonologist, Research Center of Chemical Injuries, Baqiyatallah Medical Sciences University, Tehran, Iran and Innovation center, Pasteur Institute of Iran, Tehran, Iran
7. Professor of Medical Microbiology, Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran and Innovation center, Pasteur Institute of Iran, Tehran, Iran
8. Ph.D of Medical Bacteriology, Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran and Innovation center, Pasteur Institute of Iran, Tehran, Iran
9. Ph.D of Medical Microbiology, Department of Microbiology, Pasteur Institute of Iran, Tehran, Iran
10. M.Sc of Clinical Biochemistry, Department of Mycobacteriology and pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
11. M.Sc of Microbiology, Department of Medical Biotechnology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Klebsiella pneumoniae is the most common cause of nosocomial infection over the world wild, causing infections that range from mild urinary infections to severe bacteremia and pneumonia with a high rate of mortality and morbidity. Management of these infections is often difficult, due to the high frequency of strains that are resistant to multiple antimicrobial agents. In current decades, anti-microbial peptides due to their therapeutic effects on multi-drug resistant (MDR) strains of various bacteria have been attractive. Detecting a panel of peptides with anti-bacterial effects against K.pneumoniae.

Methods: After applying several rounds of biopanning with peptide phage library on MDR strains of K.pneumoniae, a pool of enriched peptides against K.pneumoniae as isolated. Fifty colonies of the final biopanning round were selected, their single-stranded DNA were extracted and sequenced. The amino acids sequences were evaluated by Gene Runner program and then by Blastp. Peptides with different sequences were synthesized and then enzyme-linked immunosorbent (ELISA) assay was performed for each synthesized peptide on K.pneumoniae and controls (empty well and irrelevant bacteria).

Results: We found the panning process is possible on live bacteria. In this way, a panel of phages identifying K.pneumoniae was isolated. DNA sequencing results showed that the selected phages carried on the peptides with correct sequences. Data obtained from ELISA revealed that the significant binding intensities of synthesized peptides to K. pneumonia compared with controls.



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Conclusion: Anti-microbial peptides are gaining importance as probes for detection and therapeutic purposes and thereby offer excellent templates for future drug design.

Keywords: Klebsiella pneumonia, Anti Microbial Peptide, Biopanning, Phage display

**P649 - 586: EFFECT OF LINOLEIC ACID ON ASTAXANTHIN PRODUCTION IN
MICROALGAE**

Zahra Khalili¹, hasan jalili², mostafa noroozi³

1. MSc student, Department of Life Science Engineering, Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran
2. Assistant Professor, Department of Life Science Engineering, Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran
3. Assistant Professor, Department of Life Science Engineering, Faculty of New Sciences and Technologies, alzahra university, tehran, iran

Background and Aim:Two microalgae *Clorella* and *Scenedesmus* can produce astaxanthin as secondary metabolite under certain conditions. The main aim of this study was investigated of probably inducer effect of linoleic acid (L.A) on astaxanthin production.

Methods:Cultivation of *Clorella* and *Scenedesmus* was done in BG11 medium. Linoleic acid solution with 160 µM/100ml concentration was added to cultivation medium in 2, 3 and 5 days from the beginning of inoculum. Linoleic acid solution was prepared with 0.0437 gr L.A solved in 50 µl Tween 20 and for more dispersion 4 µl NaOH 1M was added. Phototroph cultivation was run for nine day and the concentration of astaxanthin was measured with spectrophotometric method. For this purpose ten ml of homogenized biomass was centrifuged at 3000 rpm in 5 minutes duration. After elimination of the supernatant aqueous 10 ml of DMSO (Di-Methyl Sulfoxide) was added and more mixing achieved by vortex. Astaxanthin extraction was completed by incubation of the mixture in 70 °C for one hour. Absorbance of the extract was measured in 480nm.

Results:Results showed astaxanthin production in L.A treatment increased two time compared to control.

Conclusion:The main suggestion reason is the L.A is a precursor for jasmonic acid synthesis and jasmonic acid is an inducer for secondary metabolite formation.

Keywords:microalgae, astaxanthin, linoleic acid, spectrophotometry

P650 - 659: EVALUATION OF THE EFFECT OF SOMATIC ANTIGENS OF MARSHALLAGIA MARSHALI ON THE EXPRESSION OF TLR4 IN SPLENOCYTES OF ASTHMATIC MICE BY QUANTITATIVE PCR METHOD

Amin Zakeri¹, Alireza Haghparast²

1. Immunology Section, Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran
2. Immunology and Biotechnology Sections, Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran

Background and Aim: Epidemiological studies suggest an inverse relationship between helminth infections and allergic diseases. Innate immunity especially antigen presenting cells (APC) have key role for initiation of allergic responses. Numerous studies revealed the role of pattern recognition receptors (PRRs) on APCs to balance or imbalance the immune responses. It seems Toll-like receptor 4 (TLR4) is the most important PRRs that plays important role during asthma development. On the other hand several studies have shown helminth parasites are masterful modulators of TLRs. We are interested in studying the effects of somatic antigens of *Marshallagia marshalli* on expression of TLR4 in spleenocytes of asthmatic mice.

Methods: Allergic airway inflammation was induced in BALB/c mice by sensitization and challenging with ovalbumin. Somatic antigens together with ovalbumin were injected intraperitoneally during sensitization. The effect of somatic components on the development of asthma was evaluated by ovalbumin specific serum IgE titers, lung histology and cell counts.

Results: Results of quantitative real time PCR showed somatic products of *M.marshali* decreased expression of TLR4 mRNA in asthmatic mice.

Conclusion: This study provides new insights into immune modulation through TLR4 by the *M.marshali* somatic products, which attenuated airway inflammation in mice

Keywords: *Marshallagia marshalli*, TLR4, experimental asthma

**P651 - 669: ANTIBACTERIAL ACTIVITIES OF SYMBIOTIC ACTINOBACTERIA ISOLATED
FROM INVERTEBRATES IN MAZANDARAN**

Khadijeh Dehghan¹, javad hamed², mojtaba mohseni³

1. 1-Department of Microbial Biotechnology, School of Biology and Center of excellence in phylogeny of living organisms, College of Science, University of Tehran, Tehran, Iran. 2- Microbial technology and products (MTP) research center of tehran university, tehran,iran
2. 1-Department of Microbial Biotechnology, School of Biology and Center of excellence in phylogeny of living organisms, College of Science, University of Tehran, Tehran, Iran. 2- Microbial technology and products (MTP) research center of tehran university, tehran,iran
3. Department of Molecular and Cell Biology, University of Mazandaran, Babolsar, Iran.

Background and Aim: Actinobacteria have attracted a lot of interest as the main producer of secondary metabolites and industrial antibiotics in biotechnology. There are more than 22,000 known microbial secondary metabolites, 70% of which are produced by actinobacteria. The aims of this study were the isolation and characterization of symbiotic actinobacteria with some invertebrates in Mazandaran and their ability to produce antimicrobial compounds.

Methods: For isolation of actinobacteria, some invertebrate animals including crabs, earthworms, snails and shrimps were collected then the gastrointestinal tracts were separated. They were kept at temperature 50-60 °C for 24 hours. After its dilution in a saline buffer solution, the samples were inoculated on Starch Casein Agar (SCA) selective medium and tryptone soy agar (TSA). The plates were incubated for 21 days at 28 °C. Putative colonies of actinobacteria with a tough or powdery texture were isolated. Then organic extract was taken from the growth culture of active isolates. The antimicrobial activities of the extracts were examined against some pathogenic bacteria using the disc diffusion method.

Results: The results demonstrated that the fermentation broth extracts of these isolates showed well antibacterial activity against *Escherichia coli*, *Shigella sonnei*, *Salmonella typhi* and *Klebsiella pneumoniae*.

Conclusion: These results revealed that invertebrates hold the potential to have a diversity of actinobacteria with antimicrobial properties.

Keywords: Actinobacteria, invertebrates, bioactive compounds, symbiotic

**P652 - 674: EVALUATION OF ANTICANCER ACTIVITIES OF LACTOBACILLI ISOLATED
FROM TRADITIONAL CHEESES OF IRAN**

Mitra Rabiei Ghermezgoli¹

1. Laboratory of Microbiology, Department of Biology, Faculty of Natural Sciences, University of Tabriz, Tabriz, Iran

Background and Aim: Probiotics such as Lactobacilli in dairy products are considered as the effective compounds in the treatment of cancer. In this study, the anti-cancer activities of lactobacilli isolated from "Shoor" as one a traditional dairy products of north west of Iran on the human leukemia K562 cells has been evaluated.

Methods: Shoor samples was taken aseptically and transferred to microbiology lab. Different dilutions of the samples were made in physiological saline and inoculated on MRS agar. Inoculated plates were incubated anaerobically for 48 hours at 37°C. Appeared colonies were examined and lactobacilli were isolated. To prepare the bacterial extracts and the supernatants, isolated bacteria were cultured in MRS broth. Supernatants were isolated by centrifugation. To prepare the bacterial extracts, the bacterial pellets were re-suspended in distilled water and were heated to obtain lysed cells. Bacterial extracts were isolated by centrifugation. The K562 cells were cultured and growth inhibition effect of bacterial supernatants and extracts on the cells were assessed in intervals of 24, 48 and 72 hours by MTT assay.

Results: During this study, three strains of Lactobacilli were isolated. The inhibition of cancer cells proliferation, as well as cell death increased time and dose dependently in all three cases.

Conclusion: Lactobacilli isolated from dairy products have considerable anti-cancer effect. Seems to focus and study of probiotics in dairy products, is effective in achieving impressive range of anti-cancer compounds.

Keywords: Probiotics, Lactobacilli, K562 cells, anti-proliferation effect, growth inhibition effect, cell death, MTT assay

**P653 - 690: DESIGNING AND EVALUATION A NEW IMMUNOTOXIN CONSTRUCT FOR
TARGETING GASTRIC CANCER**

Zohreh Neyestani¹, Aliakbar Haddad-Mashadrizesh², Jafar Saidi³

1. Department of Biology, Science and Research branch, Islamic Azad University, Khorasan Razavi, Neyshabur, Iran
2. Cell and Molecular Biotechnology Research Group, Institute of Biotechnology and Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
3. Department of Biology, Science and Research branch, Islamic Azad University, Khorasan Razavi, Neyshabur, Iran

Background and Aim: Due to the lack of sufficient specificity of the current therapeutics approaches for targeting cancer cells, costly expenditure as well as side effects the requirement to the novel therapeutic strategies are understood clearly. So, in order to overcome these challenges, target therapy such as bacteria therapies are considered based on understanding the molecular pathogenesis of the cancer. Accordingly, the use of the bacterial toxins for immunotoxin development provided new effective approaches for cancer therapy. Bearing in mind, designing an intelligent immunotoxin construct for targeting gastric cancer were considered, based on application of toxin derived of the *Pseudomonas aeruginosa*.

Methods: In this regard, the characterization of the structural and functional feature of the selected toxin was performed. Moreover, cell surface specific antigens of the gastric cancer were gathered, and then subjected to in-silico expression assay, via Protein-atlas database. Subsequently, corresponding ligands of them were determined via String programs, and then filtered via binding affinity as well as post-translation modification, through related program such as Cluspro.

Results: Furthermore, the assembly of the selected domains were performed, and then considered for 3D structure, immunogenicity, codon optimization and in-silico expression.

Conclusion: this study led to the introduction cell surface specific antigens of gastric cancer such as GRIA2, and also 7 of the related antigens. Moreover, molecular characterization of the selected toxin led to introduce the cell death domains with the capacity of the inhibition of the protein synthesis. Finally, the assembly of the effective domains, led to designing a new construct, which are considering for experimental conditions.

Keywords: Bacterial toxins, Cancer, immunotoxins, bioinformatics

**P654 - 715: THE EFFECT OF BACILLUS ATROPHAEUS HNSQJYH170 LIPOPEPTIDES ON
GERMTUBE PRODUCTION IN CANDIDA ALBICANS**

Solmaz Moghtadi pisheh¹, Mahboobeh Madani²

1. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran
2. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran

Background and Aim: Nowadays, due to overuse antibiotics by human causes to high antibiotic tolerance, also increasing Opportunistic fungi such as *Candida* has been leading to major disease in Immunosuppressed hosts. Biocontrol agents by using antagonistic beneficial microorganisms have been promoted as the alternative way in place chemicals antibiotics. So in this research the effect of *Bacillus atrophaeus* lipopeptides on germtube production in *Candida albicans* was studied.

Methods: *Bacillus atrophaeus* HNSQJYH170, was cultured on fermentation medium. After 72 h of incubation, a cell-free supernatant of *Bacillus atrophaeus* was collected by centrifugation at 14 000×g at 5°C, to remove the biomass and then acidified by adding HCl. The precipitate obtained after 24 h was collected by centrifugation. The precipitate of metabolites was dissolved in methanol:water. Then 50.0 µl of crude precipitate was added into 0.5 ml of human serum containing *C.albicans* (10⁶ cfu/ml). One tube without crude precipitate was used as the control. After incubation in 37 °C for 3 hours, germtube production under light microscope was studied.

Results: According to this research, inhibition of germtube production in %95 of *C.albicans* cells was showed by *Bacillus atrophaeus* lipopeptides. In control tube, all *C.albicans* yeast produce germtube.

Conclusion: *Bacillus atrophaeus* HNSQJYH170, isolated from soil sample, was displayed antifungal activity against *C.albicans* by producing cyclic lipopeptide-type antibiotics. Therefore, these compounds can be used as antifungal drug.

Keywords: Germtube production, lipopeptides, *Bacillus atrophaeus*, *Candida albicans*

**P655 - 765: THE EFFECT OF BACILLUS AMYLOLIQUEFACIENS M13RW01
METABOLITES ON GERM TUBE FORMATION IN CANDIDA ALBICANS**

Mahsa Aghaali Marnani¹, Mahboobeh Madadani²

1. . Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran
2. . Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran

Background and Aim: Various strains of Bacillus can produce cyclic lipopeptides in the culture media with a antifungal activity against several important yeasts pathogens including Candida albicans. The present research was aimed to study the effect of Bacillus amyloliquefaciens M13RW01 metabolites on germ tube formation in Candida albicans.

Methods: Bacillus amyloliquefaciens was cultured in Nutrient Broth medium and centrifuge at 16 000 ×g at 4°C, to remove the biomass. Then HCl was added and after centrifugation (16,000×g, 4°C), precipitate was collected and dissolved in methanol:water. 50.0 µl of crude precipitate was added into 0.5 ml of human serum containing C. albicans (10⁶ cfu/ml). Iturin A was used as positive control. After incubation in 37 °C for 3 hours, germ tube production under light microscope was studied.

Results: Similar to iturin A, in the presence of Bacillus amyloliquefaciens M13RW01 metabolites, germ tube formation was inhibited in all C. albicans yeast.

Conclusion: As a conclusion, the results reported here indicate that Bacillus amyloliquefaciens M13RW01 metabolites play a vital role in the antagonistic activity against Candida albicans.

Keywords: Bacillus amyloliquefaciens, Candida albicans, germ tube, lipopeptides

P656 - 828: SURVEY ANTIMICROBIAL EFFECT OF BOILING WATER AND ALCOHOLIC EXTRACT OF SCROPHULARIA STRIATA ON ESCHERICHIA COLI

Mitra Chalabzardi¹

1. *MSc in Microbiology, Faculty of Sciences, Faculty of Sciences, ILAM University, ILAM, Iran,

Background and Aim: With to the growing resistance to chemical antibiotics Bacterial strains Against plants have side effect less of have their drugs chemical be replaced Power .Years away from having a Scrophularia striata plant on an experimental basis in various forms in the treatment of different diseases, including inflammation and infection eye, digestive disorders and skin burns were used.[1,2] . In this study survey the antimicrobial properties of boiling water and alcoholic extract and water Scrophularia striata on strains clinical and is standard of E.coli is investigated.

Methods: In this study Scrophularia striata plant after collecting dried in shade. boiling water, water ,and ethanol extract individually prepared. extract different concentrations (25, 50-100-200-400- mg/ml) using the diffusion disc amikacin and gentamicin as positive control and DMSO was used as negative control and the MIC and MBC were dilution method found was on E.coli.k and agar diffusion and spread of E.coli standard and clinical strains the effect was and antibiotic.

Results: The results obtained from the water extract of this plant has no antimicrobial effect on standard and clinical strains. ethanol extract at concentrations of 800 and 400 mg/ml and boiling water extract at all concentrations had antimicrobial effect. Spread on agar disk diffusion method has a significant inhibitory effect on the E.coli have. MIC and MBC quantity of 100 and 400 mg respectively obtained.

Conclusion: Boiling water extract effect antimicrobial good on bacteria clinical and standard strains. boiled Scrophularia striata plant causes it was more complex isolated

Keywords: Scrophularia striata, Escherichia coli ,Antimicrobi

**P657 - 846: ANTIBACTERIAL PROPERTY OF A CAMEL RECOMBINANT PEPTIDE
(LACTOFAMPYN- LACTOFERRIN) - AN IN-VITRO STUDY**

Mahdie Sayadi¹, Marjan azghandi², Zahra mosavi³, sepideh hasan zadeh⁴, Kiarash Ghazvini⁵, hadi Sekhavati⁶

1. Masters student of medical bacteriology, Department of Microbiology and Virology Mashad University of Medical Sciences, Mashhad, Iran
2. Masters Student of Genetics and Animal Breeding, Department of Animal Science, Faculty of Agriculture, Ferdowsi University of Mashhad
3. Masters Student of Genetics and Animal Breeding, Department of Animal Science, Faculty of Agriculture, Ferdowsi University of Mashhad
4. Phd student of medical bacteriology, Department of Microbiology and Virology Mashad University of Medical Sciences, Mashhad, Iran
5. MD PhD Associate Professor of Microbiology Department of Microbiology and Virology Mashad University of Medical Sciences, Mashhad, Iran
6. Assistant Professor, Department of Animal Science, Faculty of Agriculture, Ferdowsi University of Mashhad

Background and Aim: Regarding the increasing trend of antibiotic resistance among bacteria, finding a proper antibacterial agent for infection treatment is necessary. In this study we evaluate the activity of new synthetic antibacterial peptide which seems to have some capability for preventing the growth of most of the pathogens.

Methods: In order to study the antibacterial property of this recombinant peptide the MIC was determined by the micro broth dilution method. The recombinant peptide was provided in DMEM medium. Several serial dilutions up to 1/1024 of the peptide were prepared in Mueller-Hinton Broth. Each dilution was encountered with bacteria and after 24 hours of incubation, the growth inhibitory property of the peptide was studied. The test was conducted for three standard strains *Staphylococcus aureus* ATCC 25923 and *Escherichia coli* ATCC 25922 and *Mycobacterium smegmatis* CIP 73.26

Results: This peptide showed ability of growth inhibition, *Staphylococcus aureus* up to 1/256. But when confronting with *Escherichia coli*, it presented lesser inhibitory effect and demonstrated almost no antibacterial property. Moreover, *Mycobacterium smegmatis* showed a weak antibacterial effect and it was only capable of growth inhibition of this bacterium up to 0.5 density.

Conclusion: This peptide demonstrated considerable antibacterial activity on growth of Gram-positive bacteria. Regarding the fact that this peptide with amphipathic property belongs to the cationic peptide groups can exhibit better performance on attaching to peptidoglycan in Gram-positive bacterial cell wall. Considering the specific effect of the peptide, it deserves more attention for usage in conditions which only special groups of bacteria are supposed to be controlled and have less destruction on the human microbiota

Keywords: cationic Peptide, antibacterial, MIC

**P658 - 911: ANTIBACTERIAL ACTIVITY OF PIGMENTS PRODUCED FROM NATIVE
ISOLATED MICROORGANISMS**

Mitra sadat Alihosseini¹, Mohammad Mir- Derikvand², Ashrafalsadat Hatamian-Zarmi³, Bahman
Ebrahimi-Hosseinzadeh⁴

1. Department of Life science Engineering, Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran
2. Department of Life science Engineering, Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran
3. Department of Life science Engineering, Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran
4. Department of Life science Engineering, Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran

Background and Aim: Regarding to emergence of bacterial resistance to antibiotics, identification and development of new antimicrobial compounds is essential. Pigments as biological products are one of the best options to identify antimicrobial compounds. Soil microorganisms recently have been considered to produce microbial products, such as pigments. Microbial pigments are preferred due to rapid growth of microorganisms and higher yields and easier extraction. In this study, it was isolated and identified some native microorganisms to investigate antibacterial pigments.

Methods: The soil samples collected from different areas of Iran were serially diluted and plated on Nutrient Agar (NA) and Potato dextrose agar (PDA). Then, pigment-producing colonies were selected. Extraction of pigments was performed from sediment with DMSO. The antibacterial properties of pigments were examined.

Results: Thirty pigment-producing strains were isolated, of which pigments of 7 strains had antibacterial properties. *Bacillus subtilis*, *Staphylococcus aureus* and *Escherichia Coli* were highly sensitive bacteria to pigments and *Pseudomonas aeruginosa* had lowest sensitivity. This study will be followed by new screenings.

Conclusion: Since the natural pigment in the appropriate dose is healthier than chemical type, their use in various industries such as pharmaceutical and food are useful.

Keywords: Microbial screening, Antibacterial pigment, Microorganisms

**P659 - 945: EVALUATION THE PREVALENCE AND OF ANTIBIOTIC RESISTANT PATTERN
IN AEROMONAS ISOLATED FROM BURN PATIENTS IN HOSPITAL TALEGHANI ILAM
CITY**

Mitra Chalabzardi¹

1. *MSc in Microbiology, Faculty of Sciences, Faculty of Sciences, ILAM University, ILAM, Iran,

Background and Aim: Aeromonas are ubiquitous water borne bacteria these gram -negative rod shaped bacteria comprise mesophilic motile and psychophilic nonmotile organisms which can cause important diseases in human and animals . Aeromonas them A. hederophila A. caviae and A. veronii has been considered as mainly associated with gastrointestinal disease and wound infection[1]. The aim of this study was to Evaluation the prevalence and of antibiotic resistant pattern in Aeromonas isolated from burn patients in Hospital Taleghani Ilam City

Methods: Total of 83 samples were collectiong from burn patients wounds. samples were cultured on Aeromonas specific media and sheep ampicillin blood agar following of samples cultured were confirmed by biochemical testing. according to clsi of 13 antibiotics were determined. the antibiotic resistance of the isolated strains was to antibiotics include antibiotic: Cephalothin 13.95%, Ceftriaxone 34.92%, Cefotaxime 51.81%, Cefazolin 61.22%, sulfamethoxazole 21.52%, Cephalexin 9.63%, nitrofurantion 40.32%, Trimoxazole 86.74%, 61.22%, Gentamicin 18.92%, Erythromycin 37.15%, Imipenm 69.52%, Amoxycillin 49%, oxacillin 31.94% was applied The following testing combined disk detect ESBL producing strains. Finally, PCR was performed to examine the prevalence of genes PER and OXA with used specific primers .

Results: The results of antibiogram showed that the highest amount of resistance is for Trimoxazole 72 sample (%86.74) and the least amount of resistance is for Cephalexin 9.63% Also, 50 (60.24%) were ESBL producing strains. The results of PCR showed that 33(66%) of the studied strains included OXA gene and 17 (34%) strains were PER gene.

Conclusion: of this study showed highly distribution of resistant among pseudomonas isolated different antibiotic in Ilam City, so select of proper treatment procedure is necessary.

Keywords: Pseudomonas, Antibiotic Resistance , ESBL, Ilam City , PCR

**P660 - 986: DESIGNING A GENETICS CONSTRUCT BASED ON A-SARCIN APPLICATION
FOR TARGETING COLON CANCER VIA IN-SILICO EVALUATION**

Mozhdeh Moghimi kakhki¹, Aliakbar Haddad-Mashadrizesh², Alireza Haghparast³

1. Department of Biology, Science and Research branch, Islamic Azad University, Khorasan Razavi, Neyshabur, Iran
2. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
3. Immunology section, Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran

Background and Aim: α -sarcin, a fungal ribotoxin, with the appropriate propertise in the size, thermostability, immunogenicity, resistance to the proteases as well as cell death induction via ribosome inactivation, is a suitable candidate for anti-cancer drugs development. the characterization of the structure, function of the toxin were considered in this study for development a new generation of immunotoxins for targeting colon cancer.

Methods: NCBI, Uniprot and ExPASy were used for accessing to the protein and nucleotide. CD search and Motif scan programs were used for detection active domins. cell surface specific antigens of the colon cancer were gathered based on literature and evaluated by Proteinatlas database. corresponding ligands of the selected antigens through String program. the Cluspro, Pymol, MOE and Rampage programs as well as IEDB, ProPred-I and Propred databases were used for calculating the binding affinity of the ligand to the corresponding antigene, determine the quality of the structure and immunogenicity character of the constructs, respectively.

Results: the results of this study led to the introduction a cell death domain in the a-sarcin, as well as GPA33 as a cell surface specific antigens of the colon cancer with seven corresponding ligands. physicochemical characterization of the amino acids which are involved in the interaction of the ligand to the selected antigens led to introduced several small ligands. seven novel genetic constructs were designed based on the assembly of the selected domains.

Conclusion: α T-(GGGGS)3-HSF showed the highest quality in the structure and immunogenicity among designed constructs, which for experimental confirmation is under more investigation in our group.

Keywords: α -sarcin, Ribotoxins, Colon cancer, GPA33, Immunotoxin

**P661 - 1004: SCREENING AND ISOLATION OF PHENYLALANINE AMMONIA LYASE
FROM IRANIAN CYANOBACTER ANABAENA90**

Reyhaneh Baradaran ghaffary¹, Dr.Mehrooz Dezfoulan²

1. Department of Microbiology Karaj Branch Islamic Azad University
2. Department of Microbiology Karaj Branch Islamic Azad University

Background and Aim: The enzyme Phenylalanine ammonialyase is originally a plant enzyme. But the remarkable fact about PAL is the usage of this enzyme in the treatment of human diseases. Cyanobacterial PAL is the best candidate to achieve this aim.. PAL convert phenylalanine into a harmless metabolite calls trans cinamic acid. The aim of this research was to detect the presence of Phenyl alanine ammonia lyase in Iranian Isolates of cyanobactery Anabaena 90

Methods: Enzyme extraction from cyanobacterial Mass and after freeze-thaw, vortex and centrifuging, separating the supernatant and adding "Ammonium per sulfate" observed precipitated protein includes the enzyme. The precipitate solved in Tris-HCl buffer and the activities were measured in different three temperatures "25, 37 & 42°C" in two periods of time half and one hour, with spectrophotometry so in eleven pH (2-12)

Results: Anabaena 90's best activity is in: pH 4, in 37°C during an hour with L-phenylalanine substrate and in 25°C during half an hour with L-tyrosin substrate.

Conclusion: Despite the valuable finding of this survey therapeutic effects of the extracted enzymes must be evaluated after purification and clinical trials

Keywords: cyanobacter, Anabaena 90, Phenylalanine ammonia lyase, (PAL; EC 4.3.1.24), Phenylalanine, tyrosin

**P662 - 1034: THE MONITORING OF STRUCTURAL AND FUNCTIONAL
CHARACTERISTICS OF COMBOTOX IN ORDER TO DEVELOP A NEW GENERATION OF
MEDICINE EFFECTIVE FOR LYMPHOMA.**

Seyyede fatemeh Ahmadpour moghaddam¹

1. Aliakbar Haddad-Mashadrizesh

Background and Aim: Combotox is such an immunotoxins (ITS). It is a 1:1 mixture of two immunotoxins (ITS), prepared by coupling deglycosylated ricin A chain (dgRTA) to monoclonal antibodies directed against CD22 (RFB4-dgRTA) and CD19 (HD37-dgRTA). RTA inhibits protein synthesis by catalytically inactivating the ribosomal RNA.

Methods: Combotox protein sequencing occurred based on CD-search and motif scan program. 3D structure components immunotoxins based on modeling methods. Modeling methods were determined on homology included (Modeller, Swiss model) domain connection through linker and similar linker occurred with using of Modeller software. Optimization using with Gromacs- 5.07, gromacs 96 43al force field during the 20 ns and determined quality assessment model structure with program PAMPAGE, MOE.

Results: At the first steps: The 3D structure of the immunotoxin with PDB ID: IXTD was received. Modeller analysis result indicate that of 190 aminoacids the catalytic domain to about 11% aminoacids relative to the main toxin levels are more Modeller and other aminoacids have less RMSF to about 89%. The hydrogen bond present in hydrogen bond network in the active site at position via a heterobifunctional, thiol-containing cross linker, N-succinimidyl-Oxycarbonyl-a-methyl-a-(2-pyridyldithio)toluene (SMPT).

Conclusion: The results remonstrate that sequential administration of the cytotoxic agent cytarabine and the immunotoxin combotox has synergistic anti leukemic activity in invivo model of advanced B lineage all. On direct comparison, sequential administration of both drugs at doses calculated to simulate human maximum tolerated dose resulted in increased survival when compared to concurrent administration.

Keywords: Combotox, lymphoma, GROMACS-5.0.7, PAMPAGE, MOE

Molecular Detection

P663 - 22: ISOLATION AND DETERMINATION OF ANTIBIOTIC RESISTANCE PATTERNS IN ENTEROCOCCUS FAECALIS ISOLATED FROM MEAT

Elahe Tajbakhsh¹

1. Department of Microbiology, Faculty of Basic Sciences, Shahrekord Branch, Islamic Azad University, Shahrekord

Background and Aim:Antibiotics are widely used to prevent or cure the microbial infections in human and animals. The presence of resistant bacteria in an environment is considered as a serious threat to the health. The broad antibiotic resistance of bacteria causes the failure of antibiotic treatment to these infections

Methods:In this research 104 meat samples (cows, calves, sheep and goats) were studied to isolation of Enterococcus faecalis and determine antibiotic resistance pattern. biochemical tests and PCR method were done for All samples .Antimicrobial susceptibility test was performed by the Kirby-Bauer disc diffusion method using Mueller–Hinton agar, according to the CLSI guidelines.

Results:Amonge 104 samples, 42 (40.38%) were detected as Enterococcus faecalis. Resistance to Stereptomaysin, Cefotaxim, Meropenm, Erythromaysin, Tetracycline, Amicycin, Gentamycin, Choloramephnicle, Ciproflocsacine, Amoxicylin and Vancomycin was, 95.2%, 85.6%, 80.95%, 61./9%, 26%, 23.8%, 11.9%, 9.5%, 4.76%, 4.8% and 0% respectively. Prevalence of antibiotic resistance genes such as aac (6[○])/aph (2[○]), erm A, ant (2[○] ○ ○)-I, tet M genes were reported 80%, 71.42%, 80% and 63.64%,respectively

Conclusion:All of isolated Enterococcus faecalis in the present research showed the resistance to some types of antibiotics but fortunately, they were sensitive to the most important related clinical antibiotics (Ciprofloxacin, Amoxicillin and Vancomycin) and a small resistance to Chloramphenicol, Tetracycline and Gentamicin

Keywords:Antibiotic resistance, Enterococcus faecalis, Meat. Gene

**P664 - 26: DETECTION OF CTX-M GENES IN ESBL-PRODUCING ESCHERICHIA COLI
CLINICAL ISOLATES BY COMBINED DISC TEST AND REAL-TIME POLYMERASE CHAIN
REACTION**

Fatemeh Zaboli¹, Mojtaba MohsenPour², Samaneh Rouhi³

1. Microbiology Department, Ayatollah Amoli Branch, Islamic Azad University of Amol, Amol, Iran.
2. Microbiology Department, Ayatollah Amoli Branch, Islamic Azad University of Amol, Amol, Iran.
3. Student Research Committee, Kurdistan University of Medical Sciences, Sanandaj, Iran. Cellular & Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran. Department of Microbiology, Kurdistan University of Medical Sciences, Sanandaj, Iran.

Background and Aim: Real-time polymerase chain reaction (Real time PCR) is a molecular technique based on the PCR for quantitative analysis of gene expression. Also CTX-M extended-spectrum β -lactamases (ESBLs) are increasingly among *Escherichia coli* bacteria in urinary tract infections. Aim of this study is survey on blaCTX-M genes in *E. coli* clinical samples with molecular and phenotypic test.

Methods: This cross-sectional study was performed for 6 months (July to December 2014) on urine samples of patients admitted to Shahid Yahyanejad hospital, Babol city, Mazandaran Province, Iran. Combined Disc Test (CDT) with Cefotaxime (30 μ g) and Cefotaxime (30 μ g) /Clavulanic Acid (10 μ g) and Real time PCR were performed for ESBLs and blaCTX-M genes detection. SPSS VER20 and Chi-Square test were applied for data analysis.

Results: From 1842 patient specimens, 84 (%4.56%) *E. coli* isolates were isolated. Phenotypic test showed that 29/84 (%34.52) of them were ESBLs producer. 15/29 *E. coli* isolates were selected in order to confirm blaCTX-M genes with Real-time PCR test. In the Real-time PCR test, 10/15 (66.7%) isolates were positive for blaCTX-M genes expression.

Conclusion: The results showed that the molecular and phenotypic test results were very close together. In order to accurately identify of genes, incorporation of molecular and phenotypic tests is useful.

Keywords: CTX-M Genes, ESBL-Producing *Escherichia coli*, Combined Disc Test, Real-Time Polymerase Chain Reaction

**P665 - 31: HUMAN MALIGNANCY ASSOCIATED WITH Y CHROMOSOME: GENOTYPES
AND HAPLOTYPES ASSOCIATED WITH SUSCEPTIBILITY TO COLORECTAL CANCER
PATIENTS**

Ali Almarzoqi¹, Raad abbas²

1. babylon university- college of science for women
2. babylon university- college of science for women

Background and Aim:Background: Methylenetetrahydrofolate reductases (MTHFR) considered as a critical character in digestion system of folate furthermore collaborate with union of nucleic corrosive, repair arrangement of DNA and methylation. Our study was meant to investigate the essence between MTHFR polymorphism and the danger of CRC.

Methods:Methods: The study populace included 77 disease male patients with CRC (mean of age in years 64 ± 8.7) separated as; (41 with colon malignancy and 36 with rectal growth) and 55 as controls admitted to the Merjan Healing center in span stretched out from October 2015 until March 2016.

Results:Results: The outcomes uncovered that hereditary polymorphisms of all qualities incorporating into this study for MTHFR 677 quality in CRC patients; the recurrence of MTHFR C677 genotypes were as kindred TT 12.0 (15.6%), CT 24.0 (31.2%), and CC 41.0 (53.2%) in CRC, and in the control was 19.0 (34.5%), 14.0 (25.5%), and 22.0 (40.0%) individually. Amalgamation frequencies for MTHFR 677 TT homozygous and CT 677 heterozygous watched were 31.2% in CRC and 47.3% in the controls. The Genotype dissemination for MTHFR 1298 quality in CRC patients; the recurrence of MTHFR C677 genotypes were as kindred CC 9.0 (11.7%), CA 21.0 (27.3%), and AA 47.0 (61%) in CRC, while in the control was as individual 8.0 (14.5%), 21.0 (38.2%), and 26.0 (47.3%) separately. The recurrence for MTHFR 1298 quality AA homozygous and AC 1298 heterozygous watched was 74.7% in CRC and 66.4% in the controls.

Conclusion:Conclusion: MTHFR; XRCC1 SNPs is connected with expanded CRC hazard.

Keywords:Keywords: Y-chromosome; CRC; Genotype; Haplotype; MTHFR; XRCC1.

**P666 - 44: IN-HOUSE, QUALITATIVE BASED MULTIPLE PCR: DIAGNOSIS OF
PAPILLOMA VIRUS TYPES 16 & 18 IN SUSPECTED SAMPLE**

Mohammadreza Shafaati¹, Akhavan Elnaz², Mobini Saeed³, Yazdani Shaghayegh⁴

1. Department of cellular & molecular biology IAU, Hamadan Branch, Hamadan, Iran
2. Department of Microbiology IAU, Damaghan Branch, Damaghan, Semnan, Iran
3. Department of Immunology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
4. Department of Virology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: The human papilloma virus was introduced as the major factor in outbreak of cervix cancer in 1970. Since it is impossible to recognize this virus and these types using the serological and cell culture, molecular methods such as PCR are of great importance. Therefore in this study, our goal is using a multiple specific PCR assay on L1 and E6 genes of HPV for molecular detection of this virus and its common type's detection in the society.

Methods: After collecting the samples from malignant lesions of various patients, the viral DNA was done from paraffin blocks of 50 clinical samples and the PCR method was done on the mentioned samples by specific primers for L1 and E6 genes together with β -globin (as internal control). After surveying the PCR product on agarose gel 2%, the specificity and sensitivity of this test was examined.

Results: From among 50 samples of the patients, 33 cases were HPV positive and 17 ones were negative. The results of specificity assay was positive for HPV samples and sensitivity of this test was 20 copies from recombinant construct containing target genes for each reaction.

Conclusion: This study confirmed PCR with specific primers on L1 and E6 genes of HPV to be an accurate and proper method for detecting and determining the types of HPV

Keywords: HPV, cervix cancer, L1 gene, E6 gene, PCR, molecular detection

**P667 - 53: SEROPREVALENCE OF HEPATITIS A IN HEMODIALYSIS PATIENT
CANDIDATE FOR KIDNEY TRANSPLANT YOUNGER THAN FORTY YEARS**

Ensieh Arabsaghari¹, Sara Abolghasemi^{1,2}, Shahnaz Sali^{1,3}, Yasan Sadeghian⁴, Fariba Samadian⁵, Amirhesam Alirezaie⁶, Shirin Manshouri⁷, Mahmoud Parvin⁸, Mohammad Hassan Shabani⁹

1. 1. Infectious Diseases and Tropical Medicine Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
2. 1. Infectious Diseases and Tropical Medicine Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. 1. Infectious Diseases and Tropical Medicine Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
4. 1. Infectious Diseases and Tropical Medicine Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
5. 2. Department of Nephrology and kidney transplantation, Shahid Beheshti University of Medical Sciences, Tehran, Iran
6. 2. Department of Nephrology and kidney transplantation, Shahid Beheshti University of Medical Sciences, Tehran, Iran
7. 1. Infectious Diseases and Tropical Medicine Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
8. 3. Department of pathology, Labbafinejad Medical Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
9. Head of Transplant and Certain Diseases of Tehran University

Background and Aim:Worldwide, hepatitis A is a common infection during childhood especially in developing countries. It can cause severe complications in Immunocompromised patients, including kidney transplants patients and chronic liver disease. Due to the increasing number of kidney transplants in the country and epidemiologic shift of HAV which was observed in previous studies, we're going to review the epidemiology of hepatitis A in hemodialysis patients less than forty years serving kidney transplant candidates to follow vaccination policy for them.

Methods:In a cross sectional study during 1393-1394 hepatitis A antibody levels in hemodialysis patients less than forty years of kidney transplant candidates examined in 12 hospitals in Tehran, Iran. Their serums were tested for anti HAV IgM & IgG by ELISA kits.

Results:Hepatitis A virus antibody was positive in 66 (72.5%) of 91 patients. The prevalence of HAV was 0 % at the range of younger than 20 and 45% in under 25 years age group. This significantly increased prevalence by increasing the age, and there was according to epidemiological shifts which were shown in other studies.

Conclusion:Due to the availability of vaccine and hepatitis severe complications in immunocompromised individuals, as well as a low prevalence of positive serology in individuals under 25 years, it seems check of antibodies in patients undergoing kidney transplantation and vaccination in seronegative persons is a logical.

Keywords:dialysis patients; hepatitis A; seroprevalence

P668 - 101: DETECTION OF ACINETOBACTER BAUMANNII ISOLATES BY ELASA

Samaneh Rasoulinejad¹, Seyed Latif Mousavi Gargari²

1. Department of Biology, Faculty of Basic Sciences, Shahed University, Tehran, Iran
2. Department of Biology, Faculty of Basic Sciences, Shahed University, Tehran, Iran

Background and Aim: One of the serious and important problems in hospitals is Nosocomial infections caused by drug-resistant bacteria such as *Acinetobacter baumannii*, due to its remarkable ability of surviving on hospital surfaces equipment and resistance to most of the antibiotics. *Acinetobacter baumannii* pass through the body via wounds or invasive medical devices and cause meningitis, osteomyelitis, pneumonia, bacteremia, septicemia and urinary tract infections in the hospital patients with critically illnesses, in the intensive care and burn unit. Fast and accurate detection is challenging in many microbial diagnostic applications. Nucleic acid aptamers are alternative ligands to capture pathogens.

Methods: Selected aptamer sequence are generated through the Systematic Evolution of Ligands by Exponential Enrichment (SELEX) process, a technique used for the screening of large libraries of oligonucleotides by an iterative process of in vitro selection and amplification. Herein we report a SELEX based assay to screen DNA aptamer-conjugated fluorescein (FITC) that recognizes *Acinetobacter baumannii* (ATCC 19606) with high affinity and specificity. A sandwich enzyme linked aptamer sorbent assay (ELASA) was designed with the biotinylated aptamer and our previously developed nanobody against biofilm associated protein (Bap). The assay system was optimized with *A.baumannii* (ATCC 19606) and 47 clinical isolates of *A.baumannii* were tested.

Results: After 12 rounds of selection, the highly enriched DNA pool was sorted using flow cytometry. The threshold of detection in sandwich ELASA process was 103 CFU/ml. The sensitivity of test toward the clinical isolates was 95.47%.

Conclusion: Collectively, these data suggest that ELASA assay is a promising technique for the accurate detection of microbial cells.

Keywords: ELASA, antibody, Aptamer, SELEX

**P669 - 120: RAPID DETECTION OF HIV-1 INFECTION BY LOOP-MEDIATED
ISOTHERMAL AMPLIFICATION(LAMP)**

Hamid Saadati¹, Mehdi Golshan²

1. Department of Biology, Estahban Higher Educational Center, Estahban, Iran
2. Department of Biology, Estahban Higher Educational Center, Estahban, Iran

Background and Aim: The human immunodeficiency virus (HIV) is a retrovirus that causes acquired immunodeficiency syndrome (AIDS), that requires sophisticated clinical management. This infection is identified either by the detection of HIV-specific antibodies in serum or plasma or by demonstrating the presence of the virus by nucleic acid detection using PCR. In this study, we distinguished the ability of LAMP assay to detect HIV infection and compared the sensitivity of LAMP with PCR.

Methods: A total of 35 blood samples from HIV infected patients were analyzed with six primers targeting conserved sequences of the HIV RT gene within 70 min, under isothermal conditions at 60°C. Then, visualized by gel electrophoresis with safe staining and detected by the UV doc after adding SYBR Green I.

Results: All samples positive for HIV by PCR were confirmed by LAMP method. When visualized by gel electrophoresis and safe staining, The HIV LAMP assay products appeared in a ladder pattern, with many bands of different sizes. The HIV LAMP product could also be detected by the UV doc after adding SYBR Green I to the reaction tube and observing a color change from colorless to sharp green in positive samples.

Conclusion: The HIV LAMP had the same sensitivity as a PCR assay, the detection limit for the both systems were found to be 10 copies per mL of HIV RNA. The LAMP assay reported here is superior for rapid amplification, simple operation, and easy detection and will be useful for rapid and reliable clinical diagnosis of HIV in developing countries.

Keywords: LAMP, PCR, HIV

**P670 - 123: THE SCREENING PARAGONIMUS SPP.ON FRESHWATER CRAYFISH FROM
ARAS DAM RESERVIOR BY MOLECULAR METHOD PCR**

Soheila Fazeli¹, Ali Nekuie Fard(PH.D)², Amir Amniat talab(PH.D)³

1. Faculty of Sciences, Biotechnology Department, Islamic Azad University, Urmia Branch, Urmia, Ira
2. Faculty of Veterinary , Aquatic Animal Health & Disease Department, Islamic Azad University, Urmia Branch, Urmia, Iran
3. Faculty of Veterinary , Patohology Department, Islamic Azad University, Urmia Branch, Urmia, Iran

Background and Aim:The limit number of digenea parasite of fresh water crayfish involved in zoonotic diseases has been reported.one of the most important in this field is paragonimus spp genusand its species paragonimus westermani,which is a flatworm lung and human brain is very important.identification of pathogenic microorganisms by PCR,consider as an important and achievable strategies for Health monitoring of large number of sample in ashort time

Methods:In order to study infection in Aras river fresh water crayfish to P.westermani from mehr 2014 to Kordad 2015 from 4 harvesting station.Totally 1219 freshwter crayfish (625 male and 594 feamale)were harvested and transferred to laboratory for parasitology study

Results:From hole harvested,150 freshwater crayfish(82 male and 68 female)with 12/33prevalence which have observed or suspected metacercariae cyst in fillet tail or gill isolated for morphological and molecular survey.The result of molecular analysis whit PCR in 520bp approved infection to paragonimus westermani in allsample .to ensure the result,PCR product were transferred to sinaclon for sequencing .The data surveyed and compared in Gene bank

Conclusion:The results with more than 91% reliability in whole samples,and search more than 10 times in blast run database and 100% overlap owned by paragonimus westermani parasite .

Keywords:fresh water crayfish ,Aras Dam,paragonimus westermani ,metacercer,ITS,PCR

**P671 - 128: DESIGN OF A MULTIPLEX REAL TIME PCR WITH INTERNAL CONTROL
METHOD TO DETECT YERSINIA PESTIS**

Khatereh Kabiri¹, Keivan Majidzadeh- A²

1. Department of Microbiology, Islamic Azad University, Tehran North Branch, Tehran, Iran
2. Tasnim Biotechnology Research Center (TBRC), AJA University of Medical Sciences, Tehran, IR

Background and Aim:Yersinia pestis, the agent of bubonic and pneumoni plague, has caused many millions of human deaths and still poses a serious threat to global public health. Classical methods to detect the organism are time consuming and expensive. in spite of high speed and accuracy Real time PCR, false negative results which are caused because of PCR inhibitors, are the important problems of this technic that can reduce its efficiency. In this study, an internal control was constructed for caf1 gene of Yersinia pestis.

Methods:Allele ID 7.6 software was used to design specific primers and FAM/BHQ1dual labeled probe based on caf 1 gene of the organism. Setup reactions were performed using an ABI 7500 Fast Real-Time Amplification system. Composite primers for PCR amplification of Pichia pastoris AOX1 gene sequence were designed and optimized to use as IC- AOX1. To evaluate the IPC, Real-time PCR test was conducted in the tubes containing caf1 probe and primer pair and probe for caf1-IPC (TET labeled) .

Results:Sensitivity of PCR for caf1 gene was 4ng and the specificity was 100%. The optimized IC- AOX1 concentration that was used in each test was 1fg plasmids containing IC- AOX1. The fluorescent signal was recorded by using the FAM (caf1) and TET (caf1-IPC) optic channel set at a wave length of 520 nm and 536 nm respectively.

Conclusion:The results indicate that the IPC effective tool for avoid false negative results and confirm the results.

Keywords:multiplex Real time PCR, Yersinia pestis

**P672 - 136: SURVEYING THE GENE CASSETTES OF CLASS 1 INTEGRON AMONG MULTI-
DRUG RESISTANT ESCHERICHIA COLI ISOLATES FROM URINARY TRACT
INFECTIONS COLLECTED IN ISFAHAN**

Seid Shervin Shariat Panahi¹, Seyed Shervin Shariatpanahi², Najmeh Farahani³, Ebtahaj Pishva⁴, Rasoul Salehi⁵

1. -
2. Department of Genetics and Molecular Biology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
3. Department of Genetics and Molecular Biology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
4. Department of Microbiology and Virology, Isfahan University of Medical Sciences, Isfahan, Iran
5. Department of Genetics and Molecular Biology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran

Background and Aim: Antibiotic resistance in urinary tract infection is considered an expanding public health problem in the world. Bacteria can transfer genetic information to get protection against most antibiotics. The acquisition of resistance genes involves genetic mobile elements such as plasmids and transposons. The present study aimed to determine the susceptibility and detect gene cassettes of coli forms bacteria isolates from patients with urinary tract infections (UTIs).

Methods: The number of 370 patients with UTI from both ICU (In Case group) and outpatients (in control group) were selected from two hospitals. Initially antimicrobial susceptibility testing was performed and then integrons were detected using multiplex-polymerase chain reaction (PCR), with primers targeting conserved regions of integron-encoded integrases intI1, intI2, and intI3. Integrase positive strains were further analysed for the detection of resistance gene cassettes using 5'CS and 3'CS primers and finally were sequenced.

Results: The most prevalent integron was class1 integron which was detected in 94(59.1%) and 94(58%) of case and control patients. PCR showed that the class1 integron-bearing strain contained two distinct gene cassettes, dfrA5 and dfrA1-aadA1 gene arrangement and they are encoding aminoglycoside adenylyltransferase A (aadA) and dihydrofolatereductase A (dfrA) that confer resistance to streptomycin and Trimethoprim/sulfamethoxazole, respectively.

Conclusion: The gene cassettes arrays dfrA5, dfrA1 and aadA1 were found in 60% and 58% of isolates in case and control group specimens of E.coli isolates. The presence of these integrons and cassette genes indicates conferring resistance to several classes of antibiotics in E. coli isolates collected in cases of urinary tract infection.

Keywords: Integrons, gene cassette, UTI, E.coli, PCR

P673 - 148: SINGLE-COPY AND MULTIPLE-COPY TARGET GENES FOR DETECTION OF MYCOBACTERIUM TUBERCULOSIS COMPLEX: COMPARISON OF ANALYTICAL AND DIAGNOSTIC SENSITIVITIES OF NESTED PCR

Seyede zohre Mirbagheri¹, Zahra Meshkat², Ehsan Aryan³

1. Mashhad Uni of Med Sci
2. Mashhad Uni of Med Sci
3. Mashhad Uni of Med Sci

Background and Aim: Rapid and efficient detection is one of the most important factors in controlling the spread of tuberculosis. Current common methods for detection of tuberculosis are not easily performed and do not have sufficient sensitivity. In the present study, for the first time, analytical sensitivity and diagnostic sensitivity and specificity of the two target genes IS6110 and mpt64 were evaluated using nested-PCR for detection of Mycobacterium tuberculosis complex.

Methods: In a cross-sectional study, 60 clinical specimens were collected from patients suspicious of having tuberculosis. After digestion and decontamination, microscopic smear and culture tests were employed on the specimens. After final detection, clinical samples were divided into tuberculosis (TB) and non-tuberculosis (Non-TB) groups. Extracted DNA from all samples was tested using nested-PCR for target genes IS6110 and mpt64. Analytical sensitivity of nested-PCR for both target genes was also determined

Results: Diagnostic sensitivity and specificity, PPV and NPV of nested-PCR for mpt64 were 96%, 93%, 93.1% and 96.4%, respectively. Also, those of IS6110 target gene were 89%, 96%, , 96.1% and 90.3%, respectively. Analytical sensitivity of nested PCR for both targets was the same and equal to 1 fg of Mycobacterium tuberculosis genomic DNA per reaction.

Conclusion: In conclusion, it can be inferred from the present study that mpt64 may be a more suitable target for detection of the members of M. tuberculosis complex than IS6110 in regions where the isolates of M. tuberculosis lack the latter target gene.

Keywords: Mycobacterium tuberculosis - nested polymerase-analytical sensitivity -diagnostic sensitivity - diagnostic specificity

**P674 - 192: DISTRIBUTION OF ALKANE HYDROXYLASE GENES INTO CRUDE-OIL
DEGRADING BACTERIAL POPULATION IN PERSIAN GULF**

Ziba Mehdipour¹, Hossinali Sasan², Mehdi Hassanshahian³

1. Department of Biology, Faculty of Sciences, Shahid Bahonar University of Kerman, Kerman, Iran
2. Department of Biology, Faculty of Sciences, Shahid Bahonar University of Kerman, Kerman, Iran
3. Department of Biology, Faculty of Sciences, Shahid Bahonar University of Kerman, Kerman, Iran

Background and Aim:Crude-oil bioremediation is an efficient and economical method for remove of oil pollution in marine environment. Alkane hydroxylase gene divided into two phylogenic groups. Group (II) alkane hydroxylase encode enzyme that degraded medium chain alkanes (C6-C12) and Group (III) alkane hydroxylase gene encode enzyme that degraded long chain alkanes (up to C12).

Methods:DNA was extracted from strains by miniprep method and PCR performed with primers of Group (II) and Group (III) alkane hydroxylase genes.

Results:Fifty crude-oil degrader bacterial strains were isolated. The most strains belong to Pseudomonas, Acinetobacter and Rhodococcus genus. Thirty strains have 330 bp PCR product by amplification with Group (III) primers and fifteen strains have 270 bp PCR product by amplification with Group (II) primers. Five strains haven't any PCR product. Group (III) gene has 60 % frequency and Group (II) has 30 % frequency in Persian Gulf ecosystem. Ten percent of frequency belongs to strains that have Group (II) and Group (III) genes. Group (III) alkane hydroxylase gene encodes enzyme with substrate range up to C12 that this accordance with composition of oil pollutant in Persian Gulf.

Conclusion:These conditions induce select pressure toward prevalence of Group (III) alkane hydroxylase gene. But presence of bacterial with two alkane hydroxylase genes is interest and indicated that bacterial can growth on medium and long chain alkanes. Presence of bacterial without any alkane hydroxylase indicated that these bacteria use other system for biodegradation of petroleum hydrocarbons.

Keywords:Alkane, Enzyme, Crude oil, Gene, Degradation

**P675 - 298: RAPID DETECTION OF ENTEROCOCCUS FAECALIS USING PCR BY
AMPLIFICATION OF EF0737, A NOVEL GENE**

Samira Sabzi¹, Sabzi Samira², Pourmand Mohammad Reza³, Mashhadi Rahil⁴

1. -
2. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences
3. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences
4. Urology Research Center, Tehran University of Medical Sciences

Background and Aim: Enterococcus faecalis can cause a variety of diseases in human especially in immunocompromised patients. The traditional detection of E. faecalis on the basis of phenotypic characteristics is generally not as accurate as identification based on genotypic methods. Therefore, use of molecular methods for detection of E. faecalis has been considered. The purpose of this study was to consider efficacy of ef0737 gene in the detection of E. faecalis isolates.

Methods: In this study, 100 clinical isolates including 50 E. faecalis, 25 E. faecium and 25 Staphylococcus aureus were collected and identified by biochemical methods. A pair of forward primers for the rapid detection of ef0737 were designed and optimized. All of isolates were examined for the presence of ef0737 gene by using polymerase chain reaction.

Results: The PCR assay showed an efficiency of ef0737 for 100% E. faecalis isolates, while none of S. aureus and E. faecium PCR results were positive.

Conclusion: Identification of conserved ef0737 gene in clinical samples may determine infections caused by E. faecalis. Delayed diagnosis of such infection can result in more serious disease caused by E. faecalis.

Keywords: Enterococcus faecalis, pcr, ef0737

**P676 - 308: DEVELOPMENT OF A TAQMAN REAL TIME PCR ASSAY FOR RAPID
DETECTION OF HAEMOPHILUS INFLUENZAE**

Sedigheh Taghinezhad Saroukalaei¹, Keivan Majidzadeh-A², Mohammad Soleimani³, Amir Hossein Mohseni⁴

1. Department of Microbiology, Faculty of Basic Sciences, Science and Research Branch, Islamic Azad University, Tehran, IR Iran
2. Breast Cancer Research Center (BCRC), Iranian Center for Breast Cancer (ICBC), Academic Center for Education, Culture & Research (ACECR), Tehran, IR Iran
3. Tasnim Biotechnology Research Center (TBRC), AJA University of Medical Sciences, Tehran, IR Iran
4. Department of Microbiology, Faculty of Basic Sciences, Science and Research Branch, Islamic Azad University, Tehran, IR Iran

Background and Aim:Haemophilus influenzae type b (Hib) can cause severe disease mainly in children with high morbidity and mortality. Fast early diagnosis of this bacterium is important. We evaluated a highly sensitive and specific assay based on TaqMan real-time PCR to detect Haemophilus influenzae.

Methods:The specific primers based on ompp6 were designed. TaqMan probe was labeled with TAMRA fluorescent reporter dye at the 5' end and BHQ1 as a quencher at the 3' end. The ompp6 PCR product was cloned in the pTZ57R/T plasmid to create a stable positive control plasmid. The TaqMan real-time PCR method was done. The sensitivity and specificity were evaluated. Also, detection range of the assay was determined by generation of standard curves.

Results:In contrast to DNA of H. influenzae, negative control genomes didn't show detectable signal in the assay. The lowest concentration of the pTZ-ompp6 showing fluorescent signal was 0.089fg or 240 copies of the target gene. The depicted standard curve showed R² value, efficiency and slope of 0.997, 95% and -3.43 respectively. Also, the dynamic range of the quantitative TaqMan assay was between 24 and 240 copies of ompp6 gene.

Conclusion:We concluded that this assay is specific, sensitive and really faster than conventional identification method. Therefore this taqman assay provides a potential reliable diagnostic tool for Haemophilus influenza.

Keywords:Haemophilus influenzae, TaqMan real time PCR, ompp6

**P677 - 310: IDENTIFICATION OF MOLLUSCUM CONTAGIOSUM VIRUS (MCV) FROM
VAGINAL SWAB SAMPLES BY USING TAQMAN REAL TIME PCR**

Sedigheh Taghinezhad Saroukalaei¹, Amir Hossein Mohseni², Hossein Keyvani³

1. Department of Microbiology, Faculty of Basic Sciences, Science and Research Branch, Islamic Azad University, Tehran, IR Iran
2. Department of Microbiology, Faculty of Basic Sciences, Science and Research Branch, Islamic Azad University, Tehran, IR Iran
3. School of Medicine, Iran University of Medical Sciences, Tehran, IR Iran

Background and Aim: Molluscum contagiosum virus (MCV) is a causative agent of Molluscum contagiosum infection. Molluscum contagiosum usually attacks children, but is frequently associated with compromised immunity. This infection occurs in epidermis with various tumor-like lesions and is also an increasing problem in sexually active individuals. so many clinicians recommend early diagnosis and treatment of genital molluscum. The aim of this study was to develop a technique for detection of molluscum contagiosum virus.

Methods: Fifty swab samples from Iranian female patients sent to the keyvan virology specialty laboratory to test for the confirmation of the MCV infection. Primers and probe were selected based on the MC021L gene. Taqman Real Time PCR assay was performed for molecular identification of the positive MCV samples.

Results: The existence of amplification signal in the FAM channel represented the specific amplification of MC021L gene. Of the 50 samples, 42 were identified with specific probe corresponding to the Molluscum contagiosum virus. Seven other specimens were positive for Human papillomavirus (HPV). Sequence analysis of the MCV samples by BLAST programs showed a significant homology of positive specimens with the MC021L gene (100%).

Conclusion: The results of the present study showed that Taqman Real Time PCR according to the MC021L gene of the MCV is a rapid, sensitive and specific method for detection of the MCV infection.

Keywords: Molluscum contagiosum, MCV, TaqMan Real Time PCR

**P678 - 331: UNDERSTANDING MOLECULAR IDENTIFICATION AND POLYPHASIC
TAXONOMIC APPROACHES FOR GENETIC RELATEDNESS AND PHYLOGENETIC
RELATIONSHIPS OF MICROORGANISMS**

Alireza Jahani¹, saeed enayatollahi², mehdi dehghani zahedani³

1. Islamic Azad UniversityYazd Branch
2. Islamic Azad UniversityYazd Branch
3. Islamic Azad UniversityYazd Branch

Background and Aim:ABSTRACT The major proportion of earth's biological diversity is inhabited by microorganisms and they play a useful role in diversified environments. However, taxonomy of microorganisms is progressing at a snail's pace, thus less than 1% of the microbial population has been identified so far. The major problem associated with this is due to a lack of uniform, reliable, advanced, and common to all practices for microbial identification and systematic studies. recA gene sequence provides a useful tool for differentiation at interspecies level. recA gene apparently occurs in all bacteria and is responsible for DNA damage repair, induction of SOS repair and homologous DNA recombination. As a part of the SOS response, it coordinates more than 20 genes that are involved in DNA repair, DNA recombination, DNA synthesis and cell division. Many Gram-negative and Gram positive bacteria have been reported to be classified based on the result obtained from the recA gene sequences. have been reported for recA gene sequence based identification procedures. When the amplification of recA gene is combined with restriction fragment length polymorphism methods, it becomes more accessible for identification and typing of any bacterial entity.

Methods:Molecular identification, Gene sequencing, Polyphasic taxonomy

Results:Molecular identification, Gene sequencing, Polyphasic taxonomy

Conclusion:Molecular identification, Gene sequencing, Polyphasic taxonomy

Keywords:Molecular identification, Gene sequencing, Polyphasic taxonomy

**P679 - 332: IDENTIFICATION OF MYCOPLASMA HOMINIS, MYCOPLASMA GENITALIUM
AND UREAPLASMA UREALYTICUM IN PATIENTS WITH URINARY TRACT INFECTION
BY MULTIPLEX PCR**

Hassan Piri¹, Masood Ghane ², Reza Goleyjani moghadam³

1. Department of Biotechnology, Faculty of Science, Damghan Branch, Islamic Azad University, Damghan, Iran
2. Department of Microbiology, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran
3. Department of Microbiology, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran

Background and Aim: Considering role of Mycoplasmas in occurrence of the genital infections, rate of frequency of these organisms based on separation of species of the M.Hominis, M.genitalium and U.urealyticum in appearance of the urinary infections was investigated in this study by the multiplex PCR technique.

Methods: In this study conducted from March 2014 to February, 2015, 120 urine samples were collected from the individuals with genital system infection. Criterion of entrance of the patients into this study was existence of one sign or a few signs related to Urinary Tract infection. After DNA extraction, diagnosis of the bacteria from the patients, urinary samples using PCR multiplex technique was analyzed by use of the specific primers, and the achieved results using the Fischer accurate test were analyzed by SPSS software.

Results: Using PCR multiplex technique, out of 120 tested samples, presence of M.hominis, M.genitalium, U.urealyticum was reported, 12.5%, 3.33% and 6.67 respectively. From viewpoint of the joint contamination with both two bacteria of M.hominis and U.urealyticum, 9 samples (7.5%) were reported positively, and in terms of existence of common contamination with all three bacteria of M.hominis, M.genitalium and U.urealyticum, 1 sample (0.837) was reported positively.

Conclusion: Also, Usage of PCR multiplex method is a valuable and useful technique with a high and reliable sensitivity and accuracy in order to identify contamination of Mycoplasma and Ureaplasma, and these organisms can be followed in the clinical samples by this method simultaneously.

Keywords: Mycoplasma hominis, Mycoplasma genitalium, Ureaplasma urealyticum, Urinary tract infections, Multiplex PCR

**P680 - 334: ANALYSIS OF SALMONELLA ENTERICA BY USING TWO DIFFERENT
METHODS**

Narges Golab¹, Pejvak Khaki², Soheila Moradi Bidhendi³

1. Islamic Azad Uni, Karaj
2. Department of Microbiology, Razi Vaccine & Serum Research Institute, Karaj, Iran
3. Department of Microbiology, Razi Vaccine & Serum Research Institute, Karaj, Iran

Background and Aim: Salmonella species are recognized as agents of illness and disease in both humans and animals with greater than 2000 serotypes recognized; the gastrointestinal tract of animals is considered the primary reservoir of the pathogen with human illness usually linked to exposure to contaminated animal-derived products such as meat or poultry. Therefore, establishing a reliable and powerful method for molecular subtyping of Salmonella is significantly a need for the detection of certain serovars circulating in population. Pulsed-field gel electrophoresis (PFGE) is a golden standard for genotyping of many of bacteria such as salmonella spp.

Methods: All Salmonella human and poultry isolates were obtained from Microbial Culture Collection of Microbiology Department, Razi Vaccine & Serum Research Institute, Karaj, Iran. The isolates were subjected genotyping by PFGE. PFGE data was input into BioNumerics and GelCompare II analysis software to generate two dendrograms of relatedness among the isolates.

Results: In this study, PFGE were used to subtype 48 Salmonella isolates belonging to 27 different serovars. PFGE analysis by GelCompar II softwares identified 39 profiles among the 48 isolates examined. Generally BioNumerics and GelCompar are similar softwares except that GelCompar is limited to the analysis of gel fingerprint data but BioNumerics can analyse phenotypic characters and sequence data as well as gel data. BioNumerics is used by several networks around the globe to share and identify strain information

Conclusion: According to the results, we concluded that Any type of PFGE data that can be analyzed into a dendrogram is considered a fingerprint type in the BioNumerics and GelCompar II software

Keywords: PFGE, salmonella enterica, Bionumeric, GelCompare II

**P681 - 338: DETECTION OF HUMAN PAPILLOMAVIRUS IN CERVICAL SAMPLES AND ITS
ASSOCIATION WITH CERVICAL CANCER**

Seid Shervin Shariat Panahi¹, Seyed Shervin Shariatpanahi², Bahare Tabanifar³, Rasoul Salehi⁴

1. Department of Genetics and Molecular Biology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
2. Department of Genetics and Molecular Biology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
3. Department of Genetics and Molecular Biology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran

Background and Aim: Cervical cancer is one of the most significant reasons of death among women around the world. The role of Human Papillomavirus (HPV) has been demonstrated as a cause of cervical cancer. However the results of different studies are conflicting. The main aim of the current study is to examine the association between this microorganism and cervical neoplasia among women with normal and abnormal cervical cytology from Isfahan, Iran.

Methods:: the number of 73 blocks of formalin fixed, paraffin wax embedded cervical tissues from women with different stage of cervical neoplasia and sixty cervical samples from women with normal cytology were evaluated for having ability of amplification with beta-globin primers. The positive specimens have been tested for the presence of HPV using PCR-based assays. Detection of HPV was carried out by PCR using HPV genome-specific oligonucleotide primers, GP5+/GP6+.

Results: the sixty numbers (82.2%) of blocks and all Pap smear specimens were able to be amplified with beta-globin primers. HPV DNA was detected in 8.3 % , 48.1% and 63.6% of women with normal cytology, Precancerous lesions and invasive cervical cancer (ICC) respectively.

Conclusion: HPV DNA prevalence ascended with increasing severity of the cervical lesions that confirms the role of this virus in the development of cervical neoplasia.

Keywords: HPV, cancer, Cervical neoplasia, PCR

**P682 - 339: INVESTIGATION OF THE ASSOCIATION BETWEEN CHLAMYDIA
TRACHOMATIS INFECTION AND CERVICAL CANCER**

Seid Shervin Shariat Panahi¹, Seyed Shervin Shariatpanahi², Bahare Tabanifar³, Rasoul Salehi⁴

1. Department of Genetics and Molecular Biology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
2. Department of Genetics and Molecular Biology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
3. Department of Genetics and Molecular Biology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran

Background and Aim: Cervical cancer is one of the paramount reasons of mortality among women around the world including Iran. Some epidemiologic studies suggest that Chlamydia trachomatis (Ct) has been implicated as a risk factor in cervical carcinogenesis. However the results of different studies are contradictory. The main aim of the current study is to compare the prevalence of C. trachomatis in cervical samples between women with normal and abnormal cervical cytology and investigating the association between this microorganism and cervical neoplasia.

Methods: the number of 73 blocks of paraffin wax-embedded cervical tissues from women with different stage of cervical neoplasia and sixty cervical samples from women with normal cytology were evaluated for having ability of amplification with beta-globin primers. The positive specimens have been tested for the presence of C. trachomatis DNA using PCR-based assays. Detection of C. trachomatis was carried out by PCR using Chlamydia genome-specific oligonucleotide primers, KL1/KL2.

Results: the sixty numbers (82.2%) of blocks and all Pap smear specimens were able to be amplified with beta-globin primers. 1.7% of normal individuals and 13.3% of cases were affected with C. trachomatis. Out of total number of cases, 22.2% at precancerous lesions and 6.1% at ICC infected with C. trachomatis.

Conclusion: C. trachomatis prevalence was higher in precancerous lesions than cancerous lesions and it showed a significantly higher prevalence as compared to normal cytology samples. C. trachomatis DNA positivity appeared to impose the risk of precancerous lesions independently without considering the presence of HPV genome. It can be concluded that C. trachomatis act as risk factor in earlier steps of cervical disease.

Keywords: cancer, Chlamydia trachomatis, Cervical neoplasia, PCR

**P683 - 343: MOLECULAR STUDY OF THE P40 GENE OF MYCOPLASMA AGALACTIAE
ISOLATES FROM 13 PROVINCES OF IRAN**

Maedeh Babazadeh¹, seyed Ali Pourbakhsh²

1. Poultry disease Research Department, Razi Vaccine and Serum Research Institute, Karaj, Alborz, Iran
2. Poultry disease Research Department, Razi Vaccine and Serum Research Institute, Karaj, Alborz, Iran

Background and Aim: Mycoplasma agalactiae is one of the etiological agents of contagious agalactiae (C.A). The gene encoding P40 is specific for M. agalactiae and has not been found in other Mycoplasma species. P40 is a membrane protein that involved in the adhesion of M. agalactiae in lamb synovial membrane cells. In this study we attempted to molecular monitoring of P40 gene, finding genetic variation and selecting the best vaccine candidate in Iranian isolates of M. agalactiae.

Methods: A total of 125 samples were collected. All samples were cultured in PPLO broth and The bacteria DNAs were extracted. M-PCR and MA-PCR performed for detecting of genus and species of Mycoplasma agalactiae based on 16SrRNA and P80 genes respectively. P40- PCR method was used for amplification of 920bp fragment of P40 gene. Nucleotide sequencing was done by Sanger method

Results: Out of the 125 samples, 38 cultures were shown positive. 94 were scored positive by M- PCR and 17 of the samples were scored positive by using M.A-PCR and P40 gene was amplified in all of them. The nucleotide sequences were alignmented, results showed the most important differences between our samples and the vaccinal sample that used in Iran. Furthermore, an Iranian vaccine isolate and the samples from France, Spain and Ivory coast were in the close branches of phylogenetic tree.

Conclusion: The result showed that the P40 detected in M. agalactiae isolated from Iran as a specific gene and also we evaluated the genomic diversity in the P40 gene of Iranian M. agalactiae isolates.

Keywords: Mycoplasma agalactiae, p40 protein, PCR

P684 - 360: MOLECULAR DETECTION OF FUNGI IN SYNOVIAL FLUID BY PCR METHOD

Azam Batoei¹, Mohammad Hassan Shahhosseiny², Mahsa Malekmohammadi Kalahroudi³

1. Iranian Gene Fanavar Institute (IGF), Tehran/Iran
2. Department of Microbiology- Shahr-e-Qods Branch-Islamic Azad University-Tehran/Iran. Iranian Gene Fanavar Institute (IGF), Tehran/Iran
3. Iranian Gene Fanavar Institute (IGF), Tehran/Iran

Background and Aim: Arthritis may have multiple causes, one of the factors it can sometimes be some fungi. Most fungal skin tissue, subcutaneous and rarely internal organs, bones and joints involves. Given the prevalence of arthritis and fungal possibility of some common arthritis and synovial fluid cultures may be negative, PCR method is used when a fast and accurate method for the detection of fungi. The aim of this study is rapid diagnosis of fungi in synovial fluid by PCR method.

Methods: 50 synovial fluid samples collected from Shariati Hospital Division of Rheumatology, and DNA was extracted by standard methods of phenol / chloroform. PCR test optimized, the limit of detection (LOD) and specificity were examined. Amplicon cloned by T/A Cloning method and all samples were tested by PCR optimization test

Results: in this study PCR test optimized and 430 bp products amplified and observed in agarose gel. In specificity test, primers only were positive by positive control DNA and other microorganisms were negative. High LOD test was approved. 7 samples (%14) were positive of 50 samples tested.

Conclusion: In this study, 14% of the samples were positive which shows the important role of fungi in the development of infectious arthritis. Consequently, the PCR technique is accurate, rapid and sensitive for identifying of fungi

Keywords: PCR, Arthritis, Detection, Fungi, synovial fluid

P685 - 386: DIAGNOSIS OF CANDIDA ALBICANS SINUSITIS BY PCR

Fatemeh Fardi¹, Mohammad hassan shahhosseiny², Tahereh naji³

1. Department of Molecular and Cellular sciences, Faculty of Advance Science & Technology Pharmaceutical Sciences Branch , Islamic Azad University , Tehran, Iran(IAUPS).
2. Department of Microbiology- Shahr-e-Qods Branch-Islamic Azad University-Tehran/Iran. Iranian Gene Fanavar Institute (IGF), Tehran/Iran
3. Department of Molecular and Cellular sciences, Faculty of Advance Science & Technology Pharmaceutical Sciences Branch , Islamic Azad University , Tehran, Iran(IAUPS).

Background and Aim: Various species of Candida, among Candida albicans is human optional symbioses that human Life is founding always in the environment and where host resistance to infection is reduced by local or systemic disease. Sinusitis is one of the most common problems that every year was spent a huge budget on diagnosis and treatment of this problem The aim of this study is investigate and diagnosis of candida albicans in sinusitis by PCR molecular method.

Methods: 50 samples were collected from patients suspected sinusitis in the operating room, and DNA of samples was extracted by DNG Plus. PCR test was optimized by using of ALPHA INT1 GENE target primers and were examined by On-Line way attributed to Candida albicans organisms DNA, in terms of specificity and limit of detection (LOD). Amplicon was cloned by T/A cloning method in pTZ57R plasmid for positive control.

Results: In this study PCR test was optimized and 441 bp amplicon was amplified by using of Candida albicans specific primers. Amplicon cloned and plasmid was extracted and was confirmed by PCR. In specificity test, primers were formed band only by Candida albicans DNA and weren't observed band by any other microorganism DNA. LOD test was obtained 100 copy/reaction. After PCR test on samples, from 50 samples of patients suspected sinusitis 2 were candida albicans positive.

Conclusion: The Results of this study show that the percentage of Sinusitis samples may be have other factors such as Candida albicans PCR is accurate, rapid method for detection of this fungal.

Keywords: Candida albicans, PCR, sinusitis, diagnosis.

P686 - 387: MOLECULAR DETECTION OF MYCOPLASMA SPP. IN SERUM OF MULTIPLE SCLEROSIS (MS) PATIENTS

Ghasempur Kobra¹, Kobra Ghasempur², Mohammad Hassan Shahhosseiny³, Ali Mohammad Asgharian⁴

1. -
2. Department of Molecular Cell Biology- Tonekabon Branch-Islamic Azad University-Mazandaran/Iran
3. Department of Microbiology- Shahr-e-Qods Branch-Islamic Azad University-Tehran/Iran. Iranian Gene Fanavar Institute (IGF), Tehran/Iran
4. Department of Molecular Cell Biology- Tonekabon Branch-Islamic Azad University-Mazandaran/Iran

Background and Aim: Multiple Sclerosis is complex disease which is still secret as an agent. Factors such as microorganisms are studied as candidates. In this respect, may be relationship between bacteria of Mycoplasma Spp and MS disease. Purpose of this study, rapid detection of Mycoplasma Spp. in serum of Multiple sclerosis (MS) patients in comparison with healthy controls by PCR molecular method.

Methods: 50 samples from healthy people and 50 samples were collected from Serum of MS patients. DNA was extracted by DNG PLUS method. PCR test optimized by using of specific primers and limit of detection (LOD) and specificity were examined.

Results: in this study PCR test optimized and amplicon was amplified by using of specific primers of Mycoplasma Spp. In specificity test, primers were positive only by Mycoplasma Spp DNA and no band observed with other microorganisms DNA. LOD of test were determined 100 copy/reaction. From 50 samples of patients only 1 sample was observed with Mycoplasma Spp.

Conclusion: results indicate that low percentage (2%) of MS patients were positive in Comparison of healthy controls by sensitive and rapid PCR method in Mycoplasma Spp. This results were not statistically significant, but the importance of further study is warranted.

Keywords: PCR, Mycoplasma SPP, samples of multiple sclerosis , diagnosis

P687 - 445: MOLECULAR TYPING OF METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS ISOLATES BASED ON COAGULASE GENE BY PCR-RFLP

Elahe Soltani Fard¹, Mohammad Roayaei Ardakani², Hossein Motamedi³

1. Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Iran
2. Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Iran
3. Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Iran

Background and Aim: Increased frequency of methicillin-resistant *Staphylococcus aureus* (MRSA) in hospitalized patients requires rapid and reliable characterization of isolates for its control. The aim of this study was to determine the genotypic characteristics of MRSA isolates based on PCR-RFLP of coagulase gene typing.

Methods: A total of 100 isolates of *S. aureus* were collected from clinical specimens in two hospital in Ahvaz (Golestan and Razi hospitals). The primary diagnosis of isolates was done based on biochemical tests. MRSA isolates were determined according to the presence of *mecA* gene, using specific primers. The *coa* gene of MRSA strains was amplified and then these strains were analyzed using PCR-RFLP of this gene by *AluI* restriction enzyme.

Results: Finally, 50 isolates were identified as MRSA. The amplification of the *coa* gene of MRSA strains generated 8 different genotypes (I-VIII) based on different size of polymorphism ranging from 450-900bp. PCR-RFLP of *coa* gene exhibited 13 patterns which were obtained following digestion with *AluI*. The number of fragments varied between 1-4 with 80 to 900 bp length. Type III was the most common and accounted for 44% of the isolates.

Conclusion: PCR-RFLP analysis of *coa* gene with good discriminatory power, reproducibility and easy interpretation can be considered as a promising alternative for the epidemiological typing of *S. aureus* isolates. The relationship between different isolates of this agent can be determined through genotyping and according to this we be able to plan for the prevention procedures to control the spread of *S. aureus* infection.

Keywords: *Staphylococcus aureus*, coagulase gene, PCR-RFLP.

P688 - 462: WOLBACHIA ENDOBACTERIA IN NATURAL POPULATION OF PAEDERUS FUSCIPES: THE AGENT OF HUMAN DERMATITIS

Niloofer Akhavan¹, Naseh Maleki-Ravasan², Navid Dinparast Djadid³, Fahimeh Nemati Mansoor⁴

1. Department of Biotechnology , Faculty of Advanced Science & Technology , Pharmaceutical Science Branch , Islamic Azad University , Tehran-Iran
2. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran (PII), Tehran, Iran
3. Malaria and Vector Research Group (MVRG) Biotechnology Research Center (BRC) Pasteur Institute of Iran Tehran, Iran
4. Department of Biotechnology , Faculty of Advanced Science & Technology , Pharmaceutical Science Branch , Islamic Azad University , Tehran-Iran

Background and Aim: Rove beetles of the *Paederus fuscipes* (Coleoptera: Staphylinidae) cause linear dermatitis when they meet human. Also they act as scavengers and predators in the natural ecosystems. Wolbachia endobacteria are discovered in arthropods and nematodes where alter the host biology in various modes. The reciprocal interaction between Wolbachia and *Paederus* has not investigated yet to determine winner-loser partner. Herein we aimed at to screen Wolbachia infection rates in *P.fuscipes*.

Methods: The presence and frequency of Wolbachia in rove beetle populations in two Northern provinces of Iran (Gilan and Mazandaran) was surveyed using a nested PCR assay targeted wsp gene.

Results: A total of 124 rove beetles were hunted primarily from rice fields and identified as *P.fuscipes* relying on molecular and morphological methods. The wsp gene survey of *P.fuscipes* indicated that 48 out of 73 (65.75%) in males and 42 out of 51 (82.35%) in females were positive for Wolbachia. Infection rate in females was $\approx 17\%$ higher than in males and the overall prevalence were 74% in both sexes.

Conclusion: Wolbachia are versatile bacteria that can transmit via vertical or horizontal modes. They infect at least 20–76% of all insects. The infection rate in current study was lower than mosquito's infection rate (90-100%) where Wolbachia induce feminization, parthenogenesis, male killing and cytoplasmic incompatibility in this group. The first step in understanding the potential role of Wolbachia in the *Paederus* biology is determining their prevalence. We took the first step in this essay but supplementary investigations are required to discover Wolbachia cost-benefits to the *Paederus*.

Keywords: Wolbachia, *Paederus fuscipes*, Nested-PCR, Iran

P689 - 477: MOLECULAR IDENTIFICATION OF A GDSL FAMILY OF LIPASE-ENCODING GENES IN NATIVE LACTIC ACID BACTERIA ISOLATED FROM IRANIAN DAIRY PRODUCTS

Samira Pirmanesh¹, Rooha Kasra Kermanshahi², Sara Gharavi³, Elahe Mobarak Ghamsari⁴

1. Department of Biotechnology, Faculty of Biological Sciences , Alzahra University, Tehran, Iran
2. Department of Microbiology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
3. Department of Biotechnology, Faculty of Biological Sciences , Alzahra University, Tehran, Iran
4. Department of Microbiology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran

Background and Aim: GDSL esterases/lipases are a newly discovered subclass of lipolytic enzymes that are attractive research subjects because of their multifunctional properties, such as broad substrate specificity and regiospecificity. Unlike other lipases, GDSL hydrolases have a flexible active site and change conformation in the presence of different substrates; hence, some GDSL enzymes have broadly diverse enzymatic activities, including esterase and protease activity in the same enzyme. The purpose of this study was the identification of a GDSL family of lipase-encoding genes in native lactic acid bacteria isolated from yogurt and cheese. Four isolates were identified as *Lactobacillus fermentum*.

Methods: Based on previous research conducted, all four isolates were considered as lipase positive. A pair of primers was designed to cover the coding region of GDSL lipase genes using the sequences from *L. fermentum* deposited in NCBI gene bank. Genomic DNA from lipolytic isolates was first screened using a pair of internal detection primers. Positive isolates in this step were further examined using a pair of outer primers. One of the PCR products sequenced using outer primers was aligned with sequences in NCBI databank.

Results: The identified gene was 918 base pairs in length and encoded a peptide of 305 amino acids with calculated molecular mass of 34342.1 Da, and theoretical pI 9.66. The results show that the target sequence belongs to GDSL lipase gene family in *L. fermentum*.

Conclusion: The 3-D structure and biochemical functions (structure-function relationships) of the enzyme is still unknown and require further investigation therefore Molecular detection is the first step to recognition more.

Keywords: GDSL, Lipase, LAB, *L. fermentum*

P690 - 482: THE USEFULNESS OF HYPERVARIABLE REGIONS OF 16S RRNA GENE FOR IDENTIFICATION OF BACTERIAL MICROFLORA OF LUCILIA SERICATA

Zahra Soroushadeh¹, Naseh Maleki-Ravasan², Abbasali Raz³, fahimeh nemati mansor⁴

1. Department of biotechnology, Faculty of Advanced Sciences & Technology , Pharmaceutical Sciences Branch, Islamic Azad University ,Tehran – Iran (IAUPS)
2. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran (PII), Tehran, Iran
3. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran (PII), Tehran, Iran
4. Department of biotechnology, Faculty of Advanced Sciences & Technology , Pharmaceutical Sciences Branch, Islamic Azad University ,Tehran – Iran (IAUPS)

Background and Aim:16S-rRNA gene of bacteria includes nine “hypervariable regions” (V1–V9) that their species-specific sequences have distinct value for scientific investigations. Due to relative advantage of each region it is necessary to evaluate their usefulness in different types of bacteria. Herein the utility of V1-V9 were examined for identification of bacterial microflora of *Lucilia sericata* medicinal maggots.

Methods:The 16S-rRNA gene sequences of 12 species of bacteria previously identified from *L.sericata*, was retrieved from ATCC type strain depository. These bacteria belonged to the enterobacteria, CFB-group bacteria and firmicutes. The boundary of V1-V9 was determined for all species and corresponding sequences were subjected to alignment and phylogenetic tree construction using bioinformatics softwares. The comparison of dendrograms was done visually.

Results:The sequence analyses of considered bacteria were revealed that V7 could provide more accurate identification than V3 and V1 respectively. V7 was the best differentiated among closely related bacteria species such as *Proteus* group. The V3 and V5 regions were most suitable for distinguishing the gram stain classification of the bacteria. V1, V2, V4, V6 and V9 were less useful targets for genus or species-specific differentiations. In combined system, V1-V3 region gave more accuracy than V3-V5 in separation of groups.

Conclusion:Determinations of hypervariable sequence-specific regions will provide useful tools to design primers and specific probes which decrease time and cost for the detection and study of bacteria. Although a larger sample size produces a smaller margin of error but current brief survey will be an initial step for evaluation of larger groups of bacteria.

Keywords:16S-rRNA gene, hypervariable regions, diagnosis, bacteria

P691 - 517: MOLECULAR TYPING OF ESCHERICHIA COLI ISOLATES FROM URINARY TRACT INFECTIONS BY USING ENTEROBACTERIAL REPETITIVE INTERGENIC CONSENSUS (ERIC-PCR) IN MASHHAD

Mehrnaz Rad¹, Gholam Reza Hashemi Tabar ², Zakieyh Iman panah³

1. Ferdowsi University, Faculty of Veterinary Medicine, Professor of Microbiology, Department of Pathobiology
2. Ferdowsi University, Faculty of Veterinary Medicine, Biotechnology PhD, Professor, Department of Pathobiology
3. Ferdowsi University, Faculty of Veterinary Medicine, postgraduate student Bacteriology

Background and Aim: Escherichia coli is one of the causative agents of urinary tract infections (UTIs) in humans. The aim of this study was to assess genotyping of Escherichia coli isolates from urinary tract infections by using enterobacterial repetitive intergenic consensus (ERIC-PCR) in Mashhad.

Methods: A total of 69 isolates of E. coli were isolated from urine samples of non-hospitalized patients with urinary tract infections referred to the diagnostic laboratory in Mashhad. Escherichia coli isolates were confirmed by standard microbiology methods. Genetic diversity of isolates was examined using ERIC-PCR. The products of proliferation were electrophoresed on 1.5% agarose gel, and their dendrograms were drawn. The data were analyzed by SPSS software.

Results: The method used in this study proliferated numerous bands (1-9 bands) ranging from 100 to 1700 base pairs. All E. coli strains were typable by this method and classified into 13 clusters.

Conclusion: The results of study revealed that 69 E. coli isolates were genetically diverse and comprise a heterogeneous population. We found the ERIC-PCR as a useful method for molecular typing of uropathogenic E. coli.

Keywords: Molecular typing, Escherichia coli, ERIC-PCR

**P692 - 532: BIOINFORMATICS ANALYSIS OF SORTASES OF CLOSTRIDIUM
PERFRINGENS PUTATIVE**

Seyed Mehdi Qafari¹, Gholamreza Ahmadian², Mehdi Mohammadi³, Nasim Rezaeinezhad⁴

1. National Institute of Genetic Engineering and Biotechnology Shahrak-e Pajooresh, km 15, Tehran - Karaj Highway, Tehran, Iran
2. National Institute of Genetic Engineering and Biotechnology Shahrak-e Pajooresh, km 15, Tehran - Karaj Highway, Tehran, Iran
3. National Institute of Genetic Engineering and Biotechnology Shahrak-e Pajooresh, km 15, Tehran - Karaj Highway, Tehran, Iran
4. National Institute of Genetic Engineering and Biotechnology Shahrak-e Pajooresh, km 15, Tehran - Karaj Highway, Tehran, Iran

Background and Aim:: Sortase is known as a transpeptidase enzyme which is produced by some gram positive bacteria like *Clostridium perfringens*. Sortase has the ability of conjugating the surface proteins to the bacterial cell walls. This enzyme is classified into 6 different classes (i.e. A, B, C, D, E and F) based on their substrate. It has been shown that *Clostridium perfringens* has 2 gene loci for coding sortase. In present study, these two sortases were classified using bioinformatics tools.

Methods: Conserve domain search and MEGA software were used for bioinformatics analysis.

Results: Analyses showed that one of these sortases has the ability to recognize LPXTG, then it could be classified at class A. Second sortase has a domain belongs to sortase family domain, but the motif or motifs that could be recognized by this sortase could not be identified.

Conclusion: we can conclude first gene loci classified in sortase Family group A and second gene loci can not be classified and need more information.

Keywords: Sortase, classification, Sortase family

P693 - 548: RAPID DETECTION OF STAPHYLOCOCCUS AUREUS BY PCR IN SYNOVIAL FLUID OF PATIENTS WITH ARTHRITIS

Zahra Gomarian¹, Mohammad hassan shahhosseiny², Mahsa Malekmohammadi Kalahrودي³

1. Iranian Gene Fanavar Institute (IGF), Tehran/Iran
2. Department of Microbiology- Shahr-e-Qods Branch-Islamic Azad University-Tehran/Iran. Iranian Gene Fanavar Institute (IGF), Tehran/Iran
3. Iranian Gene Fanavar Institute (IGF), Tehran/Iran

Background and Aim: Arthritis or joint inflammation is not a specific disease but to set more than one hundred disease, all of them characterized by inflammation of the joints. Septic arthritis is a common cause of joint destruction which caused pyogenic micro-organisms. Staphylococcus aureus is the most common bacterial cause of the disease. Detection of septic arthritis is very important. The aim of this study was to investigate the presence of Staphylococcus aureus in the joint fluid of patients with arthritis through PCR as a rapid test.

Methods: This study was done on 60 patients with arthritis synovial fluid and referred to Shariati Hospital in Tehran. DNA of samples were extracted with phenol-chloroform and PCR testing was performed with a NUC target gene. The limit of detection (LOD) and specificity of this test was performed

Results: PCR product of 279 bp was observed in agarose gelelectrophoresis. The specificity test with genome of different organisms resulted only with the genome of Staphylococcus aureus. LOD of test was calculated 100 copy/reaction. From total of 60 synovial fluid samples, 11 samples (33/18%) were infected with Staphylococcus aureus

Conclusion: Septic arthritis is the most common and most important infectious arthritis. Rapid diagnosis resulted to start of therapy. Culture is a slow and time consuming method for detection of agents. Antibiotic consumption before of culture and multiple factors involving of accurate detection of agents in synovial fluids. As a result, PCR is a rapid and sensitive method for detection of microorganisms responsible for patients with arthritis.

Keywords: synovial fluid, Staphylococcus aureus, Detection, PCR

**P694 - 551: COMPARISON OF 16SRRNA TARGET GENE PRIMERS IN DETECTION OF
MYCOPLASMA SPP**

Naeimeh Farhoudinasab¹, Mohammad Hassan Shahhosseiny², Zeinab Khazaei Koohpar³

1. Department of Biology, Tonekabon Branch, Islamic Azad University, Tonekabon, IR Iran
2. Department of Microbiology- Shahr-e-Qods Branch-Islamic Azad University-Tehran/Iran.Iranian Gene Fanavar Institute (IGF), Tehran/Iran
3. Department of Biology, Tonekabon Branch, Islamic Azad University, Tonekabon, IR Iran

Background and Aim: Mycoplasmas are a kind of bacteria which pass through the bacteriological filter and contamination. These unique organisms in nature produce disease in a wide range of animals, including humans. Cell line and biological products contamination is one of major problems in producing these products, so a safe method to distinguish the Mycoplasma genus in production centers is required. The aim of this research is to evaluate and compare 16srRNA target gene primers in Mycoplasma spp diagnosis.

Methods: In this research, 50 cultures suspected to Mycoplasma spp which had been separated from biologic products were collected from Razi institute of IRAN, and then DNA samples were extracted by DNG plus method. Two PCR tests were checked and they were optimized according to 16SrRNA, and limit of detection (LOD) and specificity of the both tests were reviewed.

Results: Both PCR tests were optimized and amplicones of 715 and 272 bp, propagated and were observed in agarose gels. In checking primers features the intended bands were formed only by DNA of Mycoplasmas spp. The LOD of both tests were approximately equal. Among 50 sample of tested, 42 positive with 715 bp product and 36 positive with 272bp product

Conclusion: Due to the time consuming and costly in other ways, rapid method such as PCR can have a significant impact on the early detection of Mycoplasma genus precise.

Keywords: Mycoplasma spp, 16SrRNA, PCR, Detection

**P695 - 556: DETECTION OF MYCOPLASMA PNEUMONIAE IN BRONCHOALVEOLAR
LAVAGE (BAL) SUSPECTED WITH TUBERCULOSIS**

MAHNAZ AMERI¹, Mohammad hassan shahhosseiny², Tahereh naji³

1. cell and molecular Department, pharmaceutical sciences Branch, Islamic azad university, Tehran,Iran
2. Department of Microbiology- Shahr-e-Qods Branch-Islamic Azad University-Tehran/Iran. Iranian Gene Fanavar Institute (IGF), Tehran/Iran
3. cell and molecular Department, pharmaceutical sciences Branch, Islamic azad university, Tehran,Iran

Background and Aim: Mycoplasma are breeders some diseases in humans and animals. Mycoplasma pneumoniae is responsible for 10-20% of pneumonia and respiratory infections in humans. Common methods of detection of M. pneumoniae has limitations, therefore is required to apply rigorous methods. This study aimed to investigate the molecular and rapid diagnosis of Mycoplasma pneumoniae by using of designed specific primers in P1 adhesin gene by PCR in BAL samples that was performed as negative for tuberculosis (TB)

Methods: In this study, 50 BAL of suspected in TB, were collected for tuberculosis. Then, their DNA was extracted by DNG Plus. PCR test was optimized by using of P1 adhesin target gene primers and DNA standard strains. Specificity test was examined by using of online and offline ways and DNA attributed to Mycoplasma pneumoniae organisms. Finally, limit of detection (LOD) was evaluated; amplicon was cloned by T/A cloning in PTZ57R plasmid for sequencing and create a positive control

Results: PCR test optimized and 345 bp amplicon observed in agarose gel by specific primers. Amplicon cloned, plasmid extract and was confirmed by PCR. In specificity test primers were positive only by Mycoplasma pneumoniae DNA. LOD obtained 100 copy/reaction of genome. 4 samples (8%) were positive for Mycoplasma pneumoniae from 50 suspected cases of tuberculosis.

Conclusion: Specifically, some with suspected tuberculosis and negative samples containing the pathogen, Mycoplasma pneumoniae infection was using. This result confirms the role of bacteria and attention to the breath samples, such as samples suspected to be tuberculosis.

Keywords: PCR, BAL, Mycoplasma pneumoniae, Detection.

**P696 - 569: ASSOCIATION OF CHLAMYDIA TRACHOMATIS CT681 AND CT135 GENES, IN
INFERTILITY INDUCTION IN INFERTILE PATIENTS OF TEHRAN CITY**

Akram Sabouri¹, Dr. Ali-Reza Ahmadi², Dr. Said Jalil Hosainil³

1. Department of Biology, Faculty of Science, Payam Noor University Tehran Shargh Center
2. Department of Biomedical Sciences, Alzahra University, Tehran, Iran
3. Department of Urology, Shahid Beheshti University of Medical Sciences. Tehran, Iran

Background and Aim: Infertility is the most important and influence disease in human society. It influences 60 -80 million couples in all over the world; annually and its increasing. Injury to men and women's fertile system is reason for infertility; is due to urinary tract infection and sexually transmitted diseases. Chlamydia's infections influence on infertility's treatment and since this infection in men and women is very important; survey for Chlamydia's infections is the first step in infertility's treatment. The aim of present research was to evaluate prevalence of, of Chlamydia trachomatis CT681 and CT135 Genes, in infertility induction in Tehran city.

Methods: Screening and genotyping of genital Chlamydia trachomatis in urine specimens from 55 infertile patients (25 men and 30 women) have been done. Then DNA was extracted and purified using a DNA Extraction Kit (Cinnagen, Tehran, Iran) from 55 urine samples and amplified by PCR. The nucleotide sequences were analyzed using the BLAST program (<http://www.ncbi.nlm.gov/BLAST>).

Results: The molecular investigation of samples showed that %45 of cases was Chlamydia trachomatis infection positive. Out of them, %35 of samples was determined CT681, %65 CT135.

Conclusion: This study can be considered a contribution in increasing knowledge on C. trachomatis genotype distribution and sequence variations within each genotype in Tehran city. Further studies are need to better find molecular epidemiology of C. trachomatis strains and to investigate its genotype variations in Iran.

Keywords: Molecular Diagnosis, Chlamydia trachomatis, Urinary Genital Tract Infection, Infertility Induction.

P697 - 576: HIGH FREQUENCY OF BIOFILM RELATED GENES AND PREDOMINANCE OF AGR TYPE III AMONG STAPHYLOCOCCUS AUREUS ISOLATED FROM BOVINE WITH SUBCLINICAL MASTITIS IN YASUJ, IRAN

Seyed Sajjad Khoramrooz¹, Fariba Mansouri², Masoud Marashifard³, Seyed Ali Asghar Malek Hosseini⁴, Fereshteh Akbarian Chenarestane-Olia⁵, Banafsheh Ganavehei⁶, Farzaneh Gharibpour⁷

1. Medicinal Plants Research Center, Yasuj University of Medical Sciences, Yasuj, Iran
2. Department of Basic Sciences, Islamic Azad University, Yasooj Branch, Yasooj, Iran
3. Student Research Committee, Yasuj University of Medical Sciences, Yasuj, Iran
4. Student Research Committee, Yasuj University of Medical Sciences, Yasuj, Iran
5. Department of Basic Sciences, Islamic Azad University, Yasooj Branch, Yasooj, Iran
6. Department of Basic Sciences, Islamic Azad University, Yasooj Branch, Yasooj, Iran
7. School of veterinary Medicine, Shiraz University, Shiraz, Iran

Background and Aim: Staphylococcus aureus by producing biofilm and facilitating chronic infection is a common cause of mastitis in cows and thereby can cause food poisoning by production of enterotoxins in milk. The agr typing method is an important tool for epidemiological investigation about S. aureus. The aims of the present study were to detect biofilm related genes, 5 classical enterotoxin genes and the agr types among S. aureus isolates.

Methods: The ability of S. aureus isolates to produce biofilm was evaluated by modified CRA plate. Six biofilm related adhesion genes (icaD, icaA, fnbA, bap, clfA and cna), five classical enterotoxin genes (sea, seb, sec, sed and see) and tst-1 gene were detected by PCR methods. Multiplex-PCR was used to determination of the agr groups.

Results: 55 out of 80 (68.8%) S. aureus isolates were biofilm producer. The icaD gene was detected in 70 (87.5%) of isolates. The prevalence rates of fnbA, icaA, clfA, cna and bap were 72.5, 56.25, 50, 22.5, and 5% respectively. The agr group I and III were detected in 57.5% 25% of studied isolates. The sea, sed and tst-1 genes were found in 10%, 7.5% and 1.25% of isolates respectively.

Conclusion: The majority of S. aureus were able to produce biofilm. Significant associations were observed between presence of the icaD, icaA, fnbA, clfA and the cna genes as well as biofilm formation. The present study revealed that isolates with the agr type III are more potent for biofilm production. Our data supported a possible link between the agr types and certain SE genes.

Keywords: Staphylococcus aureus; Mastitis; Biofilm; enterotoxin genes; agr typing

P698 - 593: PHYLOGENETIC STUDY OF E.COLI IN COW MEAT

Azadeh Alivandi¹, Afshin Javadi²

1. M.Sc Student of Microbiology, Cellular and Molecular Biology Department, Institute of Rabe-Rashidieh, Tabriz, Iran.
2. Associate Professor of Food Hygiene, Bio-technology Research Center, Tabriz Branch, Islamic Azad University, Tabriz, Iran.

Background and Aim: Escherichia Coli is a Bacterial index of water and food contamination, and its presence in drinking water and food show that this materials are infected by other intestinal pathogens. Due to the meat importance and determine the source of meat contamination, this study was aimed for isolation, identification and enumeration of E.Coli in Cow meat and on the other hand, to recognized the phylogenetic groups of E.Coli.

Methods: In this study 30 meat samples was prepared from Tabriz slaughter house. According to the Iranian national standard, MPN 3 tubes possible counting method and biochemical and microbial tests were used for determine identity of the isolated bacteria. Classification of Phylogenetic groups of E.Coli Isolates were done, by using Multiplex-PCR technique of two genes (chuA,yjaA) and one DNA segment (TspE4.C2).

Results: From 22(73%) detected Isolates of E.Coli, the most common identified groups were classified as B2(86.36%), A(13.63%) and D(5%). However none of the mentioned Isolates have belonged to the B1 group.

Conclusion: Overall the results show that the most of Cow meat contamination is belong to B2 phylogenetic group. This reflects that at the time of slaughter, Health standards were not considered, so the possibility of human contamination is obvious. Therefore this technique can helps us to learn more about pathogenesis and control of meat products in the manufacturing and regulatory organizations.

Keywords: Escherichia Coli, Phylogenetic, Cow meat

P699 - 605: HETEROGENEITY OF ESCHERICHIA COLI ISOLATES WITHIN DIFFERENT AGE GROUPS OF PATIENTS WITH URINARY TRACT INFECTIONS IN MASHHAD

Mehrnaz rad ¹, Gholam Reza Hashemi tabar ², Zakieyh Iman panah³

1. Ferdowsi University, Faculty of Veterinary Medicine, Professor of Microbiology, Department of Pathobiology
2. Ferdowsi University, Faculty of Veterinary Medicine, Biotechnology PhD, Professor, Department of Pathobiology
3. Ferdowsi University, Faculty of Veterinary Medicine, postgraduate student Bacteriology

Background and Aim: Escherichia coli is recognized as one of the most important bacterial pathogens of urinary tract infections (UTIs) affecting both male and female individuals with different age. The aim of this study was to assess genetic diversity of Escherichia coli isolates from urinary tract infections in different age groups of patients by enterobacterial repetitive intergenic consensus (ERIC-PCR) technique.

Methods: A total of 70 E. coli isolates from urine samples were obtained from hospitalized patients who were diagnosed with urinary tract infection in Ghaem hospital in Mashhad. Urinary E. coli isolates from woman aged and from man aged were confirmed by standard microbiology methods. Genetic diversity of isolates in different age groups were evaluated by using ERIC-PCR analysis.

Results: The ERIC-PCR profiles allowed typing of all 70 isolates which were grouped into 11 clusters based on different banding pattern ranging, numerous bands (1-8 bands) ranging from 100 to 2700 base pairs. 8 cluster was the most common cluster (32.86%). In 8 cluster, women different aged (73.91%) and man different aged (26.09%).

Conclusion: Our results showed high genetic diversity of isolates between and within different age groups of patients.

Keywords: Heterogeneity, Escherichia coli, ERIC-PCR

**P700 - 623: EVALUATE AND COMPARE TECHNIQUES OF DIAGNOSIS HELICOBACTER
PYLORI AND INTRODUCT SUITABLE METHODS THAT HAVE RESULTS OF FAST AND
ACCURATE LABORATORY**

Ezzat Nourizadeh¹, Zargar,S.J², Riazi-Rad, Farhad³, Ali Nagafi Dastenaee⁴, Ahmad Shirkhani⁵

1. Faculty of Biology, College of Science, University of Mohaghegh Ardabili , Ardabil, Iran
2. Faculty of Biology, College of Science, University of Tehran, Tehran, Iran
3. Department of Immunology, Pasteur Institute of Iran, Tehran, Iran
4. Department of Immunology, Pasteur Institute of Iran, Tehran, Iran
5. Department of Immunology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim:Background:Over 80% of individuals infected with the *Helicobacter pylori*(Hp) are asymptomatic, and it may play an important role in the natural stomach ecology. More than 50% of the world's population harbor Hp in their upper gastrointestinal tract. Due to the this important aforesaid items, rapid detection of Hp organisms is very important, that should be the appropriate method to search. The purpose of this investigation study of new applied solutions in the diagnosis producing agent of Hp and introduct suitable methods that have results of fast and accurate laboratory.

Methods:Methods: In this field study of the results of national and international conferences and congresses have been used more widely . This investigate, a new diagnostic methods were developed for the identification of Hp which is based on the Application of specific monoclonal antibodies (mAbs) for characterization,Immunoperoxidase tests , indirect immunofluorescent assay, detection of bacteria antigens Hp by , mAb-piezoelectric-based immunosensor, detection of biopsy ,that include of quick urease and culture REP - PCR.

Results:Results : Among the methods studied, mAb-piezoelectric-based immunosensor method(ISM) as an appropriate way better ,Is recommended for the diagnosis of Hp disease .

Conclusion:Discussion : The benefit of using mAb-piezoelectric-based ISM as follows ; high sensitivity,specificity, low cost, and easy portability, based on the detection of bacteria products, may constitute an important achievement to improve the clinical management of suspected Hp cases.

Keywords:Keywords: Evaluate and compare methods , diagnosis *Helicobacter pylori* , introduct suitable methods

**P701 - 627: UNCONCEIVABLE PREVALENCE OF TOXIN ANTI –TOXIN SYSTEMS IN
ACINETOBACTER BAUMANNII**

Ali Hematian¹, sobhan ghafourian², Iraj pakzad³

1. Department of Micobiology/school of medicine, Ilam University of Medical Sciences, Ilam, Iran
2. Department of Micobiology/school of medicine, Ilam University of Medical Sciences, Ilam, Iran
3. Department of Micobiology/school of medicine, Ilam University of Medical Sciences, Ilam, Iran

Background and Aim:In fact, nowadays, modern microbiology suggested that because of, toxin antitoxin (TA) systems have a curial role in antibiotic resistance and pathogenesis, so, the prevalence of these systems in nosocomial bacteria is notable

Methods: Firstly, a total of 80 *Acinetobacter baumannii* clinical isolates were obtained from Tehran hospitals as standard sampling protocol. Secondly, the samples were transported to clinical microbiology research center for future analysis. To identify *mazEF* and *higBA* TA loci, DNA were subjected for Polymerase Chain Reaction (PCR) by specific primers. Data were analyzed using spss version 16 by both descriptive and analytical statistics(X² test were subjected).

Results:Embraced findings in the current study make a disappointment about highlighting database of the *mazEF* and *higBA* TA systems; while we expected the same results but our results only demonstrated 62.5% (n=50) and 37.5% (n=30) for *mazEF* and *higBA* TA loci, respectively. The results of our study that were 62.5% (n=50) and 37.5% (n=30) for *mazEF* and *higBA* TA loci, slightly stopped the others for next evaluation of these two TA loci.

Conclusion:Debatably, previous fortunate *mazEF* and *higBA* TA loci and recent unfortunate *mazEF* and *higBA* TA targets demonstrated that we should revise our knowledge about TA systems. Our past and recent analysis emphasis that TA loci seriously should be under snow with more sample collection in various area to resolve the first part of drug discovery.

Keywords:*mazEF* and *higBA*; *Acinetobacter baumannii*;Toxin antitoxin system

**P702 - 658: MLVA MOLECULAR TYPING OF HAEMOPHILUS INFLUENZAE ISOLATED
FROM TWO IRANIAN UNIVERSITY HOSPITALS**

Faranak Nejati¹, Faranak Nedjati², Seyed Davar Siadat³, Farzam Vaziri⁴, Seyed Ali Nojoumi⁵, Fatemeh Sakhaie⁶

1. Department of Biology, Islamic Azad university of Damghan, Semnan, Iran
2. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
3. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
4. Microbiology Research Center, Pasteur Institute of Iran, Tehran, Iran
5. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Different serotypes of *Haemophilus influenzae*, are now divided into two divisions of encapsulated and unencapsulated. Multiple locus variable number tandem repeat analysis (MLVA) containing specifications including extra power of separation, ease of data interpretation, and epidemiological data accordance have made it an appropriate molecular device for good typing and phylogenetic analysis for bacterial pathogens.

Methods: In this research, the study of cultured samples and recognition of strains identified through biochemical tests was carried out, followed by the extraction of DNA and quantitative and qualitative study of the extracted DNA. The design of four pairs of specialized primer related to *H. influenzae* variable number tandem repeat (VNTR) and preparation of PCR according to its regulated program and also electrophoresis of PCR products were performed. Finally, the interpretation of electrophoresis gel in respect to the observable bands showing the presence or absence of the required sequences in the samples related to every primer was carried out.

Results: In this study, among 30 mentioned strains for which MLVA profile is obtained in this research, 25 different MLVA types were observed. Likewise, there was no repetition in VNTR sequences resulting from PCR in few *H. influenzae*. The highest diversity of repeats was for VNTR5 (7types), then VNTR6 with 6 types of repeats followed by VNTR12-1 and VNTR12-2 with three different types.

Conclusion: Based on this observation, the use of MLVA method considering its high resolving power in molecular typing can be a better choice in comparison to similar methods, it's an economical method as well.

Keywords: *Haemophilus influenzae*, MLVA, VNTR

**P703 - 680: CORRELATION BETWEEN HELICOBACTER PYLORI AND MBL RS1800450
POLYMORPHISM IN COLORECTAL CANCER**

Somaye Ajdamfekar¹, Hossein Rassi², Taher Mohammadian³

1. Department of Biology , Karaj Islamic Azad University
2. Department of Biology , Karaj Islamic Azad University
3. Department of Biology , Shahre Qods Islamic Azad University

Background and Aim:Colorectal cancer (CRC) is one of the most common malignancies worldwide and genetic and environmental factors are important in the incidence and mortality rates of CRC in Iran that have increased in recent years. here it is investigated the prevalence rate of H. pylori infection and the MBL rs1800450 polymorphism in CRC.

Methods:In this retrospective study, 30 patients with CRC and 30 healthy controls were studied. Also, age and histopathologic parameters were performed in all patients. The DNA from archival samples was analysed by PCR for detection of H pylori . The MBL rs1800450 polymorphism was detected by PCR-RFLP.

Results:MBL2 gene encodes the mannose-binding lectin, which is a key player in the innate immune system , H. pylori infection and development of CRC.

Conclusion:our results demonstrated that the testing of H. pylori and MBL rs1800450 polymorphism in combination with clinical parameters can serve as risk factors in the early detection of CRC.

Keywords:Helicobacter pylori , MBL rs1800450 polymorphism , Colorectal cancer

P704 - 687: PREVALENCE OF EXFOLIATIVE TOXIN A GENE AND ANTIMICROBIAL RESISTANCE PATTERNS IN STAPHYLOCOCCUS AUREUS STRAINS ISOLATED FROM PATIENTS AND HEALTHY INDIVIDUALS IN NORTHERN IRAN

Pegah Abbasi¹, Ali Mojtahedi², Nour Amirmozafari³

1. Microbiology Department, Faculty of Basic Science, Lahijan Branch, Islamic Azad University, Guilan, Lahijan, Iran
2. Assistant Professor, Microbiology Department, Faculty of Medicine, Guilan University of Medical Sciences Rasht, Iran
3. Professor, Microbiology Department, Faculty of Medicine, Iran University of Medical Sciences, Tehran, Iran

Background and Aim: The exfoliative toxins are among the most common virulence determinants of *Staphylococcus aureus*. This study aimed to survey the distribution of eta gene among *S. aureus* strains isolated from hospitalized patients and healthy individuals and their antibiotic resistance patterns in northern Iran.

Methods: During 2014 – 2015, a total of 126 strains of *S. aureus* (63 strains from clinical samples and 63 isolates from healthy individuals) were collected. Antibigram was performed and methicillin resistant strains (MRSA) were detected using oxacillin disk. Moreover, eta gene was detected by PCR reaction.

Results: All clinical isolates were resistant to ampicillin. Vancomycin was the most effective antibiotic against *S. aureus* (1.6%) followed by norfloxacin and nitrofurantoin (11.1%). Also, all isolates from healthy individuals were resistant to ampicillin and penicillin and resistance to other antibiotics was lower than 10%. The prevalence rate of MRSA strains were 34.9% and 3.2% among patients and healthy individuals respectively. The prevalence of eta gene among *S. aureus* strains isolated from patients and healthy individuals was 34.9% and 28.6% respectively. The presence of eta gene had no effect on antibiotic resistance

Conclusion: The prevalence of eta gene in this study was higher than most other studied regions. Interestingly, there was no significant difference in prevalence of eta gene among strains isolated from patients and healthy people. It could be related to variety of a geographical and health conditions. Resistance rate of isolates from patients was significantly higher than those isolated from healthy individuals.

Keywords: *Staphylococcus aureus*, Exfoliative toxins, eta, Antibigram, PCR

**P705 - 720: TOXINOTYPING OF CLOSTRIDIUM PERFRINGENS ISOLATED FROM
HEALTHY BROILERS AND BROILERS WITH MILD NECROTIC ENTERITIS IN EAST
NORKH OF IRAN**

Mohammad Yousefi¹

1. Department of poultry Diseases, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran

Background and Aim: Clostridium perfringens is a Gram-positive, anaerobic rod and spore forming pathogene, causing necrotic enteritis. (NE) disease in poultry. NE in poultry is associated with subpopulation of C. perfringens type A and rarely type C with numerous toxins and bacteriocins like netB, Tpel and perfrin

Methods: In this study we characterized toxin profile of Twenty strains isolated from six broiler flocks (10 isolates from suspected NE outbreak and 10 isolates from healthy flocks) using Multiplex and single PCR assays

Results: The results showed that all isolates from healthy (n=10) and NE (n=10) chickens were positive only for cpα, representing type A and were negative for netB, Tpel and perfrin.

Conclusion: Our results suggest that type A is the most prevalent type in east north of Iran. It seems that further investigations are required to determine the role of toxins and risk factors in development of NE.

Keywords: Clostridium perfringens, netB, Tpel, perfrin.

**P706 - 746: INVESTIGATION OF CHLAMYDIA TRACHOMATIS IN PATIENTS REFERRED
TO URMIA SHAHID MOTAHHARI HOSPITAL BY PCR**

Mohamadreza Mahzounieh¹, Azam Mokhtar², Amir Ebrahimzadeh³

1. Department of Pathobiology, Faculty of Veterinary Medicine, Shahrekord University.
2. Department of Pathobiology, Faculty of Veterinary Medicine, Shahrekord University.
3. Faculty of Veterinary Medicine, Shahrekord University

Background and Aim:: Chlamydia trachomatis is an obligate intracellular gram-negative bacteria and Chlamydia infection is a sexually transmitted diseases. Chlamydia trachomatis is prevalent worldwide and infects both sexes; however, its high prevalence among sexually active young women and adults has been reported. Several methods for detecting Chlamydia trachomatis include polymerase chain reaction or PCR and ELISA. PCR has been more interested by the researchers because of its very high sensitivity and specificity. The objective of this study was to determine the prevalence of Chlamydia trachomatis in urine samples taken from outpatient patients referred to Urmia Shahid Motahhari hospital

Methods:For this purpose, 71 urine samples from 24 men and 47 women were prepared and tested by PCR method for detection of Chlamydia trachomatis.

Results:: of these samples, 5/63% was positive for Chlamydia trachomatis. Of 24 men's samples, one case was positive (4/16%) and of 47 women's samples 3 cases (6/38%) was positive for Chlamydia trachomatis.

Conclusion:in this study, the samples were taken from people with no clinical symptoms. People who have less hygiene and having high-risk sexual activities are the main carriers of chlamydia in the community. The presence of Chlamydia trachomatis in the studied samples emphasizes that this microorganism can be considered as a potential health threat in a society.

Keywords:Chlamydia trachomatis,sexually transmitted diseases,PCR.

**P707 - 795: BIOINFORMATIC AND IN-VITRO CHARACTERIZATION OF SCAF AS A
NOVEL GENE FOR IDENTIFICATION OF STAPHYLOCOCCUS AUREUS ISOLATES**

Elaheh Salimi¹, Mohammad Reza Pourmand^{1,2}, Jalil Fallah Mehrabadi³, Azar Hadadi⁴, Rahil Mashhadi⁵

1. Urology Research Center, Tehran University of Medical Sciences, Tehran, Iran
2. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
3. Department of Bioscience and Biotechnology, Malekashtar University of Technology, Tehran, Iran
4. Department of Infectious Diseases, Sina Hospital, Tehran University of Medical Sciences, Tehran, Iran
5. Urology Research Center, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: Rapid detection of *Staphylococcus aureus* in clinical specimens is essential to minimize the transfer and spread of this pathogen. An appropriate method for rapid and suitable detection of *S. aureus* is detection of one of its genes. The aim of this study was to identify the *S. aureus* using *scaF* gene.

Methods: The study was conducted on 45 isolates of *S. aureus* separated from clinical specimens of patients who referred to hospitals affiliated with Tehran University of Medical Sciences in 2013. At first, *scaF* gene was analyzed by bioinformatic tools. *S. aureus* isolates were confirmed using biochemical and diagnostic tests. Following DNA extraction, *scaF* gene was amplified by polymerase chain reaction using gene-specific primers. The results of PCR were examined by gel electrophoresis.

Results: The *scaF* gene was present in all studied isolates. Bioinformatics evaluation revealed that this gene encodes a protein with a molecular weight of 33kDa and contains 297 amino acids with a PI value of 6.3.

Conclusion: The *scaF* gene belongs to Staphylococcal conserved antigen family which is conserved in *S. aureus* strains recorded in JCVI database. Furthermore, due to lack of the same gene in *Staphylococcus epidermidis* and other species, it could be used for detection of *S. aureus* infections.

Keywords: *Staphylococcus aureus*, polymerase chain reaction, detection, *scaF*

**P708 - 822: MOLECULAR INVESTIGATION OF MBL RS1800450 POLYMORPHISM AND
HELICOBACTER PYLORI IN TYPE II DIABETES**

Behnaz Eslami¹, Hossein Rassi², Taher Mohammadian³

1. Department of Biology , Karaj Islamic Azad University
2. Department of Biology , Karaj Islamic Azad University
3. Department of Biology , Shahre Qods Islamic Azad University

Background and Aim: Helicobacter pylori (H. pylori) infection has been associated with increased levels of inflammatory cytokines and subsequent insulin resistance and epidemiologically linked to type 2 diabetes. This disease causes an estimated 3.8 million adult deaths globally. In other sides, MBL2 gene encodes the mannose-binding lectin, which is a key player in the innate immune system and has recently been found to play a role in insulin resistance and development of diabetes. here it is investigated the prevalence rate of H. pylori infection and the role of MBL2 in type II diabetes susceptibility.

Methods: In this cross-sectional case-control study, 174 patients with type II diabetes and 185 healthy controls were studied. Also, demographics, physical and biochemical parameters were performed in all patients. The DNA from blood specimens was analysed by H pylori specific and cagA specific polymerase chain reaction (PCR). The MBL rs1800450 polymorphism was detected by PCR-RFLP.

Results: The results show that H. pylori positivity was detected in 42.82% of the diabetic patients and in 22.16% of the control group and H. pylori infection was closely correlated with MBL rs1800450 (Gly54Asp) when compared with healthy controls.

Conclusion: The MBL rs1800450 BB genotypes was significantly related to infection with the H pylori cagA subtype in Iranian patients with type II diabetes.

Keywords: MBL rs1800450 polymorphism , Helicobacter pylori , type II diabetes

**P709 - 823: MOLECULAR INVESTIGATION OF COMMON TNF A -308 G /A
POLYMORPHISM AND HELICOBACTER PYLORI IN TYPE II DIABETES**

Parisa Aghahosseini¹, Hossein Rassi², Taher Mohammadian³

1. Department of Biology , Karaj Islamic Azad University
2. Department of Biology , Karaj Islamic Azad University
3. Department of Biology , Shahre Qods Islamic Azad University

Background and Aim: Helicobacter pylori (H. pylori) infection has been associated with increased levels of inflammatory cytokines and subsequent insulin resistance and epidemiologically linked to type 2 diabetes.

Methods: Here it is investigate the prevalence rate of H. pylori infection in type 2 diabetes and its relation with TNF α -308 G /A polymorphism. In this cross-sectional case-control study, 154 patients with type II diabetes and 160 healthy controls were studied. Also, demographics, physical and biochemical parameters were performed in all patients. The DNA from blood specimens was analysed by H pylori specific and cagA specific polymerase chain reaction (PCR). The TNF α polymorphism at positions -308 was detected by ARMS PCR.

Results: The results show that H. pylori positivity was detected in 46.10% of the diabetic patients and in 23.75% of the control group and H. pylori infection was closely correlated with G to A transition at position -308 of the TNF α promoter when compared with healthy controls.

Conclusion: Furthermore, TNF α -308 polymorphism in patients with H pylori was significantly different from that in patients without H pylori, the -308A polymorphism was strongly associated with H pylori cagA subtype infection when compared with the polymorphism in cagA negative H pylori infection.

Keywords: TNF α -308 G /A polymorphism , Helicobacter pylori , type II diabetes

**P710 - 825: PREVALENCE OF HUMAN PAPILLOMAVIRUS GENOTYPES ASSOCIATED
WITH CERVICAL CANCERS AND ITS RELATION WITH TNF A -308 G /A
POLYMORPHISM IN IRAN**

Azar Gharonpor¹, Hossein Rassi², Behzad Hemati³

1. Department of Biology , Karaj Islamic Azad University
2. Department of Biology , Karaj Islamic Azad University
3. Department of Biology , Karaj Islamic Azad University

Background and Aim: Cervical cancer is a multi-step disease, and infection with a DNA virus could play a role in one or more of the steps in this pathogenic process. High-risk human papillomaviruses (HPV) are the causative agent of cervical cancers. In this study, we determined the prevalence and genotype distribution of HPV infection and its relation with TNF α -308 G /A polymorphism among Iranian patients with cervical cancer.

Methods: The study group consisted of 58 samples from patients diagnosed with cervical cancer. Verification of each cancer reported in a relative was sought through the pathology reports of the hospital records. The DNA from blood specimens was analysed by multiplex HPV specific polymerase chain reaction (PCR). The TNF α polymorphism at positions -308 was detected by ARMS PCR.

Results: Overall prevalence of HPV infection was 4.53 % in the SM group, 58.33% in the CIN,I-II group, 66.66% in the CIN,III group, 80% in the CC group. Furthermore, the predominant genotype detected in all cancers was the oncogenic variant HPV16/18. In addition, frequency of TNF α -308 GG genotypes among cancer groups with HPV infection was 53.33%.

Conclusion: Our results demonstrate that infection with HPV was prevalent among Iranian women with cervical cancer and the testing of TNF α -238 GG genotype and HPV genotyping in combination with clinical parameters can serve as major risk factors in early detection of cervical cancer.

Keywords: Human Papillomavirus Genotypes , Cervical Cancers , TNF α -308 G /A polymorphism

**P711 - 892: IDENTIFICATION OF THERMOPHILIC STRAINS NATIVE TO MOLECULAR
METHODS TO IDENTIFY DNA POLYMERASE GENE CODER**

Zahra Emami¹, Zahra²

1. Emami

Background and Aim: Identification of strains of thermophilic DNA polymerase enzyme in order to use them

Methods: Strains were cultured in temperature conditions of 55 ° C and then incubated in medium 42 hours TBS.. then go through the procedure set buffer for extraction DNA and then using the primer 42F and R 1496, and then product sent to sequencing

Results: After investigation it was found in the NCBI database GHM15 strain strain *Geobacillus* sp. GAM23 with access code JX262995.1 and GHM4 strain *Geobacillus* sp. TP-1 with access code JQ319387 more closely

Conclusion: DNA polymerase is the key enzyme in all living organisms and is responsible for DNA replication in them. In addition to the main role of DNA polymerase in living organisms, they are widely used for in vitro DNA manipulation. was discovered. That some of them have reached the stage of commercial production, due to the presence of hot springs in Iran And the presence of thermophilic microorganisms in them, could be the potential for identification of appropriate used.

Keywords: dna polymerase, thermophil strain

**P712 - 893: THE MULTI LOCUS SEQUENCE TYPING (MLST) OF PASTEURELLA
MULTOCIDA, A TECHNICAL APPROACH**

SAHAR ABBASI¹, KEYVAN TADAYON², RAINAK GHADERI³, MOHAMMAD SEKHAVATI⁴,
MEHDI SHARIARI NOUR⁵, MASOUMEH ANVARI⁶, MAHIA IRANSHAHI⁷, ALIREZA
SANCHOU⁸, ALIREZA ARAB⁹, JAMILEH NASERI HAVIZAVI¹⁰

1. Islamic Azad University of Rasht, Science & Research Branch of Guilan, Rasht, Iran
2. Razi Vaccine Serum Research Institute
3. Razi Vaccine Serum Research Institute
4. Razi Vaccine AND Serum Research Institute
5. Islamic Azad University of Rasht, Science & Research Branch of Guilan, Rasht, Iran
6. Islamic Azad University of Rasht, Science & Research Branch of Guilan, Rasht, Iran
7. Islamic Azad University of Rasht, Science & Research Branch of Guilan, Rasht, Iran
8. Razi Vaccine AND Serum Research Institute
9. Razi Vaccine AND Serum Research Institute
10. Islamic Azad University of Karaj, Karaj, Iran

Background and Aim:Currently, there are two *Pasteurella multocida* MLST schemes including the British Multiple host MLST that holds isolates from variety of animal hosts, including cattle, sheep, pigs and birds. This database is more concentrated on evolutionary relationships between the isolates. The second database is Australian and was developed by the Rural Industries Research and Development Corporation so-called RIRDC MLST with an initial focus on avian isolates and epidemiological theme. Both systems assay polymorphism in limited stretches of 7 housekeeping genes among which four are shared by both. The fact that there is no previous MLST experience on *P. multocida* in Iran, a principle scope of the present work was establishment of the technique.

Methods:Using the Primer 3 program, seven new primer pairs recommended by RIRDC MLST were designed against the genome of *P. multocida* P70 reference strain. This was performed in a way that 7 PCR products matching with the corresponding target sections of the of *adk*, *est*, *gdh*, *mdh*, *pgi*, *pmi* and *zwf* genes were all within the range of 500-700 bp.

Results:Amplification protocols were optimized and set as a single identical protocol could be used for all the 7 loci. Feasibility of these modifications was successfully tested against a single field isolate and two vaccinal strains of *P. multocida*.

Conclusion:Our observations proved suitability of the employed modifications that can be easily used in any MLST work on *P. multocida*.

Keywords:*Pasteurella multocida*, MLST, housekeeping genes

**P713 - 909: ISOLATION AND MOLECULAR IDENTIFICATION (SEROTYPING) NEISSERIA
SPECIES ISOLATED FROM CHILDREN UNDER 5 YEARS**

Mehrad Vosough¹, Seyed Davar Siadat², Bagher Yakhchali³, Seyed Fazlollah Mousavi⁴

1. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
2. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
3. Department of Industrial and Environmental Biotechnology, National Institute of Genetic Engineering and Biotechnology, Tehran, Iran
4. Department of Bacteriology and Microbiology Research Center, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: *Neisseria meningitidis* (*N. meningitidis*) is a pathogen which colonizes in the nasopharynx without any clinical manifestations. Among the 13 different serological groups, only the serogroups A, B, C, W135, Y, X play a major role in disease development. This study aimed to determine *N. meningitidis* cases carrying these serological groups using the multiplex PCR method in the nasopharynx of the healthy children under five years old age

Methods: In current study, 450 nasopharyngeal samples isolated from healthy children under 5 years old in children's care center in Tehran during 2015-2016. In the next step they were cultured on modified Thayer martin agar. Identification was performed by biochemical tests such as oxidase, catalase, CTA. And also was confirmed by molecular methods and then the serological groups were determined using the multiplex PCR method

Results: The results illustrate that 137 cases (30.44%) were the carrier of *Neisseria* spp (42.1% girls and 57.9% boys). 4 cases (2.9%) of them were positive for *N. meningitidis* (25% girls and 75% boys) and 133 cases (97.1%) of them were *Neisseria* spp. In addition, the highest rate of carriers (75%) was in the 3 to 4 year age group. In this study, only the serological groups A (1 cases) and B (3 cases) were detected

Conclusion: The identification and detection of serotypes which are presented in Iran will enable us to estimate the magnitude of the meningitis problem in our country and would make it possible to set up the appropriate treatment measures and apply specific vaccines in our population

Keywords: *Neisseria*, nasopharynx, multiplex PCR

**P714 - 923: THE RECA INTERACTION WITH COMPETITIVE MODULATORS DINI AND
RECX**

Sareh Mohammadi¹, Razieh Pourahmad²

1. MSc student in Genetics at university of shahrekord
2. Associate Professor of Genetics at university of shahrekord and corresponding author

Background and Aim: RecA has a key role in maintaining the integrity of the bacterial genome. It is crucial for DNA repair via homologous recombination and induction of the SOS response in bacteria. The RecA protein of E.coli contains 352 amino acid and consists of a large core domain and a smaller C-terminal domain. Both DinI and RecX proteins of Escherichia coli modulate the function of RecA protein, but have very different effects. DinI protein stabilizes RecA filaments and prevents disassembly. The RecX protein inhibits RecA filament extension, leading to net filament disassembly. The two proteins act as competitive modulators of RecA performance. The aim of this study was to investigate RecA interaction with DinI and RecX competing modulators.

Methods: For this purpose, the NCBI site and PubMed were used.

Results: The results showed DinI binds to the active RecA filament in two distinct structural modes. Removal of the C-terminal 17 amino acid residues of RecA strongly enhances the interaction between the two proteins and also significantly alters the ability of RecX to inhibit the strand exchange reaction and DNA-dependent ATPase activity.

Conclusion: Thus, it can be stated that C-terminal of RecA Plays a significant role in the interaction with moderators.

Keywords: RecA protein , Escherichia coli, DinI , RecX

P715 - 951: DETERMINATION OF THE PREVALENCE OF THE GENES ENCODING OUTER MEMBRANE SIDEROPHORE RECEPTORS IN UROPATHOGENIC ESCHERICHIA COLI ISOLATED FROM URINARY TRACT INFECTIONS AS NEW VACCINE CANDIDATES

Mohammad Reza Asadi Karam¹, Mehri Habibi², Saeid Bouzari³

1. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
2. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
3. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran; saeidbouzari@yahoo.com

Background and Aim: Uropathogenic *Escherichia coli* (UPEC) cause the majority of urinary tract infections (UTIs). The prevalence of antimicrobial resistance in patients with UTI is increasing, making treatment of these infections ever more complicated and costly. To date, there is no ideal vaccine against UTI and there is a need to test other target antigens to develop an ideal vaccine against UTI. Siderophore receptors play an important role in pathogenicity of ascending UTIs by UPEC. In this study, we evaluated the presence of six siderophore receptor genes in Iranian UPEC isolates, in order to examine them as new vaccine candidates against UTI caused by UPEC.

Methods: One hundred UPEC clinical isolates were investigated in this study. In addition, 30 *E. coli* isolates collected from feces of healthy humans were used as control. Bacterial identification was performed by microbial and biochemical tests. Genomic DNA from the samples was extracted using the Phenol& Chloroform method and PCR amplification of six siderophore receptor genes was performed by specific primers.

Results: Among the 100 UPEC isolates, 30%, 94%, 57%, 87%, 75% and 6.7% and from 30 commensal *E. coli*, 5%, 5%, 15%, 30%, 30% and 0% isolates presented *iroN*, *fyuA*, *hma*, *chuA*, *iutA*, and *ireA* genes, respectively.

Conclusion: Prevalence of the siderophore receptor genes in UPEC isolates was more than those belonging to flora groups. Thus, we concluded that siderophore receptors might be ideal vaccine candidates for the prevention of UTI in human. Evaluation of the efficacy of the receptors as vaccine candidates is under study.

Keywords: Urinary tract infection, Uropathogenic *E. coli*, Virulence factors, Siderophore receptors, Vaccine candidate

**P716 - 981: MULTIPLEX PCR ASSAY TARGETING THE MECA AND SPA GENE FOR RAPID
DETECTION OF METHICILLIN RESISTANCE STAPHYLOCOCCUS AUREUS**

Sara Kashani¹, ramin abiri², amirhoshang alvandi³

1. presenter
2. Corresponding
3. Corresponding

Background and Aim: Over the last decades, methicillin-resistant *Staphylococcus aureus* (MRSA) have emerged as a significant pathogen in community and hospital environments and is associated with high mortality. The aim of this study was to develop a detection assay for staphylococcal *mecA* and *spa* by using multiplex PCR method

Methods: Analytical Sensitivity and specificity of a newly developed multiplex PCR were assayed for the detection of methicillin resistant *Staphylococcus aureus*. A serial dilution of extracted DNA from different isolates of methicillin-resistance and methicillin-sensitive *Staphylococcus aureus* were subjected to assessment by multiplex PCR

Results: The analytical sensitivity of the multiplex PCR for *mecA* was 1fg/ml DNA (2DNA copies) and *spa* was 0.01pg/ml (4DNA copies) respectively.

Conclusion: According to our results, sensitivity and specificity of multiplex PCR comparing to culture were 100%, 100%, respectively. In this study Multiplex PCR assay is suitable for the rapid detection of *mecA* and *spa* gene *staphylococcus aureus*.

Keywords: MRSA, Multiplex PCR, *mecA*, *spa*

**P717 - 1017: IDENTIFICATION AND ASSESS THE GENETIC DIVERSITY OF
AGROBACTERIUM STRAINS ISOLATED FROM DIFFERENT HOST PLANTS IN WEST
AZARBAYJAN**

Jino Karimi¹, Nabi Khehrinejad², Abdorahman Khalki³, Ramin Mohamadi⁴, Hojat Hatami⁵

1. Department of Plant Protection, college of Agriculture, Mahabad branch, Islamic Azad University, Mahabad, Iran
2. Department of Plant Protection, college of Agriculture, Mahabad branch, Islamic Azad University, Mahabad, Iran
3. Department of Plant Protection, college of Agriculture, Mahabad branch, Islamic Azad University, Mahabad, Iran
4. Department of Plant Protection, college of Agriculture, Mahabad branch, Islamic Azad University, Mahabad, Iran
5. Department of Plant Protection, college of Agriculture, Mahabad branch, Islamic Azad University, Mahabad, Iran

Background and Aim: *Agrobacterium tumefaciens* causes crown gall disease in a wide range of plants by transferring the transferred DNA (T-DNA) from its large tumor-inducing (Ti) plasmid to the nuclear genome of the host plants. To identification and assess the genetic diversity of bacteria inciting tumors on crowns and stems of various host species, 30 strains were isolated from galls on cherry, plum and grapevine in West Azarbaijan province in 2015.

Methods: The heterogeneity of the strains was assessed by comparing their morphological, biochemical and physiological characteristics and ERIC-PCR fingerprints. Comparison of the phenotypic characteristics and ERIC-PCR generated fingerprints with those of the reference strains led to the identification of *Agrobacterium* species inciting tumors on each plant host sampled and presence of the heterogeneity among strains of each species. In pathogenicity tests, tomato seedling were inoculated with all strains and tumors started to appear two weeks after inoculation.

Results: All strains produced a 224bp fragment of *virD2* gene in PCR reactions using *VirD2A/VirD2C* primer pair. Strains isolated from galls formed on apple, plum and cherry stems and crowns were identified as *A. tumefaciens* but were differentiable by their unique and their levels of similarity, 62% , 57% and 55% respectively, with the fingerprinting of the reference strain.

Conclusion: Strains isolated from galls on crown and vines of grapevine also heterogenic consisting of a major group with subgroups clustered at 65% similarity level with the type strain of the *A. vitis*. The strains of group B had 48% similarity to the type strain of *A. tumefaciens*.

Keywords: crown gall, bacterial disease, fruit trees, phenotypic and genotypic identification

**P718 - 1019: MOLECULAR SURVEY OF THE FREQUENCY OF PVL, SEA AND SEB GENES
IN STAPHYLOCOCCUS AUREUS ISOLATED FROM SKIN INFECTIONS IN RAZI
HOSPITAL OF TEHRAN.**

Katayoon Abolghasemi¹, Nasser Harzandi², Mehroz Dezfolian³

1. Departeman of Microbiology, Karaj Branch, Islamic Azad University, Alborz, Iran
2. Departeman of Microbiology, Karaj Branch, Islamic Azad University, Alborz, Iran
3. Departeman of Microbiology, Karaj Branch, Islamic Azad University, Alborz, Iran

Background and Aim: Staphylococcus aureus is one of the most common pathogens of wide range of nosocomial and community acquired infections and diseases such as skin and soft tissue infections, respiratory tract infections, endocarditis and urinary tract infections. The bacterium has different virulence factors and provides aggressive conditions to the host with secretion of toxins such as Superantigen enterotoxins. A and B enterotoxins (SEA, SEB) have the most pathogenicity effect among these toxins. Pantone Valentin Leukocidin (PVL) is important virulence factors that causes white blood cells destruction, necrosis and accelerated apoptosis. The aim of this study was to determine the frequency of (pvl, sea and seb) in Staphylococcus aureus isolated from skin infections

Methods: A total of 65 isolates of Staphylococcus aureus from skin samples were confirmed with phenotypic methods. Then the frequency of the sea, seb and pvl genes were detected with PCR using specific primers

Results: The PCR results showed that 84.61 % of Staphylococcus aureus isolates carry the sea gene and the frequency of seb and pvl genes in the tested isolates were 13.84 % and 64.61% respectively.

Conclusion: According to the importance of Staphylococcus aureus enterotoxins and also PVL and their role in the development and exacerbation of the staphylococcal diseases, the presence and expression of the corresponding genes in clinical isolates must be considered in management of the diseases.

Keywords: Staphylococcus aureus, PVL, enterotoxins

**P719 - 1077: DETECTION OF PAP, AFA AND FIM GENES IN UROPATHOGENIC
ESCHERICHIA COLI ISOLATES FROM PATIENTS WITH URINARY TRACT INFECTION
IN SHAHREKORD**

Zahra Kherghepoush¹, Ali Davarzani², Sara Barati³

1. Student of veterinary medicine, Islamic Azad University of Garmsar, Garmsar, Iran
2. Student of veterinary medicine, Islamic Azad University of Garmsar, Garmsar, Iran
3. Department of bacteriology, Member of young researcher club, Ahvaz, Iran

Background and Aim: Urinary tract infections (UTIs) are common bacterial infections associated with considerable morbidity and health care cost. Uropathogenic *Escherichia coli* (UPEC) with its virulence factors is the most prevalent cause of urinary tract infection (UTI). This study aimed to determine the occurrence of fim, pap, afa genes among 122 UPEC isolates collected from patients diagnosed with UTI in shahrekord.

Methods: A total of 122 UPEC isolates were collected from urine samples of patients with UTI. The prevalence of virulence genes encoding type 1 fimbriae (fimH), pili associated with pyelonephritis (pap) and afimbrial adhesins (afa) were determined by PCR method.

Results: The prevalence of genes encoding for fimbrial adhesive was 82% for fim, 41% for pap. The operons encoding for afa afimbrial adhesins were identified in 15% of isolates. Conversely, significant differences were observed in relation to pap and afa operons.

Conclusion: These results indicate that the PCR method is a powerful genotypic assay for the detection of adhesin-encoding operons. This method can be recommended for clinical use or epidemiological studies.

Keywords: Uropathogenic *Escherichia coli*; Urinary Tract Infections; Adhesion Proteins-Encoding Operons

**P720 - 1080: DEVELOPING MLVA TECHNIQUE AS A COMPROMISED APPROACH
TOWARD MOLECULAR CHARACTERIZATION OF PASTEURELLA MULTOCIDA**

Jamileh Naseri Hovizavi¹, Rainak Ghaderi², Keyvan Tadayon³, Ahmadreza Jabbari⁴, Gholamreza Shokri⁵,
Majid Valadan⁶, Mohammad Sekhavati⁷, Reza Banihashemi⁸, Alireza Arab⁹, Alireza Sanchouli¹⁰

1. Islamic Azad University of Karaj
2. Razi Vaccine & Serum Res Institute, Karaj
3. Razi Vaccine & Serum Res Institute, Karaj
4. Razi Vaccine & Serum Res Institute, Karaj
5. Razi Vaccine & Serum Res Institute, Karaj
6. Razi Vaccine & Serum Res Institute, Karaj
7. Razi Vaccine & Serum Res Institute, Karaj
8. Razi Vaccine & Serum Res Institute, Karaj
9. Razi Vaccine & Serum Res Institute, Karaj
10. Razi Vaccine & Serum Res Institute, Karaj

Background and Aim: Multi locus variable number tandem repeat analysis as a PCR-based technique scrutinizes short tandem repeats within amplified DNA. These tandem repeat units show frequent variation in the number of copies by slippage strand misalignment throughout DNA synthesis. Different numbers of tandem repeat units makes different fragment lengths in a way that each discrete sized fragment called as unique "allele" for the locus under study. Razi Vaccine and Serum Institute has a long history of production of vaccine against fowl cholera and Haemorrhagic septicemia using indigenous strains. In order to genetically characterize these vaccine strains, it was tried to set-up this technique over *Pasteurella multocida* while there had been no evidence of any similar attempts so far.

Methods: Employing Tandem Repeat Finder software, *Pasteurella Multocida* strain PM70 as the main complete genome was gone under TRs investigation process. More over 9 other complete genome strains including: ATCC43137, HB01, OH4807, PMTB2.1, 3480, HB03, HN06, NC-006300-fna, and NC-016808-fna were compared by selected tandem repeats.

Results: Three microsatellites markers with 6, 9 and 12 bp size were selected entitled VNTR6, VNTR9 and VNTR12. Using Primer 3 software under NCBI website 3 pairs of primers were designed to incorporate Amplicons less than 800 bps in length encompassing the Tandem repeat region in the middle. Optimization process was done to harmonize all 3 amplification protocols. 2 vaccine strains and 4 field isolates were successfully gone under MLVA investigations.

Conclusion: Our findings proved the feasibility of this technique that can be employed as an appropriate way to characterize *Pasteurella Multocida* isolates.

Keywords: *Pasteurella Multocida*, MLVA, PM70

**P721 - 1092: ISOLATION, IDENTIFICATION AND HOST RANGE DETERMINATION OF
THE CAUSAL AGENT OF CROWN GALL DISEASE ON STONE FRUIT CULTIVARS**

Nabi Khezhinejad¹, Hamed Zeinali²

1. Department of Plant Protection, college of Agriculture, Mahabad branch, Islamic Azad University, Mahabad, Iran
2. Department of Plant Protection, college of Agriculture, Malakan branch, Islamic Azad University, Malakan, Iran

Background and Aim: In 2014, Orchards and nurseries of West Azarbayjan province of Iran, including the suburbs of Ourmieh, Miandoab and Mahabad were surveyed for the incidence, identification and host range determination of crown gall disease.

Methods: Samples from different host plants whitish young tumors were transferred to the laboratory. A standard set of physiological and biochemical tests were performed for differentiation of *Agrobacterium* spp. The 16S rRNA sequences of strains obtained were compared with those from GenBank, using the BLASTN program, and EzTaxon-e server. These sequences and those of related bacteria were aligned using the Clustal W program. In pathogenicity tests, Two plants of each stone fruit cultivars were inoculated for each strain and the test was repeated once.

Results: From the symptomatic crown and stem tissues 30 strains with white, mucoid and convex colonies on NA medium were isolated. Strains were catalase and oxidase positive. The strains were positive in tests urase, nitrate reduction and production of ketolactose but negative in tests of hydrolysis starch and indole. In pathogenicity tests, tomato seedlings were inoculated with all strains and tumors started to appear two weeks after inoculation. The strains were tested for utilizing Adonitol, Dulcitol, Arabinose, sorbose, Mannitol, Lactate and Malonate as Carbon sources. 2 months after inoculation, it was determined that galls appeared on most plant crowns.

Conclusion: Based on physiological, biochemical and sequencing of 16s rRNA genes, the strains were identified as *Agrobacterium tumefaciens*. Some varieties of stone fruits including Khony peach cultivar, Takdane cultivar of cherry and Bokharaei of plum were less sensitive to *Agrobacterium* and showed little galls.

Keywords: host range, resistance, plant bacterial disease, detection,

**P722 - 1127: DETECTION OF THE BOVINE VIRAL DIARRHEA VIRUS IN POOLED BOVINE
SERUM BY RT- PCR**

Sajjad Najafi mosleh¹, Dr Sajjad Najafi mosleh², Dr Farhad Mosakhani³, Dr Arya Badiiee⁴

1. Department of Clinical Sciences School of Veterinary Medicine Ferdowsi University Of Mashhad
2. Karaj Islamic Azad University, faculty of veterinary medicine
3. Karaj Islamic Azad University, faculty of veterinary medicine

Background and Aim: The Bovine viral diarrhea virus is one of the most widespread and important virus infections in cattle throughout the world and Iran. This situation results in severe economic losses to the dairy and beef cattle industries.. Persistently infected cattle are capable of shedding large quantities of virus throughout their lives and are considered the primary reservoirs for BVDV. Currently available methods to detect PI cattle are verity of procedures include virus isolation, (AC-ELISA), IHC and RT-PCR

Methods: 60 negative cattle sera specimens were collected & were surveyed by AC-ELISA & RT-PCR tests for reliable specimens' negativity. Serial dilution from 1\25 titer through 1\200 titers were prepared by addition of BVDV to these specimens. The prepared specimens then tested by one step-RT-PCR for detection of the BVDV in sera with individual titers

Results: The results of RT-PCR evaluation for screening and detection of the PI animals were showed that pooled serum sample with 1/200 serial dilution titer prepared with a identified amount of PI serum is enable to detect the amplified specific DNA band in gel agarose electrophoresis after RT-PCR performance test

Conclusion: Identification and elimination of PI cattle is an essential component of a control program in an infected herd. The RT-PCR assay was shown to be sensitive and specific test for detection of BVDV in bovine serum pooled in lots of up to 200 samples

Keywords: BVDV – pooled – RT-PCR

**P723 - 1135: MOLECULAR DETECTION OF G1691A MUTATION AND ITS RELATION
WITH TNF A -308 G /A POLYMORPHISM IN ABORTION HUMAN**

Samaneh Kehani¹, Hossein Rassi², Taher Mohammadian³

1. Department of Biology , Damgan Islamic Azad University
2. Department of Biology , Karaj Islamic Azad University
3. Department of Biology , Shahre Qods Islamic Azad University

Background and Aim: Abortion is the most common of pregnancy complications and in the pathogenesis of abortion genetic factors and environmental factors are related. Factor 5 Leiden (G1691A) is one of the most important factors is the hereditary coagulation thrombosis. Many studies have been directed towards the relationships between SNPs in the promoter region of TNF- α at -308G/A and abortion. This study aimed to investigate the relationship between G1691A and TNF α -308 genotypes with abortion.

Methods: In this case-control study, 47 patients with a history of abortion and 58 controls without a history of abortion were selected. DNA extracted from the venous blood and then to determine the genotypes of G1691A and TNF α -308 G /A polymorphism were used ARMS-PCR .

Results: In connection with the polymorphism G1691A, GG and GA genotype frequencies in controls, respectively 95% and 5% and 87% and 13% respectively in patient samples. About TNF α -308 genotype frequencies GA, GG and AA in the control samples, respectively 54%, 31% and 15% in patient samples, 19%, 45%, 36%. The result show that relationship between case and control groups was significant in genotypes of G1691A and TNF α -308.

Conclusion: In general it can be concluded that molecular analysis of mutations in Factor 5 Leiden G1691A polymorphism and 308- TNF α in early detection and early treatment is effective in abortion.

Keywords: G1691A mutation , TNF α -308 G /A polymorphism, abortion human

**P724 - 1155: STUDY THE PRESENCE OF REGULATORY SEQUENCE OF FHLA PROTEIN IN
GYRB UPSTREAM REGION**

Hoda Akhavan armaki¹, Razieh Pourahmad²

1. MSc student in Genetics at university of shahrekord
2. Associate Professor of Genetics at university of shahrekord and corresponding author

Background and Aim: FhlA protein is the transcriptional activator of formate hydrogen lyase system genes in *Escherichia coli*. This regulatory protein binds to a specific sequence. The aim of this study was to search the presence of this specific sequence in the *gyrB* upstream region

Methods: For this purpose, the bioinformatics software, promoter Analysis, was used to analyze the presence of this sequence in the promoter region of *gyrB*. The promoter hunter was used to predict promoter for this gene.

Results: Results showed the presence of FhlA binding site in upstream region of this gene, placed 45 nucleotides before the transcription start site .

Conclusion: It is concluded that FhlA protein can be effective in regulation of *gyrB* expression

Keywords: FhlA -binding site - *gyrB* - *Escherichia coli*

**P725 - 1169: USE OF MULTI LOCUS SEQUENCE TYPING METHOD FOR MOLECULAR
DETECTION OF SALMONELLA ENTERICA SEROTYPE ENTERITIDIS**

Faegheh Sarfi¹, Reza Ranjbar², Nasser Harzandi³

1. Microbiology Department, Azad Islamic University, Karaj, Iran
2. Molecular Biology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran
3. Microbiology Department, Azad Islamic University, Karaj, Iran

Background and Aim:: Salmonellosis is considered as the public health problem worldwide. This study evaluated the housekeeping genes to screen and identify *Salmonella enterica* serotype Enteritidis.

Methods:: In this study, the strains of *Salmonella enterica* serotype Enteritidis were collected from suspicious patients admitted to different hospitals in Tehran. Bacterial isolation and identification was carried out using standard microbiological and serological methods. Housekeeping genes (*sucA*, *thrA*, *purE*, *hisD*, *aroC*, *hemD*, *dnaD*) were chosen as target genes for PCR amplification of *Salmonella enterica* serotype Enteritidis

Results: The results obtained from PCR showed that housekeeping genes were amplified with size of 643 for *sucA*, 630 for *thrA*, 488 bp for *purD*, 651 bp for *hisD*, 639 bp for *aroC*, 666 bp for *hemD* and 833 bp for *dnaD* genes in all *Salmonella enterica* serotype Enteritidis. There was any positive reaction while the test was done on *Shigella* and *E. coli* strains which indicated that these genes are specific for *Salmonella*

Conclusion:: According to our results, housekeeping genes used in this study were efficient and suitable targets for screening of *Salmonella enterica* serotype Enteritidis

Keywords:: *Salmonella enteritidis*, housekeeping genes, *sucA*, *thrA*, *purE*, *hisD*, *aroC*, *hemD*, *dnaD*.

**P726 - 1185: MOLECULAR DIAGNOSIS OF CHLAMYDIA TRACHOMATIS IN SUSPECTED
PSEUDOMONAS AERUGINOSA KERATITIS BY PCR**

zeynab Dalirgoli¹, Mohammad hassan shahhosseiny ², Reza Hosseini Doost³

1. Department Of Microbiology Faculty Of Advanced Sciences & Technology Pharmaceuticalis Sciences
Branch Islamic Azad university Tehran Iran (IAUPS)
2. Department of Microbiology- Shahr-e-Qods Branch-Islamic Azad University-Tehran/Iran. Iranian Gene
Fanavar Institute (IGF), Tehran/Iran
3. Department Of Microbiology Faculty Of Advanced Sciences & Technology Pharmaceuticalis Sciences
Branch Islamic Azad university Tehran Iran (IAUPS)

Background and Aim:keratitis refers to part of eyes sphere inflammation. Keratitis involved endogenous and exogenous reasons. In happening of keratitis infection reasons such as bacteria, fungi and viruses can be mentioned. Chlamydia trachomatis causes infections for eyes-genital system and rectal organization. By considering the importance of this bacteria in production of infectious disease especially eye problems, in this study has tried to research its role and analyzing the bacteria in suspected keratitis of Pseudomonas. Actually the main purpose of this research is to molecular detection of Chlamydia trachomatis in pseudomonas aeruginosa suspected keratitis by PCR method

Methods:This project was held on about 50 pseudomonas aeruginosa suspected keratitis samples collected in Tehran's Labafinejad hospital. The DNAs were extracted by DNG –Plus method from samples and PCR test optimized and specificity was checked by genomic DNA of other organisms. Limit of detection (LOD) test carry out by genomic DNA of standards strains.

Results:PCR product with 517 bp observed in 1.5% agarose gel electrophoresis. In specificity test with the other multiple organisms any amplicon was not detected in electrophoresis. From 50 samples of suspected keratitis by Pseudomonas aeruginosa, in 6 samples (12%) , Chlamydia trachomatis observed by PCR method.

Conclusion:C. trachomatis is the most important and widespread reason of trachoma. This study approved certain pseudomonas aeruginosa suspected keratitis have another agent such as C.trachomatis.

Keywords:Chlamydia trachomatis, PCR, Diagnosis, pseudomonas aeruginosa suspected keratitis

P727 - 1264: REAL-TIME PCR ANALYSIS OF P21 GENE EXPRESSION IN JURKAT E6.1 T-LYMPHOCYTE LEUKEMIA CELL LINE IRRADIATED WITH LOW POWER LASER IRRADIATION (635NM AND 780NM)

Layla Alamery¹, Layla M. H. Al-Ameri², Ali H. Ad'hiah¹³

1. institute of laser for postgraduate studies, Baghdad University, Baghdad, Iraq
2. Real-time PCR Analysis of p21 Gene Expression in Jurkat E6.1 T-lymphocyte Leukemia Cell Line Irradiated with Low Power Laser Irradiation (635nm and 780nm)
3. Real-time PCR Analysis of p21 Gene Expression in Jurkat E6.1 T-lymphocyte Leukemia Cell Line Irradiated with Low Power Laser Irradiation (635nm and 780nm)

Background and Aim: The effect of low power laser irradiation (LPLI) on the expression of p21 gene in cultured Jurkat E6.1 T-lymphocyte leukemia (JELT) cell line was investigated in vitro.

Methods: The cells were irradiated with LPLI at 635nm and 780nm wavelengths (energy density 9.174 J/cm² P), and the gene expression was analyzed by real-time PCR after 24, 48 and 72 incubation time periods (ITPs).

Results: The analysis revealed that the expression of p21 was higher in 780nm irradiated cultures (2P - ??CT P = 1.62) than in 635nm cultures (2P - ??CT P = 1.07) at 24 hours ITP. The same manner of increased expression was observed 48 hours post-irradiation (2P - ??CT P: 2.14 vs. 1.41). In both cases, the difference was not significant. However, a pronounced effect of LPLI on p21 expression was observed 72 hours post-irradiation. For 635nm, the LPLI at energy density 9.174 J/cm² P caused two-fold increase expression (2P - ??CT P = 2.30), but at 780nm much more increased expression was observed, and reached more than six-fold (2P - ??CT P = 6.50), and such increase was significant (P ? 0.01).

Conclusion: It is possible to conclude that the LPLI at the wavelength 780nm might be associated with an increased expression of a gene involved in regulation of cell cycle and apoptosis.

Keywords: Low power laser irradiation, Leukemia cell line, p21 gene.

Molecular Epidemiology

P728 - 30: THE NECESSITY OF OBSERVING HEALTH CARE IN AVOIDING THE PATIENT'S INFECTION

Behnaz Samiee¹, Marzieh Azar Faza², Ali Nezhad Esmaeel³, zahra Ghandehari⁴, Shamsol molok Khoshbakht⁵, sakineh rooki⁶, fatemeh Imani⁷, najmeh abdolbaghi⁸, nahid sahgi⁹, Asieh Heidarian¹⁰

1. Infection Control Supervisor
2. Director of Nursing
3. Clinical Supervisors
4. Educational Supervisor
5. hed nurse
6. hed nurse
7. nurse
8. nurse
9. nurse
10. nurse

Background and Aim: Caring about hygiene is one of the easiest, most effective and least expensive methods to prevent and building up resistance against gems. Today, washing hand in order to remove the micro-organisms attached to them due to the contact with the surroundings and preventing infection is usually considered as one of the most important fundamental actions taking in controlling infections. However in most health institution, advising to care about hand hygiene is unacceptably rare,

Methods: we checked our staff in Kamyab hospital washing their hands based the World Health Organization's rules of washing hands in 2015.

Results: Hand hygiene was observed between 20 staff, who were aware of observation, in each unit per month. The situations of observation were The World Health Organization's rules of washing hands in 2015- 3010 staff of different job titles (nurses, doctors, nurse aids, staffs, paramedics including laboratory samplers and physiotherapists) were observed in Shahid Kamyab Hospital which 707 cases were from group C (doctors), 1126 cases from group A (nurses and nurse students), 1022 cases from group B (nurse aids and staffs) and 155 cases from group D (paramedics). Totally 83753 cases were observed which 46% obeyed the rules of hand hygiene and 54% didn't. 41% of doctors obeyed the rules, 51% of nurses, 42% of nurse aids and staffs and 40% of paramedics.

Conclusion: Thus becoming aware of hand hygiene rate is the first step of nosocomial infection control and knowledge about agents linked will be the next

Keywords: Hand hygiene, Microorganisms, Andication

**P729 - 133: PREVALENCE OF VARIOUS HEPATITIS C (HCV) GENOTYPES AMONG
CHRONIC HCV PATIENTS IN A PRIVATE LABORATORY, TEHRAN, IRAN**

Sara Nemati vahedi¹, Fatemeh Jahedi², Solmaz Agha Amiri³

1. 1- Ph.D student of Cell and Molecular Biology, Islamic Azad University of Sirjan
2. 2- M.Sc in Virology, Shiraz University of Medical Sciences
3. 3- Ph.D student of Pharmaceutical Biotechnology, Shahid Beheshti University of Medical Sciences

Background and Aim: Hepatitis C (HCV) is a public health problem in many part of the world. Since HCV has different genotypes that showing different responses to treatment, determination of patient's HCV genotype is critical prior to antiviral therapy. The aim of this study was to determine the prevalence of various HCV genotypes among patients who were referred to a private laboratory.

Methods: 100 patients with chronic hepatitis was enrolled from 2011-2016. RNA was extracted using standard commercial kits from patient's serum. After CDNA synthesis HCV RNA was detected using reverse transcriptase nested PCR (RT- nested PCR) and then HCV genotypes were analyzed with restriction fragment length polymorphism (RFLP) assay.

Results: Out of 100 samples, 45(45%) were positive for subtype 1a, and 41 (41%) were subtype 3a, followed by 11 (11%) showed genotype 1b, and genotypes 2a, 2b and 4 were 1 (1%), each. there is no mixed HCV genotypes found in the patients.

Conclusion: This study showed that the most frequent genotype among patient was 1a followed by 3a.

Keywords: HCV genotyping ,HCV ,Iran

P730 - 204: THE FREQUENCY OF PLASMID MEDIATED QUINOLONE RESISTANCE (PMQR) DETERMINANTS IN URINARY ISOLATES OF EXTENDED-SPECTRUM B-LACTAMASE-PRODUCING ESCHERICHIA COLI

Alisha Akya¹, Roya chegene lorestani², Azam Elahi³

1. Kermanshah Uni of Med Sci, Kermanshah, Iran
2. Kermanshah Uni of Med Sci, Kermanshah, Iran
3. Kermanshah Uni of Med Sci, Kermanshah, Iran

Background and Aim: Plasmid-mediated quinolone resistance genes (PMQR) play an important role in the development of resistance to quinolones in *Escherichia coli*. The aim of this study was to determine qnr, aac (6') -Ib-cr and qepA genes in the extended spectrum β -lactamase-producing (ESBL) *E. coli* Isolates.

Methods: A total of 240 *E. coli* were isolated from the urine of outpatients with urinary tract infections in Kermanshah. The isolates were screened for ESBL phenotypes followed by testing the minimum inhibitory concentration (MIC) for ciprofloxacin, levofloxacin and Nalidixic acid using microdilution assay. PCR was performed to identify qnrA, qnrB, qnrS, aac (6')-Ib and qepA genes. All PCR products for aac(6')-Ib were digested by BstCI and electrophoresed to confirm the aac (6')-Ib-cr variant.

Results: Of 240 isolates, 66 (27.5%) were ESBL positive. Of them, 45 (68.1%) and 56(84.4%) isolates were resistant to ciprofloxacin and / or levofloxacin and Nalidixic acid, respectively. The qnrA, qnrB, qnrS and qepA genes were found in 28.7, 40.9, 4.5 and 3 percent of 66 isolates, respectively. The 57.7% of aac (6')-Ib gene was aac (6')-Ib-cr variant involved in the resistance to quinolones.

Conclusion: Our results indicated a relatively high frequency of PMQR genes in ESBL producing *E. coli* isolates. The aac (6') -Ib-Cr and qnrB genes are more common than others genes tested, which reflects the dissemination of resistance to quinolones in our area. The data analysis suggests that PMQR genes are associated with resistance to quinolones and may increase the MIC levels.

Keywords: Quinolone resistance, *Escherichia coli*, Plasmid mediated genes

P731 - 304: DISTRIBUTION OF STAPHYLOCOCCAL CASSETTE CHROMOSOME MEC (SCCMEC) TYPES I, II, III AND IV IN STAPHYLOCOCCUS EPIDERMIDIS AMONG PATIENTS REFERRED TO EDUCATIONAL HOSPITALS ESFAHAN, IRAN.

Seyed Asghar Havaei¹, Ashkan Karimi², Parisa Shoaie³, Mohammadreza Nahaei⁴, Sina Mobasherizadeh⁵, Behrooz Ataei⁶, Mehrdad Halaji⁷

1. Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
2. . Nosocomial Infection Research Center, Isfahan University of Medical Sciences, Isfahan, Iran
3. Infectious Diseases and Tropical Medicine Research Center, Isfahan University of Medical Sciences, Isfahan, Iran
4. Drug Applied Research Center, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran; Department of Medical Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran.
5. . Nosocomial Infection Research Center, Isfahan University of Medical Sciences, Isfahan, Iran
6. Infectious Diseases and Tropical Medicine Research Center, Isfahan University of Medical Sciences, Isfahan, Iran
7. Nosocomial Infection Research Center, Isfahan University of Medical Sciences, Isfahan, Iran

Background and Aim:Coagulase-negative staphylococci (CoNS) are now recognized as the etiological agents of an important range of infections in humans. Most developed countries have reported an increase in CoNS infections in hospitalized patients that are resistant to meticillin and other antibiotics. Staphylococcal cassette chromosome mec (SCCmec) typing is essential for understanding the molecular epidemiology of meticillin-resistant Staphylococcus strains. SCCmec elements are currently classified into types I to VI based on the characteristics of the mec and ccr gene complexes and are further classified into subtypes according to their 'junkyard DNA' region. We evaluated the distribution of SCCmec types in CoNS from patients referred to educational hospitals Esfahan, Iran.

Methods:One hundred and thirty isolates were collected from clinical samples from different teaching hospitals in Esfahan, Iran, and identified by biochemical tests. SCCmec typing was performed using the PCR schemes previously published.

Results:Among the 130 isolates, 30 (43 %) harboured SCCmec type I, 8 (11 %) harboured SCCmec type II, 24 (34 %) harboured SCCmec type IV. Sixty eight isolates were not typable. SCCmec type I was the most prevalent among isolates of *S. epidermidis* (43 %). None of the isolates harboured SCCmec type III.

Conclusion:Our results indicate that SCCmec type I was the most prevalent among the of *S. epidermidis*. Isolates with SCCmec type I were more resistant to non-beta-lactam antimicrobials than isolates harbouring SCCmec types, II and IV.

Keywords:Coagulase-negative staphylococci (CoNS) -SCCmec-Staphylococcus epidermidis

**P732 - 491: MICROBIOLOGY OF PRE-DIURESIS IN ANOPHELES STEPHENSI, THE ASIAN
MALARIA MOSQUITO**

Maryam Rahimi¹, Naseh Maleki-Ravasan², Fahimeh Nemati Mansoor³

1. Department of biotechnology, Faculty of Advanced Sciences & Technology , Pharmaceutical Sciences Branch, Islamic Azad University ,Tehran – Iran (IAUPS)
2. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran (PII), Tehran, Iran
3. Department of Biotechnology, Faculty of Advanced Sciences and Technology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, Iran (IAUPS)

Background and Aim:Pre-diuresis, the excretion of droplets from the anus of hematophagous insects aims at concentrating erythrocytes, restoring the water balance and thermoregulation. Bacterial communities have a significant influence on the insect development. Herein, we delved deeper understanding into the bacteria of repelling liquid of *Anopheles stephensi* to infer the nature of transient bacteria and their possible significance on the mosquito biology.

Methods:Two biological forms of *An.stephensi* (mysorensis and intermediate) were fed on healthy and *Plasmodium berghei* infected BALB/c. Droplets from the anus of the feeding *Anopheles* were directly entrapped into the BHI broth medium. Colonies with different morphology were separated on agar plates and pure colonies were subjected to 16S-rRNA sequencing. The body of BALB/c was swabbed to identify skin resident bacteria.

Results:Totally, 42 bacterial isolates including 12 species were isolated from the *Anopheles* passing droplets (n=6) and their feeding mice (n=10). In non-infected *An.stephensi*-mysorensis, *Serratia marcescens* originating from mouse skin passed through pre-diuresis. In *P.berghei*-infected *An.stephensi*-intermediate, *Bacillus cereus*, originating from mouse skin passed through pre-diuresis as well. *Bacillus pumilus* was the common bacterium in the droplets of both biological forms. *B.pumilus*, *B.cereus* and *Enterobacter cloacae* restricted to the droplets of *P.berghei*-infected *Anopheles* while *Acinetobacter junii*, *Staphylococcus xylosus* and *S.marcescens* expelled via pre-diuresis of non-infected ones.

Conclusion:For the first time, this study revealed the presence of transient/indigenous bacteria in excretions of *An.stephensi*. Both *S.marcescens* and *B.cereus* are previously introduced as natural facultative pathogens of *Anopheles* and herein repelled out alongside the pre-diuresis. Therefore pre-diuresis could be considered as an immune response.

Keywords:Pre-diuresis, *Anopheles stephensi*, *Serratia marcescens*, *Bacillus cereus*, immune responses

P733 - 495: DETECTION OF CIRCULATING HUMAN NOROVIRUS IN CHILDREN LESS THAN 5 YEARS WITH ACUTE GASTROENTERITIS BY GENOGROUP SPECIFIC REAL TIME PCR

Behrooz Nejati¹, Fatemeh Roodbari², Arash Arashkia³, Somayeh Jalilvand⁴, Alireza Nateghian⁵, Mitra Mehrazma⁶, Aliakbar Rahbarimanesh⁷, Zabihollah Shoja⁸

1. Department of Biology, Faculty of Basic Sciences, University of Mazandaran, Iran; Department of Virology, Pasteur Institute of Iran, Tehran, Iran
2. Faculty of Basic Sciences, University of Mazandaran, Iran
3. Department of Virology, Pasteur Institute of Iran, Tehran, Iran
4. Department of Virology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
5. Iran University of Medical Sciences, Ali-Asghar Children's Hospital, Tehran, Iran
6. Iran University of Medical Sciences, Ali-Asghar Children's Hospital, Tehran, Iran
7. Department of Pediatric Infectious Diseases, Bahrami Children Hospital, Tehran University of Medical Sciences, Tehran, Iran
8. Department of Virology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Norovirus (NoV), as non-enveloped viruses of the Caliciviridae family, is a major etiologic agent responsible for non-bacterial sporadic and epidemic gastroenteritis worldwide in humans. Genetically, NoV can be subdivided into five separate genogroups (genogroup I [GI], GII, GIII, GIV, and GV), and viruses belonging to GI, GII, and GIV have been detected in humans. GII contains most of the currently circulating strains, which are able to infect humans. The aim of this study was to determine the prevalence of GI and GII NoV in children suffering from gastroenteritis.

Methods: Fecal samples (N = 100, Male=61 and Female=39) were collected from children under 5 years of age who were suffering from gastroenteritis. All the children were referred to Aliasghar and Bahrami Hospitals located in Tehran, Iran. NoV RNA was extracted by RNA extraction kit, and NoV RNA was detected using genogroup specific Real-time reverse transcription polymerase chain reaction (RT) PCR assays.

Results: NoV infection was detected in 16 (16%) of the 100 collected samples. All positive samples belonged to GII.

Conclusion: Our results indicated that NOV GII was dominant circulating genogroup and must be considered as one of the infectious causes of acute gastroenteritis among Iranian children. To the best of our knowledge there is limited data about the role of NoV in children's acute gastroenteritis among Iranian children and this report can be remarkable for further studies.

Keywords: Norovirus, Gastroenteritis, Real time

**P734 - 497: MOLECULAR ANALYSIS OF PSEUDOMONAS AERUGINOSA STRAINS
ISOLATED FROM BURN PATIENTS BY REPETITIVE EXTRAGENIC PALINDROMIC-PCR
(REP-PCR) IN AHVAZ TALEGHANI HOSPITAL**

Mansooreh Abbasi¹, Niloufar Rashidi², Leily Shokuhizadeh³, Elahe Tajbakhsh⁴

1. Master of Science student in Microbiology, Department of Microbiology, Islamic Azad University of Shahrekord, Iran
2. Assistant Professor, Department of laboratory sciences, Paramedical school, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
3. Assistant Professor, Department of laboratory sciences, Paramedical school, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
4. Assistant Professor, Department of Microbiology, Islamic Azad University of Shahrekord, Iran

Background and Aim: *Pseudomonas aeruginosa* is an important pathogen which causes nosocomial infections in immunocompromised patients, especially in hospitalized burn patients. Among DNA analysis methods used for investigating genetic diversity, rep-PCR typing has been introduced as a rapid, low cost method with high discriminatory power. The aims of this study were to investigate genotypic relatedness and antibiotic resistance in clinical isolates of *P. aeruginosa*.

Methods: Totally 75 Strains of *Pseudomonas aeruginosa* were isolated from burn patients. Antimicrobial susceptibility testing was performed using disk diffusion method. Also genetic analysis of the palindromic sequence amplified by polymerase chain reaction (rep-PCR) was performed.

Results: Antibiotic resistance pattern with disk diffusion method showed high resistance to ceftriaxone (94.66%), cefotaxime (90.66%), Piperacillin/Tazobactam (88%), meropenem (88%), and low resistance to amoxycillin/clavulanic acid (5.33%) and azithromycin (6.66%). The number of bands in rep typing varied from 2 to 18, with the length of 100 bp to 1000 bp. Rep fingerprinting results of *P. aeruginosa* showed 20 clusters and 40 different groups. Different antibiotic resistance patterns were observed among the members of the same cluster.

Conclusion: Based on findings in this study we suggest rep-PCR is a useful method for assaying genetic diversity among *Pseudomonas aeruginosa* strains. This is a rapid, low cost method with high discriminatory power. Moreover our findings suggest that genotyping by rep-PCR, may play an important role in routine epidemiological surveillance, and in the identification of the source of transmission of *P. aeruginosa* in the hospitals.

Keywords: *Pseudomonas aeruginosa*, burns, antibiotic resistance, rep-PCR

**P735 - 521: DETECTION OF BOVINE SALMONELLA CARRIERS AS A POTENTIAL
THREAT FOR HUMAN NON-TYPHOIDAL SALMONELLOSIS IN SANANDAJ CITY**

Towhid Sarbaz Janfada¹, Elham Ahmadi², Karim Mardani³

1. Undergraduate Student of Veterinary Medicine, Sanandaj Branch, Islamic Azad University, Sanandaj, Iran
2. Department of Veterinary Pathobiology, Sanandaj Branch, Islamic Azad University, Sanandaj, Iran
3. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Urmia University, Urmia, Iran

Background and Aim: Non-typhoidal Salmonella represents an important human pathogen world-wide. The source of environmental contamination is invariably animal feces and the feco-oral route is the most important mode of transmission of Salmonella in animals and humans. The aim of this research was to access the burden of colonizing gastro-intestinal tract of healthy cows with Salmonella spp. in Sanandaj city as its zoonotic importance.

Methods: In one field trial, 100 bovine fecal samples were collected randomly and aseptically during January-June 2016 from 10 dairies in Sanandaj city. The samples were tested by culture following pre-enrichment and selective enrichment steps in buffered pepton water and rappaport vassiliadis medium. Identification of suspected Salmonella isolates on Brilliant-green Phenol-red Lactose Sucrose (BPLS) agar was carried out by the biochemical method and invA PCR. The isolates were further serotyped using polyvalent O and H antiserum.

Results: Of the 100 fecal samples, 26 (26%) were shown to be infected with Salmonella organisms detected both phenotypically and molecularly (based on a 284 bp amplicon). Serotypes which were classified by the Kauffman-White scheme includes 17 (53.84%) Salmonella typhimurium, 7 (26.92%) Salmonella enteritidis, and 2 (7.69%) Salmonella dublin.

Conclusion: Basic hygiene practices and the implementation of scientific based management strategies can efficiently mitigate the risks associated with animal contacts. However, the general public is frequently unaware of the specific disease risks involved and high-risk behaviors are common. The disease can be also controlled by vaccination of cattle.

Keywords: Sanandaj, Salmonella carrier, cow, public health

**P736 - 528: PREVALENCE OF VIRULENCE ASSOCIATED GENES IN BRUCELLA SPECIES
ISOLATED FROM HUMAN AND ANIMAL SOURCES IN IRAN**

Iman Hashemifar¹, Abbas Yadegar², Faramarz Masjedani Jazi³, Noor Amir Mozafari⁴

1. Microbiology Department, School of Medicine, Iran University of Medical Sciences, Tehran, Iran
2. Foodborne and Waterborne Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran Gastroenterology and Liver Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. Microbiology Department, School of Medicine, Iran University of Medical Sciences, Tehran, Iran
4. Microbiology Department, School of Medicine, Iran University of Medical Sciences, Tehran, Iran

Background and Aim: *Brucella* spp. are gram negative facultative intracellular bacteria that are causative agents of brucellosis. At present, ten species are identified in the genus *Brucella* including *B. abortus* and *B. melitensis* as important animal and human pathogens. The genome of *Brucella* species carries several putative virulence genes. In this context, we investigated the prevalence of several virulence genes of *B. abortus* and *B. melitensis* isolates in Iranian patients and cattle.

Methods: Totally, 120 samples including 60 human and 60 animal specimens were collected during 2010-2015 from different parts of Iran. All samples were cultured in blood culture media and subcultured in *Brucella* agar medium. Identification of *Brucella* species were confirmed by colony morphology, Gram staining, oxidase, catalase and also by molecular assays. PCR and sequence analysis was carried out with nine primer pairs for *BtpA*, *BtpB*, *BetB*, *PrpA*, *VirB5*, *VceC*, *BPE275*, *BSPB*, and *VirB2* virulence genes designed in this study.

Results: A total of 68 *Brucella* strains were isolated from humans (37) and animals (31) including *B. abortus* (8 strains) and *B. melitensis* (60 strains). Overall, all *B. abortus* and *B. melitensis* strains were positive (100%) concerning the *BtpA*, *BtpB*, *VirB5*, *VceC*, *BPE275*, *BSPB*, and *VirB2* genes except *PrpA* and *BetB* that were detected respectively in 86% and 97% of the strains studied.

Conclusion: Our results showed that Iranian *Brucella* strains, regardless of human or animal sources, are highly virulent due to presence of several virulence-associated genes in almost all strains studied. In conclusion, characterization of overmentioned virulence genes can promote further understanding of pathogenic mechanisms of these bacteria.

Keywords: *Brucella abortus*, *Brucella melitensis*, virulence genes, patients, animal source

**P737 - 558: INVESTIGATION OF PNEUMOCOCCAL COCOLONIZATION IN
NASOPHARYNX OF CHILDREN UNDER 6 YEARS BY MULTIPLEX PCR**

Sanaz Asgarian¹, Mohammadali Malekan², Nour Amirmozaffari, PhD³, Seyed Hamid Mousavi⁴, Shadi Aghamohammad⁵, Seyed Fazlollah Mousavi, PhD⁶, Fatemeh Ashrafian⁷

1. Science and Research Branch , Islamic Azad University, science faculty
2. Iran Pasteur Institute , Department of Microbiology
3. Science and Research Branch , Islamic Azad University, science faculty
4. Science and Research Branch , Islamic Azad University, science faculty
5. Iran Pasteur Institute , Department of Microbiology
6. Iran Pasteur Institute , Department of Microbiology
7. Iran Pasteur Institute , Department of Microbiology

Background and Aim: Streptococcus pneumoniae is among the most important of human pathogen and is responsible for bacterial meningitis, sepsis, pneumonia, and acute otitis media. Colonization with more than one distinct strain of the same species or sometimes different species, also termed cocolonization, is a prerequisite for horizontal gene transfer between pneumococcal strains that may lead to change of the capsular serotype. Capsule switch has become an important issue since the introduction of conjugated pneumococcal polysaccharide vaccines. A problem for study of cocolonization is lack of techniques to detect multiple colonization by Streptococcus pneumoniae strains directly from nasopharyngeal samples. The aim of this study is to determine of different serotypes of colonized S. pneumoniae in Iranian children under 6 years.

Methods: Two hundred eighty-one nasopharyngeal swabs were collected from unvaccinated children under six years during one year (2015-2016) and they were transferred in STUART (transfer media) to Pasteur Institute and then they were analyzed by PCR and Multiplex PCR, to detect CpsA gene and different colonized serotypes. The number of strain and their relative abundance in cocolonized sample were determined by final Multiplex PCR.

Results: According to PCR results: from 281 swab samples, 181 strain include CpsA gene and according to Multiplex PCR we had 50/54% total cocolonization and about cocolonization: 13/18% for 2 serotypes cocolonization, 2/74% for 3 serotypes cocolonization, 28/02% for 1 serotype colonization and the prevalence of 19F, 5 and 6A/6B, 19F, 5 serotypes are 2/76% and 1/1% respectively.

Conclusion: This new technique allows for the rapid and economical study about pneumococcal cocolonization in nasopharynx samples. It will be valuable for the control of Streptococcus pneumoniae epidemiology under vaccine selection pressure.

Keywords: Streptococcus pneumoniae - Multiplex PCR - Cocolonization

**P738 - 578: HIGH FREQUENCY OF SCCMEC TYPE III AND SPA TYPE T037 AND T631
AMONG MULTI DRUG RESISTANT STAPHYLOCOCCUS AUREUS ISOLATED FROM
BURN PATIENTS IN SOUTHWEST OF IRAN**

Seyed Sajjad Khoramrooz¹, Najmeh Parhizgari², Asghar Sharifi³, Seyed Abdolmajid Khosravani⁴, Seyed Ali Asghar Malek Hosseini⁵, Masoud Marashifard⁶, Mahboobeh Yazdanpanah⁷, Farzaneh Gharibpour⁸

1. Cellular and Molecular Research Center, Yasuj University of Medical Sciences, Yasuj, Iran
2. Department of Virology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
3. Cellular and Molecular Research Center, Yasuj University of Medical Sciences, Yasuj, Iran
4. Cellular and Molecular Research Center, Yasuj University of Medical Sciences, Yasuj, Iran
5. Student Research Committee, Yasuj University of Medical Sciences, Yasuj, Iran
6. Student Research Committee, Yasuj University of Medical Sciences, Yasuj, Iran
7. Department of Genetics, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran
8. School of veterinary Medicine, Shiraz University, Shiraz, Iran

Background and Aim: Methicilin resistance *Staphylococcus aureus* (MRSA) infections are major challenge in hospital especially in burn units. The use of molecular typing methods is essential for tracking the spread of *S. aureus* infection and epidemiological investigations. The aim of this study was to find the profile of the spa types and also the prevalence of each SCCmec types of *S. aureus* strains in a central burn hospital in south west of Iran.

Methods: A total of 82 non-duplicate *S. aureus* isolated from burn patients between April 2011 to February 2012. Susceptibility of isolates against 13 different antibiotics was tested by Disk Agar Diffusion (DAD) method. Phenotypic test were used for identification of MRSA strain and they confirmed by molecular detection of *mecA* gene. Multiplex-PCR technique used for determines the SCCmec typing of MRSA strains and all of the *S. aureus* isolates were typed by spa-typing method.

Results: Seventy (86.4%) of isolates were MRSA. The highest rate of resistance was observed to penicillin (97.5%) and erythromycin (77.8%). Sixty seven of 70 MRSA isolates harbored only SCCmec type III and 3 untypeable isolates. Five different spa-types were detected. The most common spa-type were t037 (42.5%) and t631 (34.5%) that only found in MRSA isolates.

Conclusion: Only SCCmec type III was found in burn patients that emphasize the HA-MRSA origin of these strains. Only five different spa-types identified in this study that in accordance with one SCCmec type indicating a limited number of bacterial clones is circulated in the burn unit in this hospital.

Keywords: *S. aureus*, burn patient, SCCmec type, spa type

**P739 - 581: PREVALENCE OF DIFFERENT ESCHERICHIA COLI PATHOTYPES IN
DIARRHEAL PATIENTS FROM ZANJAN AND FARS PROVINCES, IRAN**

Mehrnaz Yadani milajerdi¹, Saied Bouzari ², Saied Mostaan ³, Mana oloomi ⁴

1. M.Sc. student of General Microbiology, Islamic Azad University
2. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
3. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
4. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran; saeid bouzari@yahoo.com

Background and Aim:Diarrhea is one of the most prevalent diseases in the world, especially in developing countries. Diarrheogenic *Escherichia coli* cause gastroenteritis and involving ETEC (Enterotoxigenic *Escherichia coli*), EPEC (Enteropathogenic *Escherichia coli*), EAEC (Enteraggregative *Escherichia coli*), EHEC (Enterohemorrhagic *Escherichia coli*), EIEC (Enteroinvasive *Escherichia coli*), and DAEC (Diffusely adherent *Escherichia coli*). The aim of this study was to determine the prevalence of these pathotypes in Zanzan and Fars provinces in Iran.

Methods:Stool specimens were collected based on inclusion and exclusion criteria. For *E. coli* isolation, stool samples were streaked on to MacConkey agar and incubated overnight at 37°C then cultured for enteric pathogen by standard methods. In brief, selected colonies from MacConkey agar were cultured on TSI, Citrate, MR/VP and motility medium. Identified *E. coli* samples were stocked for further investigations. Phenol-chloroform method was used for bacterial DNA extraction and PCR for detecting the ST and LT genes for ETEC, eae and bfp for EPEC, invE for EIEC, aa for EAEC and stx₁, stx₂ and eae for STEC isolates.

Results:From 134 samples, 96 (71.6 %) were identified as *E. coli*, 84 (87.5%) as STEC, 1 (1.04%) as EIEC, 2 (2.08%) as EPEC and 9 (9.3%) as nonpathogenic *E. coli*. No EAEC and ETEC were identified using PCR technique.

Conclusion:Based on this study, it was shown that all the pathotypes are not prevalent in the regions and only some are present.

Keywords:*Escherichia coli* pathotypes, ETEC, EPEC, EHEC, STEC, EIEC, EAEC

**P740 - 592: DETERMINATION OF INTESTINAL ESCHERICHIA COLI PATHOTYPES
FREQUENCY IN TEHRAN PROVINCE BY PCR**

Mohammad Hossein Zarei¹, Saeid Bouzari², Saeid Mostaan³, Amir Dashti⁴, Moein Shahidi⁵, Elaheh Mokarrami⁶

1. Pasteur Institute Of Iran
2. Pasteur Institute Of Iran
3. Pasteur Institute Of Iran
4. Pasteur Institute Of Iran
5. Pasteur Institute Of Iran
6. Pasteur Institute Of Iran

Background and Aim: Escherichia coli (E.coli) is an important member of the normal intestinal microflora for mammals, including humans. Diarrheagenic Escherichia coli (DEC) is an emerging agent among pathogens that cause diarrhea. E.coli categorized into six major groups according to virulence factor profiles, severity of clinical manifestations and prognosis. Diarrheagenic E.coli such as enterohaemorrhagic E.coli, enteroaggregative E.coli, enteropathogenic E.coli, enteroinvasive E.coli, enterotoxigenic E.coli and shiga toxin producing E.coli strain are among the most prevalent causative agents in acute diarrhea.

Methods: totally 325 isolates (5 colonies of each 65 samples) were collected from patients with diarrhea in Tehran province of Iran, during 2013. E.coli strains were isolated by traditional culture and standard biochemical identification test, the diarrheagenic genes isolated by polymerase chain reaction (PCR) technique to detect presence of virulence genes. eae, stx1 and stx2 for EHEC, bfp and eae for EPEC, LT and ST for ETEC, AA for EAEC, invE for EIEC, STX1 or STX2 for STEC.

Results: 50 samples of 65 (77%) were identified E.coli by traditional cultures and biochemical identification test. EPEC 5(7.7%), STEC 27(41.5%), ETEC 1(1.5%), EAEC 3(4.6%) and non pathogenic E.coli 14(21.5%) were identified using PCR technique.

Conclusion: STEC mostly affected children less than 5 years old but EPEC and ETEC and EAEC were seen in any age groups. It seems that in Tehran province, prevalence of these pathotypes are less than other regions that have hot or dryer weather. On the other hand the prevalence of different pathotypes was variable and some pathotypes were more prevalent than others. It could be suggested to pay serological studies for the better treatment and access to vaccine.

Keywords: Diarrheagenic Escherichia coli polymerase chain reaction intestinal

P741 - 610: RELATIONSHIP BETWEEN TOXIN ENCODING GENES AND ANTIBIOTIC RESISTANCE PROPERTIES IN UROPATHOGENIC ESCHERICHIA COLI ISOLATED FROM IRAN

Zohreh Payamani¹, mohsen mirzaee², Nooshin Kamrani Hemat³

1. Department of Cell and Molecular Biology, Boroujerd Branch, Islamic Azad University, Boroujerd, Iran.
2. Department of Medical Laboratory Sciences, Boroujerd Branch, Islamic Azad University, Boroujerd, Iran.
3. Department of Cell and Molecular Biology, Boroujerd Branch, Islamic Azad University, Boroujerd, Iran.

Background and Aim:Background and aims: Escherichia coli are the most common cause of complicated as well as uncomplicated urinary tract infections (UTIs). Most of these uropathogenic E. coli (UPEC) strains exhibit certain virulence factors (VFs), including fimbrial adhesins, toxins, sidero-phores and capsular polysaccharide. The present investigation was performed to study the toxigenic genes and antimicrobial resistance properties in UPEC isolated from Iranian patients with UTIs.

Methods:Material and Methods: This cross sectional investigation was performed on 210 urine samples collected from hospitalized patients in Boroujerd, Sanandaj and Tehran hospitals, Iran. All samples were cultured and those with positive results were subjected to polymerase chain reactions (PCR) to detect antibiotic resistance genes and toxigenic genes. Also, antimicrobial susceptibility testing was performed according to the instruction of Clinical Laboratory and Standard Institute.

Results:Results: From the total of 210 urine samples examined, 150 samples (71.42%) were positive for E. coli. High resistance levels to tetracycline (68%), sulfonamide (60%) and trimethoprim (58%) were also observed. 7.33% of tested strains were resistant to 8 antibiotics. The incidence of genes encoding resistance against aminoglycosides (aadA1 and aac(3)-IV), sulfonamide (sul1), beta-lactams (blaSHV and CITM), tetracycline (tetA and tetB), trimethoprim (dfrA1), chlor-phenicol (cat1 and cmlA) and quinolones (qnr) were (8%, 5.33%), 44.66%, (42.66%, 8%), (58.66%, 55.33%), 48.66%, (8%, 3.33%) and 30%, respectively. The frequency of toxigenic genes were hlyA (40%), cnf1 (38.66%), set-1 (24%), sen (1.33%), astA (16%), vat (10%), tsh (2%) and pic (6%).

Conclusion:Conclusion: Resistant strains of uropathogenic E. coli had the lower incidence of uropathogenic virulence factors.

Keywords:Keywords: Uropathogenic Escherichia coli; Toxigenic Genes; Antimicrobial; Iran

**P742 - 654: PCR-SEROTYPING OF LISTERIA MONOCYTOGENES ISOLATED FROM
CLINICAL, FOOD AND CATTLE SAMPLES**

Lida Lotfollahi¹, Ardalan Chaharbalesh², Mohammad Ahangarzadeh Rezaee³, Alka Hasani³⁴

1. Department of Microbiology, faculty of medicine, Urmia University of Medical Sciences, Urmia, Iran.
2. Immunology Research Center, Tabriz University of Medical Sciences, Tabriz, IR Iran
3. Tabriz Infectious and Tropical Diseases Research Center, Tabriz University of Medical Sciences, Tabriz, IR Iran
4. Tabriz Infectious and Tropical Diseases Research Center, Tabriz University of Medical Sciences, Tabriz, IR Iran

Background and Aim: *Listeria monocytogenes* and listeriosis due to it, is an important hazard for human being because of high mortality rate and ubiquitous nature of bacteria that grows on different environments. Of 13 serotypes known for *Listeria monocytogenes*, 4 of them directly related to human disease. Because routine serotype determination kits are expensive and the process is time consuming, using molecular methods to serotype determination is an accepted and reliable way to characterization of bacterial serotypes.

Methods: The number of 22 *L. monocytogenes* isolated from women with abortion, dairy and meat products and goat and sheep carcasses were used for assessment of serotypes by PCR. 5 primer pairs for detection of phosphoribosyl pyrophosphate synthetase gene (*prs*) (for genus *Listeria*), *0737* gene, transcriptional regulator gene, secreted protein gene and *lmo1118* was used for PCR. After PCR, electrophoresis was performed

Results: Among 22 *L. monocytogenes* isolates, 20 (91%) belonged to serotype 1/2a, 1/2c, 3a, remaining 2 isolates were identified as 4b, 4d, 4e. Serotype 1.2 c was predominant among clinical, food samples but serotype 4b was recovered from 2 of 3 cattle samples.

Conclusion: detection of 4b serotype among domestic animals is important because most of listeriosis epidemics occur due to this serotype

Keywords: pcr-serotyping, *Listeria monocytogenes*, human

**P743 - 697: MOLECULAR TYPING OF STREPTOCOCCUS PYOGENES ISOLATES FROM
IRANIAN CHILDREN BY RAPD-PCR METHOD**

Akram Rahimi moghaddam¹, Siavosh Salmanzadeh-Ahrabi², Tahereh Falsafi³, Mahvash Seifali⁴

1. Department of Biotechnology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
2. Department of Microbiology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
3. Department of Microbiology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
4. Department of Plant Sciences, Faculty of Biological Sciences, Alzahra University, Tehran, Iran

Background and Aim: Streptococcus pyogenes is the most frequent cause of bacterial pharyngitis. Several molecular typing methods for identification of DNA polymorphism in Streptococcus pyogenes species are established. However, Random Amplified Polymorphic DNA (RAPD), a PCR based technique, is a rapid, easy and inexpensive method that can be performed in a moderate laboratory. In this study, Streptococcus pyogenes isolates from throat of children aging from 5 to 15 years old were genotyped by RAPD-PCR.

Methods: Ten isolates of Streptococcus pyogenes obtained from throat of children aging from 5 to 15 years old were cultured in sheep blood agar and incubated in candle jar at 37°C overnight. DNA were extracted by set buffer method. The amplification conditions were optimized using H2 primer and isolate-specific fingerprints were generated. PCR products were analyzed by electrophoresis in 1.5% agarose gel. Analysis of PCR products on agarose gel was performed using NTSYSpc program.

Results: The optimized protocol generated 24 bands within the range of 400–5000 bp for primer H2. The patterns of amplification demonstrate DNA polymorphism among all isolates of Streptococcus pyogenes used in this study. We noted that for producing the reproducible RAPD-PCR results which is main disadvantage of this method, it is unavoidable to optimize correctly the conditions of RAPD-PCR. Streptococcus pyogenes isolates from this work were classified into 2 main clusters. Most of the isolates belonged to cluster 2.

Conclusion: RAPD-PCR is an effective, rapid, easy and inexpensive technique for molecular typing of bacteria. Results of RAPD-PCR may be reproducible by correct optimization of RAPD-PCR conditions.

Keywords: Molecular typing, RAPD-PCR, Streptococcus pyogenes

P744 - 726: GENETIC ANALYSIS OF STAPHYLOCOCCUS AUREUS STRAINS ISOLATED FROM PATIENTS ADMITTED TOM EMAM REZA HOSPITAL IN BOJNURD

Amir Azimian¹, Seyed Ahmad Hashemi ², Majid Ghafouri ³, Saghar Safamanesh ⁴, Sara Nojoomi ⁵, Mahsa Khosrojerdi⁶, Reza Besharati ⁷

1. Department of Pathobiology and Laboratory Sciences, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran
2. Department of Internal Medicine, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
3. Department of Internal Medicine, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
4. Department of Pathobiology and Laboratory Sciences, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran
5. Emam Reza Hospital Medical Laboratory, North Khorasan University of Medical Sciences, Bojnurd, Iran
6. Department of Pediatrics, Semnan University of Medical Sciences, Semnan, Iran
7. Department of Pathobiology and Laboratory Sciences, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran

Background and Aim:Staphylococcus aureus is a major human pathogen associated with a wide range of community and hospital acquired infections. Therefore studying its origin and resistance is of utmost importance for determining an appropriate treatment pattern. The aim of this study was to detect methicillin resistance gene by PCR and demonstrate it's type with SCCmec and agr typing typing method.

Methods:a total of 150 clinical samples were collected from patients admitted to different wards of Emam Reza Hospital. Resistance to Cefoxitin was determined with disk diffusion method. Thereafter the samples containing mecA gene were subjected to SCCmec and agr typing.

Results:frequency of mecA gene in Staphylococcus aureus strains was found to be 54% using PCR method. Resistance to Cefoxitin was 52% by disk diffusion method. Results with SCCmec typing revealed that the majority of strains were type IV and the minority were type I whereas agr typing showed type I to be predominant with the minority belonging to type IV.

Conclusion:the resistance of Staphylococcus aureus strains to antibiotics is increasing. In addition, SCCmec type IV isolates, being CA-MRSA themselves, are continuing to spread in communities. It should be noted that Staphylococcus aureus strains in different regions have different agr patterns.

Keywords:Staphylococcus aureus, Cefoxitin, SCCmec, agr, mecA

P745 - 730: THE FIRST REPORT OF ISOLATION OF PVL/ACME POSITIVE COMMUNITY ACQUIRED-METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS (USA300) IN IRAN

Amir Azimian¹, Seyed Asghar Havaei², Kiarash Ghazvini³, Mahsa Khosrojerdi⁴, Siamak Mirab Samiee⁵, Saghar Safamanesh⁶, Reza Besharati⁷

1. Department of Pathobiology and Laboratory Sciences, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
2. Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran.
3. Department of microbiology, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran.
4. Department of Pediatrics, School of Medicine, Semnan University of Medical Sciences, Semnan, Iran.
5. Reference Health Laboratories, Ministry of Health and Medical Education, Tehran, Iran.
6. Department of Pathobiology and Laboratory Sciences, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
7. Department of Pathobiology and Laboratory Sciences, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.

Background and Aim: Methicillin Resistant *Staphylococcus aureus* (MRSA) is responsible for an increasing number of serious hospital and community acquired infections. USA300 strains are known to be significant in community associated infections even though recently there are reports that they are introducing themselves into health care settings.

Methods: Totally 171 isolates of *S. aureus* were collected from different clinical samples in selected hospitals in Isfahan, Mashhad and Tehran. Then, they were evaluated by agar screening and disk diffusion methods to determine their resistance to Methicillin. The isolated MRSA strains were confirmed with detection of *mecA* gene. *mecA* positive strains were subjected to evaluation of SCCmec, agr, spa type and PVL and ACME genes. MLST performed on PVL/ACME positive MRSA strains.

Results: We found PVL/ACME positive MRSA isolate. Genetic evaluation results for this strain produced the following profile: positive for the *mecA*, *pvl*, *arcA* and *hla* genes and negative for *vanA*, *sec* and *tst1*, belonged to agr I, SCCmec IV, ST8, spa t008.

Conclusion: Our data suggests a finding of USA300 CA-MRSA isolate in Mashhad, Iran. This is an uncommon finding, because USA300 was routinely found in areas other than Middle East. A notable point about these isolates is that they belonged to American Endemic clones.

Keywords: *Staphylococcus aureus*, Methicillin, USA300, PVL, ACME, community Associated

P746 - 772: DIAGNOSTIC METHODS OF HELICOBACTER PYLORI IN GASTRIC BIOPSY

Narges Badi¹, zahra badi², sasan badi³, masomeh.mazaheri⁴

1. A graduate student in microbiology. , Ayatollah Amoli Branch, Department of Biology, Tehran, Iran.
2. Expert, hospital nurse Amiralmomenin city Kordkuy, Medical Sciences, Golestan Province
3. A graduate student in genetics, Islamic Azad University, Department of Biology, Iran
4. A graduate student in microbiology. , Ayatollah Amoli Branch, Department of Biology, Tehran, Iran.

Background and Aim: Helicobacter pylori, the major cause of gastritis, peptic ulcer disease, gastric Vadvnkarsynvmay, gastritis is a global expansion. Given the importance of the prevalence of these bacteria is different in different areas of Iran, the aim of this study was to identify the prevalence of H pylori in Golestan province.

Methods: Materials and Methods: This study was a cross - sectional study on 80 patients suffering from gastrointestinal disorders descriptive referred to the Endoscopy Department Amiralmomenin city were Kordkuy. At the beginning of Zsry-urea breath test (RUT) was used to detect bacteria after planting and from polymerase chain reaction (PCR) was used to confirm the identification of Helicobacter pylori. Then the software spss chi-square tests for the relationship between Helicobacter pylori infection properties patients was used.

Results: Of the patients studied, 93.75% and 68.75% by PCR method using culture and RUT 74.76% Bvdnd.ntayj infected with H pylori showed that between gender, education level, age group and infection disease symptoms there is a significant correlation bacteria.

Conclusion: Considering the high prevalence of H. pylori infection resulting from complications in those infected, the need for continuous monitoring, health education and control of infection in this population there.

Keywords: Helicobacter pylori, gastrointestinal disorders, RUT, culture, PCR

P747 - 830: CONSIDERATION OF SEPTICEMIA IN NEONATAL IN NICU SECTION OF SINA HOSPITAL.

Seyyed askar Roghani¹, ali khorasanizade²

1. Laboratory Sciences Group, Paramedical Faculty, JundiShapur University of medical science ,Ahvaz, Iran
2. Laboratory Sciences Group, Paramedical Faculty, JundiShapur University of medical science ,Ahvaz, Iran

Background and Aim:Septicemi is one of the most common reasons of mortality and morbidity around the world. Antibiotic is the main approach for curing this disease and quick diagnosis can decrease level of mortality. The aim of this study is to investigate the frequency of the bacteria isolated from neonatal and diagnosis sensitivity or antimicrobial resistance in patients with septicemia.

Methods:In this study 287case of neonatal in NICU section of Sina in1392 (2013- 2014). have been studied. Blood extraction from neonatal has been performed using sterile method and blood has been cultured in TSB medium, then subculture in MAC and blood Agar for 24 hours. Finally we considered cultures and in some cases, bacteria types have been identified by using bacteriological biochemical tests. Antibigram has been performed using disc diffusion method.

Results:We considered 34 patients affected by septicemia among 287 neonatal. The abundance of isolated bacteria is as following: staphylococc 25 case (73/52%), E coli(8%), Klebsiella (8 %), reptococci(4%), proteus (4%) the results, it has been showed that Staph has the greatest sensitivity to vancomycin and Amikacin high resistance to Ceftraxon.

Conclusion:Frequency of Staph coagulase Posetive has been found more than other bacteria. therefore more epidemiologic studies in sensitivity of this bacteri to antibiotics and its frequency should be performed.

Keywords:Septicemia, Antibiotic, neonatal.

**P748 - 910: DETERMINATION OF FIM H GENE AND MANNOSE SENSITIVE
HAEMAGGLUTINATION ABILITY AMONG ESCHERICHIA COLI ISOLATES IN EXTRA-
INTESTINAL IN RAFSANJAN CITY**

Sanaz Dehdashti¹, Reza ghanbarpour², Majid hemati³, asma askari⁴

1. The department of Pathobiology shahid Bahonar university of Kerman
2. The department of Pathobiology shahid Bahonar university of Kerman
3. The department of Pathobiology shahid Bahonar university of Kerman
4. The department of Pathobiology shahid Bahonar university of Kerman

Background and Aim: Escherichia coli strains are the major cause of urinary tract infections (UTI). Bacterial adherence mediated by fimbriae is an essential prerequisite for colonization of the urinary tract. Uropathogenic Escherichia coli express a number of different adhesive organelles. Type 1, or mannose-sensitive, fimbriae are produced by 80% of all uropathogenic E. coli. The purposes of this study were to determine of the virulence genes of Escherichia coli isolates from human extraintestinal diseases in Rafsanjan city.

Methods:: 218 urine samples were obtained from patients. Samples were cultured on appropriate mediums to identify Escherichia coli. The isolates were tested for haemagglutination with human O group erythrocytes in the presence and absence of mannose. DNA was extracted from all of the isolates and was examined for detection of fim H gene by using PCR technique.

Results: fim H gene were found in 83.2% of isolates. In fimbrial haemagglutination tests 52 and 77 isolates showed mannose resistant and mannose sensitive haemagglutination respectively.

Conclusion:. In this study more than 83.2% of fim H gene was detected in E. coli isolates. It has possible to design vaccines that responses against specific bacterial proteins such as fim H adhesion of type 1 fimbriae.

Keywords: Escherichia coli , fim H, rafsanjan city

**P749 - 915: ISOLATION OF STREPTOBACILLUS MONILIFORMIS FROM LABORATORY
RAT (RATTUS NORVEGICUS)**

Sanaz dehdashti¹, Baharak akhtardanesh², majid hemati³, zinat lotfi⁴, Asma askari⁵

1. The department of Pathobiology shahid Bahonar university of Kerman
2. Clinical Sciences Department shahid Bahonar university of Kerman
3. The department of Pathobiology shahid Bahonar university of Kerman
4. The department of Pathobiology shahid Bahonar university of Kerman
5. The department of Pathobiology shahid Bahonar university of Kerman

Background and Aim:Worldwide, millions of people are bitten by animals each year and Rats are responsible for 1% of these bites. Streptobacillus moniliformis is the most common cause of Rat bite fever (RBF) occurring worldwide. Laboratory personnel's and chides as owners of pet rats are now account for over 50% of the reported cases.

Methods:To estimate the occupational hazard associated with S. moniliformis infection in individuals working in conventional animal houses, random sampling from 180 adult rats were performed. Nasopharynx swabs were cultured on blood Agar, trypticase soy agar and trypticase soy broth media.

Results:S. moniliformis were isolated from 76 rats (42.2%). Typical colonies appeared after 6 days with a puff ball appearance on broth media and were circular, convex, grayish, smooth, and glistening on agar media. According to standard biochemical test, isolated bacteria were defined as S. moniliformis.

Conclusion:Current findings suggest that at least there may be an occupational risk of rat bite fever in conventional animal houses. Persons should wear gloves, practice regular hand washing, and avoid hand-to-mouth contact when handling rats or cleaning rat cages. If bitten by a rat, persons should promptly clean and disinfect the wound, seek medical attention, and report their exposure history.

Keywords:Streptobacillus moniliformis, rat, animal house.

**P750 - 949: CLONING AND IDENTIFICATION OF SINGLE NUCLEOTIDE
POLYMORPHISMS(SNP) OF POR A GENE FROM NEISSERIA MENINGITIDIS CLINICAL
SPECIMENS**

Mehrad Vosough¹, Seyed Davar Siadat², Bagher Yakhchali³, Seyed Fazlollah Mousavi⁴

1. Department of Mycobacteriology and Pulmonary Research, Microbiology Research Center, Pasteur Institute of Iran, Tehran, Iran
2. Department of Mycobacteriology and Pulmonary Research, Microbiology Research Center, Pasteur Institute of Iran, Tehran, Iran
3. Department of Industrial and Environmental Biotechnology, National Institute of Genetic Engineering and Biotechnology, Tehran, Iran
4. Department of Bacteriology and Microbiology Research Center, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: *Neisseria meningitidis* is a major causative agent of bacterial septicemia and meningitis in humans. There are no vaccines to prevent diseases caused by strains of *N. meningitidis* serogroup B at the present time. The fundamental component of *N. meningitidis* outer membrane protein is PorA which function is such as a cationic porin. In current study, Sequencing, cloning and also finding the differences in the sequence of PorA were performed

Methods: In this study, the serogroup A and B of *N. meningitidis* isolated previously by the same author was used and cultured on chocolate agar. Afterward, Genomic DNA was extracted by commercial kit. Then, specific primers were designed for complete cds of *porA* and PCR product was purified. PCR product was inserted into the PTG19-T plasmid and the recombinant plasmids were transferred to *Escherichia coli* (Top10). For screening the recombinant cells from others, they were cultured on LB agar which had ampicillin and tetracycline antibiotics. Recombinant cells were purified by a specific kit. The presence of complete cds of *porA* was confirmed by colony-PCR, double digest and sequencing

Results: In comparison with the corresponding sequences of original genes, the nucleotide sequence homology of the cloned *porA* gene was 97%. As expected, the greatest difference was observed in the sequence of the variable region of *porA* gene, and the variable regions were located in Loop 1 and 4

Conclusion: Designing of highly effective vaccines is mediated by protein PorA. Therefore, this selected region could be an appropriate candidate in order to design effective vaccines

Keywords: *Neisseria meningitidis*, PorA, Colony-PCR

**P751 - 1082: ANTIBIOTIC RESISTANCE OF 12 PSEUDOMONAS SPP. ISOLATED FROM
CLINICAL SPECIMENS OF KERMAN HOSPITALS**

Sohrab Rajaei¹, : Nadia Kazemi-pour², Farokh Rokhbakhsh-Zamin³

1. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
2. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
3. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.

Background and Aim: *Pseudomonas aeruginosa* is one of the most common human pathogens. It is the causative agent for 10% of nosocomial infections. Accordingly, Identification of these bacteria helps public health programs in the shortest time. With the rapid detection of virulence genes related to these bacteria and enhancing our information about resistant genes in each area, treatment of patients can be done in a better way. So, by evolution of our information about virulence gene as well as specific detection of bacteria, treatment of patients can be done more efficiently and on time.

Methods: In this study, 12 *Pseudomonas aeruginosa* strains were isolated from patients in Kerman hospitals from various sources of clinical wounds caused by burns. By Multiplex PCR assay and specific primers, antibiotic resistant genes qnr BM, qnr SM, qnr AM were identified among test bacteria .

Results: According to Multiplex PCR samples, 1 samples (8/33%) of qnr B positive, 0 (0%) of qnr S positive and 7 samples (58/33%) qnr A were positive, which qnr A of the rest statistically higher than that with most Peugeot hash results for the same.

Conclusion: Rapid detection and accurate reporting of these bacterial strains in hospitals can lead to better control and more effective dissemination of these strains. The use of molecular methods for diagnosis of resistant genes in pathogenic bacteria including hospital-acquired infections such as *Pseudomonas aeruginosa* could be helpful to know the epidemiology of resistant bacteria and to find a better way to defend by suitable drugs.

Keywords: *Pseudomonas aeruginosa*, Multiplex PCR, qnr BM, qnr SM, qnr AM

**P752 - 1126: PATHOGENIC BACTERIA ON CELL PHONES TOUCH AND KEYBOARD: A
SYSTEMATIC REVIEW**

Mehran Farzaneh¹, Hossein Akhgar²

1. Jahrom University Of Medical Science
2. Jahrom University Of Medical Science

Background and Aim: A microbiologist at the University of Arizona in 2012 published a study showing that cell phones, the more bacteria than the toilet are normal. Due to advances in technology and the necessity of using mobile phones, transmission of pathogenic bacteria is important.

Methods: This study was to systematically review the 45 articles selected since the keyword 2000-2015 bacteria, pathogenic bacteria, phones touch, keyboard among them, 20 articles were selected and results were extracted. Sites include: Google Scholar, PubMed, SID, Margin and many related topics.

Results: Most studies have been found in samples transfer to enrich the nutrient broth and lactose broth and was incubated for 24 h at 37 ° C. Then the medium for the isolation of EMB, MacConkey and were cultured Blood Agar. Then were incubated for 24 h at 37 ° C. The results indicate that the majority of bacterial contamination was positive again, most of which is related to touch and keyboard input. In between mobile phones touch was the most common Staphylococcus, Escherichia coli and Streptococcus belongs. This type of bacteria also found in cell phones, respectively, including Pseudomonas, Serratia, Bacillus, Klebsiella and is Entrobact.

Conclusion: Research reveals a host of pathogens that cause disease in humans and living beings are, during a telephone conversation with different people makes the device a perfect environment for the growth of various bacteria become. According to the results, the contamination of cell phones pathogenic bacteria, especially touch, more. Therefore it is recommended to wash hands after each use of mobile phones should be considered.

Keywords: bacteria, pathogenic bacteria, phones touch, keyboard

**P753 - 1191: PREVALENCE OF ESCHERICHIA COLI PATHOTYPES IN KURDISTAN
PROVINCE 1391-1392**

Latifeh Panahandeh¹, Mitra Salehi², Saied Mostaan³, Amir dashti⁴, Moein shahidi nejad monfared
tehrani⁵, Saeid bouzari⁶

1. Molecular biology Department, Pasteur institute of iran
2. Islamic Azad University North Tehran Branch
3. Molecular Biology department, Pasteur institute of iran
4. Molecular Biology department, Pasteur institute of iran
5. Molecular Biology department, Pasteur institute of iran
6. Molecular Biology department, Pasteur institute of iran

Background and Aim: Diarrhea is one of the basic problems for children's health in Iran and other developing countries. diarrhea-causing *Escherichia coli* (*E. coli*) is one of the main causes of mortality in developing countries under in 5 year old children. Pathotypes of *E. coli* that cause diarrhea include EPEC, ETEC, EIEC, EHEC, DAEC and EAEC. The present study aimed to investigate the prevalence of *E. coli* pathotypes in Kurdistan province using molecular diagnostic techniques

Methods: Sampling was conducted using questionnaires completed by 100 patients of all ages suffering from diarrhea in hospitals and health centers in Kurdistan province and its cities throughout a year. The samples were cultured on the MacConkey agar and then, the identification of *E. coli* samples was performed using standard biochemical methods. *E. coli* isolated were tested by PCR method

Results: Of the total samples analyzed, 80 (80%) *E. coli* were isolated from the culture and as a result of this testing, 16 samples (20%) were EAEC with the highest prevalence in fall season and 10 samples (12.5%) were ETEC with the highest prevalence in winter and spring, 23 samples (29%) were STEC with the highest prevalence in winter and autumn, and 8 samples (10%) were EPEC, with the highest prevalence in autumn and winter, and no samples of EIEC was observed

Conclusion: This study shows the importance of these pathotypes of *E. coli* to diarrhea in people in different seasons and necessity of physicians' attention to this group of bacteria.

Keywords: *Escherichia coli*, Pathotype, diarrhea

**P754 - 1236: GENETIC DIVERSITY OF HELICOBACTER PYLORI STRAINS ISOLATED
FROM PATIENTS WITH GASTRODUODENAL DISEASES USING MULTILOCUS
SEQUENCE TYPING IN KERMANSHAH**

Nasrin Souri¹, amirhoshang alvandi², ramin abiri³

1. presenter
2. Corresponding
3. Corresponding

Background and Aim: Helicobacter pylori is etiological agent gastritis, peptic ulcer disease, gastric cancer, duodenal ulcer and MALT Lymphoma. It is estimated that about 70% of people are infected with H. pylori. Peptic ulcer and gastric cancer are influenced by ethnic and geographic conditions, and also great diversity among strains of H pylori. By 2010, ten different populations of H pylori has been identified using Mlst. The geographic differences among strains might explain differences in the prevalence of H. pylori-related diseases in some areas. Various methods have been provided for typing of H. pylori Such as PFGE, REA Ribotyping, Rep-PCR and MLST. This study investigates the molecular epidemiology and genetic diversity of H. pylori isolates obtained from patients Gastroduodnal of Kermanshah in 2013 by MLST

Methods: Two biopsies were taken from patients with digestive disorders. sample was cultured on colombia agar containing %10 sheep blood. DNA extraction was carried out on identified colonies. The seven house keeping genes was amplified and sequences, and submitted in MLST and Genbank database. Allele Number and sequence type of each isolate were characterized and analysed using START v2 and MEGA v6 for drawing dendrogram

Results: Allele number and sequence type of H. pylori strains, isolated in Kermanshah were new and were not registered in the mlst database previously

Conclusion: Due to the uniqueness of the strain and their diverse sequence, the H.pylori isolates were characterized in separate .

Keywords: Helicobacter pylori, MLST,

Nanotechnology and Nanomicrobiology

P755 - 70: ISOLATION AND MOLECULAR IDENTIFICATION OF GOLD NANOPARTICLE-PRODUCING MICROORGANISMS

Mandana Jafari¹, hamid forootanfar², farokh rokhbakhsh-zamin³, mojtaba shakibaei⁴, mohammad hasan moshafi⁵, atefeh ameri⁶

1. Pharmaceutics Research Center, Institute of Neuropharmacology, Kerman University of Medical Sciences, Kerman, Iran
2. Pharmaceutics Research Center, Institute of Neuropharmacology, Kerman University of Medical Sciences, Kerman, Iran
3. islamic azad university ,kerman branch ,kerman , iran
4. Pharmaceutics Research Center, Institute of Neuropharmacology, Kerman University of Medical Sciences, Kerman, Iran
5. Pharmaceutics Research Center, Institute of Neuropharmacology, Kerman University of Medical Sciences, Kerman, Iran
6. Pharmaceutics Research Center, Institute of Neuropharmacology, Kerman University of Medical Sciences, Kerman, Iran

Background and Aim: In recent decades, nanotechnology has been developed in medical field, and most of the nanoparticles are highly valuable in hygienic care. Nanoparticle synthesis methods based on biological procedures due to its high compatibility with the environment, particles and have a special place. The aim of this study was to investigate the biological production of gold nanoparticles by microorganisms isolated from mine soil in order to localize gold nanoparticles biological synthesis.

Methods: An Au ion reducing bacterial strain was first isolated from soil samples and then was identified by morphological and biochemical tests according to the Bergey's Manual of Systematic Bacteriology. In the next step, the 16S rDNA gene from the isolate was amplified with PCR method using the specific primers and then after the sequencing.

Results: the result was compared with other sequences previously submitted in the GenBank. The obtained results showed that one bacterial strain, identified as *Pseudomonas pseudoalcaligenes* was able to reduce Au³⁺ ions.

Conclusion: The 16S rDNA gene sequence of the isolated strain was deposited under accession number of KF055346 in the GenBank.

Keywords: Biological synthesis, Gold nanoparticles, *Pseudomonas pseudoalcaligenes*

**P756 - 117: PREPARATION OF PLGA NANOPARTICLES FOR ORAL VACCINE DELIVERY
OF A. BAUMANNII BIOFILM ASSOCIATED PROTEIN (BAP)**

Elham Darzi eslam¹, iraj rosooli²

1. biology department of shahed university
2. biology department of shahed university

Background and Aim: *Acinetobacter baumannii* is a drug-resistant Gram-negative bacterium causing nosocomial infections. Vaccination is one of the effective procedures for infection control. The aim of mucosal vaccination is to make protective immunity by particular antibodies at mucosal surfaces and by induction of cellular immunity. Oral vaccination is an attractive mode of immunization because of its acceptability and the ease of performance. PLGA (poly(lactic-co-glycolic acid)) nanoparticles are suitable protein carriers offering antigen protection, increased permeation across mucosal surface and controlled release of encapsulated antigen.

Methods: Loaded PLGA nanoparticles were prepared by double emulsion solvent evaporation method. All the process was done at room temperature. 15 mg of PLGA was dissolved in dichloromethane and 1 ml of Bap (1mg/ml) added drop wise. After 3 times sonication, PLGA-antigen solution was added to polyvinyl alcohol. The solution was sonicated 4 times. Its volume reached to 50ml and was centrifuged after evaporation of its solvent. Supernatant was collected and the pellet was washed twice and lyophilized to storage at -70°C. The entrapment efficiency and loading capacity was determined using Bradford protein assay. The loaded Bap release profile was evaluated invitro.

Results: The EE and LC were 90% (W/W) and 6% (W/W). After 5 h of incubation in GI medium, 2.7% of Bap was released from PLGA-NPs. Release reached 80% at 24 h.

Conclusion: The results represented this method to be efficient for oral delivery of our protein. Further analyses such as mucosal and systemic immune responses are needed for confirmation of its application.

Keywords: PLGA, nanoparticle, mucosal immunization, Bap, *A. baumannii*

P757 - 118: BIOSORPTION OF LEAD BY SPORES OF BACILLUS ATROPHAEUS

Afrouzossadat Hosseini Abari¹

1. Department of Biology, Faculty of Science, University of Isfahan

Background and Aim: Contamination of lead in the environment is a major threat to human life and environment. The high concentration of lead in the water and food supply causes a direct hazard to human and animals. Nowadays, several physical and chemical methods are used for restriction of heavy metals from environment which are expensive and may cause adverse effects. However, bioremediation of heavy metals by microorganisms are more cost effective and affordable. In this study, spores of a new marine bacillus, *Bacillus atrophaeus* NSP were used for biosorption of lead in water.

Methods: *Bacillus atrophaeus* NSP (accession number of Gene Bank , NCBI: HQ414235.1) was incubated in 30 °C in DSM sporulation medium for 48hours. The spores were then purified by renografin. The purified spores were added to 1 M Pb(NO₃)₂ in distilled water. Absorption of Pb on the spore surface was detected after 1 hour by Atomic Absorption Spectroscopy (Perkin-Elmer 3030).

Results: The results revealed that 83.7% of lead was absorbed on the spores after 1 hour.

Conclusion: Since spores are resistant form of bacteria in high temperatures, extreme pH values, UV radiation and also they are survive in nature for a long time, they are valuable tools for removal of heavy metals from environment.

Keywords: Biosorption, *Bacillus atrophaeus*, Lead, Spore

**P758 - 143: THE ANTIBACTERIAL EFFECT OF DIFFERENT SIZES OF SILVER
NANOPARTICLES ON STAPHYLOCOCCUS AUREUS ISOLATES AND THEIR PLASMID
PATTERN**

Nasrin Jahandideh¹

1. Malahat Ahmadi

Background and Aim: Silver nanoparticles as an alternative to antibiotics are in consider in recent years. It seems that sizes may affect their antibacterial properties. The present study aimed to investigate the effect of different sizes of silver nanoparticles on *Staphylococcus aureus* isolates and their plasmid pattern.

Methods: Twenty five *Staphylococcus aureus* isolates from the skin around the groin dog samples, were identified. Their plasmid pattern determined using alkaline lysis method. MIC and MBC of the isolates determined against different sizes of 20, 40 and 70 nm silver nanoparticles at concentrations of 500-1000 µg/ml. The plasmid pattern of all isolates determined after the effect of different sizes of silver nanoparticles also.

Results: The concentrations of 500, 550, 600 µg/ ml of different sizes of silver nanoparticles had no antibacterial effect on *Staphylococcus aureus* and in fact, all the isolates showed sensitivity in the concentrations higher than 650 µg/ mL.

Conclusion: The results showed that the antibacterial effect of silver nanoparticles with different of sizes 20, 40 and 70 nm had no significant differences. In spite the different sizes of silver nanoparticles had different effect on plasmid pattern of the isolates. As it can be concluded that by reducing the sizes of silver nanoparticles, their effect on plasmid pattern were more obvious.

Keywords: *Staphylococcus aureus*, silver nanoparticles, plasmid pattern

**P759 - 160: ENGINEERING OF BACILLUS SUBTILIS SPORES TO DISPLAY OF
PHENOLOXIDASE ON SPORE SURFACE**

Afrouzossadat Hosseini Abari¹

1. Department of Biology, Faculty of Science, University of Isfahan

Background and Aim: Spore display in *Bacillus subtilis* spore is an interesting alternative to other bacterial surface display systems because the fusion proteins do not need to cross the cytoplasmic membrane, and several chaperones are present in spores to assist correct folding of the fusion proteins. In the present study, our aim was to immobilize a type of bacterial phenol oxidase (tyrosinase) on spores of *B. subtilis* to develop a cost- and labor-effective process for efficient production of tyrosinase with nano- and bio-technologically remarkable features.

Methods: The cotE of *Bacillus subtilis* was used as an anchor motif to display of tyrosinase from *B. megaterium* on the spore surface. The pSDJH-cotE-linker-tyr vector was constructed and transformed to *Bacillus* by the two-step (SP I, SP II) method. Western Blotting and Flow Cytometry were used to verify surface expression of tyrosinase on the purified spores. Moreover, tyrosinase activity was monitored in the presence of L-tyrosine (substrate) and CuSO₄ (inducer).

Results: The purified spores of *B. subtilis* DB104 (pSDJH-cotE-tyr) and wild type *B. subtilis* DB104 were stained with FITC-labeled anti-His-tag antibody. Display of tyrosinase also verified by Western Blotting and assay of tyrosinase activity. This indicates that tyrosinase was efficiently expressed, and displayed on the surface of the spores by CotE anchoring protein.

Conclusion: This genetically immobilized tyrosinase on the spores would make a new advance in industrial, medical, and environmental applications.

Keywords: Phenol oxidase/ Spore surface display/ Tyrosinase / CotE

**P760 - 170: VEGFR2-HIGG SPECIFIC DIABODY GENE CONSTRUCTION AND EXPRESSION
IN E.COLI EXPRESSION SYSTEM**

Fatemeh Bayat¹, Reza Shapouri², Mahdi Behdani³

1. Department of Microbiology, Faculty of Sciences, Zanjan Islamic Azad University, Zanjan, Iran
2. Department of Microbiology, Faculty of Sciences, Zanjan Islamic Azad University, Zanjan, Iran
3. Department of Molecular Medicine, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Vascular endothelial cell growth factor receptor-2 or VEGFR-2, one of the molecules involved in the formation of new blood vessels, or angiogenesis, which block an important role in preventing tumor formation and metastasis in cancer, respectively. Camels produce single heavy-chain antibodies (VHH) in addition to usual antibodies. These minimal-sized binders are very robust and bind the antigen with high affinity in a monomeric state.

Methods: In this study, plasmid containing a proprietary Nanobody against human IgG was purified by PCR, using specific primers was amplified. Then the amplified product was cloned into the piece nano-specific antibodies against VEGFR2. After confirmation of cloning, fragments was transformed into strain of E.coli bacteria wk6 for expression of recombinant protein. Cloning was confirmed by means of, PCR clony, digestion and sequencing. Finally expression of diabody was confirmed by western blotting.

Results: We describe the construction, expression, and purification VEGFR2-specific Diabody. Two variable fragments of nobodies, 3VEGR19 and hIgG were linked together by the upper hinge segment of antibody to make diabody.

Conclusion: Using recombinant antibody fragments expressed in E.coli in medical research, biotechnology and pharmaceutical sciences due to the inherent characteristics of these components on the rise. The aim of this project is to increase the half-life of our proprietary Nanobody against endothelial cells of blood vessels Nanobody binding to human IgG.

Keywords: Diabody, Nanobody, vascular endothelial growth factor recepror-2

**P761 - 171: THE EVALUATION OF NANOGOLD FOR UTILIZATION IN SALMONELLA
SENSING**

Narges Maleksabet¹, Mohamadreza Masoumian², Majid Zeinali³

1. Department of Bioscience and Biotechnology. Malek-Ashtar University of Technology-Tehran.Iran
2. Department of Bioscience and Biotechnology. Malek-Ashtar University of Technology-Tehran.Iran
3. Biotechnology Research Center, Research Institute of Petroleum Industry (RIPI). Tehran.Iran

Background and Aim: Food safety is the most concern in food industry. One of the numerous application of nanotechnology is nanobiosensor developing for contaminants sensing in food including toxins , microbial agents and others. Salmonella is one of the major threats for food and water safety. In this study, the synthesized nanogold is stabilized by HRP conjugated antibody as a model protein to be used in a salmonella detection system in future study.

Methods: The 500 μ l nanogold solution 30 nm that was synthesized by citrate reduction, already, was mixed with HRP conjugated antibody (100 nM) and incubated in 4°C. After, the solution was centrifuged and protein fixation on nanogold in supernatant was evaluated by spectroscopy. The enzyme activity was assayed for efficiency determination of modified nanogold. For this, ABTS as substrate and H₂O₂ was used and a spectroscopy scanning in 280-500 nm was performed.

Results: Due to surface Plasmon resonance, a red shift is produced from near 520 to near 550 nm in absorbance spectrum of supernatant as a result of nanogold coupling to antibody. The HRP activity of conjugated antibody after coupling to nanogold was monitored in 1-8 min and results show the absorbance peak of ABTS in 340 nm shifts to 415 nm that is related to efficient protein modified nanogold.

Conclusion: In this study, to evaluation of synthesized colloidal gold solution, its coupling to HRP-conjugated antibody as a model was performed and the results, promise that the produced nanogold is efficient for stabilization by antisalmonella to develop a sensitive salmonella nanobiosensor.

Keywords: Nanogold- synthesis- evaluation

P762 - 172: THE EFFECT OF PH IN CONTROL OF NANOGOLD SYNTHESIS

Narges Maleksabet¹, Mohamadreza Masoumian², Majid Zeinali³, Asieh Aramvash⁴

1. Department of Bioscience and Biotechnology. Malek-Ashtar University of Technology-Tehran.Iran
2. Department of Bioscience and Biotechnology. Malek-Ashtar University of Technology-Tehran.Iran
3. Biotechnology Research Center, Research Institute of Petroleum Industry (RIPI). Tehran.Iran
4. Department of Bioscience and Biotechnology. Malek-Ashtar University of Technology-Tehran.Iran

Background and Aim: Among the metal nanoparticles, nanogold is attractive for biological applications due to optical properties and easy synthesis. One of this ,is usage of gold nanoparticles (GNPs) in nanobiosensors by colorimetric assays. (1) The final scope of our study is focused on nanobiosensor development for salmonella detection based on GNPs. For this, we synthesized gold colloids by citrate reduction method. In this study, the effect of pH on nanogold synthesis was evaluated and determined that in low pH, GNPs were aggregated so as its color and uv-vis spectra was changed.

Methods: In the fixed concentration of chloroauric acid (10 mM stock) and sodium citrate gold nanoparticles 30 nm, pH 6 was synthesized (spectroscopy & SEM results), while adding Hcl , the solution pH varied from 6 to 3. The absorbance peak of nanogold solution was monitored in 0-140 minutes interval.

Results: The results show , the synthesized nanogold is monodispersed distribution with 30 nm size in pH 6 . After changing pH to 3, corresponding to reduction of the specific peak of nanoparticle in 520-550 nm, the increasing of it in 600 nm region is observed . The color of solution shift from red to violet, too.

Conclusion: These finding suggest that the changes is related to aggregation of GNPs in low pH. Finally , it can be concluded that one of the important points in uniform nanogold synthesis based on citrate reduction is the pH control. It would seem , the optimized pH is near to neutral pH.

Keywords: Gold nanoparticle, pH variation, nanobiosensor, aggregation, salmonella

**P763 - 176: STUDY OF ANTIBACTERIAL CHARACTERISTICS OF SILVER
NANOPARTICLES ON STAPHYLOCOCCUS AUREUS**

Ehsan Zayerzadeh¹, Azadeh Fardipour ²

1. Department of Biology, Faculty of Food Industry and Agriculture, Standard Research Institute, Karaj, Iran
2. Department of Vaccine Quality Control, Razi Vaccine and Serum Research Institute, Karaj, Iran.

Background and Aim: Microbial antibiotic resistance is a challenging medical problem nowadays. Silver have strong inhibitory and bactericidal effects as well as a antimicrobial property for bacteria, fungi, and virus. Hence, it is of considerable interest to develop antibacterial with a new mechanism of action which can potentially evade the emergence of drug resistance. In this work, we investigated antibacterial activity of silver nanoparticles against Staphylococcus aureus bacteria.

Methods: In the present study, we assessed antibacterial effects of silver nanoparticles against Staphylococcus aureus bacterial strain. Several concentrations of silver nanoparticles were tested for antibacterial activity against Staphylococcus aureus by disc-diffusion susceptibility at different time intervals.

Results: The results of our study showed that high concentrations of silver nanoparticles have significant antibacterial properties against Staphylococcus aureus following incubation period.

Conclusion: In conclusion, results of the present study demonstrated silver nanoparticles has antibacterial activity on Staphylococcus aureus and may be use as new agent for treatment of disease induced by Staphylococcus aureus..

Keywords: silver nanoparticles, Staphylococcus aureu, antibacterial activity.

**P764 - 199: PREPARATION AND STUDY OF ANTIBACTERIAL PROPERTIES OF
VANCOMYCIN-LOADED POSITIVELY AND NEGATIVELY CHARGED MESOPOROUS
SILICA NANOPARTICLES AGAINST STAPHYLOCOCCUS AUREUS**

Elham Nematzadeh¹, Ayyoob Arpanaei², Mehdi Alavi³, Parvin Shariati⁴

1. Department of Industrial and Environmental Biotechnology, National Institute of Genetic Engineering and Biotechnology, Tehran, Iran
2. Department of Industrial and Environmental Biotechnology, National Institute of Genetic Engineering and Biotechnology, Tehran, Iran
3. Department of Agricultural Biotechnology, National Institute of Genetic Engineering and Biotechnology, Tehran, Iran
4. Department of Industrial and Environmental Biotechnology, National Institute of Genetic Engineering and Biotechnology, Tehran, Iran

Background and Aim: The emergence of life-threatening multi-drug resistant *Staphylococcus aureus* and other antimicrobial-resistant pathogens has become a major concern both in the community and health-care facilities. Development of novel antibiotic formulation procedures is of great importance in enhancing the stability and efficiency of commonly used antibiotics, thereby solving problems and concerns regarding the applications of antibiotics and their emerging resistance

Methods: vancomycin-loaded mesoporous silica nanoparticles (VAN-MSNs) were prepared. The MSNs of negatively or positively charged surfaces were synthesized and then were characterized. Thereafter, antibacterial activity, stability of the loaded drug and cytotoxicity of VAN-MSNs were evaluated and compared with those of the free VAN by exposure to VAN-semi resistant *Staphylococcus aureus*, as a model pathogen and mouse fibroblast cells (L929) as a model eukaryotic cell.

Results: The average nanoparticle size and pore size of the as-synthesized MSNs were 113 and 4 nm, respectively. The loading efficiency values of positively and negatively charged MSNs were measured to be 36.82% and 85.31% respectively. MIC of VAN-MSNs was half of that of the free Van in the in vitro studies. In addition, it was found that physical adsorption of Van on functionalized and non-functionalized MSNs significantly increases drug stability during storage in acidic and alkaline pH. The results of the cytotoxicity tests on nanoparticles obtained by the MTT assay showed that the prepared antibacterial nanosystems do not have significant cytotoxicity against eukaryotic cells

Conclusion: MSNs can be recommended as suitable carriers for delivery of vancomycin into infection site.

Keywords: Mesoporous silica nanoparticles, Vancomycin, *Staphylococcus aureus*, Minimal inhibitory concentration, MTT assay

**P765 - 211: EVALUATION OF ANTIBACTERIAL ACTIVITY OF SILVER NANOPARTICLES
PRODUCED BY MELIA AZEDARACH**

Shahab Ojani¹, Leila Safari², Fatemeh Safari³

1. Young Researchers and Elite Club, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran.
2. Master of Microbiology, Department of Biology, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran.
3. Master of Microbiology, Department of Biology, Ayatollah Amoli Branch, Islamic Azad University, Amol, Iran.

Background and Aim: Development of a biologically inspired experimental process for synthesis of nanoparticles is evolving into the area of nanotechnology research. Green synthesis of nanoparticles is very simple, non-toxic, cost effective and eco-friendly. The present study reports the synthesis of silver nanoparticle using *Melia azedarach* leaves extract were used as reducing agent for reduction of silver nitrate solution in short period.

Methods: The silver nanoparticles formation was confirmed by the colour change of plant extracts and further confirmed with the help of UV-Vis, FT-IR, XRD and TEM. These phytosynthesized silver nanoparticles were tested for antibacterial activities using minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) method. The test cultures such as *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Staphylococcus aureus* of bacteria was used.

Results: The surface Plasmon resonance peak, centered near 450 nm, affirmed the reduction of Ag⁺ to Ag⁰. Stability of synthesized silver nanoparticles was analyzed using UV-visible absorption spectra. The FTIR measurement was carried out to identify the possible biomolecules responsible for efficient stabilization of silver nanoparticles. X-ray diffraction analysis showed that the particles were crystalline in nature with face centred cubic (FCC) structure. TEM showed the formation of silver nanoparticles with an average size of 8-30 nm.

Conclusion: Biosynthesized silver nanoparticles showed potent antibactericidal activity against human pathogenic bacteria. It can be concluded that the leaves of *Melia azedarach* can be good source for synthesis of silver nanoparticle which shows antibacterial activity against human pathogens.

Keywords: *Melia azedarach* - Green synthesis - TEM - *Escherichia coli* - antibactericidal activity - human pathogens.

**P766 - 212: THE ANTIBACTERIAL EFFICACY OF SILVER NANOPARTICLES DERIVED
FROM INULA ROYLEANA LEAVES**

Shahab Ojani¹, Leila Safari², Fatemeh Safari³

1. Young Researchers and Elite Club, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran.
2. Master of Microbiology, Department of Biology, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran.
3. Master of Microbiology, Department of Biology, Ayatollah Amoli Branch, Islamic Azad University, Amol, Iran.

Background and Aim: The biological approaches for synthesis of nanoparticles using plants and their extract are better than chemical and physical procedures because of low energy and time expenditure. Green synthesis of nanoparticles is an eco-friendly method and uses natural solvent. In this research, extracellular biosynthesis of the silver nanoparticles was carried out by using extract of *Inula royleana* that treated with aqueous silver nitrate solution extracts.

Methods: Synthesized silver nanoparticles were characterized by UV-visible, Fourier transform infrared Spectroscopy (FTIR), X-ray diffraction (XRD) and Transmission Electron Microscopy (TEM). Antibacterial activity of silver nanoparticles was measured using disk diffusion on gram positive (*Staphylococcus aureus*) and gram negative (*Escherichia coli*) bacteria.

Results: The formation of silver nanoparticles was confirmed by an absorption peak at 465 nm. TEM and XRD analysis showed the average particle size of 20 nm as well as revealed their cubic structure. FTIR results showed the role of compounds phenols, carbohydrates and proteins in synthesis of silver nanoparticles. Biosynthesized silver nanoparticles showed potent antibactericidal activity against human pathogenic bacteria.

Conclusion: Thus, the synthesis of AgNPs using whole plant aqueous extract leaves of *Inula royleana* would be helpful for the preparation of pharmaceutically useful drugs to destroy pathogenic microbes.

Keywords: *Inula royleana* - Silver nanoparticles - XRD - Antibactericidal activity - Disk diffusion - *Staphylococcus aureus*.

**P767 - 220: ANTIBACTERIAL AND ANTIBIOFILM CHARACTERISTICS OF SILVER
NANOPARTICLES LOADED AGAR HYDROGEL AGAINST STAPHYLOCOCCUS AUREUS**

Leila sadat Bouryabaf¹, Leila sadat², Mehran³, Hossein⁴, Maryam⁵, Negin⁶

1. Bouryabaf
2. Moradi
3. Tajik
4. Shirdel
5. Heydarian

Background and Aim: Gel technology known as an innovative approach to food plant sanitation. Antibacterial and antibiofilm effect of agar hydrogel incorporating silver nanoparticles (SNP) at various concentrations was studied in vitro.

Methods: In first step, the minimum inhibitory concentrations (MICs) of SNP was determined against *S. aureus* via agar dilution method. In second step, hydrogels were prepared from a mixture of 0.8% w/v agar and SNP ($\frac{1}{2}$ MIC, MIC and 2 MIC) and their inhibitory efficacy against planktonic and biofilm forms of bacteria were measured using agar spot and microtiter test, respectively. The MIC value was 125 $\mu\text{g mL}^{-1}$.

Results: The results of this study confirmed the strong ability of SNP loaded hydrogel against one day old *S. aureus* biofilm at contact times of 15 min. By increasing SNP, antibiofilm activity of hydrogels decreased.

Conclusion: We recommended SNP incorporated agar hydrogel as an effective antibiofilm sanitizer.

Keywords: Agar, Hydrogel, Nanoparticles, Biofilm, Antibacterial.

P768 - 223: BIOSYNTHESIS OF ZNO NANOPARTICLES USING LUMINESCENT VIBRIOS

Maryam Barani¹, Mansour Mashreghi², Ali Makhdoumi³

1. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
2. Cellular and Molecular Research Group, Institute of Biotechnology, Ferdowsi University of Mashhad, Mashhad, Iran
3. Cellular and Molecular Research Group, Institute of Biotechnology, Ferdowsi University of Mashhad, Mashhad, Iran

Background and Aim: Microorganisms have been introduced as eco-friendly Nano factories for biosynthesis of nanoparticles in a clean and low-cost way. Usage of luminescent bacteria for production of ZnO nanoparticles have not been documented yet.

Methods: Therefore in this study luminescent bacteria (*Vibrio* spp.) isolated from shrimp farm located in south east of Iran were used for in vitro biosynthesis of ZnO NPs. Luminescent *Vibrio* strains (VLA, VLB identified as *Vibrio harvey* using 16s rRNA gene analysis) were grown overnight on seawater-based complete (SWC) medium and then 5 mM ZnSO₄.H₂O solution was added into flasks containing minimal media of fourth dilution of above overnight bacterial suspension, heated on a water bath up to 80 °C for 30 min. A white precipitation was appeared at the bottom of the flask as indication for nanoparticles formation. Then, flasks were incubated at 30 °C in shaking condition of 120 rpm for 24 hours. The product was filtered and then dried in a vacuum oven at 70 °C for 3 hours.

Results: The initial formation of nanoparticles was studied by UV-vis spectroscopy in absorption peak at 360 nm. Further characterizations were applied using XRD, FTIR and DLS instruments. XRD pattern showed that ZnO nanoparticles were properly formed. Also the obtained FTIR spectra of ZnO NPs exhibited peak at 420 cm⁻¹ (standard peaks for ZnO NPs are normally between 400–500 cm⁻¹) and the size of particles was around 60 nm according to DLS analysis.

Conclusion: Therefore we concluded that luminescent Vibrios are able to produce ZnO nanoparticles, fast and extracellular.

Keywords: microbial biosynthesis, ZnO nanoparticles, luminescent bacteria, UV-vis, XRD, FTIR

**P769 - 230: ANTICANDIDAL ACTIVITY OF FLUCONAZOLE CONJUGATED GOLD
NANOPARTICLES AGAINST FLUCONAZOLE RESISTANT STRAINS OF CANDIDA
ALBICANS**

Ali Javadi¹, Mehrdad Memarian ², Roohollah Fateh ³

1. PhD Student, Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
2. Assistant Professor of Microbiology, Department of Microbiology, Islamic Azad University, Qom, Iran.
3. Assistant professor of Medical Mycology, Department of Microbiology and Immunology, Faculty of Medicine

Background and Aim: A number of women with vulvovaginal candidiasis suffer from recurrent infection that affects the quality of their life. Other hand, increased use of antifun-gals especially azolic drugs for treatment of recurrent candidiasis is the important factor for drug resistance among Candida iso-lates from patients with vulvovaginitis candidiasis. The aim of this study was evaluation of antifungal effects of fluconazole conjugated gold nanoparticles in order to achieve better antifungal drugs for treatment of patients with vaginal candidiasis especially, recurrent vulvovaginitis

Methods: After collection of 300 specimens by vaginal swabs, culture and isolation of primary colonies and determination of Candida species, fluconazole resistant strains of Candida albicans was recognized using disc diffusion method. Finally, antifungal effects of fluconazole conjugated gold nanoparticles were evaluated using broth microdilution method in comparison with fluconazole.

Results: Only, one fluconazole resistant strains of C. albicans was isolated from patients (MIC=64µg/ml). The results obtained from antifungal susceptibility testing showed that this strains was sensitive to fluconazole conjugated gold nanoparticles (MIC=2µg/ml).

Conclusion: According to favorite antifungal effects of fluconazole conjugated gold nanoparticles on resistant strains of C. albicans, it looks promising to achieve the new drug with excellent anticandidal effects in future.

Keywords: recurrent vaginitis, Candida albicans, gold nanoparticles, fluconazole

**P770 - 239: NANOTECHNOLOGY APPROACHES FOR DEVELOPMENT OF NOVEL
NATURAL ANTIBACTERIAL PRODUCTS; PROS AND CONS**

Hasan Rafati¹, Atousa AliAhmadi², Roya Moghimi³

1. Dep. Pharm. Eng., Medicinal Plants and Drugs Research Inst., Shahid Beheshti Univ.
2. Dep. Biology, Medicinal Plants and Drugs Research Inst., Shahid Beheshti Univ.
3. Dep. Phytochem., Medicinal Plants and Drugs Research Inst., Shahid Beheshti Univ.

Background and Aim: The growing concern about the antibiotic resistance demonstrated by many microorganisms has recently inspired nanotechnology scientists for designing innovative biomaterials with antibacterial properties. Metal based nanoparticles are among the well-established antibacterial nanomaterials, which suffer from the increasing number of toxicological reports (1).

Methods: Natural antibacterial agents, on the other hand, are among the most interesting compounds for new antibiotic discovery which also can benefit from nanotechnology approaches. It is estimated that 40% of the new chemical entities in drug discovery stages are poorly water soluble which is a key property in dissolution, absorption and thus the in vivo efficacy. Therefore, enhancing the solubility, dissolution rate and bioavailability of a drug candidate is a very challenging task in drug development which may all be provided by nanotechnology approaches [2].

Results: Essential oils (Eos) are among the most widely used class of antibacterial agents in food, drug and cosmetics. In the last few years, we have used new approaches for preparation and characterisation of nanoemulsions of EOs to investigate the impact on the antibacterial activity against pathogenic and foodborne bacteria. Our results showed an interesting improvement in the antibacterial activity using the above mentioned nanocarriers. The mechanism of antibacterial activity was investigated by measuring potassium, protein, and nucleic acid leakage from the cells, and electron microscopy.

Conclusion: The nanoemulsions appeared to amplify the antibacterial activity of essential oils by increasing their ability to disrupt cell membrane integrity (3-4).

Keywords: Nanotechnology, Nanoemulsions, Cell membrane

**P771 - 320: PROTEIN VACCINATION WITH HPV16 E7/PEP-1 NANOPARTICLES INDUCES
STRONG PROTECTIVE IMMUNITY**

Golnaz Mardani¹, Azam Bolhassani², Elnaz Agi³, Sepideh Shahbazi⁴

1. Department of Biotechnology, Islamic azad university of pharmaceutical sciences, Tehran, Iran
2. Department of Hepatitis and AIDS, Pasteur Institute of Iran, Tehran, Iran
3. Department of Hepatitis and AIDS, Pasteur Institute of Iran, Tehran, Iran
4. Department of Hepatitis and AIDS, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Human papillomavirus type 16 (HPV16) protein E7 is the major factor of human cervical cancer. Since current vaccines have not therapeutic effects, developing therapeutic strategies is crucial. In current study, we used a short amphipathic peptide carrier, Pep-1, for delivery of HPV16 E7 protein in vitro and evaluated immune responses and protective effects in C57BL/6 mice model.

Methods: HPV-16 E7 gene fused to 6XHis-tag was cloned and expressed in the pQE30 vector and SDS-PAGE analysis verified the expression. Purification of the recombinant protein was performed by Ni-NTA affinity chromatography. E7/Pep-1 complexes at the ratios of 1:5, 1:10, 1:20 were produced and compared by SDS-PAGE analysis. The characteristics of E7/Pep-1 complex at the ratio of 1:20 were monitored using Atomic Force Microscopy (AFM) and zeta sizer. HEK-293 T cell line grown in RPMI medium was transfected by 10 µg E7 protein and E7/Pep-1 complex (1:20). Transfection was confirmed by western blotting. Cell cytotoxicity was determined using MTT assay. C57BL/6 Mice were immunized with three injections (10 µg each) of E7 protein and Pep-1 peptide. Three weeks later, antibody and cytokine detection assays performed by ELISA. Mice were challenged with 1×10^5 TC-1 tumor cells, then were monitored for tumor growth by palpation twice a week.

Results: Immunization of mice with Pep-1/E7 nanoparticles at a ratio of 20:1 induced high levels of IgG2a antibody and IFN-γ responses and protected all mice from tumor growth.

Conclusion: These data suggest that Pep-1 peptide would indicate promising applications for improvement of HPV therapeutic vaccines.

Keywords: E7; Pep-1; cell penetrating peptide; cervical cancer; human papillomavirus

P772 - 354: ANTIBACTERIAL EFFECT OF EUGENOL AND SILVER NANOPARTICLES AND THEIR INTERACTION WITH FOOD COMPONENTS

Negin Heydarian Dehkordi¹, Hossein Tajik², Mehran Moradi³

1. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine Urmia University, Urmia, Iran
2. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine Urmia University, Urmia, Iran
3. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine Urmia University, Urmia, Iran

Background and Aim: The food matrix can represent a physical hurdle and affect the antibacterial activity of antimicrobial agents. This study was conducted to represent the role of food components (fat, protein and carbohydrate) on antibacterial activity of eugenol and silver nanoparticles (SNP) on *Staphylococcus aureus* and *Salmonella Typhimurium*.

Methods: Minimal inhibitory concentrations (MIC) of eugenol and SNP were determined in Luria-Bertani medium using a broth micro-dilution assay, then antibacterial effect of eugenol and SNP and their interaction with different concentrations (2, 5 and 10 %) of sunflower oil, meat extract and potato starch with eugenol and SNP were tested.

Results: The MIC of eugenol and SNP against both bacteria were 2500 and 25 µg mL⁻¹, respectively. The MICs of SNP were not changed during exposure to different concentrations of sunflower oil and potato starch for both bacteria, but meat extract made an increase in MICs of SNP. Generally, potato starch and sunflower oil significantly increased MICs of eugenol on both bacteria and meat extract only increased MIC of eugenol against *S. aureus*. Variations in MICs of SNP and eugenol for both bacteria were not associated with the concentrations of ingredients.

Conclusion: The findings suggested that antibacterial activity of antimicrobial food additive and also sanitizers affect by food ingredient or food residue on surfaces.

Keywords: Eugenol; Silver nanoparticles; Antibacterial; Food components.

P773 - 356: ANTIMICROBIAL EFFECTS OF SILVER NANOPARTICLES

Zahra Ebrahimi¹, Ayyoob Arpanaei², Habbib Abbasi³, Kambiz Akbari Noghabi⁴

1. Islamic Azad Uni, Jahrom
2. Department of Industrial and Environmental Biotechnology, National Institute of Genetic Engineering and Biotechnology (NIGEB).
3. Department of Chemical Engineering, Jundi-Shapur University of Technology, Dezful, Iran
4. Department of Industrial and Environmental Biotechnology, National Institute of Genetic Engineering and Biotechnology (NIGEB).

Background and Aim: Silver is known for its antimicrobial properties and has been used for years in the medical field for antimicrobial applications. Recently, because of the increasing incidence of antimicrobial resistance against topically applied “conventional” antibiotic agents, numerous silver-containing products have been developed, mainly for the treatment of wound infections.

Methods: The antimicrobial effect of AgNPs was assessed against a variety of pathogens including *Staphylococcus aureus*, *Salmonella typhi*, were propagated in LB broth and the rest of tested bacteria including *Klebsiella pneumonia* and *Bacillus subtilis* with agar diffusion technique. The bacterial cells were allowed to grow in 10 ml broth to give a bacterial concentration of about 4.5×10^8 CFU/ml, which were incubated at 37°C for 12 h. After incubation centrifugation was done at 4000 rpm. For agar diffusion technique, 50 µl of diluted bacterial suspensions was dispensed to the series of agar plates. Wells were cut in the center of the plates and 50 µl of dispersion of AgNP solution at different concentration from 100ppm to 2000ppm was dispensed in each well (6 lg/well). The bacterial cultures and MHB alone and deionized water with NaBH₄ were used as controls. The plates were incubated after 24 h of incubation at 37°C, Zones of inhibition were measured in millimeter and recorded.

Results: The antibacterial activity of silver nanoparticles against *Salmonella typhi* and *Staphylococcus aureus* were higher than that against *Klebsiella pneumonia* and *Bacillus subtilis*.

Conclusion: In conclusion, Ag nanoparticles prepared by the cost effective reduction method described here have great promise as antimicrobial agents

Keywords: Silver nanoparticle, Antimicrobial, Muller Hinton agar

**P774 - 367: THE SYNTHESIS OF SILVER NANOPARTICLES AND EVALUATION OF THEIR
IN VITRO ANTIBACTERIAL ACTIVITIES WITH GENTAMICIN AGAINST MRSE**

Mahsa Esmaeillou¹, Gholamreza Zarrini², Mohammad Ahangarzadeh Rezaee³, Javid Shahbazi Mojarad⁴,
Ali Bahadori⁵

1. Department of Biology, Faculty of Natural Sciences, University of Tabriz, Tabriz, Iran.
2. Department of Biology, Faculty of Natural Sciences, University of Tabriz, Tabriz, Iran.
3. Immunology Research Center, Tabriz University of Medical Sciences, Tabriz, Iran.
4. Department of Medicinal Chemistry, Faculty of Pharmacy, Tabriz University of Medical Sciences, Tabriz, Iran.
5. Department of Medical Microbiology, Faculty of Medicine, Cukurova University, Adana, Turkey.

Background and Aim: The spread of antibiotic resistance, originating from the widespread and limitless use of antibiotics in humans and livestock over the past decades has emerged as a global health issue. Advances in nanotechnology have opened new horizons in nanomedicine, allowing the synthesis of nanoparticles that can be assembled into complex structures such as antibiotics. In this investigation synergistic antibacterial activity of combined silver nanoparticles with gentamicin was tested against the methicillin-resistant *Staphylococcus epidermidis* (MRSE).

Methods: spherical silver nanoparticles are prepared by wet chemical reduction method and stabilized by Thioglycolic acid. The synthesis of silver nanoparticles was confirmed by using UV-vis spectrophotometer and scanning electron microscopy (SEM). The antibacterial activity of AgNPs in combination with gentamicin, was determined in vitro, using minimum inhibitory concentration (MIC) determination method.

Results: The results of this study showed that, the minimum inhibitory concentration (MIC) for pure AgNPs was 0.8 µg NP per ml and for pure gentamicin was more than 3.2 µg/ml (?3.2 µg/ml) and in combination use of AgNPs with gentamicin, MIC was 0.4 µg/ml.

Conclusion: The consequences of this investigation suggest that the combination of the ineffective gentamicin with AgNPs effectively inhibits the growth of MRSE.

Keywords: antibiotic resistance; silver nanoparticles; gentamicin; synergistic effect; gentamicin, MRSE

**P775 - 380: EVALUATION OF ANTIFUNGAL EFFECT OF IRON OXIDE NANOPARTICLE
AGAINST CANDIDA ALBICANS ISOLATES**

Samira Salari¹, Nazanin Seddighi², Pooya Ghasemi Nejad Almani³

1. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran
2. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran
3. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran

Background and Aim: *Candida albicans* is dimorphic fungal species with a number of pathogenic capabilities, including biofilm formation, systemic infection and development of fluconazole resistance. Given the increased incidence of candidiasis in the past decade, limits on the use of antifungal drugs, emergence of azole-resistant *Candida* species, and increased incidence of treatment failures, it is necessary to identify a novel agent with antifungal properties. The purpose of this study was to evaluate the effect of Iron Oxide nanoparticles on *Candida albicans* isolates.

Methods: In the present study, the antifungal susceptibility of Iron Oxide nanoparticles compared with fluconazole was investigated against *Candida albicans* isolates by broth microdilution test.

Results: The average MIC and MFC Iron Oxide nanoparticles on *Candida albicans* isolates were 62.5 and 500 µg/ml, respectively. Whereas these isolates showed MIC and MFC 64 and 128 µg/ml for fluconazole.

Conclusion: Our data indicated that the Iron Oxide nanoparticle was less active than fluconazole but it had anti- *Candida* effect.

Keywords: Iron Oxide nanoparticles, antifungal efficacy, *Candida albicans*

P776 - 381: ANTIFUNGAL EFFICACY OF IRON-OXIDE NANOPARTICLE ON CANDIDA GLABRATA ISOLATES

Samira Salari¹, Nazanin Seddighi², Pooya Ghasemi Nejad Almani³

1. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran
2. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran
3. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran

Background and Aim: Candida a common commensal fungus of humans, may convert to an opportunistic pathogen causing superficial or deep infections in susceptible hosts including neonates, patients undergoing immunosuppressive or broad-spectrum antibiotic therapy, or those with indwelling catheters, human immunodeficiency virus infection and diabetes. Nanotechnology is applied to various fields such as biological, physical, chemical and engineering sciences where novel techniques are being developed to probe and manipulate single atoms and molecules. The metallic have applications in various areas such as coating, packaging electronics, cosmetics and biotechnology. The aim of this study was to evaluate the antifungal efficacy of Iron-Oxide nanoparticle on *C. glabrata* isolates.

Methods: In the present study, the antifungal susceptibility of Iron Oxide nanoparticles compared with fluconazole was investigated against *C. glabrata* isolates obtained from patients with different forms of candidiasis were evaluated using Clinical and Laboratory Standard Institute (CLSI) guidelines.

Results: The average MIC and MFC Iron-Oxide nanoparticles on *C. glabrata* isolates were 125 and 1000 µg/ml, respectively. Whereas these isolates showed MIC and MFC 32 and 256 µg/ml for fluconazole.

Conclusion: The antifungal activity results shown by Iron-Oxide nanoparticles suggests their potential against infections caused by *C. glabrata*.

Keywords: Antifungal Efficacy , Iron-Oxide nanoparticle , *Candida glabrata*

P777 - 394: SYNTHESIS OF SILVER-COPPER NANOALLOYS BY THE BIOLOGICAL METHOD AND INVESTIGATION OF ITS ANTIBACTERIAL EFFECTS ON SOME OF THE PATHOGENIC GRAM-POSITIVE AND GRAM NEGATIVE BACTERIA

Sheyda Mohammadi¹, Mehri Kouhkan², Nima Hosseini Jazani³, Leila Ashrafi Babaganjeh⁴

1. Student Research Committee, Urmia University of Medical Sciences, Urmia, IRAN
2. Faculty of Pharmacy, Urmia University of Medical Sciences, Urmia, Iran
3. Department of Microbiology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran
4. Student Research Committee, Urmia University of Medical Sciences, Urmia, IRAN

Background and Aim: Metallic nanoparticles, an important group of nanomaterials, may consist only of one or more than one metallic element, which in this case are called nanoalloy. Various methods for the production of nanomaterials are currently in use. In biological methods, microorganisms are used for producing of nanoparticles. Antimicrobial effects of silver and copper nanoparticles and silver- copper nanoalloy produced by chemical synthesis have been shown previously. The aim of this study was to produce silver- copper nanoalloy by the biological method and investigation of its antibacterial effects on standard strains of some pathogenic bacteria.

Methods: Silver-copper nanoalloys was produced by *Lactobacillus casei* ATCC39392 in MRS broth containing Tween 80 by using different concentrations of silver nitrate and copper Sulfate salts. The presence of nano-structures was confirmed by imaging with TEM, FESEM and X-ray diffraction. Antibacterial activities of synthesized nanoalloys were investigated on *S. aureus*, *B. subtilis*, *K. pneumoniae*, *P. aeruginosa* and *A. calcoaceticus* with three different methods.

Results: The presence of two different elements was confirmed by TEM and FESEM photography. X-ray diffraction confirmed the presence of the copper and silver particles. Silver-copper nanoalloys which were synthesized by using three different doses of copper and silver salts showed inhibitory effects at different concentrations on tested bacterial strains. The most antimicrobial effects of nanoalloy were on gram positive bacteria.

Conclusion: In this study silver-copper-nanoalloy was green synthesized using *Lactobacillus casei* ATCC39392. Results showed the antibacterial effects of the synthesized compounds.

Keywords: silver-copper nanoalloy, antibacterial, *Lactobacillus casei*, pathogenic bacteria

**P778 - 432: LOW CYTOTOXICITY EFFECT OF DENDROSOMAL CURCUMIN ON
MACROPHAGE ISOLATED FROM BALB/C MICE : IN VITRO STUDY**

Abazar Razavinia¹, Majid Sadeghizadeh ², Mehdi Mahdavi ³, Farzaneh Balkanian ⁴, shokofeh zadeh-
nasir⁵

1. Department of Genetics, School of Biological Sciences, Tarbiat Modares University, Tehran, Iran
2. Department of Genetics, School of Biological Sciences, Tarbiat Modares University, Tehran, Iran
3. Department of Immunology, Pasteur Institute of Iran, Tehran, Iran
4. Islamic Azad University, Qom Branch, Qom, Iran
5. Department of Genetics, School of Biological Sciences, Shahid Beheshti University, Tehran, Iran

Background and Aim:Curcumin, the active ingredient in curcuma rhizomes, has a wide range of therapeutic effects. While curcumin does have potential therapeutic efficacy, both solubility and bioavailability must be improved before it can be more successfully translated to clinical care. We have previously reported a novel formulation of nano particles in capsulated curcumin as dendrosomal curcumin. At present there is not a fully effective and non-toxic supplement treatment for biological effect . In this study the viability effect of dendrosomal curcumin has been studied on mice isolated Macrophage in the in vitro condition.

Methods:thioglycollate medium was injected into the Mice the peritoneal area and after 5 days incubation period at temperature-controlled colony room . on day 5, mice was killed and after describing, cold RPMI solution was injected into the peritoneal area and liquid was removed from mice body . the macrophage was cultured in 96 well plates with different concentration of nano-curcumin, curcumin or without treatment. Also amphotericin B was used as positive control. Culture continued for 24, 48, and 72hrs. The viability effect was evaluated via MTT assay.

Results:Treatment with nano- curcumin, Free curcumin and also amphotericin B shows suppress proliferation and low cytotoxicity effect in a dose dependent manner.

Conclusion:Nano-curcumin shows good viability effect at in-vitro analysis, compare with free curcumin and positive control . Because of immunomodulatory effect of nano-curcumin, maybe it shows better viability effect at the in-vivo condition.

Keywords:dendrosomal curcumin, nano-curcumin , mice macrophage

**P779 - 439: ONE STEP PHYTOSYNTHESIS OF SILVER NANOPARTICLES USING
REDUCING AGENT OBTAINED FROM NATURAL SOURCES FLOWERS EXTRACT OF
CALENDULA OFFICINALIS AND ITS ANTIBACTERIAL ACTIVITY**

Fatemeh Safari¹, Leila Safari², Shahab Ojani³

1. Master of Microbiology, Department of Biology, Ayatollah Amoli Branch, Islamic Azad University, Amol, Iran.
2. Master of Microbiology, Department of Biology, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran.
3. Young Researchers and Elite Club, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran.

Background and Aim: The synthesis of metal nanoparticles is a growing area for research due to its potentiality in the application and development of advanced technologies.

Methods: Here, we have used a fast, convenient and environment-friendly method for the synthesis of silver nanoparticles by reducing silver nitrate with flowers extract of *Calendula officinalis*. Characterization of the silver nanoparticles was done by UV-Vis Spectroscopy, Fourier Transform Infrared Spectroscopy (FTIR), X-ray Diffraction (XRD), Transmission Electron Microscopy (TEM). The antibacterial activity of these nanoparticles was studied against *Bacillus subtilis* and *Escherichia coli*.

Results: The surface plasmon resonance (SPR) found at 435 nm confirmed the AgNPs synthesis. The phytochemical like phenolic compounds and etc play a vital role in the nanoparticles synthesis was identified using the FT-IR. The as-synthesized AgNPs were phase pure and well crystalline with a face centered cubic (FCC) structure. The particle size of the AgNPs was studied by TEM and showed the presence of AgNPs in the size range 30–50 nm. The synthesized AgNPs exhibited good antibacterial potential against gram positive and gram negative bacterial strains.

Conclusion: Thus, the synthesis of AgNPs using whole plant aqueous extract of flowers of *Calendula officinalis* would be helpful for the preparation of pharmaceutically useful drugs to destroy pathogenic microbes.

Keywords: *Calendula officinalis*, Antibacterial activity, Nanoparticles, pharmaceutical, Pathogenic microbes

**P780 - 440: GREEN SYNTHESIS, CHARACTERIZATION AND ANTIBACTERIAL ACTIVITY
OF SILVER NANOPARTICLES BY USING MENTHA PULEGIUM LEAVES AQUEOUS
EXTRACT**

Fatemeh Safari¹, Leila Safari², Shahab Ojani³

1. Master of Microbiology, Department of Biology, Ayatollah Amoli Branch, Islamic Azad University, Amol, Iran.
2. Master of Microbiology, Department of Biology, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran.
3. Young Researchers and Elite Club, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran.

Background and Aim: Nanobiotechnology is an emerging field in biotechnology and it has vast applications in all fields. In this report a simple and eco-friendly biosynthesis of silver nanoparticles using leaves of *Mentha pulegium* extract as the reducing agent from 1 mM AgNO₃ had been investigated.

Methods: The formation of silver nanoparticles was characterized by UV-Vis spectrum, Fourier Transform Infrared Spectroscopy (FT-IR), X-ray diffraction (XRD) and transmission Electron Microscopy (TEM) analysis.

Results: The UV-Vis spectra results show a strong resonance centered on the surface of silver nanoparticles (AgNPs) at 470 nm. The Fourier Transformation Infrared Spectroscopy spectral study demonstrates leaves of *Mentha pulegium* extract acted as the reducing agent. X-ray diffraction (XRD) pattern displayed typical peak of crystalline silver at (111), (200), and (220). The transmission electron microscopy (TEM) analysis showed nanoparticles with the average particles size ranges about 5-50 nm. Further the antibacterial activity of AgNPs was evaluated against *Staphylococcus aureus*, and *Escherichia coli* pathogens. The synthesized nanoparticles showed significant antibacterial activity against both Gram positive and Gram negative bacteria.

Conclusion: This route is rapid, simple, without any hazardous chemicals as reducing or stabilizing agents and economical to synthesize silver nanoparticles.

Keywords: Nanobiotechnology, *Mentha pulegium*, XRD, *Escherichia coli*, Silver nanoparticles

**P781 - 541: COMPARATIVE EVALUATION OF THE EFFECTS OF IRON-OXIDE
NANOPARTICLE COMPARED WITH FLUCONAZOLE ON C. KRUSEI ISOLATES**

Samira Salari¹, Nazanin Seddighi², Pooya Ghasemi Nejad Almani³

1. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran
2. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran
3. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran

Background and Aim: Nanotechnology is the science that deals with manipulating matter at the atomic and molecular scale and the size range between 1- 10 nm. Magnetic nanoparticles of iron oxides (Fe₃O₄ and Fe₂O₃) are now extensively used throughout the medicine, drug delivery systems, superparamagnetism, antimicrobial, non-toxicity, biocompatibility, biodegradability properties and low price. In this study the antifungal effect of iron oxide nanoparticles was evaluated against c. krusei isolates.

Methods: In this experimental study, antifungal effect of Iron-Oxide nanoparticle compared with fluconazole was investigated on C. Krusei isolates using Clinical and Laboratory Standard Institute (CLSI) guidelines.

Results: MIC of Iron-Oxide nanoparticle was 250 µg/ml while MFC was determined to be 1000 µg/ml. These values for the fluconazole were 32 and 128 µg/ml for MFC.

Conclusion: Iron-Oxide nanoparticle showed a suitable antifungal property against C. Krusei isolates. Thus it can be a new strategy in prevention of fungal infection.

Keywords: Candida Krusei, fungal Infection, Iron-Oxide nanoparticle

**P782 - 564: CHEMICAL FUNCTIONALIZATION OF SILICA PARTICLES FOR
PURIFICATION OF PROTEINS FUSED GLUTATHIONE S-TRANSFERASE**

Nasim Rezaeinezhad¹, Mehdi Mohammadi², Gholamreza Ahmadian³, Seyed Mehdi Qafari⁴

1. Department of Industrial and Environmental Biotechnology National Institute of Genetic Engineering and Biotechnology
2. Department of Industrial and Environmental Biotechnology National Institute of Genetic Engineering and Biotechnology
3. Department of Industrial and Environmental Biotechnology National Institute of Genetic Engineering and Biotechnology
4. Department of Industrial and Environmental Biotechnology National Institute of Genetic Engineering and Biotechnology

Background and Aim: Separation and purification of proteins is a common practice in biotechnology. Glutathione S-transferase (GST) is a protein found in eukaryotic cells. GST gene fusion protein is an efficient method for purification of inducible, high level expressed recombinant proteins. GST (26 KD) can be fused to the N-terminus of the target proteins which has a high affinity for binding to glutathione supports. After binding, the fusion proteins can be competitively eluted from the reduced glutathione supports. The main purpose of this study is to prepare glutathione S-transferase modified carriers for purification of proteins.

Methods: In this study, the fusion protein consists of Cyan Fluorescent protein (CFP) and GST tag was cloned in pGEX plasmid and expressed in a bacterial host. In order to prepare glutathione supports, chemical modification of silica was performed by (3-Mercaptopropyl)trimethoxysilane followed by covalent immobilization of reduced glutathione on its surface. Finally, fusion protein was eluted and purified from glutathione support.

Results: This study shows that glutathione support can be efficiently used for purification of recombinant proteins. Therefore this support can aid to purification of any protein fused to the GST tag.

Conclusion: Affinity Chromatography is a method of purification biomolecular. Each affinity tag is necessary for isolation of proteins of interest. Therefore it is efficient approach to purified human proteins or protein domains for studies.

Keywords: Glutathione s- transferase, pGEX, Affinity Chromatography, silica

**P783 - 574: INVESTIGATION OF THE ANTIMICROBIAL EFFECT OF SILVER DOPED ZINC
OXIDE NANOPARTICLES**

Farzaneh Hosseini Dolat Abadi¹, Farzane Hoseyni-Dowlatabadi², Gholamreza Amiri³, Maryam
Mohammadi-Sichani⁴

1. Islamic Azad University, Falavarjan Branch, Esfahan, Iran
2. Islamic Azad University, Falavarjan Branch, Esfahan, Iran
3. Islamic Azad University, Falavarjan Branch, Esfahan, Iran

Background and Aim: The antimicrobial effect of metal nanoparticles such as zinc oxide and silver nanoparticles has been taken into great consideration separately during recent years. The useful application of these nanoparticles in the areas of medicine, biotechnology, and professional prevention of microbes motivated us. The aim of this study was to evaluate antibacterial activity properties of silver doped zinc oxide nanoparticles (ZnO: Ag) by synthesizing them.

Methods: The silver doped zinc oxide nanoparticles (ZnO:Ag) were provided with wet chemical method in an aqueous solution, and mercaptoethanol. The physical properties of the sample were investigated with UV, XRD, and TEM techniques. Then, the antibacterial activity of 50 to 3.12 concentrations of the silver doped zinc oxide nanoparticles (ZnO:Ag) was investigated against *Escherichia coli*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Enterococcus faecalis* by well diffusion method. Moreover, the MIC and MBC values of these nanoparticles were assessed by microdilution method.

Results: The sizes of the nanoparticles was obtained as between 4 and 5 nanometers in average. The optical study of the nanoparticles demonstrated that the band gap of the silver doped nanostructures is higher than that of the pure sample. The zone of inhibition diameter in the presence of 50 mg/ml density was 19, 15 and 8 mm against *S.aureus*, *E.coli*, and *P.aeruginosa*, respectively.

Conclusion: The results showed that silver doped zinc oxide nanoparticles prevented *E.coli*, *S.aureus*, and *P.aeruginosa*, but did not affect *E.faecalis*. The zone of inhibition diameter increases as the density of the nanoparticles does.

Keywords: ZnO:Ag nanoparticles, wet chemical method, Antibacterial activity

P784 - 589: THE EFFECT OF TOBRAMYCIN WITH INCORPORATION BISMUTH-ETHANEDITHIOL LOADED ON NIOSOMES ON BIOFILM PRODUCED BY PSEUDOMONAS AERUGINOSA.

Faeze Mahdiun¹

1. Department of Microbiology, School of Medicine, Kerman University of Medical Sciences

Background and Aim: *P. aeruginosa*, a gram negative, opportunistic pathogen that high resistance to various antibiotics. we study the effect of tobramycin with incorporation bismuth-ethanedithiol loaded on niosomes on the biofilm produced by *P. aeruginosa*

Methods: Thin layer hydration method with different concentrations of cholesterol, Span and Tween for making of niosomes. Physical properties and particle size of the niosomes investigated. Micro dilution method used to determinate of MIC. In addition, biofilm formation evaluated by using of the micro-titer methods.

Results: The suitable formulation for drug loading of niosomes included, Span 40, Tween 40 and concentration of 30% cholesterol. The results of the inhibition of *P. aeruginosa* grown in various concentrations was for TOB: 16.64 µg/ml, Nio-TOB: 1.3 µg/ml, BiEDT: 163 µM, Nio- BiEDT: 163 µM, TOB- BiEDT: 0.006 µg /ml, 0.6 Mµ and Nio-TOB- BiEDT: 0.0002 µg / ml, 0.02 µm, respectively. The concentration of 1/2 MIC and 1/4MIC for TOB-BiEDT and Nio-BiEDT-TOB inhibit %80 of biofilm formation.

Conclusion: These nano-carrying layer containing non-ionic surfactants, can kept the drug and gradually release the drug. This way increase the effectiveness of antibiotics in treating *P. aeruginosa* infection.

Keywords: Niosomes, Tobramycin, Bismuth ethanedithiol, *pseudomonas aeruginosa*.

P785 - 617: ANTI BACTERIAL EFFECT OF QUANTUM DOTS NANOPARTICLE

Faride Sadeghkhan¹, Neda Soleimani²

1. B.Sc Student, Department of Microbiology , Shahid Beheshti University, Tehran, Iran.
2. Assistant Professor, Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, Tehran, Iran.

Background and Aim: Synthesis of new antibacterial agents is becoming increasingly important in light of the emerging antibiotic resistance. Inorganic nano materials have large specific surface area and high bio activity which made them promising alternatives to the traditional organic antimicrobial agents that are extremely irritant and toxic. The aims of research is Effect of the antibacterial activity of Cadmium Tellurium Quantum Dots (QDs) nano particle on *Staphylococcus aureus*, *Staphylococcus epidermidis* (PTC1114), *Pseudomonas aeruginosa* (PTCC1181), *Proteus mirabilis* and *Serratia marcescens*.

Methods: The CdTe QDs were synthesized in two type, CdTe core without any shell (QD10) and CdTe/ZnS core/shell QDs nanoparticle with a Kappa Biopolymer coat (QD12). Size and zeta potential of nanoparticle was determined by DLS and SEM microscope method. The antibacterial activity of Quantum Dot nanoparticle derivatives prepared on Bacterial strains were examined according to CLSI.

Results: Quantum Dot nano particle have antibacterial activity on *Staphylococcus aureus*, *Staphylococcus epidermidis* , *Pseudomonas aeruginosa*, and Partially on *Serratia marcescens* but they Have little effect on *Proteus mirabilis* .

Conclusion: This nano particle can be used as antibacterial agent. It can effect synergism with Disinfection. Quantum Dot nano particle will be applied to antibacterial environment.

Keywords: Quantum Dot; nano particle; Anti-Bacterial Agents.

P786 - 622: APPLICATION OF NEW STRATEGIES FOR DIAGNOSIS OF THE CAUSATIVE AGENT OF KALA-AZAR

Ezzat Nourizadeh¹, Zargar,S.², Farhad Riazi-Rad³, Ali Najafi Dastenaie⁴, Mosayeb Rostamian⁵, Ahmad Shirkhani⁶

1. Faculty of Biology, College of Science, University of Mohaghegh Ardabili , Ardabil, Iran
2. Faculty of Biology, College of Science, University of Tehran, Tehran, Iran
3. Department of Immunology, Pasteur Institute of Iran, Tehran, Iran
4. Department of Immunology, Pasteur Institute of Iran, Tehran, Iran
5. Department of Immunology, Pasteur Institute of Iran, Tehran, Iran
6. Department of Immunology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Leishmaniasis are endemic in 88 countries. Kala-azar is a severe form of Leishmaniasis, a disease is typically caused by *L. infantum*. one of the largest parasites-borne illnesses, this disease could be fatal, if untreated. Due to these important aforesaid items the purpose of this investigation was study of new applied solutions in the diagnosis of causative agent of kala-azar.

Methods: In this review, a new array of diagnostic methods were discussed for the identification of Leishmania parasites which is based on the application of specific monoclonal antibodies for characterization , Immunoperoxidase tests , indirect immunofluorescent assay (IFA), detection of Leishmania antigens by monoclonal antibody-piezoelectric-based immunosensor, PCR, ELISA

Results: Among the methods studied, mAb-piezoelectric-based immunosensor method (ISM) as an appropriate way better ,Is recommended for the diagnosis of kala-azar disease ,because for this method, there are certain factors that include; An ISM is a device made up of an antigen or antibody specdetects the binding of the complementary species coupled to a signal transducer that.

Conclusion: Biosensors based on piezoelectric transducers can replace commonly used tests, decreasing the time of performance and cost, by using serum and tissue samples. The immunosensor-based assay using aLimAbs that has been described in the present work is a promising tool for the detection of Leishmania antigens in infected experimental animals, and it may be useful for the development of a diagnostic method based on antigen detection, of Visceral leishmaniasis in humans .

Keywords: new applied strategies, diagnosis, causative agent of kala-azar

**P787 - 649: THE STUDY OF ANTIFUNGAL AND ANTI ADHESIVE PROPERTIES NIO
THINFILMS POLYMER-MATRIX NANOCOMPOSITE**

Monir Douli¹, Nasrin Talebian²

1. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Falavarjan, Isfahan, Iran.
2. Department of Chemistry, Shahreza Branch, Islamic Azad University, Shahreza, Isfahan, Iran.

Background and Aim: Nickel oxide thin films of various preferred orientations were deposited by sol-gel methods using different solvents including methanol, ethanol and isopropanol.

Methods: The resulting films were analyzed by-ray different (XRD), scanning electron microscopy (SEM), contact angle measurement, UV-vis spectroscopy, atomic force microscopy (AFM). Nickel-oxide-based films antifungal activities against Pathogenic both Candida and Standard Candida have been evaluated by drop test method under UV light irradiation and dark condition

Results: The relationship among solvent polarity, preferred orientation, optical, and structural properties of the NiO films and dependent antifungal activity were investigated. Surface play a vital role in the functioning of a biomaterial. Cellular adherence and growth onto biomaterials can be enhanced in biomaterial modification of their surface, Polymeric coating may present some disadvantages. As a result, embedding of bioactive compounds and biomolecules within inorganic coatings is attracting significant attention. In this work, to improve antifungal and anti-adhesive properties of NiO thin films, organic polymer-matrix nanocomposite coating were prepared by layer by layer self-assembly. Here we used chitosan as an antifungal and heparin as anti-adhesive agent as alliteratively deposited on NiO films. As another polymer-based nanocomposite coating, polyethyleneimine was self-assembled on NiO films.

Conclusion: NiO surface NiO surfaces were successfully modified toward higher inactivation efficiency in comparison with bare NiO films especially against Candida. The most likely reason for the higher polymeric coating's activities was its sufficient hydrophobicity and/ or positive charge.

Keywords: Nickel oxide-sol-gel Thin films-Polymer-matrix nanocomposite- layer by layer self-assembly-Antifungal.

**P788 - 650: CONTROLLED SYNTHESIS OF ZNO NANOSTRUCTURE AND THEIR
MORPHOLOGY-DEPENDENT ANTIFUNGAL ACTIVITIES**

Monir Douadi¹, Nasrin Talebian²

1. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Falavarjan, Isfahan, Iran.
2. Department of Chemistry, Shahreza Branch, Islamic Azad University, Shahreza, Isfahan, Iran.

Background and Aim: In this research, ZnO nanostructure were synthesized using solvothermal and sol-gel in the presence of three solvents including 1-hexanol, ethylene glycol and water in the two forms of powder and thin film.

Methods: Then characterized and used as catalyst toward inactivation of some pathogenic *Candida* and Standard *Candida*. The prepared samples were characterized using the X-ray diffraction, Scanning electron microscopy (SEM) and UV-vis spectrophotometry. Structural and morphology studies show that all samples include wurtzite hexagonal phase with high crystalline and relatively homogeneous distribution of average particle diameters.

Results: The obtained results showed that the synthesized ZnO nanostructured powder in water and ZnO thin film in 1-hexanol as solvent have highest photocatalytic activity. The factors as crystalline structure and preferential growth habit, special cross section, size distribution and band gap were discussed as influencing parameters.

Conclusion: ZnO surfaces were successfully modified toward higher inactivation efficiency in comparison with bare ZnO films specially against pathogenic *Candida* and Standard *Candida*.

Keywords: ZnO nanostructures, Solvothermal, Optical property, Antifungal activities.

**P789 - 688: PROCEDURE OPTIMIZATION FOR GREEN SYNTHESIS OF SILVER
NANOPARTICLES BY AQUEOUS EXTRACT OF MENTHA LANGIFOLIA L. USING AS
ANTIMICROBIAL AGENT.**

Zahra Aghajani kalaki¹, Dr. Raheleh Safaei javan², Dr. masumeh mahdavi ortakand³

1. Department of Biology, College of Biological Sciences, Varamin-Pishva Branch, Islamic Azad University, Varamin, Iran
2. Department of Biology, College of Biological Sciences, Varamin-Pishva Branch, Islamic Azad University, Varamin, Iran
3. Department of Biology, College of Biological Sciences, Varamin-Pishva Branch, Islamic Azad University, Varamin, Iran

Background and Aim: This study is dealing with Optimization of the green synthesized silver nanoparticles (AgNPs) using the Taguchi design. Orthogonal array of L9 type was used as an experimental design to detect the optimum conditions. Nine Experiments were designed with three levels including aqueous solution (1, 5 and 10 mM as level 1, 2 and 3) of Silver nitrate, temperature (40, 60, 80°C as level 1, 2 and 3), PH (5, 7, 9 as level 1, 2, 3) and aqueous extract (3%, 5%, 7% as level 1, 2, 3).

Methods: Silver nanoparticles was synthesized by a simple, fast and eco- friendly biological method using an extract of Mentha langifolia as a reducing agent. Nanoparticles formation were observed by the color changes of medium and was confirmed by UV-Vis spectrum, FT-IR and Scanning Electron Microscopic (SEM) analysis. The average particle size of produced AgNPs was determined by dynamic light scattering (DLS) technique. For statistical calculations Minitab (version 16) software was used.

Results: UV-Visible spectrophotometer showed absorbance peak in 340 nm. The results of Scanning Electron Microscopy (SEM) showed that synthesized AgNPs are spherical in shape. DLS analysis showed that the average synthesized AgNPs diameter was 21.1nm in optimum condition.

Conclusion: The results demonstrated that AgNPs can be synthesized by controlling silver nitrate and plant extract concentration, pH and temperature. The minimum diameter predicted by statistical model was 35nm while the obtained diameter was 21.1nm which is very close to the experimental designed measure. This indicates that the statistical predicated proposed by Taguchi was correct.

Keywords: Silver nanoparticles, Mentha longifolia, Green synthesis, Taguchi Design.

P790 - 693: COMPARATIVE STUDY BASED ON MICRO-DILUTION AND PLATE COUNT METHOD FOR SYNERGISM ANTIBACTERIAL EFFECT OF MOF-5 NANOPARTICLES AND BROCCOLI EXTRACT AGAINST PSEUDOMONAS AERUGINOSA

Vahid Pezeshkpour¹, ramin jannesar², seyed abdolmajid khosravani³

1. Cellular and Molecular Research Center, Yasuj University Of Medical Sciences, Yasuj, Iran
2. Department of pathology, Yasuj University Of Medical Sciences, Yasuj, Iran
3. Cellular and Molecular Research Center, Yasuj University Of Medical Sciences, Yasuj, Iran

Background and Aim: The aim of this work was comparison study of dilution and plating method for evaluation of the synergism effect of metal-organic framework nanoparticles (MOF-5 NPs) and broccoli extract (*Brassica oleracea*) on antibacterial activity of standard and clinical *Pseudomonas aeruginosa* strains. For this purpose, synthesis and characterization of MOF-5 NPs were performed using instrumental techniques including X-ray diffraction (XRD), FT-IR analysis and scanning electron micro-copy (SEM). Maceration extraction (ME) and ultrasound assisted extraction (UAE) methods were used and compared for the preparation and evaluation of total phenolic content, reducing power, radical scavenging and antioxidant activity in three different solvents. The HPLC/UV analysis was applied for separation, identification and evaluation of phenolic acids in broccoli extract in two methods of UAE and ME. Then, antimicrobial activity of MOF-5 NPs and broccoli extract against gram-negative bacteria

Methods: *Pseudomonas aeruginosa* was evaluated by detection of minimal inhibition concentration (MIC), minimal bactericidal concentration (MBC) and zone of inhibition (ZOI).

Results: MIC of broccoli extract and MOF-5 NPs together on *Pseudomonas aeruginosa* strains were 7.81 mg.mL⁻¹ and 3.13 mg.mL⁻¹, respectively

Conclusion: The results of in vitro assays showed that dilution method could not be able to estimate MBC. The reason for false estimation of 4% viability percentage which is not logic by consideration of MBC well. Therefore, plate count method was performed for precise calculation of MBC.

Keywords: Metal-Organic frameworks, Ultrasonic assisted extract, Broccoli, Antibacterial activity, Plate count.

P791 - 712: ANTIBACTERIAL PROPERTIES OF GRAPHENE BASED MATERIALS

Hazhir Tashan¹, Fatemeh Yazdian², Meisam Omid³

1. Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran
2. Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran
3. Department of Tissue Engineering and Regenerative Medicine, School of Advanced Technologies in Medicine, Shahid Beheshti University, Tehran, Iran

Background and Aim: Graphene nanosheets which have carbonic structure is a carbon allotrope with sp² bonds. graphene-based materials show unique properties in electronic, thermal, and mechanical and have applications in conductive thin films, supercapacitors, nanoelectronics, nanosensors, and nanomedicine. Recently several studies indicate the cytotoxicity and antimicrobial properties of graphenic nanosheets. It has demonstrated that different factors impress the antimicrobial effects of these nanosheets such as concentration, time of incubation, surface engineering, etc. Graphenic sheets with different surface engineering may have different antibacterial effects in various mechanisms such as wrapping bacterial cells oxidative stress and etc.

Methods: In this study Graphene (Gn), Graphene Oxide (GO) and reduced Graphene Oxide (rGO) was provided. E.coli bacteria was grown up with the use of Tryptic Soy Broth (TSB) medium and the antibacterial effects of each nanosheets using Minimum Inhibitory Concentration (MIC) was evaluated.

Results: All of the sheets decrease cell viability demonstrate the antibacterial effects of each sheet. GO has further antibacterial effect compared to Gn and rGO. In addition, rGO have further antibacterial effect compared to Gn.

Conclusion: According to this study graphenic nanosheets have antimicrobial properties that prove their future usage in medical such as antibacterial Bandages, coating of Biomedical Devices, antibacterial Clothing and Coating of Public Toilet Seats.

Keywords: Antibacterial; Graphene; Graphene Oxide; reduced Graphene Oxide; Nanosheet

**P792 - 716: ANTIBACTERIAL EFFECTS OF SILVER NANOPARTICLES ON PSEUDOMONAS
AERUGINOSA**

Hamed Charkhian¹, Abdollah Ghasemian², Zahra Moradpour³, Mohammad Esmaeillou⁴

1. Department of Biotechnology urmia branch, Islamic Azad University, urmia, Iran.
2. Urmia university of medical sciences, Faculty of pharmacy, Department of pharmaceutical Biotechnology, urmia, Iran
3. Urmia university of medical sciences, Faculty of pharmacy, Department of pharmaceutical Biotechnology, urmia, Iran
4. Università degli Studi di Siena Department of medical Biotechnology Siena, Italy

Background and Aim: Background: Hospital infections are a major problem in the treatment and care systems. Moreover, increasing bacterial resistance to antibiotics as well as the relatively high cost and side effects of them threaten the health of human society. *Pseudomonas aeruginosa* is one of the bacteria involved in hospital infections, and in recent years has a significant growth of resistant strains. Recently, it has been demonstrated that nanoparticles can be used to overcome bacterial resistance due to promising antibacterial effect. In this study, antibacterial activity of silver and copper oxide nanoparticles was evaluated on *P. aeruginosa*.

Methods: Antimicrobial susceptibility testing was performed by disk diffusion and spot test. The inhibition zone diameter and the clear zone were measured respectively. Also, the inhibitory action of nanoparticles was monitored in liquid media culture based on recording the optical density of the cultures at 600 nm.

Results: According to the results, nanoparticles of silver and copper oxide had antibacterial effects on *P. aeruginosa* cultivated on plates of disk diffusion and spot test. Our data also revealed increasing concentration of silver and copper oxide, leads to increase in nanoparticles antibacterial effects significantly.

Conclusion: It was found that silver nanoparticles show notable bactericidal properties against the bacteria.

Keywords: antibacterial, silver, nanoparticles, *Pseudomonas aeruginosa*

P793 - 717: EFFECT OF IRON-OXIDE NANOPARTICLE ON GROWTH OF CANDIDA TROPICALIS ISOLATES COMPARED WITH FLUCONAZOLE

Samira Salari¹, Nazanin Seddighi², Pooya Ghasemi Nejad Almani³

1. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran
2. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran
3. Department of Medical Mycology and Parasitology, School of Medicine, Medical University of Kerman, Kerman, IR Iran

Background and Aim: *Candida tropicalis* is one of the more common *Candida* causing human diseases in tropical countries; the frequency of invasive disease varies by geography causing 3-66% of candidaemia. *C. tropicalis* is taxonomically close to *C. albicans* and shares many pathogenic traits. During recent years there is an increased interest in magnetite nanoparticles for their wide use in biomedical applications, as prevention of microbial colonization and targeted drug delivery systems. The aim of this study was to evaluate the effect of Iron Oxide nanoparticles compared with fluconazole on *C. tropicalis* isolates.

Methods: The antifungal activity of the Iron Oxide NPS was evaluated for opportunistic human fungal pathogen *C. tropicalis* isolates. The antifungal effect was determined by minimum inhibitory concentration (MIC), minimum fungicidal concentration (MFC), and disk diffusion assay.

Results: The average MIC and MFC Iron Oxide nanoparticles on *C. tropicalis* isolates were 62.5 and 500 µg/ml respectively. Whereas these isolates showed MIC and MFC 128 and 256 µg/ml for fluconazole.

Conclusion: These results display the potential of Iron Oxide nanoparticles to be used as an effective anti-*Candida* agent capable of acting upon *C. tropicalis* infections.

Keywords: Effect, IRON-OXIDE NANOPARTICLE , *CANDIDA tropicalis*

**P794 - 719: IN VITRO INHIBITORY EFFECT OF CHROMIUM NANOPARTICLES ON AMPC
BETA-LACTAMASE PRODUCING KLEBSIELLA STRAINS**

Lyla Rahimi¹, Azam Haddadi², Somayeh Makarem³

1. Department of Biology, Karaj Branch, Islamic Azad University, Karaj, Iran,
2. 1 Department of Biology, Karaj Branch, Islamic Azad University, Karaj, Iran,
3. Department of chemistry, Karaj Branch, Islamic Azad University, Karaj, Iran,

Background and Aim: Unfortunately, antibiotic resistance has become an increasingly critical problem among Enterobacteriaceae in many countries like Iran. AmpC β -lactamases are important cephalosporinases chromosomally encoded in many of Enterobacteriaceae, where they mediate resistance to cephalothin, cefazolin, cefoxitin and penicillins. Recent years have witnessed unprecedented growth of research and applications in the area of nanoscience and nanotechnology. There is increasing optimism that nanotechnology, as applied to medicine, will bring significant advances in the treatment of disease

Methods: This study was performed on 80 clinical Klebsiella isolates. Phenotypic combined disc test (CDT) was used for detection of AmpC beta-lactamase producing Klebsiella isolates. MICs of chromium nanoparticles were determined using sterile 2ml 96-well plates. The tested dilutions ranged from 2500 to 9 $\mu\text{g/mL}$ using dimethyl sulfoxide (DMSO) as solvent. MBC was determined by subculturing the contents of wells that showed no visible growth of bacteria onto Muller Hinton agar plates and incubating at 37°C for 18 h.

Results: AmpC screening of strains by phenotypic combined disc test showed that out of 80 samples 3.75% (3) were AmpC positive. All AmpC-producing isolates were tested for MIC value and chromium nanoparticles showed antibacterial activity with MIC values of 2500 $\mu\text{g/mL}$. Furthermore our MIC was equal to MBC.

Conclusion: Nanoparticles provide a versatile platform in designing materials for antimicrobial therapy. However, further studies at the fundamental, biological, and pharmacological level are required to enable systemic administration of these antimicrobials. In conclusion, nanoparticles have offered promising avenues to design effective next-generation therapeutics against bacterial threats.

Keywords: AmpC beta-lactamases, Klebsiella, nanoparticles

**P795 - 801: FIRST REPORT ON BIOSYNTHESIS OF SILVER NANOPARTICLES USING
ACHROMOBACTER SPANIUS**

Hoda Dezhkhi¹, Elika Faraj Tabrizi², Reza Najafpour³, Mandana Salehizadeh⁴, Sajjad Yazdansetad⁵

1. Department of Microbiology, Faculty of Basic Sciences, Karaj Branch, Islamic Azad University, Alborz, Iran
2. Department of Microbiology, Faculty of Basic Sciences, Qom Branch, Islamic Azad University, Qom, Iran
3. Department of Microbiology, Faculty of Basic Sciences, Qom Branch, Islamic Azad University, Qom, Iran
4. Department of Microbiology, Faculty of Basic Sciences, Science and Research Branch, Islamic Azad University, Tehran, Iran
5. Department of Microbiology, School of Medicine, Golestan University of Medical Sciences, Gorgan, Iran

Background and Aim: A promising usage of Silver nanoparticles (AgNPs) as antimicrobial agent is well known and has already found applications in antimicrobial paint coatings, textiles, water treatment, wound healing, and medical devices. In this study, we have reported the successful synthesis of silver nanoparticles by *Achromobacter spanius*, as a novel silver nanoparticles producing isolate.

Methods: *A. spanius*, a silver nanoparticles producing organism was isolated from vinegar. The isolate was confirmed by standard biochemical tests and 16S rDNA typing method. The ability of the organism was evaluated by adding 1 M solution of silver nitrate (AgNO₃) to the microorganism culture medium. Production of the silver nanoparticles was investigated by X-ray diffraction (XRD), spectrophotometry, transmission electron microscopy (TEM), and fourier transform infrared spectroscopy (FTIR) analysis.

Results: The biosynthesis of silver nanoparticles was observed with the color change of the microorganism culture medium from yellow to dark brown. XRD indicated the silver nanoparticles diffraction peaks which were ranged from $2\theta=20^\circ$ to $2\theta=100^\circ$. A peak at 430 nm for silver nanoparticles was seen by spectrophotometer. TEM micrograph revealed the fairly uniform size and spherical shapes of silver nanoparticles in the range of 30 to 65 nm. FTIR absorption spectra with range of 350 to 3000 cm⁻¹ were also observed for silver nanoparticles.

Conclusion: Biosynthesis of nanoparticles by microorganism is a green and eco-friendly technology. Our study indicated that the isolate has robust potential in production of silver nanoparticles. Further study is required to explore the silver nanoparticles production of *A. spanius*.

Keywords: silver nanoparticles, *Achromobacter spanius*, biosynthesis

**P796 - 856: EVALUATION OF IRON OXIDE NANOPARTICLE ON THE PROTOSCOLECES
OF ECHINOCOCCUS GRANULOSUS IN IN VITRO CONDITION**

Pooya Ghasemi Nejad Almani¹, Samira Salari²

1. Department of Medical Parasitology and Mycology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran
2. Department of Medical Parasitology and Mycology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran

Background and Aim: Cystic echinococcosis (CE) caused by the metacestode stage of *Echinococcus granulosus* is an important public health problem in many countries. New protoscolicidal agents are needed to reduce CE relapse rate at the time of surgery. In this study, Effectiveness of Iron Oxide Nanoparticle on the protoscoleces of *Echinococcus granulosus* in in vitro condition has been evaluated.

Methods: G1 genotype *E. granulosus* protoscoleces from Sheep hydatid cysts were used in this study. Cyst fluid was aspirated and transferred into conical glasswares and the protoscoleces were collected from the sediment. Protoscoleces were washed with saline and their viability was evaluated by Eosin staining test. Concentrations of 6.25, 12, 25 and 50 mg/ml of Iron Oxide Nanoparticle has been prepared and were treated with the same volume of protoscoleces suspension for 1, 5 and 10 minutes in order to evaluate the survival of protoscoleces by Eosin staining. Saturated salt solution has been used as positive control and physiological saline solution has been used as negative control.

Results: At these concentrations and times used in this study the Iron Oxide Nanoparticle could not be effectively caused the deaths of the protoscoleces.

Conclusion: Based on the current study, it seems that this material is not suitable for use in surgery. Although more study in this area with a different concentration and different compounds is needed.

Keywords: protoscoleces, *Echinococcus granulosus*, Iron Oxide Nanoparticle, in vitro

**P797 - 874: STUDY OF THE EFFECT OF SILVER NANOPARTICLES ON BIOFILMS
FORMATION BY URINARY ESCHERICHIA**

Ailin Ahmadi¹, Teena Dadgar², Ania Ahani Azari³

1. MSc of Microbiology, Department of biology, Golestan Science and Research Branch, Islamic Azad University, Gorgan, Iran
2. Assistant professor of Microbiology, Department of biology, Golestan Science and Research Branch, Islamic Azad University, Gorgan, Iran
3. Assistant professor of Microbiology, Department of biology, Golestan Science and Research Branch, Islamic Azad University, Gorgan, Iran

Background and Aim: The purpose of this study was to evaluate the effects of silver colloidal nanoparticles on biofilm formation of urinary *Escherichia coli*.

Methods: In this empirical study, experiments were performed on 100 clinical isolated specimens of *Escherichia coli*. The minimum inhibitory concentration (MIC, subMIC) and antibiofilm activities of colloidal nanosilver (average size: 30 ± 10 nm, concentration: $4000 \mu\text{g/ml}$) prepared in Tehran Nano Pars Company were determined by micro titer plate method.

Results: Our result showed that silver exhibited considerable antimicrobial property against *E. coli* where the minimum inhibitory concentration (MIC) was found at $7.8 \mu\text{g/ml}$. The result was showed that all the tested sub MIC doses of silver exhibited considerable anti biofilm activity against *E. coli*. Therefore 5% of all isolates were weak biofilm producers and 95% were biofilm non producers.

Conclusion: The results showed that colloidal silver nanoparticles have the ability to inhibit the *E. coli* biofilm formation. It is offered to use these compounds to coat prosthetic devices which are placed in the body or to cover environmental surfaces in medical centers.

Keywords: *E. coli*, Biofilm, silver nanoparticles

**P798 - 880: STUDY OF MONOCLONAL ANTIBODY DEDICATED PRODUCTION
TECHNIQUES AGAINST ANTIGENS OF LEISHMANIA INFANTUM AMASTIGOTE**

Ezzat Nourizadeh¹, Zargar,S.J², Mohammad H. Alimohammadian³, Soheila Ajdary⁴, Farhad Riazi-Rad⁵,
Mosayeb Rostamian⁶, Ali Najafi Dastenaee⁷, Ahmad Shirkhani⁸

1. 1 . Faculty of Biology, College of Science, University of Mohaghegh Ardabili , Ardabil, Iran-Faculty of Biology, College of Science, University of Tehran, Tehran, Iran
2. Faculty of Biology, College of Science, University of Tehran, Tehran, Iran
3. Immunology Department; Pasteur Institute of Iran; Pasteur St. Tehran; IR.IRAN
4. Immunology Department; Pasteur Institute of Iran; Pasteur St. Tehran; IR.IRAN
5. Immunology Department; Pasteur Institute of Iran; Pasteur St. Tehran; IR.IRAN
6. Immunology Department; Pasteur Institute of Iran; Pasteur St. Tehran; IR.IRAN
7. Immunology Department; Pasteur Institute of Iran; Pasteur St. Tehran; IR.IRAN
8. Immunology Department; Pasteur Institute of Iran; Pasteur St. Tehran; IR.IRAN

Background and Aim:Introduction: Leishmania currently affects 12 million people in 98 countries. About 2 million new cases occur each year, and 21 species are known to cause disease in humans. Leishmania infantum is the causative agent of infantile visceral leishmaniasis in the Mediterranean region. Leishmania causes several different diseases such as cutaneous leishmaniasis that is self-limiting, and Kala-azar. Due to importance of the disease there is a need for an effective Diagnosis. Monoclonal antibody is a suitable method to recognize and purify the Leishmania antigens. The purpose of this study is investigation of techniques for production of monoclonal antibodies against antigens of Leishmania infantum amastigote.

Methods: Methods: Axenic amastigotes of Leishmania infantum were cultured in specific medium at 35°C and 5% CO₂. Amastigote antigens together with complete Freund's adjuvant and incomplete Freund's adjuvant were injected into 6-week old female mice. There after spleen lymphocytes were fused with myeloma SP2/0 in ratio of 10:1 by polyethylene glycol. Positive hybrids in HAT and HT medium were identified with ELISA and subsequently subcloned.

Results:Results: In this study we produced several Hybridoma cells and monoclonal antibodies against Leishmania infantum amastigote antigens. These antibodies recognized specific antigens with different techniques.

Conclusion:Discussion: We produced several monoclonal antibodies against Leishmania infantum antigens to be used for rapid diagnosis purposes and to purify antigens to be used for vaccine production, analytical and chemical application, therapeutic purposes, and Immunoprecipitation technique development.

Keywords:: Monoclonal antibody, Hybridoma, Production techniques, Leishmania infantum amastigote

**P799 - 946: PROCEDURE OPTIMIZATION FOR GREEN SYNTHESIS OF SILVER
NANOPARTICLES BY AQUEOUS EXTRACT OF BUNIUM PERSICUM (BOISS) USING AS
ANTIMICROBIAL AGENT.**

Parisa Jafari¹, Dr. Masumeh mahdavi ortakand ², Dr. Raheleh Safaei javan ³

1. Department of Biology, College of Biological Sciences, Varamin-Pishva Branch, Islamic Azad University, Varamin, Iran
2. Department of Biology, College of Biological Sciences, Varamin-Pishva Branch, Islamic Azad University, Varamin, Iran
3. Department of Biology, College of Biological Sciences, Varamin-Pishva Branch, Islamic Azad University, Varamin, Iran

Background and Aim: In this investigation, a rapid and simple approach was applied for synthesis of silver nanoparticles (AgNPs) using *Bunium persicum* (boiss) aqueous leaf extract. To study the optimum parameters for silver nanoparticles synthesis, the Taguchi design was used as an experimental design with nine experiments which were done in various conditions included silver nitrate concentration (1, 5, 10 mM), pH (5, 7, 9), temperature (40 °C, 60°C, 80°C) and the *Bunium persicum* (boiss) aqueous extract concentration (1, 3, 5).

Methods: AgNPs were synthesized by reacting aqueous AgNO₃ with *Bunium persicum* (boiss) leaf extract at dark condition. The color change from yellow to dark brown showed the formation of AgNPs. To confirm it, UV-Visible absorption spectrophotometer between 200 and 800 nm was used. Other techniques used to characterize synthesized AgNPs were FT-IR, particle size analyzer (DLS), scanning electron microscopy (SEM). Minitab (version 16) software was used for calculations.

Results: a peak in 340 nm was shown by UV-Visible spectrophotometer. The photographs of Scanning Electron Microscopy (SEM) showed that synthesized AgNPs are spherical. The results of DLS analysis indicated that the synthesized AgNPs diameter was 21.3 nm in optimum condition.

Conclusion: The current research proved that AgNPs can be yielded in optimum conditions by controlling silver nitrate and plant extract concentration, pH and temperature. Size of the synthesized AgNPs were 21.3 nm as shown in DLS that's very close to the experimental designed size. This green synthesis method is rapid and environmentally safe to use in different biotechnological applications.

Keywords: Green synthesis, Taguchi Design, Silver nanoparticles, *Bunium persicum* (boiss)

P800 - 955: ISOLATION OF AGROBACTERIUM TUMEFACIENS STRAINS FROM CROWN GALL DISEASE ON GRAPE AND TOXICITY EFFECTS OF TYPICAL NANOMATERIALS ON ITS.

Hamid Reza Dorri¹, Maryam Ahsani Irvani²

1. Research Center of Agricultural and Natural Resources in Markazi, Arak, Iran
2. Department of Horticultural Sciences, University of Arak, Arak 38156, Iran

Background and Aim:Improvements in nanotechnology in the past decayed has created various opportunities for evaluation of biologic effects such as anti-bacterial effects of nanoparticles. Agrobacterium tumefaciense that causes crown gall diseases is one of the major problems affecting stone fruit production. The purpose of this study was Isolation and of Agrobacterium Tumefaciens Strains from Crown Gall Disease on vitis vinifera in Markazi Province And evaluation Antibacterial effect of silver nanoparticles against it.

Methods:A.tumefaciensstrains were isolated and identified from 10 different samples Crown Gall Diseases on vitis vinifera in Markazi Province.A.tumefaciens were identified with biochemical test. The Antibacterial effect of silver nanoparticles against A.tumefaciens with disc diffusion method was performed.

Results:The isolated strains were confirmed as Agrobacterium using different biochemical tests. The bacterial cells were rod shaped with rounded ends and were either single or in pairs. The isolates were Gram negative, the optimum growth was 28°C. All strains are positive for mobility, catalase, oxydase. On the other hand, these isolates had all oxidized the lactose to 3-ketolactose. On the other hand, all Agrobacterium strains oxidized Sucrose, D-mannitol, D-sorbitol, Indol, inositol, Melibiose, D-galactose, L arabinose, Rhamnose, Amygdalin, Lactose and Glucose. Furthermore, the isolates transform also the arginin, lysin, ornithin, gelatin and starch.Silver nanoparticles showed very good antibacterial effect and after 16 hours the bacteria were totally diminished.

Conclusion:Use of silver nanoparticles as an anti-microbial agent is recommended in different fields of medicine, food industry and agriculture and can be of importance considering health and economic issues.

Keywords: Agrobacterium Tumefaciens- Isolation- Crown Gall- nanomaterials

P801 - 960: BACILLUS SPECIES SCREENING FOR SILVER NANOPARTICLE SYNTHESIS

Leila Rezaei somee¹, Parinaz Ghadam², Ahya Abdi-Ali ³

1. Department of Biotechnology, Faculty of Biological sciences, Alzahra University, Tehran, Iran
2. Department of Biotechnology, Faculty of Biological sciences, Alzahra University, Tehran, Iran
3. Department of Microbiology, Faculty of Biological sciences, Alzahra University, Tehran, Iran

Background and Aim: Nanoparticles with the size range of 1-100 nm are building blocks of nanotechnology. Although some biological synthesis of nanoparticles are time-consuming and produce polydisperse nanoparticle, but they are preferred to physical and chemical methods utilizing reducing and capping agent which are harmful to the environment. Microorganisms which have reducing and stabilizing agents in their extract, have been explored as a potential biofactory for synthesis of nanosilver. In this study different strains of bacillus spp. were investigated for optimum nanoparticle synthesis.

Methods: Ten bacillus specieses (separated from soil) were cultured in optimum medium containing 0.35g potassium nitrate, 0.35g yeast extract, 1.5g glucose and 1g tryptone in 100 ml for maximum nitrate reductase enzyme expression. Bacterial extracts of each strain, harvested by centrifugation (6000 rpm, 4°C, 20 min) and assayed for nitrate reductase enzyme as reducing agent for nanoparticle synthesis. Each bacterial extract adjusted in pH 12 then dispersed in test tubes containing silver nitrate with 5mM final concentration and incubated at room temperature. The results were investigated by UV-visible spectroscopy.

Results: Color changes to yellowish brown after 30 minutes, indicate silver nanoparticle synthesis with maximum absorbance at 430 nm, which is due to the surface plasmon resonance of electrons. The samples with high absorbance and rapid color changes were selected as the best bacillus strain (*Bacillus psychrosaccharolyticus*) for nanoparticle synthesis.

Conclusion: Silver nanoparticle synthesis after 30 minutes by *Bacillus psychrosaccharolyticus* which had high nitrate reductase enzyme activity, could overcome the time-consuming problem of bacterial mediated nanosilver synthesis.

Keywords: Bacillus strain, Silver nanoparticle, Nitrate reductase

**P802 - 969: CONJUGATION OF LYSOSTAPHIN ON THE SURFACE OF DENDRIMER AS AN
ANTIBACTERIAL ENZYME**

Rahimeh Rasouli¹, Parstoo Ehsani², Reza Faridi-Majidi³

1. 1Department of Medical Nanotechnology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran.
2. Molecular Biology Unit, Pasteur Institute of Iran, Tehran, Iran
3. 1Department of Medical Nanotechnology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran.

Background and Aim:Increasing antibiotic resistance strains are major concerns for health. There is an urgent need to generate of new effective antimicrobial treatment that can eradicate them.

Methods:In this study, our goal was conjugation recombinant lysostaphin on the surface of dendrimer as a new antimicrobial enzyme against hospital infection.

Results:the first step dendrimer G2 was synthesized, after physiochemical characterization of dendrimer, Lysostaphin was conjugated on the surface of dendrimer. Lysostaphin activity after conjugation was studied.

Conclusion:So, this new carrier can be introduced as an effective and safe nanocarrier for enzyme delivery in treatment of hospital infections.

Keywords:Antibiotic resistance strains, Nanoparticle, Dendrimer

**P803 - 1013: PERFORMANCE EVALUATION OF ANTIMICROBIAL OF METAL OXIDE
NANOPARTICLES AGAINST ESCHERICHIA COLI**

Somayeh Hosseini khomeirani¹, Sara Rasouli², Mohammad Ebrahim Hosseini khomeirani³

1. Department of microbiology ,Rasht branch ,Islamic azad university ,Rasht ,Iran
2. Department of microbiology ,Rasht branch ,Islamic azad university ,Rasht ,Iran
3. Department of chemical engineering,University of Guilan,Rasht,Iran

Background and Aim: Gradual development of antibiotic resistant bacteria is producing severe global threat. Newer strategies are now being employed in order to control the microbial infections and to reduce the mortality as well as infection rates. Nanotechnology is expected to open some new aspects to fight and prevent diseases using atomic scale tailoring of materials. In this work we investigated the antibacterial properties of 3 nano-metal oxides; zinc oxide (ZnO), iron oxide (Fe₃O₄) and copper oxide (CuO) nanoparticles against the gram-negative bacterium *Escherichia coli* [ATCC 25922]

Methods: nanoparticles were prepared using chemical reduction method and characterize metal oxides nanoparticles using scanning electron microscope and X-ray diffractometer. The antibacterial activity of nano-metal oxides against *Escherichia coli* was measured by the inhibition zone methods. Minimum Inhibitory Concentration (MIC) of these nanoparticles was found to be 1000-0.48 µg/ml, respectively.

Results: The MIC values of ZnO NPs against tested bacteria were in the value of 250 µg/ml. While Fe₃O₄ showed the MIC value of 31.25 µg/ml and CuO showed the MIC values of 15.625 µg/ml.

Conclusion: The interactions of metal nanoparticles with biosystems are just beginning to be understood. It is hoped these particles are increasingly being used as microbicidal agents.

Keywords: metal oxides nanoparticles, *Escherichia coli*, antibacterial activity

**P804 - 1015: IRON OXIDE NANOPARTICLES (Fe₃O₄) ENHANCED ANTIBACTERIAL
ACTIVITY OF GENTAMICIN AGAINST STAPHYLOCOCCUS AUREUS**

Somayeh Hosseini khomeirani¹, shayan imani², Mohammad Ebrahim Hosseini khomeirani³

1. Department of microbiology ,Rasht branch ,Islamic azad university ,Rasht ,Iran
2. Department of microbiology ,kurdestan science and research branch ,Islamic azad university ,sanandaj,Iran
3. Department of chemical engineering,University of Guilan,Rasht,Iran

Background and Aim:Gentamicin sulphate is a semi-synthetic aminoglycoside antibiotic. This drug used to treat various infectious diseases. Resistance of bacterial infections has emerged in recent years and is a major health problem. Nanoparticle metal oxides offer a wide variety of potential applications in medicine has offered to the unprecedented advances in nanobiotechnology research. The aim of this work ,formulate nanoparticles of iron oxide (Fe₃O₄) Coated by gentamicin and antibacterial effects of gentamicin loaded on NPs in comparison with drug common form against Staphylococcus aureus is done.

Methods:In this study, we have used a chemical reduction method for the synthesis of iron oxide nanoparticles. Then gentamicin loaded on Fe₃O₄-NPs. The combined activity of the capped iron oxide NPs with gentamicin was assessed in comparison to antibiotic and free NPs, with disc-diffusion method. Broth macro dilution technique was used to determine the minimum inhibitory concentration (MIC) of formulations drug against s. aureus[PTCC1113].

Results:The morphology of the nanoparticles was observed using a SEM, XRD and FTIR spectrum were consistent with the structure of Fe₃O₄-NPS .the entrapment efficiency was 94% and particle size about 45nm.Experimental data showed that Iron Oxide NPs at a concentration of 25µg/ml, gentamicin solution of 6.25µg/ml and gentamicin loaded in (Fe₃O₄) 1.56 µg/ml.

Conclusion:In this result showed that iron oxide NPs may be a appropriate carrier for antibiotic therapy. The antibacterial activity of gentamicin sulphate was enhanced in presence of Fe₃O₄-NPS against S.aureus. This allows more efficient therapy compared with the antibiotic original form.

Keywords:Iron Oxide Nanoparticles (Fe₃O₄), Gentamicin sulphate, Staphylococcus aureus.

**P805 - 1020: SYNTHESIS AND ANTIBACTERIAL PROPERTIES OF SELENIUM
NANOPARTICLES AGAINST STAPHYLOCOCCUS AUREUS**

Maryam alsadat Mehrbakhsh bandari¹, leila asadpour ², Afshin Pourahmad³

1. Department of microbiology ,Rasht branch ,Islamic azad university ,Rasht ,Iran
2. Assistant Prof. of microbiology , Rasht Branch, Islamic Azad University
3. Associate Prof. of Chemistry, Rasht Branch, Islamic Azad University

Background and Aim:As bacterial resistance to antibiotic therapy is a major public health concern worldwide, recently special attention has been to antimicrobial effects of selenium nanoparticles. The present study was aimed to synthesized and investigate antibacterial properties of selenium nanoparticles (SeNPs).

Methods:Selenium nanoparticles were synthesized by the reduction of sodium selenite by L-cysteine. The size and morphology of selenium nanoparticles were investigated by using scanning electron Microscope. Antibacterial properties of produced nanoparticles against Staphylococcus aureus [PTCC1113] were tested by the disc diffusion method and broth macrodilution method was used to investigate SeNPs minimum inhibitory concentration against test bacteria.

Results:The synthesized SeNPs were characterized by their spherical shape with diameter range of 30 nm and a well –defined absorption peak at 200-250nm in UV-vis spectra. SeNPs showed antibacterial properties against S. aureus with diameter of zone of inhibition of 24mm and minimum inhibitory concentration of 28.37 µg/ml.

Conclusion:The obtained results confirmed antibacterial activity of SeNPs that is possible be used especially for the elimination of S. aureus hard-to-heal infections.

Keywords:selenium nanoparticles ,Staphylococcus aureus,minimum inhibitory concentration

**P806 - 1054: SYNTHESIS AND CHARACTERIZATION OF CHITOSAN COATED IRON
OXIDE NANOPARTICLES FOR BIOMEDICAL APPLICATION**

Ashkan Oliaei¹, Parasto zamani mazde², Dr. Raheleh safaei javan³, Dr. shohre zare karizi⁴

1. research fellow
2. research fellow
3. master
4. advisor

Background and Aim: Magnetic nanoparticles (MnPs) with biological coating exhibited many properties that can be exploited in a variety of biomedical application. In comparison with many other polymers the chitosan backbone contains number of free amine groups, which allow binding of many agents. The aim of the present study was to coat chitosan onto iron oxide nanoparticles.

Methods: MnPs synthesized by the coprecipitation of Fe (II), Fe (III) salt at 2:1 ratio in deionized water within a two necked glass balloon in 80°C paraffin bath. Ammoniac is added to the system and after 2 hours stirring the colour of mixture become black. Chitosan was dissolved in acid acetic and MnPs were mixed in chitosan solution and stirring at 2500 rpm at room temperature. The characterization of synthesized MnPs and chitosan coated MnPs was performed by XRD, FTIR and DLS analysis.

Results: Synthesis of MnPs confirmed by FTIR spectrum at 568cm⁻¹ as a result of Fe-O stretching in Fe₃O₄. The XRD analysis proved that the synthesized MnPs was magnetite (Fe₃O₄). SEM results demonstrated a spherical morphology and the average size of the MnPs was 40 nm. The layer of chitosan on the magnetite surface was confirmed by FTIR. The average diameters were generally between 194 and 197 nm for chitosan coated MnPs in DLS.

Conclusion: The synthesis of nanoparticles with small size and uniform size distribution is a subject of intensive research in recent years. In this study chitosan polymer is coated on iron oxide core for anti-biofilm properties of this nanoparticles. The Cs MnPs have many reactive functional groups for biomedical applications.

Keywords: nanoparticles, iron oxide, chitosan

**P807 - 1136: FIRST REPORT ON BIOSYNTHESIS OF SILVER NANOPARTICLES USING
ACHROMOBACTER SPANIUS**

Hoda Dezhkhi¹, Elika Faraj Tabrizi², Reza Najafpour³, Mandana Salehizadeh⁴, Sajjad Yazdansetad⁵

1. Department of Microbiology, Faculty of Basic Sciences, Karaj Branch, Islamic Azad University, Alborz, Iran
2. Department of Microbiology, Faculty of Basic Sciences, Qom Branch, Islamic Azad University, Qom, Iran
3. Department of Microbiology, Faculty of Basic Sciences, Qom Branch, Islamic Azad University, Qom, Iran
4. Department of Microbiology, Faculty of Basic Sciences, Science and Research Branch, Islamic Azad University, Tehran, Iran
5. Student Research Committee, Golestan University of Medical Sciences, Gorgan, Iran

Background and Aim: A promising usage of Silver nanoparticles (AgNPs) as antimicrobial agent is well known and has already found applications in antimicrobial paint coatings, textiles, water treatment, wound healing, and medical devices. In this study, we have reported the successful synthesis of silver nanoparticles by *Achromobacter spanius*, as a novel silver nanoparticles producing isolate.

Methods: *A. spanius*, a silver nanoparticles producing organism was isolated from vinegar. The isolate was confirmed by standard biochemical tests and 16S rDNA typing method. The ability of the organism was evaluated by adding 1 M solution of silver nitrate (AgNO₃) to the microorganism culture medium. Production of the silver nanoparticles was investigated by X-ray diffraction (XRD), spectrophotometry, transmission electron microscopy (TEM), and fourier transform infrared spectroscopy (FTIR) analysis.

Results: The biosynthesis of silver nanoparticles was observed with the color change of the microorganism culture medium from yellow to dark brown. XRD indicated the silver nanoparticles diffraction peaks which were ranged from $2\theta=20^\circ$ to $2\theta=100^\circ$. A peak at 430 nm for silver nanoparticles was seen by spectrophotometer. TEM micrograph revealed the fairly uniform size and spherical shapes of silver nanoparticles in the range of 30 to 65 nm. FTIR absorption spectra with range of 350 to 3000 cm⁻¹ were also observed for silver nanoparticles.

Conclusion: Biosynthesis of nanoparticles by microorganism is a green and eco-friendly technology. Our study indicated that the isolate has robust potential in production of silver nanoparticles. Further study is required to explore the silver nanoparticles production of *A. spanius*.

Keywords: silver nanoparticles, *Achromobacter spanius*, biosynthesis

P808 - 1179: BIOSYNTHESIS OF ZNO NANOPARTICLES USING THE AZOTOBACTER

Hamid Reza Dorri¹, Maryam Ahsani Irvani²

1. Research Center of Agricultural and Natural Resources in Markazi, Arak, Iran
2. Department of Horticultural Sciences, University of Arak, Arak 38156, Iran

Background and Aim: The use of microorganisms in the synthesis of nanoparticles emerges as an eco-friendly and exciting approach. Generally, nanoparticles are prepared by a variety of chemical methods which are not environmentally friendly. Development of biologically inspired experimental processes for the synthesis of nanoparticles is evolving into an important branch of nanotechnology. In this paper, we report on the use of Azotobacter for the green synthesis of ZnO nanoparticles.

Methods: In this work colloid of ZnO nanoparticles was prepared using Azotobacter as reducing agent by phyto-bioreduction method at room temperature. Zinc sulfate was used as the starting material for the ZnO nanoparticles. The colloidal iron nanoparticles were characterized using scanning electron microscopy (SEM) and X-ray diffraction (XRD).

Results: The results of SEM analysis proved an average diameter of 34-70 nm for ZnO nanoparticles.

Conclusion: We used Azotobacter as a reducing and capping agent to minimize the serious environmental pollution problems. ZnO were synthesised by this method having 50.6 nm average mean sizes. The preparation of nanoparticles by using Azotobacter has desired quality with low cost and convenient methods.

Keywords: Biosynthesis- Azotobacter- nanoparticles

**P809 - 1180: BIOSYNTHESIS OF ANISOTROPIC CUO NANOPARTICLES USING THE
BACILLUS CEREUS**

Hamid Reza Dorri¹, Maryam Ahsani Irvani²

1. Research Center of Agricultural and Natural Resources in Markazi, Arak, Iran
2. Department of Horticultural Sciences, University of Arak, Arak 38156, Iran

Background and Aim: The development of reliable, eco-friendly processes for the synthesis of nanoscale materials is an important aspect of nanotechnology. Application of Nano scale material and structures are usually ranging from 1-100nm and is emerging area of nanoscience and nanotechnology. Metal nanoparticles have a high specific surface area and a high fraction of surface atoms; have been studied extensively because of their unique physicochemical characteristics including catalytic activity, optical properties, electronic properties, antibacterial properties and magnetic properties.

Methods: In this work colloid of CuO nanoparticles was prepared using *Bacillus cereus* as reducing agent by phyto-bioreduction method at room temperature. Copper sulfate was used as the starting material for the CuO nanoparticles. The colloidal iron nanoparticles were characterized using scanning electron microscopy (SEM) and X-ray diffraction (XRD).

Results: The results of SEM analysis proved an average diameter of 15-42 nm for ZnO nanoparticles.

Conclusion: We used *Bacillus cereus* as a reducing and capping agent to minimize the serious environmental pollution problems. CuO were synthesised by this method having 50.6 nm average mean sizes. The preparation of nanoparticles by using bacillus has desired quality with low cost and convenient methods.

Keywords: Synthesis- nanoparticles- *Bacillus cereus*

**P810 - 1183: BIOLOGICAL SYNTHESIS OF SILVER NANO PARTICLES BY USING
PSEUDOMONAS AERUGINOSA**

Hamid Reza Dorri¹, Maryam Ahsani Irvani²

1. Research Center of Agricultural and Natural Resources in Markazi, Arak, Iran
2. Department of Horticultural Sciences, University of Arak, Arak 38156, Iran

Background and Aim: Synthesis of metallic nanoparticles has attracted by bacterial based production and alternative to physical and chemical approaches.

Methods: Synthesis of silver nanoparticles was achieved by addition of culture supernatants with aqueous silver nitrate solution, The colloidal silver nanoparticles were characterized using UV-visible spectroscopy, Transmission Electron Microscopy (TEM) and Dynamic Light Scattering (DLS) techniques.

Results: immediately it turns to brown colour solution showed a peak at 420 nm corresponding to the plasmon absorbance of silver nanoparticles by UV-vis spectroscopy. TEM study shows that silver nanoparticles formed are crystalline in nature and spherical in shape. The results of DLS analysis proved an average diameter of 12 ± 2 nm for iron nanoparticles

Conclusion: We used pseudomonas aeruginosa as a reducing and capping agent to minimize the serious environmental pollution problems. Silver nano particles were synthesised by this method having 12-29 nm average mean sizes. The preparation of nanoparticles by using pseudomonas aeruginosa has desired quality with low cost and convenient methods.

Keywords: Biological synthesis- silver nano particles- pseudomonas aeruginosa

**P811 - 1186: RAPID SYNTHESIS OF IRON NANOPARTICLES USING BACILLUS
MEGATERIUM AND ITS CHARACTERIZATION AS AN ANTIBACTERIAL AGENT**

Hamid Reza Dorri¹, Maryam Ahsani Irvani²

1. Research Center of Agricultural and Natural Resources in Markazi, Arak, Iran
2. Department of Horticultural Sciences, University of Arak, Arak 38156, Iran

Background and Aim: Iron nanoparticles have expressed significant advances owing to wide range of applications in the field of bio-medical, sensors, antimicrobials, catalysts, electronics, optical fibers, agricultural, bio-labeling and in other areas. The green synthesis of iron nanoparticles using bacteria has been reported. In this work colloid of iron nanoparticles was prepared using bacillus megaterium extract as reducing agent by phyto-bioreduction method at room temperature. Iron nitrate was used as the starting material for the Iron nanoparticles.

Methods: The colloidal iron nanoparticles were characterized using Transmission Electron Microscopy (TEM) and Dynamic Light Scattering (DLS) techniques. As an application the antibacterial activity of nanocomposite was evaluated against clinical isolates of Gram-positive (*Staphylococcus aureus*) and Gram-negative (*Escherichia coli*) bacteria. The Kirby-bauer method was accomplished for determination of zone of inhibition.

Results: TEM study shows that iron nanoparticles formed are crystalline in nature and spherical in shape. The results of DLS analysis proved an average diameter of 34-81 nm for iron nanoparticles. The results indicated that the system exhibited antibacterial activity at micro molar concentration levels. The results of antibacterial study shown that the studied structure have a 15 mm zone of inhibition on gram negative *Escherichia coli* and 17 mm on gram positive *Staphylococcus aureus* in a 75 mic gr/ml concentration.

Conclusion: This is an interesting report on the antibacterial effect of iron nanoparticles that was prepared with green synthesis method. It may be investigated as potential candidate for request in futuristic biomedical fields.

Keywords: Rapid synthesis- iron nanoparticles- bacillus megaterium- antibacterial

Nosocomial Infections

P812 - 276: EVALUATION OF BACTERIAL CONTAMINATION AND ANTIBIOGRAM IN CELL PHONES OF CLINICAL STAFF PERSONNEL : MATERNITY, INTENSIVE CARE AND NEONATAL WARDS ON IMAM SAJJAD AND SHAHID BEHESHTI HOSPITALS IN YASUJ CITY .

Mohsen Naghmachi¹, Fatemeh Ehsani², Maryam Heydari³, Ebrahim Sharifpour⁴

1. Msc of Microbiology , Faculty member of Health school of Yasuj university of medical sciences
2. Student of Environmental Health Engineering of Yasuj university of medical sciences
3. Student of Environmental Health Engineering of Yasuj university of medical sciences
4. Expert of laboratory of microbiology - Health school of Yasuj university of medical sciences

Background and Aim: The cell Phones of clinical personnel is one of the major of transmitting nosocomial infection. The aim of this study is identify present of bacteria in the cell phones in certain clinical staff in Imam Sajjad and Beheshti hospitals in Yasouj city and antimicrobial resistance patterns of them.

Methods: 104 samples were collected from mobile phones in clinical staff .The samples were cultured in blood agar and EMB agar and they were observed by Gram stain and spores stain and were identified gram negative and gram positive bacteria by biochemical standard tests , then the antibiogram pattern were determined .

Results: The isolated bacteria were included: coagulase negative staphylococci (51.5%), Bacillus (10%), Corynebacterium (10%), Pseudomonas aeruginosa (7.5%), Staphylococcus aureus (2.5%), Streptococcus spp (18.5%). Results of the resistancy in antibiogram were included : clindamycin (62.1%), erythromycin (48.3%), ceftazidime (69%), ampicillin (72.45%), penicillin (62.1%), tetracycline (51.75%), chloramphenicol (27.6%)

Conclusion: The results show that mobile phones of personnel of clinical staff in Yasouj hospitals were Contaminated with pathogenic agents, and potentially they could transmitted opportunistic bacteria and caused nosocomial infections . Antibiogram Showed a high level of microbial resistance in the detected bacteria

Keywords: Nosocomial infection , Antibiogram, Cell phone

**P813 - 306: THE ROLE OF CELL PHONES OF MEDICAL STUDENTS IN SPREAD OF
NOSOCOMIAL BACTERIAL INFECTIONS IN AMIRALMOMENIN HOSPITAL IN
SEPTEMBER 2015**

Mohammad Darvishi¹, Sana Jalalmanesh², Mohammadkarim Rahimi³

1. Associate professor, Infectious diseases and tropical medicine research center, AJA ums, Tehran, Iran
2. Medical Student, Tehran Medical Branch of Islamic Azad University, Tehran, Iran
3. Department of Medicine, Tehran Medical Branch of Islamic Azad University, Tehran, Iran

Background and Aim: Nosocomial infections are a growing problem in many health centers. Cell phones used by the medical staff, can act as a vector for nosocomial transmission of microorganisms. This study aimed to investigate the role of cell phones of medical students in spread of nosocomial bacterial infections in amiralmomenin hospital in september 2015.

Methods: Thirty medical students were enrolled using convenience sampling method. Demographic data, perspectives, attitudes, phone type, and frequency of cleaning of mobile phones were collected by questionnaires. Samples were taken from the phones using a sterile swab moistened with a nutritive medium in order to assess the possibility of bacterial growth.

Results: 53.3 percent of mobile phones were infected. Isolated bacteria were: Staphylococcus Epidermidis (26.7%), Non-Albicans Candida (16.7%), Bacillus PSP (13.3%), Micrococcus PSP (10%), non-Hemolytic Streptococcus and Enterococcus (each 6.7%), and Klebsiella and Staphylococcus Aureus (each 3.3%).

Conclusion: Mobile phones can act as potential carriers of nosocomial infections which are significantly higher in male students' phones and in smartphones. So, some restrictions should be applied to their use in sensitive areas of hospitals. Also, due to the significant impact of cleaning mobile phones in reducing the frequency of bacterial contamination, attention to their regular cleaning should be considered.

Keywords: Cell phone, medical students, nosocomial bacterial infections.

**P814 - 664: AN OLD DRUG FOR A NEW BUG: CLASS 1 INTEGRONS AMONG MULTIDRUG-
RESISTANT ACINETOBACTER BAUMANNII**

Farzaneh Ghasabi¹, Nazanin Chatrabnous², Tayebah Hashempoor³, Behnaz Soltani⁴, Nahal Hadi⁵, Hadi Sedigh Ebrahim-Saraie⁶, Hamid Heidari⁷, Mohammad Motamedifar⁸

1. Student Research Committee, Shiraz University of Medical Sciences, Shiraz, Iran
2. Department of Immunology, Medical School, Kerman University of Medical Sciences, Kerman, Iran
3. Professor Alborzi Clinical Microbiology Research Center, Nemazee Hospital, Shiraz University of Medical Sciences, Shiraz, Iran
4. Department of Bacteriology & Virology, School of Medicine, Shiraz University of Medical Sciences Shiraz, Iran
5. Department of Bacteriology & Virology, School of Medicine, Shiraz University of Medical Sciences Shiraz, Iran
6. Department of Bacteriology & Virology, School of Medicine, Shiraz University of Medical Sciences Shiraz, Iran
7. Department of Bacteriology & Virology, School of Medicine, Shiraz University of Medical Sciences Shiraz, Iran
8. Department of Bacteriology & Virology, School of Medicine, Shiraz University of Medical Sciences Shiraz, Iran

Background and Aim: *Acinetobacter baumannii* is an important cause of nosocomial infections. Multiple antibiotic resistance (MDR) nature of *A. baumannii* strains are one of the main concern of public health. Integrons are mostly associated with MDR *A. baumannii* isolates. The aim of this study was to investigate the presence of integrons in clinical isolates of the *A. baumannii*.

Methods: In this cross-sectional study, a total of 76 *A. baumannii* isolates obtained within 6 months from August 2015 at Nemazee teaching hospital in Shiraz, Iran. All isolates were identified as *A. baumannii* using standard microbiological tests and molecular methods. Antibiotic susceptibility was performed using the disk diffusion method according to CLSI recommendations. All isolates were assayed for the presence of the class 1 integrons gene by PCR. MDR defined non-susceptible to ≥ 1 agent in ≥ 3 antimicrobial categories.

Results: In overall, 35 (46.1%) *A. baumannii* isolates were positive for the presence of class 1 integrons. The most common source of integron positive isolates were sputum 25.7%, blood 17.1%, and endotracheal tube and wound sample each with 11.4%. Among integron positive isolates, 18 (51.4%) isolates were resistant to all 6 tested classes of antibiotics. The most effective antibiotics against 18 MDR isolates were polymyxin B and colistin with 100% sensitivity followed by minocycline with 44.4%. Moreover, apart from polymyxin B and colistin, minocycline showed encouraging susceptibility for integron positive isolates with 71.4%.

Conclusion: The lack of clinically effective antimicrobials to treat *A. baumannii* infections suggest to reevaluate older agents such as minocycline for the treatment of MDR isolates.

Keywords: *Acinetobacter baumannii*, Antibiotic resistance, Integrons, Nosocomial infections

**P815 - 695: STAPHYLOCOCCUS AUREUS AND ANTIMICROBIAL RESISTANCE ISOLATED
FROM ICU PATIENTS, ENVIRONMENT AND PERSONNELS IN A TEACHING HOSPITAL
IN TEHRAN, IRAN.**

Hossein Hejr¹, Alireza Badrkhani Jam²

1. Yasouj University of Medical Science, Clinical Research Development Unit Yasouj Beheshti Hospital
2. Loghman Hakim Hospital, Shahid Beheshti University of Medical Science

Background and Aim: Hospital-acquired infections have profound social, economic, and personal costs to patients in the intensive care unit (ICU). The aim of this study was detection of *S. aureus* and their antibiotic resistance in ICU patients, ICU environment and personnel in the teaching hospital in Tehran-Iran.

Methods: The study was done from April 2011 to January 2013 in a hospital in Tehran. A total of 322 samples from intensive care unit (patient, environment, personnel), were cultured on Blood agar and Mannitol salt agar plates. Colony counts of each culture and biochemical identification were done according to standard methods. Antimicrobial susceptibility of *S. aureus* isolates to 11 clinically important antibiotics was assessed on the basis of CLSI guideline by the disk diffusion method.

Results: Total rate of the *S. aureus* in the ICU samples was (24/322)7.4% (environment, 6/24 (25%); clinical samples 8/24 (33.3%); and staffs 10/24 (41.6%)). Methicillin resistant *S. aureus* (MRSA) isolates showed a frequency of 91.6% (environment 100, clinical samples 100% and staffs 80%). Sensitivity of *S. aureus* isolates to trimethoprim/sulfamethoxazole and chloramphenicol was 83.3%, 95.8% respectively. In another way the resistance of *S. aureus* isolates rates was observed to penicillin, erythromycin, imipenem and ciprofloxacin 100%, 87.5%, 70.8% and 66.6%, respectively. The frequency of antibiotic resistance among the strains isolated from patients showed higher rates of resistance compared with those from environment and personnel.

Conclusion: *Staphylococcus aureus* is an important cause of infection in ICU patients. Colonization with methicillin-resistant *S. aureus* (MRSA) is a risk factor for subsequent *S. aureus* infection.

Keywords: *Staphylococcus aureus*, Hospital-acquired infections, intensive care unit (ICU)

**P816 - 761: STUDY OF NOSOCOMIAL INFECTIONS IN PEDIATRIC INTENSIVE CARE
UNITS IN THE TEHRAN**

Mohammad Mehdi Attarpour Yazdi¹

1. Department of Microbiology, Faculty of Medicine, Shahed University, Tehran, Iran

Background and Aim: Introduction: To study the epidemiology of nosocomial infections in pediatric intensive care units (ICUs) in the Tehran is aim of this research. Patient and ICU characteristics in pediatric ICUs suggest the pattern of nosocomial infections experienced may differ from that seen in adult ICUs.

Methods: Methods: Data were collected between February 2014 and September 2015 from 4 pediatric ICUs in the Iran using the standard surveillance protocols and nosocomial infection site definitions of the National Nosocomial Infections Surveillance System's ICU surveillance component.

Results: Results: Data on 1400 patients with 156 nosocomial infections were analyzed. Primary bloodstream infections (28%), pneumonia (21%), and urinary tract infections (15%) were most frequent. Primary bloodstream infections and surgical site infections were reported more frequently in infants aged 2 months or less as compared with older children. Urinary tract infections were reported more frequently in children >5 years old compared with younger children. Coagulase-negative staphylococci (38%) were the most common bloodstream isolates, and aerobic Gram-negative bacilli were reported in 25% of primary bloodstream infections. *Pseudomonas aeruginosa* (22%) was the most common species reported from pneumonia and *Escherichia coli* (19%), from urinary tract infections.

Conclusion: Conclusions: In pediatric ICUs, bloodstream infections were the most common nosocomial infection. The distribution of infection sites and pathogens differed with age and from that reported from adult ICUs.

Keywords: Key Words: Nosocomial Infections, Pediatric, Intensive Care Unit

P817 - 791: TRENDS OF ANTIBIOTIC RESISTANCE IN METHICILLIN-RESISTANT STAPHYLOCOCCI ISOLATED FROM SHIRAZ TEACHING HOSPITALS, IRAN

Reza Khashei¹, Yalda Malekzadegan², Mahtab Hadadi³

1. Department of Bacteriology and Virology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran
2. Student Research Committee, Shiraz University of Medical Sciences, Shiraz, Iran
3. Student Research Committee, Shiraz University of Medical Sciences, Shiraz, Iran

Background and Aim: Methicillin-resistant staphylococci are one of the most common causes of nosocomial infections which associated with high morbidity and mortality. The present study aimed to determine the frequency and antibiotic resistance profile of clinical staphylococci isolates obtained from Shiraz teaching hospitals.

Methods: This cross-sectional study conducted within 6 months from September 2015 on 164 staphylococci isolates obtained from Nemazee and Faghihi hospitals in Shiraz, Iran. All isolates were identified by using standard microbiological tests and confirmed by molecular methods. Antibiotic susceptibility testing performed using disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI) guideline.

Results: Of 164 *S. aureus* isolates, 49 (29.9%) were methicillin-resistant *Staphylococcus aureus* (MRSA) and 58 (35.4%) were methicillin-resistant coagulase-negative staphylococci (MRCoNS) isolates. Inducible clindamycin resistance was detected among 9 (5.5%) isolates that out of these isolates 2 (4.1%) were MRSA and 6 (10.3%) were MRCoNS. MRSA isolates are mostly susceptible to teicoplanin (100%) and co-trimoxazole (75.5%), and mostly resistant to erythromycin (65.3%) and tetracycline (63.3%). The most effective antibiotic against MRCoNS isolates were teicoplanin (100%) and rifampin (81%). On the other hand, the majority of MRCoNS isolates were resistance to erythromycin (82.8%) and clindamycin (69%).

Conclusion: In summary, to preserve the effectiveness of antibiotics, rational prescription and application of periodic surveillance against the spread of methicillin-resistant staphylococci are recommended.

Keywords: MRSA, Coagulase negative Staphylococci, Nosocomial infection, Antibiotic resistance

P818 - 848: DETERMINATION OF ANTIMICROBIAL RESISTANCE PROFILE IN RELATION TO PHYLOGENETIC GROUPS AMONG UROPATHOGENIC ESCHERICHIA COLI ISOLATES AT A UNIVERSITY HOSPITAL IN URMIA, IRAN

Nazanin Habibi khiavi¹, Saber Yousefi², Lida Lotfollahi³, Bita Zareikar⁴

1. Student Research Committee, Urmia University of Medical Sciences, Urmia, Iran
2. Department of Microbiology and Virology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran - Cellular and Molecular Research Center, Urmia University of Medical Sciences, Urmia, Iran
3. Department of Microbiology and Virology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran
4. Imam Khomeini Hospital Laboratory, Urmia University of Medical Sciences, Urmia, Iran

Background and Aim: Escherichia coli strains are the major cause of urinary tract infections and belong to the large group of extra-intestinal pathogenic E. coli. Extra-intestinal infections due to E. coli are a major cause of morbidity, mortality, and increased health-care costs. The present study was designed to determine the phylogenetic group and antibiotic resistance pattern among uropathogenic E. coli isolates.

Methods: During July 2015 to January 2016 uropathogenic isolates of E. coli were collected from in-patients and out-patients of Imam Hospital of Urmia, Iran. Bacterial identification were done by standard microbiological test. Antimicrobial susceptibility testing was done by disk diffusion method. Detection of phylogenetic groups among E. coli isolates was carried out by triplex polymerase chain reaction.

Results: One hundred and thirty nine isolates of E. coli were collected from UTI cases. Antibiotic susceptibility testing showed that overall 88 isolates (63.3%) belonged to multiple drug resistant also the most effective antibiotics against the isolates were imipenem (89.9%), amikacin (89.9%) and gentamicin (58.3%). Majority of the isolates (45.3%) belonged to phylogenetic group B2, followed by group D (27.3%), group A (25.2%) and group B1 (1.4%).

Conclusion: Our results showed that the Phylogenetic group of B2 was the most prevalent among extra-intestinal E. coli isolates in study area. It's worth to mention that majority of these isolates were multiple drug resistant and had high antimicrobial resistance. Also since we found the high rate of resistance against some routine antibiotics such as trimethoprim/sulfamethoxazole and nalidixic acid, it's important to do antimicrobial susceptibility testing prior to empirical therapy.

Keywords: Escherichia coli, UTI, Multiple drug resistant, phylogenetic group

**P819 - 882: DISTRIBUTION OF NAN1 VIRULENCE GENE AMONG NOSOCOMIAL
ISOLATES OF PSEUDOMONAS AERUGINOSA**

Alireza Mohammadzadeh¹, Jalal Mardaneh²

1. Department of Microbiology, School of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran.
2. Department of Microbiology, School of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran.

Background and Aim: *Pseudomonas aeruginosa* is an opportunistic pathogen that is a common cause of hospital-acquired infections, particularly infecting patients with predisposing factors. It possesses various cell-associated and extracellular virulence factors. The aim of this study was to examine the distribution of nan1 virulence gene among nosocomial isolates of *Pseudomonas aeruginosa*.

Methods: In the present cross-sectional study, clinical samples from hospitalized patients were collected and culture was done on appropriate media. Final identification was performed using biochemical tests and API 20NE system. Detection of nan1 gene (encoding neuraminidase) was performed by PCR assay.

Results: In the current study, 82 isolates of *Pseudomonas aeruginosa* were obtained from hospitalized patients. As observed, the nan1 gene was detected in 56% (46 strains) of isolates.

Conclusion: The distribution of virulence genes may vary in different geographical region. Simultaneous determination of other virulence factors is a contemporary approach for examination of the microbiological and clinical aspects of infections caused by *P. aeruginosa*.

Keywords: Hospital infection, *Pseudomonas aeruginosa*, nan1, PCR.

P820 - 900: THE PATTERN OF RESISTANCE IN BACTERIA THAT RESPONSIBLE FOR NOSOCOMIAL INFECTIONS IN KHATAM-AL-ANBIA HOSPITALS OF SHUSHTAR CITY.

ALI PAYDAR¹, Masoumeh Yahyavi², Elahe shomal nasab³

1. B.S student of Medical Laboratory Sciences, paramedical faculty, Ahvaz Jundishapur University of medical sciences
2. Department of Laboratory Science, School of Paramedicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.
3. B.S student of Medical Laboratory Sciences, paramedical faculty, Ahvaz Jundishapur University of medical sciences

Background and Aim: Although great efforts have been made in the field of nosocomial infections control, but also transferable antibiotic resistance are increasing. In recent years, bacteria resistant to the usual antibiotics have been prevalent throughout the world, so that the use of antimicrobial drugs in the medical community has been raised as a major problem. Therefore, awareness of antibiotic susceptibility pattern of this organism is essential in any state or city. The aim of this study was to evaluate the resistance patterns of bacteria responsible for nosocomial infections in Khatam-al-anbia hospitals of Shushtar city.

Methods: In this retrospectively study sample of patients in different ward, in during 2014_2015 (22 months) were collected and transferred to the laboratory, after the pattern of antibiotic-resistant isolates tested by disk diffusion, results were analyzed by spss.

Results: 1507 samples were studied that 43 samples cultures were positive, 32 samples (76.7%) were Gram-negative bacteria that include: *E. coli*, *Shigella*, *Proteus*, *Klebsiella*, *Enterobacter*, *Pseudomonas*, *Arizona*. *E. coli* with 20 cases (46.5%) are the most common bacteria has been reported. Among the antibiotics used for both Gram positive and negative, cefixim has the highest sensitivity (90%) and nalidixic acid and ceftriaxon respectively 73.2% and 71.4% are in the next ranks also in antibiotic resistance, gentamycin and imipenem and ciproflaxacin respectively 50%, 46.6% and 44.4% are in the first rank. *E. coli*, respectively, compared to ceftriaxon, ceftizoxim, cefixim, nalidixic acid show the greatest sensitivity but compared to Nitrofurantion and ciproflaxacin have the most resistance.

Conclusion: Given that antibiotic resistance as a major problem in the treatment and control of infections with recognition of common bacteria and their resistance patterns can be helped to improve and accelerate the process of treating these infections.

Keywords: nosocomial infections, resistance patterns, samples

**P821 - 912: PREVALENCE OF MULTIDRUG RESISTANT ENTEROCOCCUS FAECIUM
ISOLATED FROM PATIENTS AND HOSPITALS ENVIRONMENT IN LORESTAN
PROVINCE**

Mansour Goudarzi¹, Mohabati Mobarez Ashraf², Najar-Peerayeh Shahin³, Mirzaei Mohsen ⁴

1. PhD Student in Bacteriology, Department of Medical Bacteriology, Faculty of Medical Sciences, TarbiatModares University, Tehran, Iran
2. Associate Professor, Department of Medical Bacteriology, Faculty of Medical Sciences, TarbiatModares University, Tehran, Iran
3. Associate Professor, Department of Medical Bacteriology, Faculty of Medical Sciences, TarbiatModares University, Tehran, Iran
4. Assistant Professor, Department of Laboratory Sciences, Borujerd branch, Islamic Azad University ,Borujerd, Iran

Background and Aim: Nosocomial infections caused by *E. faecium* have rapidly increased and treatment options have become more limited. This is due to increasing resistance to antibiotics. In this study we will assess antibiotic resistance in clinical and environmental isolates of multi drug resistance enterococcus faecium. In *E. faecium* isolates will identify genes associated with resistance with PCR.

Methods: In this study, after isolating and identifying 228 strains of *Enterococcus faecium* from clinical and environmental specimens in different wards of Lorestan hospitals, the pattern of antibiotic resistance of each isolate to β -lactam antibiotic, glycopeptides, aminoglycosids and other Common antibiotics by disk diffusion agar and agar dilution method determined. For PCR amplification assay, specific primers of resistance genes was used.

Results: Among 690 evaluated strains of Enterococci, 228 isolates (34.2%) were *Enterococcus faecium*. among the antibiotics studied to determine the MIC, The antibiotic resistance rate of isolated *Enterococcus faecium* was to ampicillin (74%), penicillin (78%) and vancomycin (51%) respectively. Which indicates the high antibiotic resistance to vancomycin in *Enterococcus faecium*. product sizes for resistance genes including *vanA*, *vanB*, *pbp5*, *pbpZ* and *blaZ* were found in 84 (72%), 26 (32%), 87 (74%) and 63 (53%) of the isolates respectively.

Conclusion: Based on this study, there are vancomycin-resistant enterococci in Lorestan as well as other parts of the world. Therefore, application of precautionary and management procedures are highly required. Furthermore, it is recommended to carry out the antibiogram assay for each patient, before the treatment process, in order to prescribe an appropriate antibiotic.

Keywords: *Enterococcus faecium*, resistance, Vancomycin

**P822 - 927: FREQUENCY OF PANTON-VALENTINE LEUKOCIDIN GENE AMONG
HOSPITAL ASSOCIATED METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
ISOLATES IN URMIA UNIVERSITY HOSPITALS**

Yaeghob Sharifi¹, Maryam Ghahremani², Nima Hosseini Jazani³, Homayoun babazadeh⁴

1. Assistant Professor of Bacteriology, Department of Microbiology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran
2. M.Sc. student of medical Microbiology, Student's research committee, Urmia University of Medical Sciences, Urmia, Iran
3. Professor of Microbiology, Department of Microbiology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran
4. Urmia University of Medical Sciences, Faculty of medicine, Department of Microbiology

Background and Aim: Panton-Valentine leukocidin (PVL) is a cytotoxin produced by *Staphylococcus aureus* that causes leukocyte destruction and tissue necrosis. Although produced by <5% Of *S. aureus* strains, the toxin is detected in large percentages of isolates that cause necrotic skin lesions and severe necrotizing pneumonia. Although commonly associated with community-acquired methicillin-resistant *S. aureus* (CA-MRSA), several outbreaks due to hospital associated methicillin resistant *Staphylococcus aureus* (HA-MRSA) have also been reported. This study was undertaken to determine the frequency of pvl-producing *Staphylococcus aureus* among strains isolated in our university Hospitals

Methods: A total of 177 *S. aureus* isolates obtained from different clinical specimens from June 2014 to June 2015, at university teaching hospitals in Urmia were investigated for antimicrobial susceptibility and carriage of genes for pvl elements. Antimicrobial susceptibility testing was performed by disk diffusion agar methods. The presence of pvl genes for HA-MRSA isolates was determined by PCR

Results: Of the 177 *S. aureus* isolates, 95 (53.7%) were methicillin-resistant *S. aureus* (MRSA), whereas 82 (46.3%) were methicillin susceptible (MSSA). Gene for pvl were detected in 6 (3.4%) of the MRSA isolates. The majority of the pvl-producing MRSA (66.7%) were isolated from blood specimen and Nephrology ward (40%). Multidrug resistance was observed among pvl-producing and nonproducing MRSA isolates

Conclusion: Despite the presence of pvl genes is common between the Community acquired -MRSA isolates, this study revealed the presence of genes for pvl in HA-MRSA isolates, associated mostly with Nephrology ward and blood specimens

Keywords: *Staphylococcus aureus*, pvl gene, HA-MRSA

P823 - 931: PREVALENCE OF HOSPITAL-ACQUIRED INFECTIONS AND ANTIBIOTIC RESISTANCE OF THE CAUSATIVE ORGANISMS IN PATIENTS ADMITTED TO SINA HOSPITAL

Yasaman Jamshidi¹, Mohammad Reza Pourmand², Rahil Mashhadi³

1. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
2. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
3. Urology Research Center, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: Hospital-acquired infections (HAI) are serious causes of mortality and morbidity in hospitalized patients and major concern of developing and developed countries. Immobilized and ventilator-dependent ICU patients are considered as risk groups for HAIs. The aim of our research is to analyze incidence of HAIs and antibiotic susceptibility patterns of causative agents among the patients admitted to Sina Hospital.

Methods: This was a descriptive study, conducted prospectively during 6 months from April 2015 to September 2016 in Sina Hospital. From out of 250 patients hospitalized in Sina Hospital, patients have urinary tract infection (UTI), surgical site infections (SSI), septicemia (BSI) and pneumonia (Pneu). The demographic data were collected from the hospital records and antibiotics susceptibility pattern of the isolates has been determined using disk diffusion method. The statistical data were analyzed using SPSS version 16.0.

Results: The overall prevalence of HAIs in all wards of Sina hospital was 39.3%. The incidence rates of infections were 46.18%, 60.35% and 9.4% in the Surgical ward, Intensive care unit (ICU) and Coronary care unit (CCU), respectively. The most common organisms were *Acinetobacter baumannii* with 26.7% and *Escherichia coli* with 20.4% that isolated from blood, urine, cerebrospinal fluid, wound, and surgical site.

Conclusion: All the *Acinetobacter baumannii* were multidrug-resistant and all the gram negative and gram positive bacterial species in our study showed high resistance to antibiotics. These findings provide efficiency information for future to improve the hospital infection control systems.

Keywords: Prevalence, hospital-acquired infections, Antibiotic Resistance, Tehran

**P824 - 953: ROLE OF ATTACHMENT FACTORS IN BIOFILM PRODUCER
UROPATHOGENIC ESCHERICHIA COLI**

NAGHMEH MOORI BAKHTIARI¹, shahab javad Makui²

1. assistant professor of shahid chamran university of Ahvaz, Iran
2. student of veterinary school of shahid chamran university of Ahvaz, Iran

Background and Aim: Pathogenic *Escherichia coli* strains are a common cause of extraintestinal infections such as urinary tract infections. Biofilm formation is a pathogenic mechanism that hinders the eradication of organisms. In addition, biofilm-forming strains show significantly difference in virulence and attachment factors. Such differences might be due to divergences in geographical variation or differences in association with host characteristics. In the present study, molecular, as well as biological, assays were employed to investigate the attachment-associated characteristics and biofilm production of uropathogenic *E. coli* (UPEC).

Methods: For this purpose, 35 strains of *Escherichia coli*, isolated from human urinary tract infections at the Microbiology department, Shahid Chamran university of Ahvaz, Iran, were investigated. Two attachment-associated genes were analysed, including: *fimA* (large subunit of the fimbriae type 1) and *csgA* (large subunit of curli fimbriae), by PCR. Morphological appearance of biofilm in all isolates were also studied by microtiter plate crystal violet assay.

Results: Twenty seven strains from 35 isolates could be expressed two studied attachment- associated factors but 5 and 2 strains could be expressed only *fimA* and *csgA*, respectively. Except two strains that couldn't produced biofilm, one strain was classified as moderate biofilm producer and the remaining 32 strains were regarded as weak biofilm producers.

Conclusion: Pointed out that, all positive and two negative strains from biofilm production, could be expressed two studied genes, correlation between presence of studied genes and biofilm production may not be invoked but because of high percentage of biofilm production in studied strains, the need to use good hygiene practices is recommended.

Keywords: Biofilm, *Escherichia coli*, Curli, Fimbriae

**P825 - 1064: TRENDS OF ANTIBIOTIC RESISTANCE IN ENTEROCOCCUS FAECALIS
ISOLATES OBTAINED FROM CLINICAL SPECIMENS FROM SHIRAZ, IRAN**

Somaye Hasanpour¹, Hamid Heidari², Hadi Sedigh Ebrahim-Saraie³, Mohammad Motamedifar⁴

1. Student Research Committee, Shiraz University of Medical Sciences, Shiraz, Iran
2. Student Research Committee, Shiraz University of Medical Sciences, Shiraz, Iran
3. Student Research Committee, Shiraz University of Medical Sciences, Shiraz, Iran
4. Department of Bacteriology and Virology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran

Background and Aim: *Enterococcus faecalis* is one of the most common causes of nosocomial infections that cause a broad spectrum of diseases. Increasing antibiotic resistance among *E. faecalis* isolates is a serious concern of public health. The knowledge of *E. faecalis* prevalence and the current antimicrobial resistance profile is necessary in selection of appropriate treatment for related infections. The present study aimed to determine the frequency and antibiotic resistance profile of clinical *E. faecalis* isolates.

Methods: This cross-sectional study was performed within six months from August 2015 on 51 *E. faecalis* isolates collected from different clinical specimens from Nemazee hospital in Shiraz, Iran. *E. faecalis* isolates were identified using standard microbiological procedure and molecular method. Antimicrobial resistance patterns were determined using disk diffusion method in accordance with CLSI recommendation.

Results: Overall, 30 (58.8%) of *E. faecalis* isolates obtained from female and 21 (41.2%) from male samples. The most prevalent source of *E. faecalis* isolation were urine specimens with 68.6% (35/51). Antibiotic susceptibility testing revealed that among tested isolates all were susceptible to fosfomycin. Moreover, apart from fosfomycin, the most effective antibiotic against *E. faecalis* isolates were linezolid (88.3%), followed by teicoplanin (78.4%) and nitrofurantoin (76.5%). on the other hand, the majority of *E. faecalis* isolates were resistance to tetracycline (90.2%) and erythromycin (78.4%).

Conclusion: Linezolid still is a promising antibiotic, since majority of the isolated strains were susceptible to this agent. Although, fosfomycin results are hopeful and because of some advantage compared to linezolid must be more attention as an effective treatment for enterococcal infections.

Keywords: *Enterococcus faecalis*, Antibiotic resistance, Nosocomial infection

**P826 - 1141: HOSPITAL-ACQUIRED URINARY TRACT INFECTION , MICROBIAL
CAUSATIVE AGENTS AND ANTIBIOTIC RESISTANCE PATTERN IN SOUTHERN IRAN: A
PROSPECTIVE STUDY**

kourosh khani¹, Farzaneh Dehghan², Arefe chahoofard³, Afsaneh Karmostaji⁴, Nader Zolghadri⁵

1. Student Research Committee, Hormozgan University of Medical Sciences, Bandar Abbas, Iran.
2. . Infectious & Tropical Diseases Research Center , Hormozgan University of Medical Sciences, Bandar Abbas, Iran. Iranian Social Security Organization, Hormozgan Social Security management, Khalij Fars Hospital of Social Security, Bandar Abbas, Iran
3. Student Research Committee, Hormozgan University of Medical Sciences, Bandar Abbas, Iran.
4. . Infectious & Tropical Diseases Research Center , Hormozgan University of Medical Sciences, Bandar Abbas, Iran
5. M.Sc Statistics, Department of Mathematics, Islamic Azad University, Sama college, Bandar Abbas, Iran

Background and Aim: antimicrobial resistance is a problem in Hospital-acquired urinary tract infections (HAUTIs) that is the most frequent nosocomial infection. This study was carried out to determine the prevalence of HAUTIs, aetiological microorganisms and their antimicrobial resistance to commonly used antibiotics.

Methods: This cross-sectional study was performed in bandarabbas, southern of IRAN between January 2014 and December 2015. all cases admitted to the different wards of shahidmohammadi hospital and recognised as HAUTIs 48 hours after admission, were included as targeted population. identification of isolated microorganism were done by standard microbiological test, then antimicrobial susceptibility testing of all bacterial isolates were performed by disk diffusion method and statistical analysis was done using SPSS software version 20.0.

Results: In this study, from 19768 hospitalized patient 1.57% of them acquired HAUTI. The most commonly gram negative bacteria were E.coli 26.7%(82), followed by Acinetobacter baumannii 15.3%(47) and in gram positive organisms was Candida spp 23.5%(72). The most resistant antibiotic in Gram negative bacteria was to Ceftriaxone, in non-fermenter bacteria was to Cefazolin, cotrimoxazole and Nalidixic acid, in Staphylococcus spp were to Ampicillin and in Enterococcus faecalis were to Gentamicin and Nalidixic acid while Streptococcus agalactiae didn't show any resistant pattern.

Conclusion: The results of this study are indicative of a big challenge about the prevalence of multi-drug bacteria in studied hospital that limits therapeutic options, if infection control policy and continuous monitoring of ESBL bacteria have not been used.

Keywords: Antibiotic resistance, Hospital-acquired Urinary Tract Infections

**P827 - 1146: PREVALENCE OF NASAL CARRIER STAPHYLOCOCCUS AUREUS AND
THEIR ANTIBIOTIC RESISTANCE PATTERNS AMONG HEALTH CARE WORKING IN
BOJNURD IMAM REZA HOSPITAL**

Reza Besharati¹, Majid Ghafouri², Sepideh gholami³, Sara Nojoomi⁴, Maryam Besharati⁵

1. M.Sc of microbiology ,faculty member, north khorasan university of medical science,Bojnurd,Iran
2. Assistant Professor of Infection disease, north khorasan university of medical science,Bojnurd,Iran
3. MSc of Nursing,faculty member, North Khorasan University of Medical Science, Bojnurd, Iran
4. B.Sc of microbiology,Emam Reza hospital, north khorasan university of medical science,Bojnurd,Iran
5. PhD student of microbial biotechnology,Tehran univercity,Tehran,Iran

Background and Aim: Staphylococcus aureus is the most common bacteria in nosocomial infections. Nosocomial infections which caused by this bacterium in recent years, considerably, have been increased. This study was conducted in aim of prevalence of Staphylococcus aureus nasal carriage and antibiotic resistance patterns in health care workers, in Imam Reza hospital in Bojnurd.

Methods:A cross-sectional study was conducted on a total of 200 health care workers for 4 months. Nasal swabs were collected. After detection of Staphylococcus aureus isolates, the susceptibility to commonly used antibiotics was determined by disk diffusion method. Methicillin disk diffusion method was applied for detection of methicillin-resistant strains.

Results:From 200 patients, 22 (11%) were nasal carrier of Staphylococcus aureus, and 3 of these (13.6%) were resistant to methicillin. In this study, the results indicated that from three nasal methicillin-resistant strains, two were resistant to vancomycin

Conclusion:Presence of nasal carriers, indicated presence of methicillin resistant S. aureus in hospital personnel of Imam Reza in Bojnurd. Although the prevalence of S. aureus nasal carriage was not very high, otherwise, with no attention, presence of MRSA, indicated wide distribution. We advice control measures for prevent MRSA transmission in high risk persons.

Keywords:Nasal carriage, Staphylococcus aureus, methicillinresistant strains

Other related topics

P828 - 15: RISK OF INFECTION FROM E. COLI 0157:H7 THROUGH INFORMALLY MARKETING RAW MILK IN URMIA CITY

Elham Hajilouyan¹, Naghi Taher Talatpeh², Moslem Neyriz Nagadehi³

1. Faculty of Sciences, Biology Department, Islamic Azad University, Urmia Branch, Urmia, Iran
2. Iran Faculty of Veterinary, Microbiology Department, Islamic Azad University Urmia Branch, Urmia, Iran
3. Faculty of Veterinary, Food Hygiene and Quality Control Department Islamic Azad University, Urmia Branch, Urmia

Background and Aim: E. coli 0157:H7 is a newly recognised bacterial zoonosis that originates from the gut of infected cattle. It causes potentially fatal haemorrhagic enteritis, haemolytic uraemic syndrome and kidney damage in humans. Given the high proportion of informal sales of unpasteurized milk in many tropical countries, E. coli 0157:H7 has been one of several zoonoses of concern.

Methods: survey data and raw milk samples were collected seasonally from households consuming unpasteurised milk in rural and urban locations in central Kenya. Respondents were randomly selected within production system (extensive and intensive) and human population density (urban, peri-urban and rural) strata. Laboratory samples were assessed for bacteriological quality by total and coliform counts. Selective media were used sequentially to screen for faecal coliforms and E. coli 0157:H7. Suspect E. coli 0157:H7 colonies were also serotyped and tested for production of verocytotoxins.

Results: E. coli was recovered from 91 out of 264 samples (34%) and E. coli 0157:H7 serotype identified in two samples (<1%). One of the two isolates produced verocytotoxins. As in many studies, the recovery rate of this serotype was low, but the finding is significant from a public health perspective. Our consumer studies have shown that over 95% of consumers of unpasteurised milk boil the milk before consumption and potential health risks from this zoonosis are therefore quite low.

Conclusion: As informal milk markets without pasteurisation technology are likely to remain dominant for the foreseeable future, there is the need to further emphasise the importance of boiling raw milk before consumption, especially among pastoral communities where this practice is not common.

Keywords: E. coli 0157:H7, unpasteurised milk marketing, URMIA

**P829 - 55: HANDS SKIN MICROBIOTA COMPOSITION AND BEHAVIORAL
CHARACTERISTICS**

Mohammad reza Ataie kachoee¹, Ramezan Ali Ataee ²

1. Department of Microbiology, Faculty of Medicine, Baqiyatallah University of Medical Sciences, Tehran.
Iran
2. Department of Microbiology, Faculty of Medicine, Baqiyatallah University of Medical Sciences, Tehran.
Iran

Background and Aim:The effects of hands skin microbiota composition and major behavioral characteristics are not well understood. The present study aimed to characterize the microbiota composition in the hands skin of healthy individuals and their behavioral at the species level.

Methods:In a cross-sectional study ,62 nursing students (17 Female and 45 male) were assayed. Members of both groups before hands washing the fingers sampling was conducted separately. As the same condition, after washing the hands in wet and dry state the sampling was taken out from the fingers. After 24 hours' incubation by colonies characterization, Gram staining, and biochemical identification of isolated bacteria were determined. The results were descriptively analyzed.

Results:The results showed that the population composition of microbiota women compared with men was less predominantly ($P \leq 0.001$). in addition, the number of bacterial colonies isolated from two groups were significantly different ($P \leq 0.001$). The main finding of this study were the presence of one or two Gram positive bacteria on the hands of subjects with characteristics such as: calm, placid, diligent and hard-working. These characteristics in subjects who released of several other bacteria species were abandoned different.

Conclusion:Based on this study findings, the hands bacterial population composition isolated from male were higher than females. There is a maximum of one or two particular bacteria isolates associated with some personality characteristics. Although, more research is required, the relationship of lifestyle and some behavioral characteristics with hands skin microbiota as a biomarker for some personality indexes should be consideration.

Keywords:: microbiota, hands skin, behavioral characteristics, biomarker

**P830 - 68: STADY ON EXPRESSION OF THE FULL LENGTH HCV-E2 GENE IN YEAST
PICHIA PASTORIS**

Rahele Solat¹, Pooneh Rahimi²

1. MSc in Microbial Biotechnology, Biology Group, Payameh Nour University, Tehran, Iran.
2. Assistant Professor in Medical Virology, Department of Hepatitis and AIDS, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Hepatitis C virus infection initiates through binding of E2 glycoprotein to its specific human liver cell receptor results in considering this glycoprotein as one of the important targets in drug and vaccine researches against this infection. This project was accomplished for the first time to transfer the full length of E2 gene by using the recombinant pPICZAa-E2 (HCV-2a, JFH1) vector to Pichia pastoris yeast KM71H strain and to evaluate the possibility of its expression in this expression system.

Methods: The E2 gene was amplified by using primers contained the EcoRI and XbaI restriction sites and was inserted into the (T-PTG 19) and (pPICZAa) vectors to be transferred into the E-Coli. The recombinant pPICZAa-E2 vector was transferred into the yeast through electroporation, and it was evaluated by digestion and sequencing. The yeast was grown in YNB medium contained methanol for five days. Gene expression was studied by western blot.

Results: Construction of a recombinant vector pPICZAa- (JFH1)E2, transforming the yeast and its expression in KM71H strain were successfully done.

Conclusion: This glycoprotein is a large protein with several glycosylation sites with difficulties for full-length cloning and expression in yeast. In this study, successful design and construct of an yeast recombinant vector containing the E2 gene confirmed the feasibility of that. Also, it was shown that its transfer into and being expressed in the yeast cell was possible. As a result, the ability of an yeast expression system to express this glycoprotein have been evaluated and confirmed

Keywords: Hepatitis C virus, HCV glycoprotein E2, HCV JFH1 strain, pPICZAa, Yeast Pichia Pastoris

**P831 - 76: DETECTION OF BLA NDM -1, BLA VIM AND BLA IMP GENES IN
PSEUDOMONAS AERUGINOSA AT TEHRAN HOSPITALS BY PCR AND GENE
SEQUENCING**

Yousef Erfani¹, Arezoo Rasti²

1. Department of Medical laboratory Sciences, School of Allied Medical Sciences, Tehran University Medical Sciences, Tehran, Iran
2. Oncopathology Research Centre, Iran University Medical Sciences, Tehran, Iran yerfani@sina.tums.ac.ir

Background and Aim: *Pseudomonas Aeruginosa* is non-fermentative Gram-negative bacilli which cause serious infections. Because of its ability to produce β -lactamase, this organism is often resistant to β -lactam drugs. The aim of this study is to investigate the prevalence of metallo β -lactamases (MBL) genes (bla NDM -1, bla VIM and bla IMP) among isolated multidrug-resistant (MDR) *P. Aeruginosa*.

Methods: A total of 105 imipenem and meropenem resistant *P. Aeruginosa* isolated from patients at three hospitals in Tehran were included in the study. Antimicrobial susceptibility was determined by disk diffusion agar method according to CLSI recommendation. MBL enzyme production was performed by CDDT. Polymerase chain reaction (PCR) was performed for the detection of MBL (bla NDM -1, bla VIM and bla IMP) genes. Gene sequencing was performed for representative isolates.

Results: Of 105 imipenem and meropenem resistant *P. Aeruginosa*, 93 (88.57%) were producers of MBL enzymes by CDDT phenotypic method. After conducting PCR, 69 (65.7%) were VIM positive and 36 (34.3%) were IMP positive. Furthermore bla NDM-1 was not observed in isolated *P. Aeruginosa*.

Conclusion: These data suggest that among genes encoding β -lactamase, the prevalence of bla-IMP in *P. Aeruginosa* show an increase in comparison with other countries, furthermore patients with bacteria carrying MBL cannot be treated easily, and so increased research and resources in optimising treatment, infection control and antibiotic stewardship are needed.

Keywords: *Pseudomonas Aeruginosa* , MBL genes, PCR

**P832 - 83: EVALUATION OF TABRIZ STUDENTS KNOWLEDGE AND ATTITUDES
TOWARDS AIDS**

Mirsajjad Eslamkhah¹, Mirsajjad Eslamkhah taghizad², Nastaran ghafeli³

1. M.sc student in Genetics, Islamic Azad university , tabriz Branch
2. M.sc student in Genetics, Islamic Azad university , tabriz Branch

Background and Aim: AIDS is a common and dangerous disease, which ranks first in infectious and dangerous diseases and mortality ranked fourth among the people of the world. According to statistics, about 35 million people with HIV worldwide are women. So far, little research has been done in this regard in student of the city of Tabriz. The aim of this study was to evaluate awareness about AIDS in Tabriz.

Methods: The study was cross-sectional study of 300 students in the city of Tabriz in the winter of 1394. At first questionnaires were collected. Data analyzed by SPSS version 19

Results: The results indicated that the student of Tabriz "transmission through the needle" (95.99%) and "unsafe sex" (95.59%) are the main cause of HIV transmission and low awareness of the "non-epidemic among classmates and academics "(55.91%), respectively. Also, 24.45% of people think that AIDS is an infectious disease and is not contagious

Conclusion: The results can be concluded that the media role in awareness and inform the public about their HIV

Keywords: AIDS, Tabriz students, awareness, HIV

**P833 - 96: ISOLATION OF ACTINOMYCETES PRODUCING ANTIMICROBIAL
SUBSTANCES AGAINST BENEFICIAL BACTERIA AND PATHOGENS IN PLANTS**

EBRAHIM ESHAGHI¹, Mehrad Vosough², Hossein Mirzayi ³, Rahim Nosrati ⁴

1. Department of Biology, Faculty of Science, Nourdanesh Institute of Higher Education, Esfahan, Iran
2. Department of Biology, Faculty of Science, Nourdanesh Institute of Higher Education, Esfahan, Iran
3. Department of Microbiology, Islamic Azad University of Qom, Qom, Iran
4. Department of Pharmaceutical Biotechnology, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran

Background and Aim: Actinomycetes are classified as a group of gram-positive bacteria that are unique for their spore forming abilities and formation of mycelia structures. Actinomycetes DNA are rich in G+C content with the GC % of 57 - 75%. These bacteria have been noted to serve as rich reservoirs of medicinal antibiotics and are therefore extremely relevant to scientists, pharmaceutical industries and agricultural industries. They are predominant in dry alkaline soil. Also actinomycetes isolated from farming soil of the ability to inhibit *Erwinia amylovora* a bacteria that cause fireblight to apple and *Agrobacterium tumefaciens* a casual agent of Crown Gall disease. The two major groups of soil actinomycetes that serve as important sources of antibiotics are Streptomyces and Micromonospora.

Methods: From 70 soil samples the rhizosphere of agricultural land, including: (Qom, Tehran, Arak, Kashan, Isfahan, Mazandaran, Gilan, Golestan) were collected. To isolate actinomycetes samples were cultured in medium ISP4. Anti-bacterial strains for culture in sterile packages that include actinomycetes isolated and bacteria disease-causing, useful standard and carrying, they examined for 6 months.

Results: From 70 soil samples collected, isolated were 54 bacteria, similar bacteria characteristics actinomycetes with white chalk and raised colonies. Seven strains showed antagonism against pathogenic bacteria and beneficial properties. Only two isolates of antagonistic effects against pathogenic bacteria of the display.

Conclusion: Actinomycetes which have bactericidal properties, can be used in plants against bacterial pathogens.

Keywords: Antibacterial, Bactericide, Actinomyces, ISP4, Organic products

**P834 - 114: SEROLOGICAL AND MOLECULAR DIAGNOSIS OF TOXOPLASMOSIS IN
PATIENTS WITH AIDS/HIV IN ARAK CITY, MARKAZY PROVINCE**

Zahra Eslamirad¹, Reza Aghaee², Sassan Saki³, Mojtaba Didehdar⁴, Reza Hajihosseini⁵

1. Department of Parasitology & Mycology, Arak university of Medical Sciences, Arak, IRAN
2. Department of Biology, Faculty of Microbiology, Islamic Azad University, Sciences and Research Branch, Arak, IRAN
3. Department of Medical Laboratory Sciences, Faculty of Medical Sciences, Islamic Azad University, Arak Branch, Arak, IRAN
4. Department of Parasitology & Mycology, Arak university of Medical Sciences, Arak, IRANd
5. Department of Parasitology & Mycology, Arak university of Medical Sciences, Arak, IRAN

Background and Aim: *Toxoplasma gondii* is one of the most successful parasites in the world. It is capable to infecting all warm-blooded beings. It has been estimated that about one third of the world population are infected with this parasite. Studies show that infection with *Toxoplasma gondii* exists in all parts of the world. The main routes of transmission are contact with excreted oocysts from cat, food contamination and transmission from mother to fetus. One of the major factors that caused the relapse of symptoms of toxoplasmosis is immune deficiency. For this reason in people with AIDS, chronic infections are transforming into severe and fatal infections. The aim of this study was to evaluate the acute and chronic toxoplasmosis in AIDS patients in the Arak city.

Methods:: This descriptive study was done on HIV-positive population in Arak city. 5 ml of blood samples were collected. Sera and blood cells were separated by centrifugation and kept at -20 °C. Blood sera were tested for the presence of anti- *Toxoplasma* IgG and IgM antibody. Finally, the samples were serological positive, were tested by molecular methods.

Results: In this study, 65 blood samples were tested. Ten (10) samples were containing anti-*Toxoplasma* IgG and one (1) sample was containing anti-*Toxoplasma* IgM. The molecular examination of samples was negative.

Conclusion: The results showed that in Arak city, 1.5% and 15.4% of HIV-positive patients were infected by acute and chronic toxoplasmosis, respectively. Untreated the disease can lead to severe and dangerous complications such as encephalitis and finally death of these people.

Keywords: *Toxoplasma gondii*, toxoplasmosis, IgG, IgM, AIDS, HIV

**P835 - 140: AUDIT OF URINARY TRACE INFECTIONS 1394 IN SHAHID KAMYAB
HOSPITAL –MASHHAD-KHORASAN RAZAVI**

Behnaz Samiee¹, Ali Nezhad Esmaeel², Marzieh Azar Faza³

1. Infection Control Supervisor
2. Clinical Supervisors
3. Director of Nursing

Background and Aim: Urinary infection is the most common nosocomial infections .80% of these infections are related to urinary catheters .urinary infection cause fewer side effects than other nosocomial infections but some times it causes death.

Methods: the data were collected by national soft ware of infection control .(INIS) This study shows the rate of urinary infections , between first six months and second six months in 1394

Results: In first six months 1394 ,in 119 cases of nosocomial infections (15) cases (12%) were urinary trace infections and the most common age range was (0-14) (6 cases) 40%. this rate in men (73%) is more than women (27%) the most pathogen was klebsiella (40%) and All patients in the ICU and All patients had a Foley catheter. Interventions and solutions : - Holding training classes - Considering sterile methods in catheterization - The urinary catheter care - Patient training In further audit ,in second six month ,from 79 cases of nosocomial infections 13 cases were urinary infection

Conclusion: With providing solutions and appropriate interventions the rate of urinary infection in second six months was reduced than the first six months but it should always be considered that ,whit following these items we can largely prevent urinary infections: - Limiting the time of using urinary catheter in necessary conditions. - Considering sterile methods in catheterization . - Hand washing before catheterization . - Cleaning the perinea before catheterization. - Using of suitable lubricant in catheterization. - Maintaining a closed derange system.

Keywords: nosocomial infections- pathogen- catheterization

P836 - 168: NON-INFECTIOUS DISEASES RELATED TO THE HUMAN MICROBIOME

Roya Mokhtarian¹

1. Microbial Biotechnology graduate student, Nourdash Institute of Higher Education, Meymeh, Isfahan, Iran

Background and Aim: There are microbes all over the body, that most of them are in the digestive tract. The number of known bacteria inside and outside the human body are more than human cells (The number of bacteria are $\sim 10^{24}$ and the number of human cells are $\sim 10^{13}$). In 2010, the approximate number of bacterial genes in our genome ($\sim 3,300,000$) more than the number of our genes (22,000) was announced. Although bacteria are a thousand times smaller than human cells, about two percent of adult body weight (1.5kg), the capacity of the human brain (1.4kg) or liver (1.6kg) are included and can be added as a member of the human body. In this review article we intend to investigate human microbiome studies about the relationship with the number of diseases considered non-infectious.

Methods: does not have.

Results: does not have.

Conclusion: Microbes are important in maintaining health and especially our immune system and digestion of food. Also they are the first line of immune defense against pathogens and the cause of many diseases is abnormalities in the microbiome.

Keywords: Microbiome, Non-infectious diseases, Human symbiotic microbes

P837 - 177: EVALUATION OF ANTIBACTERIAL ACTIVITY OF MULTI-WALLED CARBON NANOTUBES AGAINST SOME BACTERIAL STRAINS

Ehsan Zayerzadeh¹, Azadeh Fardipour²

1. Department of Biology, Faculty of Food Industry and Agriculture, Standard Research Institute, Karaj, Iran.
2. Department of Vaccine Quality Control, Razi Vaccine and Serum Research Institute, Karaj, Iran

Background and Aim: Due to unique mechanical, electrical, and thermal properties of carbon nanotubes, these nanomaterials have potential various applications in nanomedicine, electronics, and other industries. Carbon nanotubes (CNTs), including single walled carbon nanotubes (SWCNTs) and multi walled carbon nanotubes (MWCNTs) are allotropes of carbon from the fullerene family. Nowadays, antimicrobial resistance is recognized as a growing global threat. Hence, it is of significant interest to find new antibacterial agents with a new mechanism of action which can potentially prevent the emergence of drug resistance. The aim of the present investigation is evaluation of antibacterial activity of multi walled carbon nanotubes against some bacterial strains including *Pseudomonas aeruginosa*, *Staphylococcus aureus* and *Escherichia coli*.

Methods: In this study, in order to evaluate MWCNTs antibiotic activity against *Pseudomonas aeruginosa*, *Staphylococcus aureus* and *Escherichia coli* bacterial strains, we tested these bacterial strains with different concentrations of MWCNTs by disc-diffusion susceptibility at different time intervals. Inhibition zone diameter was measured from the clear zone of agar dish following the test.

Results: The results of these study exhibited antibacterial properties with increasing of MWCNTs concentrations against *Pseudomonas aeruginosa*, *Staphylococcus aureus* and *Escherichia coli* bacterial strains.

Conclusion: In conclusion, our findings indicated that MWCNTs have antibacterial effects on *Pseudomonas aeruginosa*, *Staphylococcus aureus* and *Escherichia coli* bacterial strains. Hence, multi walled carbon nanotubes (MWCNTs) may be an important alternative to antibiotics in dealing with drug-resistant and multidrug-resistant.

Keywords: disc-diffusion, multi walled carbon nanotubes (MWCNTs), *Pseudomonas aeruginosa*.

**P838 - 181: REDUCTIVE BIOTRANSFORMATION OF TETRACHLOROETHENE DURING
AEROBIC DEGRADATION: EXPERIMENTAL EVIDENCE AND KINETICS**

Neda Badali¹, Neda Badali Varzaghani², Abbas Farazmand³, Soheila Shokrollahzadeh⁴

1. -
2. M.S. Student of Chemical Technologies, Iranian Research Organization for Science and Technology, Tehran, Iran
3. Department of Biotechnology, Iranian Research Organization for Science and Technology, Tehran, Iran
4. Department of Chemical Technologies, Iranian Research Organization for Science and Technology, Tehran, Iran

Background and Aim: Tetrachloroethene (PCE) is one of the most common pollutants at petrochemical contaminated sites. Degradation of tetrachloroethene was reported by anaerobic bacteria.

Methods: The PCE concentration measured by gas chromatography and ion analyser with surface-induced dissociation (SID).

Results: The PCE biodegradation was enhanced by addition of glucose/yeast extract. The degree of PCE degradation was increased more than 2.3 times using glucose/yeast extract compared to PCE as sole carbon. The maximum specific dechlorination rate of 0.298 mg PCE/h.l.mg cell mass was achieved when initial PCE concentration was 119.8 mg/l in the presence of glucose/yeast extract (0.5 g/l) after 48 h. A Monod-like kinetic model provided a good fit ($R^2=0.9953$) to the PCE degradation profiles at high concentration of PCE.

Conclusion: Here, we report that an indigenous gram-negative bacterium, *Sphingopyxis ummariensis* UI2, which is isolated from wastewater treatment plant of a petrochemical company, is aerobically capable for utilizing PCE as the sole carbon source and in defined medium with glucose/yeast extract.

Keywords: Tetrachloroethene, TCE-reductive dehalogenase, kinetic

در بیمارستان تک تخصصی زنان ام البنین(س) مشهد رفتار شستشوی دست: 194 - P839

Sakine Seddighi¹, Batoul Khairkhah², Marzieh Ghazi³, Akram Jafarzade Noghani (MSC)⁴, Fatemeh Nejati Asl⁵, Maliheh Khoshahang⁶, Fatemeh MoghaddShaer am⁷, Zohreh Bagheri⁸

1. SeddighiS1@mums.ac.ir
2. KhairkhahB1@mums.ac.ir
3. GhaziM3@mums.ac.ir
4. JafarzadeNA1@mums.ac.ir
5. NejatiF2@mums.ac.ir
6. KhoshahangM1@mums.ac.ir
7. ShaerMF1@mums.ac.ir
8. BagheriZ2@mums.ac.ir

Background and Aim: موثرترین، ارزانتین نقش مهمی در انتقال عفونت بیمارستانی دارند و شستشوی دست به عنوان دستها: بررسی رفتار بهداشتی کردن دست ارائه هدف با مطالعه این لذا و راحت ترین روش پیشگیری از این عفونتها بشمار می رود انجام گرفت 1394 دهندگان خدمات سلامت ، بیمارستان تک تخصصی زنان ام البنین(س) مشهد ،در سال

Methods: تخصصی زنان ام البنین(س) مطالعه توصیفی، ۱۰۰ نفر از ارائه دهندگان خدمات سلامت شاغل در بیمارستان تک در این نا بهداشتی کردن دست در سال ۱۳۹۴ توسط مشاهده گران آموزش دیده و به طور شدند. رفتار مطالعه به طور تصادفی وارد و آزمون Spss داده ها پس از جمع آوری در نرم افزار آماری گردید ثبت لیستی چک در مشاهده نتایج و شد مشاهده محسوس مورد تجزیه تحلیل قرار گرفت مجذور کای

Results: در بخش اورژانس ۶۶,۶۲% 67.61% تحقیق نشان داده که رفتار رعایت بهداشت دست در بخش جراحی و مامائی نتایج: است.در مجموع از ۵ موقعیت رفتار بهداشت دست، میزان بروز رفتار و بخش زایشگاه ۵۵,۷۷% بوده 78.51% NICU، بخش مطالعه ۷۰,۸۱% بوده است که در بوده است که ۵۸۴ مورد رعایت شده است. رعایت بهداشت دست در سه گروه مورد ۸۲۵ مورد است. همچنین آموزشها و نظارت موثر واقع شده است دار بوده سال گذشته افزایش قابل توجه داشته است و تفاوت آن معنی است مقایسه با سال گذشته، تفاوت معنی دار بوده

Conclusion: بیمارستان نسبت به داد که رفتار بهداشت دست در میان کارکنان درمانی حین مراقبت از بیماران در نتایج تحقیق نشان: است. همچنین آموزشها و نظارت موثر واقع شده است دار بوده سال گذشته افزایش قابل توجه داشته است و تفاوت آن معنی

Keywords: بهداشت دست، پرسنل درمانی، عفونتهای بیمارستانی

**P840 - 203: KINETIC PARAMETERS FOR EXTRACELLULAR POLYSACCHARIDE
PRODUCTION BY CRYPTHECODINIUM COHNII MICROALGAE IN BUBBLE COLUMN
BIOREACTOR**

Niloofer Hosseinkhani¹, Shahin Ansari², Hassan Jalili³

1. Faculty of New Sciences and Technologies , University of Tehran, Tehran
2. Faculty of New Sciences and Technologies , University of Tehran, Tehran
3. Faculty of New Sciences and Technologies , University of Tehran, Tehran

Background and Aim: Microalgae are commercial source of high value chemical products. One of them is Extracellular polysaccharides (EPS) that have the potential to be used as antioxidant, antiviral agents and anti-inflammatory agents. Microalgae can produce wide range of polysaccharides.

Methods: The microalgae *Cryptocodinium cohnii* was cultivated in 250ml Erlenmeyer. Its media contain : 9 g/l Glucose , 1 g/l yeast extract and 27.8 g/l sea salt (PH:6-8). The media incubated at 28°C in an orbital shaker at 150 rpm in dark for 48h. Then the seed culture inoculated in bubble column bioreactor with 2L culture. Samples were obtained for determination of biomass, EPS, formation and glucose consumption. For EPS measurement samples were centrifuged at 4000 ×g for 10 min. Keep the supernatant and added 2 volumes of absolute ethanol. After 6 h at room temperature (25°C) products obtained by centrifuging at 1000 ×g for 5 min. After washed twice by ethanol 66% (v/v). Then EPS dissolved in ddH₂O and lyophilized. For glucose and biomass determination samples were centrifuged at 2800 ×g for 15 min then supernatant keep for glucose determination and sediment lyophilized for biomass.

Results: Kinetic parameters such as productivity and specific growth rate were calculated. For process design, rheological changes were investigated during fermentation.

Conclusion: Knowledge of kinetic parameters for scale up and optimization of the process is required.

Keywords: Microalgae. Extracellular polysaccharide .*Cryptocodinium cohnii*

**P841 - 229: BACTERIA IN ANTI-TUMOR THERAPY AS A NOVEL ANTICANCER
EXPERIMENTAL STRATEGY**

Faezeh Houman sadr¹, Lashgari Najmeh²

1. Department of Microbiology, Faculty of Medicine, AJA University of Medical Sciences, Tehran, Iran
2. Department of Microbiology, Faculty of Medicine, AJA University of Medical Sciences, Tehran, Iran

Background and Aim: The antitumor effect of different bacteria strains, including Bifidobacterium, Clostridium, and Salmonella spp. has been analyzed. C.novyi was selected for research on the basis of an extensive screen of anaerobic bacterial species for those with optimal properties. C.novyi proved to be particularly oxygen-sensitive as well as highly mobile within tumors due, in part, to their numerous peritrichous flagellae.

Methods: This study is a review article. In a report has here systematically assessed anaerobic bacteria for their capacity to grow expansively within avascular compartments of transplanted tumors. They created a strain of C.novyi devoid of its lethal toxin (C.novyi-NT) and showed that intravenously injected C.novyi-NT spores germinated within the avascular regions of tumors in mice and destroyed surrounding viable tumor cells.

Results: When C.novyi-NT spores were intravenously injected into mice with CT26 tumors, bacteria germinated exclusively within the tumors. By 24 h after treatment, hemorrhagic necrosis could be observed at the centers of most of the tumors. Three to four weeks later, the tumors had regrown from the small non necrotic region at the periphery in 66% (31 of 47) of the animals. In the other 34% of the mice, the tumors had completely regressed, and the mice remained tumor free until the end of the experiment (>60 days).

Conclusion: There are reasons to believe that systemic injection of C.novyi-NT into humans would lead to bacteriolysis of tumors. First, C.novyi-NT germinates within the tumors of all species tested. Second, C.novyi-NT can germinate within human tumor xenografts in the nude mouse host.

Keywords: Bacteria –Clostridium novyi -Cancer –Therapy

**P842 - 237: ASSESSMENT OF COLIFORM CONTAMINATION TRADITIONAL BUTTER IN
KERMANSHAH PROVINCE**

Behjat Namaky¹, Sinasadat Emami², Roya Montazeri³

1. Food and Drug Administration, Kermanshah University
2. Food and Drug Administration, Kermanshah University
3. Food and Drug Administration, Kermanshah University

Background and Aim: Contaminated food such as butter can transmit bacteria and cause food poisoning or infection. Coliform bacteria easy to culture and their presence is used to indicate that other pathogenic organisms of food origin may be present ,also sometimes cause serious illness in human .Health problems associated with these pathogens include: diarrhea, cramps, nausea and vomiting. This study was carried out to understand level of microbial contamination in Kermanshah city.

Methods: In this descriptive cross-sectional study 80 samples were collected and transferred to food drink cosmetic and sanitary laboratory under sterile condition and microbial test were conducted according to Iran national standards.

Results: The result of this study showed 30% samples were contaminated with coliform. According of finding the rate of microbial contamination in traditional butter is high.

Conclusion: Butter traditional must be free of coliform according to Iran national standard. when coliform detected modification of butter may be required that contamination has been eliminated .there for to prevent of microbial infection due to consumption of traditional butter, Pasteurization of milk, personal hygiene and regarding the principle of health should be taken place.

Keywords: butter traditional, coliform, bacterial contamination, Kermanshah,

**P843 - 244: A COLUMN STUDY OF BENZENE CONTAMINATED GROUNDWATER
BIOREMEDIATION**

Hamid Mosmeri¹, Ebrahim Alaie², Mahmood Shavandi³, Seyed Mohamad Mehdi Dastgheib⁴, Saeideh Tasharrofi⁵

1. Ecology and Environmental Pollution Control Research Group, Environment and Biotechnology Research Division, Research Institute of Petroleum Industry, Tehran, Iran
2. Environment and Biotechnology Division, Research Institute of Petroleum Industry, Tehran, Iran
3. Ecology and Environmental Pollution Control Research Group, Environment and Biotechnology Research Division, Research Institute of Petroleum Industry, Tehran, Iran
4. Microbiology and Biotechnology Group, Environment and Biotechnology Research Division, Research Institute of Petroleum Industry, Tehran, Iran
5. Ecology and Environmental Pollution Control Research Group, Environment and Biotechnology Research Division, Research Institute of Petroleum Industry, Tehran, Iran

Background and Aim: Groundwater contamination by petroleum hydrocarbons (especially soluble components, like benzene) is one of the most important issues in developed and developing countries. Aerobic bioremediation is a widely accepted technique for benzene removal from groundwater. Oxygen releasing compounds (ORCs) as an appropriate oxygen source can be applied to bioremediate benzene from groundwater efficiently. In present study, application of calcium peroxide (CaO₂) nanoparticles as an ORC for benzene bioremediation from groundwater in column tests has been investigated.

Methods: A column study was performed on bioremediation efficiency of synthesized CaO₂ nanoparticles. Experiment column was a plexiglass sand packed reactor (20cm length and 9cm diameter). The effect of nanoparticles on dissolved oxygen (DO), pH, microbial population and benzene concentration in groundwater were analyzed within 30days. Standard plate count (SPC) method was applied to study the microbial population on R2A agar. Benzene concentration was measured by high performance liquid chromatography (HPLC) (SPD-M10A, Shimadzu, Japan). Mira-3 FESEM (TESCAN) was used for the observation of biofilms on sands.

Results: Results indicated that CaO₂ nanoparticles were able to removed 60% of benzene from groundwater in continues experiments after 30days. It also showed an increasing in microbial population from 10⁴ to 10⁶cfu/ml of groundwater. The dissolved oxygen of the groundwater was kept more than 9mg/l and pH of the effluent was about 9 after 30days. FESEM results confirmed the growth of biofilm on the sands within the experiments.

Conclusion: The results provided an important insight into the application of CaO₂ nanoparticles in benzene bioremediation from groundwater.

Keywords: Biostimulation, oxygen releasing compound, hydrocarbon removal, remediation, calcium peroxide

**P844 - 254: CHEMICAL AND BIOLOGICAL BENZENE REMEDIATION FROM
GROUNDWATER BY CALCIUM PEROXIDE NANOPARTICLES**

Hamid Mosmeri¹, Ebrahim Alaie², Mahmood Shavandi³, Seyed Mohamad Mehdi Dastgheib⁴, Saeideh Tasharrofi⁵

1. Ecology and Environmental Pollution Control Research Group, Environment and Biotechnology Research Division, Research Institute of Petroleum Industry, Tehran, Iran
2. Environment and Biotechnology Division, Research Institute of Petroleum Industry, Tehran, Iran
3. Ecology and Environmental Pollution Control Research Group, Environment and Biotechnology Research Division, Research Institute of Petroleum Industry, Tehran, Iran
4. Microbiology and Biotechnology Group, Environment and Biotechnology Research Division, Research Institute of Petroleum Industry, Tehran, Iran
5. Ecology and Environmental Pollution Control Research Group, Environment and Biotechnology Research Division, Research Institute of Petroleum Industry, Tehran, Iran

Background and Aim: Contamination of groundwater to BTEX (benzene, toluene, ethylbenzene and xylene) is a widespread environmental issue. Calcium peroxide (CaO_2) as an oxygen releasing compound (ORC) has been efficiently used for BTEX removal from groundwater. Two main mechanisms are proposed for benzene degradation in presence of ORC, chemical oxidation (ORC as a modified Fenton agent) and bioremediation (ORC as a slowly releasing oxygen source). The aim of the present study, was to compare the efficiency of chemical oxidation and bioremediation of benzene contaminated groundwater by ORC nanoparticles in batch experiments.

Methods: Batch experiments were performed to study chemical oxidation and bioremediation of benzene from groundwater by synthesized ORC nanoparticles. Groundwater and chemicals placed in 100ml headspace vials and the effect of nanoparticles on dissolved oxygen (DO), pH, microbial population and benzene concentration in groundwater were analyzed within 70 days. Standard plate count (SPC) method was applied to study the microbial population on R2A agar. Benzene concentration was measured by high performance liquid chromatography (HPLC).

Results: HPLC results indicated that chemical oxidation and bioremediation removed 100% (50mg/l) of benzene in presence of ORC nanoparticles within 70 and 60 days, respectively. Microbial population showed an increase from 10^4 to 10^{10} and 10^8 cfu/ml for chemical oxidation and bioremediation, respectively. The abiotic control samples also resulted in 74 and 50% removal of benzene, respectively for chemical oxidation and bioremediation.

Conclusion: According to the batch experiments, bioremediation showed a great potential for benzene removal from groundwater. It also provides an insight into the efficiency of chemical oxidation and bioremediation processes for groundwater remediation.

Keywords: oxygen releasing compound, hydrocarbon removal, remediation, calcium peroxide, modified Fenton, chemical oxidation

**P845 - 255: EVALUATION OF E7-HMGB1 PROTEIN EXPRESSION IN MAMMALIAN CELLS
USING DIFFERENT METHODS**

Somayeh Talebi¹, Elnaz Agi², Sepideh Shahbazi³, Talat Mokhtari Azad⁴, Mohammad Hossein Modarresi⁵, Azam Bolhassani⁶

1. 1. Department of Hepatitis and AIDS, Pasteur Institute of Iran, Tehran, Iran , 2. Department of Biology, School of Basic Science, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. 1. Department of Hepatitis and AIDS, Pasteur Institute of Iran, Tehran, Iran
3. 1. Department of Hepatitis and AIDS, Pasteur Institute of Iran, Tehran, Iran
4. 3. Virology Centre, School of public health, Tehran University of Medical Sciences (TUMS), Tehran, Iran
5. 3. Virology Centre, School of public health, Tehran University of Medical Sciences (TUMS), Tehran, Iran
6. 4. Department of Medical Genetics, Faculty of Medicine, Tehran University of Medicine Science, Tehran, Iran

Background and Aim: Human Papilloma Viruses (HPV)-16 E7 interacts with the tumour suppressor protein pRb, promoting its degradation, leading to cell cycle dysregulation in infected cells. High mobility group box 1 (HMGB1) has been demonstrated to be a long-searched-for nuclear danger signal passively released by necrotic, as opposed to apoptotic, cells that will induce inflammation. In this study, we investigated expression of E7-HMGB1 protein in mammalian cells using different methods.

Methods: At first plasmid preparation and cloning of E7-HMGB1 was performed in pEGFP-N1 eukaryotic expression vector in order to evaluate their expression in mammalian cells. For this purpose, the HEK-293T cells were transfected by pEGFP-E7 and pEGFP-E7-HMGB1 using TurboFect delivery system. The levels of protein expression were assessed by flow cytometry and fluorescent microscopy at 48 hr after transfection as well as western blot analysis.

Results: Our data showed a band of ~ 297 bp and ~ 982 bp related to E7 and E7-HMGB1 genes in agarose gel, respectively. The expression of HMGB1-GFP and E7-HMGB1-GFP proteins was confirmed as the bands of ~ 38 kDa and ~ 64 kDa in the transfected cells using western blot analysis, respectively. The percentage of expression for E7-GFP and E7-HMGB1-GFP was 76% and 52%, in comparison with pEGFP-N1 (~82%) as a positive control.

Conclusion: The fusion protein could be efficiently expressed in mammalian cells for the next use in immunotherapy.

Keywords: E7, HMGB1, HEK-293T, Cell transfection

**P846 - 287: ISOLATION AND IDENTIFICATION OF BACTERIA ON MOBILE PHONES IN
FASA**

MohammadHosein Yazdanpanah¹, Salar HosseinPour², Ghazal Ghaznavi³, Zahra Tabesh⁴, Najmeh Namdar⁵

1. Medical student , Student Research Committee , Fasa University of Medical Science , Fasa , Iran
2. Medical laboratory science student , Student Research Committee , Fasa University of Medical Science , Fasa , Iran
3. Microbiological department , Fasa University of Medical Science , Fasa , Iran
4. Medical student , Student Research Committee , Fasa University of Medical Science , Fasa , Iran
5. Microbiological department , Fasa University of Medical Science , Fasa , Iran

Background and Aim:Today , using mobile phones is necessary due to technology progression. Combination of constant handling with the heat generated by the phones creates a good place for growth for many bacteria and transmission of them. Our aim was to isolation and identification of bacteria on mobile phones in Fasa city in year 2016.

Methods:In this cross-sectional study , 237 phones were sampled with sterile swaps. Samples were nutrient broth and then incubation was performed for 24 hours in 37 centigrade. For isolation samples were cultured on EMB , MacConkey and blood agar , then incubation was performed for 24 hours in 37 centigrade. Gram stain, catalase and oxidase test, TSI , SIM , Citrate , MRVP , LD and OD test were used for bacterial identification.

Results:113 of 237 (47%) samples were positive for bacterial growth. Staphylococcus was the most bacterial contamination . Also among gram negative bacteria , Escherichia coli was in the first place. various types of bacterial isolates from the mobile phones including Streptococcus ,Pseudomonas, Bacillus ,Klebsiella ,Serratia ,Enterobacter and Citrobacter .

Conclusion: Our study showed that bacterial growth of mobile phones were significant and can be considered as a source of contamination. We recommend cleaning mobile phones with an alcohol wipe. So it can reduce contamination rates and transmission of bacteria.

Keywords:Mobile phones , Bacteria , Staphylococcus , Escherichia Coli

**P847 - 289: COMPARISON BETWEEN BACTERIA ON TOUCH-SCREEN AND KEYPAD
MOBILE PHONES**

MohammadHosein Yazdanpanah¹, Salar HosseinPour², Ghazal Ghaznavi³, Zahra Tabesh⁴, Sohrab
NajafiPour⁵

1. Medical student , Student Research Committee , Fasa University of Medical Science , Fasa , Iran
2. Medical laboratory science student , Student Research Committee , Fasa University of Medical Science , Fasa , Iran
3. Microbiological department , Fasa University of Medical Science , Fasa , Iran
4. Medical student , Student Research Committee , Fasa University of Medical Science , Fasa , Iran
5. PhD of virology , virology department , Fasa University of Medical Science , Fasa , Iran

Background and Aim:Today , using mobile phones is necessary due to technology progression. Considering type of mobile phone , number and bacterial strain are different . So our aim was to compare bacteria contaminant on touch-screen and keypad mobile phones in Fasa in year 2016.

Methods:In this cross-sectional study , 237 phones were sampled with sterile swaps. Samples were nutrient broth and then incubation was performed for 24 hours in 37 centigrade. For isolation samples were cultured on EMB , MacConkey and blood agar , then incubation was performed for 24 hours in 37 centigrade. Gram stain, catalase and oxidase test, TSI , SIM , Citrate , MRVP , LD and OD tests were used for bacterial identification.

Results:113 of 237 (47%) samples were positive for bacterial growth. Among positive samples , 70 samples(62%) were from touch-screen and 43 samples(38%) were from keypad mobile phones. The most frequency of bacteria was related to Staphylococcus (20.5%), Escherichia coli (16%) and Streptococcus (16%) . Also various types of bacterial were isolated from the touch-screen mobile phones . According to frequency rate ,bacteria containment was Pseudomonas, Serratia, Bacillus, Klebsiella and Enterobacter.

Conclusion:Our study showed that touch-screen mobile phones are associated with a significant increased risk of bacterial contamination. According to widespread usage of touch-screen mobile phones , it is important to clean hands and mobile phones after daily usage.

Keywords:mobile phones, touch-screen , keypad , bacteria

**P848 - 301: OPTIMIZATION OF LOVASTATIN PRODUCTION USING ASPERGILLUS
TERREUS IN BUBBLE COLUMN BIOREACTOR**

Shahin Ansari¹, Niloofar Hosseinkhani², Hassan Jalili³

1. faculty of new sciences and technologies ,university of tehran, Tehran
2. faculty of new sciences and technologies ,university of tehran, Tehran
3. faculty of new sciences and technologies ,university of tehran, Tehran

Background and Aim: Lovastatin, a natural statin used as a cholesterol lowering drug, is secondary polyketide metabolite produced by such filamentous fungi as *Monascus ruber*, *Penicillium* species and, *Aspergillus terreus*. It is commercially produced by submerge fermentation using *A.terreus*. In this work the effect of aeration rate on lovastatin production using *A.terreus* was studied in Bubble column bioreactor. Furthermore fungal morphology and kinetic of biomass formation were investigated.

Methods: Fermentation was carried out at PH 6.5, temperature 28°C , aeration rate 0.5 vvm, in Bubble column bioreactor containing 2L culture media. Fermentation lasted 10 days. The samples were collected every days. The specimens centrifuged at 7000 rpm. Biomass was measured by freeze- dry of resulting sediments. Biomass-free filtered broth was used for measuring of Lovastatin in its β -hydroxyacid form using high-performance liquid chromatography (HPLC). Fungal morphology was identified by image analysis.

Results: Profiles of lovastatin production and biomass growth were achieved. We conclude that beside lovastatin production, kinetic of biomass formation and fungal morphology is generally associated with aeration rate.

Conclusion: *A.terreus* is an aerobic fungi so one of the important parameters for lovastatin production is oxygen saturation level . Holding a high concentration of dissolved oxygen (DO) is necessary for achieving a high titer of lovastatin. In this work impact of the aeration rate on production of lovastatin was investigated. Bubble column bioreactor can supply high concentration of DO without destructive effect on fungal morphology.

Keywords: lovastatin, *Aspergillus terreus*, Bubble column

**P849 - 347: PREVALENCE OF EXTENDED-SPECTRUM β -LACTAMASE-PRODUCING
ESCHERICHIA COLI IN AGRICULTURAL FIELDS OF GORGAN DISTRICT**

Arezoo Hoseini¹, Arezoo Hosseini², Ania Ahani Azari³

1. Gorgan Branch, Islamic Azad University, Gorgan, Iran
2. Department of Biology, Gorgan Branch, Islamic Azad University, Gorgan, Iran

Background and Aim: The aim of this study was to assess the prevalence of ESBL-producing *Escherichia coli* in agricultural fields of Gorgan district, Golestan province.

Methods: Two soil samples, one from surface and the other from a depth of 15cm, were collected from 20 agricultural fields that half of them had been fertilized with chemical fertilizers. The samples were examined for *E. coli* strains. The cefotaxime resistant *E. coli* isolates were identified by disk diffusion method. The resistant isolates were further confirmed by phenotypic confirmatory test. Afterwards, antibiotic susceptibility of the confirmed ESBL-producing *E. coli* strains was determined.

Results: The prevalence of *E. coli* strains in the soils fertilized with animal manure was higher than the soils strengthened with chemical fertilizers. Moreover, from the surface samples more *E. coli* strains were isolated than the depth samples. This finding was similar for the both types of soils. 68.4% of the strains isolated from the soils fertilized with animal manure were resistant to Cefotaxime and among them the frequency of ESBL-producing *E. coli* was 43%. However, 33.3% of the strains isolated from the soils strengthened with chemical fertilizers were resistant to Cefotaxime in which 75% of them were ESBL producers. The highest resistance rate was observed against Amoxicillin in all the ESBL-producing isolates.

Conclusion: The results of this study showed that the use of animal manure may increase the dissemination of the antibiotic resistant bacteria to the soil. This may transfer antibiotic-resistant genes to other bacteria, causing spreading of these genes in the environment.

Keywords: Agricultural fields, Animal manure, ESBL, *E. coli*, Prevalence.

**P850 - 406: PHYSICO-CHEMICAL ANALYSIS OF PATHOGENIC AND NON-PATHOGENIC
E. COLI OUTER MEMBRANE VESICLES (OMVS)**

Roghayeh Mohammadzadeh¹, Seyed Davar Siadat², Farzam Vaziri³, Ava Behrouzi⁴, Abolfazl Fateh⁵,
Morteza Ghazanfari⁶

1. Mycobacteriology and Pulmonary Research Department, Pasteur Institute of Iran, Tehran, IR Iran
Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, IR Iran
2. Mycobacteriology and Pulmonary Research Department, Pasteur Institute of Iran, Tehran, IR Iran
Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, IR Iran
3. Mycobacteriology and Pulmonary Research Department, Pasteur Institute of Iran, Tehran, IR Iran
Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, IR Iran
4. Mycobacteriology and Pulmonary Research Department, Pasteur Institute of Iran, Tehran, IR Iran
Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, IR Iran
5. Mycobacteriology and Pulmonary Research Department, Pasteur Institute of Iran, Tehran, IR Iran
Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, IR Iran
6. Mycobacteriology and Pulmonary Research Department, Pasteur Institute of Iran, Tehran, IR Iran
Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, IR Iran

Background and Aim: Escherichia coli like other gram-negative bacteria secretes OMV, nano-sized spherical bilayered proteolipids. OMVs have several offensive and defensive functions that allow their producing microorganisms to communicate with other live cells and overcome their hostile environment.

Methods: Standard strains of pathogenic (strain O1:K1:H7) and non-pathogenic (strain ATCC25922) E.coli were obtained from the standard Bacterial Collection of Pasteur Institute of Iran. OMVs were extracted with deoxycholate and EDTA, and purification was performed by sequential centrifugation. Physicochemical properties of extracted OMVs were analyzed by electron microscopy and SDS-PAGE.

Results: The electron microscopy showed that pathogenic and non-pathogenic E.coli were produced OMVs with an average diameter of 20–200 nm. The results revealed that the content of extracted protein were 1mg/mL in pathogenic and 0.9 mg/ml in non-pathogenic E.coli. The SDS-PAGE showed that two strains had protein bands in the range of 25 up to 100 kD. In spite of the fact that OMVs were extracted from the equal volume of the biomasses, Pathogenic E.coli had more bands in close different sizes but non-pathogenic E.coli had sharper bands.

Conclusion: The electron microscopy observations showed that OMVs were produced by both pathogenic and nonpathogenic strains of E.coli. The SDS-PAGE showed that these two strains of E.coli had different protein patterns and sizes. In the future works we want to use these data to evaluate Nod-Like Receptors (NLRs) signalling pathways in Caco2 epithelial cells.

Keywords: OMV; Physico-chemical analysis; E. coli

**P851 - 449: OPTIMIZATION OF PYRENE BIODEGRADATION BY ACHROMOBACTER SP.
ISOLATED FROM OIL -CONTAMINATED SOILS**

Ensieh Daliri¹, Bahar Shahnava², Tahereh Heidari³

1. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran.
2. Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran.
3. Department of chemistry, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran

Background and Aim:Currently, Microbial degradation is the major process to remove PAH pollutants in the environment. Pyrene is one of PAH compounds, that has been used as a model to study the biological degradation of PAHs.

Methods:Pyrene-degrading bacterial strains were isolated from oil-contaminated soils on the culture medium containing pyrene as sole source of carbon. The morphology and biochemical characteristic of the strains having the highest degradation in the shortest time was evaluated. Finally, D6 strain was selected for further study. This strain was identified as *Achromobacter* sp. by 16S rDNA gene analysis. For research purposes, five factors were studied including pH, temperature, nitrogen source and presence of glucose and NaCl to optimize pyrene degradation

Results:The results demonstrated that decreasing temperature from 37 to 30 °C had a positive impact on the biodegradation of pyrene and environment pH from neutral to acidic was more favorable for the pyrene degradation. On the other hand, using of organic nitrogen source was associated with a decrease in pyrene degradation. Using (NH₄)₂SO₄ instead of NH₄NO₃ stimulated pyrene bio degradation to 75% in 72 hours. Glucose did not affect on bio degradation and removal rate of pyrene was higher in the absence of NaCl.

Conclusion:Results indicated that native strains have high potential to removal of pollutants and environmental condition's optimization can be affected in shorten the removal time.

Keywords:Pyrene, Biodegradation, Optimization, *Achromobacter* sp.

**P852 - 505: POTENTIAL OF EARTHWORMS (EISENIA FETIDA) TO BIOLOGICAL
REMEDIATION OF THE GAS OIL CONTAMINATED SOIL**

Nazila Jafari Farjam¹, Mahdi Zarabi², Ashrafalsadat Hatamian-Zarmi³, Ghasemali Mohebbali⁴

1. Department of Life science Engineering, Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran
2. Department of Life science Engineering, Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran
3. Department of Life science Engineering, Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran
4. Department of Petroleum Biotechnology, Biotechnology Research Center, Research Institute of Petroleum Industry, Tehran, Iran

Background and Aim:Crude oil compromise variety of different compounds. Petroleum and its derivatives cause soil pollution at the time of extraction, transportation and storage. Abiotic methods of polluted soil refining are not economical and biocompatible. Bioremediation is a bioengineering technique to clean up contaminated soil using microbes, plants and earthworms. Vermi-remediation is the use of earthworms for the removal of soil pollutants and reinforcement of hard degradable compounds. Earthworms toward burrowing the soil mass; not also change soil structure but also increase bioavailability of organic materials and develop bacterial community and bioactivity so cause further removal of soil pollutants. The aim of the study was to investigate the influence of earthworms (*Eisenia fetida*) on microbial activity gas oil polluted soil.

Methods:The amount of 3% (v/w) gas oil was added to 0.5 kg of soil and transferred into pots . Then, 20 earthworms (*Eisenia fetida*) were added to each pot. The control enclosed 3% gas oli polluted soil without earthworms.

Results:: Results showed that the *Eisenia fetida* was able to increase bacterial community from 45 to 147 colonies.

Conclusion:The study demonstrated that earthworms can increase the microbial activity, which led to enhancing removal of gas oil pollutants.

Keywords:Soil pollution; earthworm; *Eisenia fetida*; vermi-remediation

**P853 - 538: CULTURE OF MICROALGAL STRAINS ISOLATED FROM PERSIAN GULF OF
IRAN IN DIFFERENT SALINE MEDIA**

Mahroo sadat Seyed jafari olia¹, Mehrdad Azin², Abbas Akhavan Sepahi³

1. Dept. of Microbiology, Faculty of Biological Sciences, Islamic Azad University, North of Tehran Branch, Tehran, Iran.
2. Department of Biotechnology, Iranian Research Organization for Science and Technology (IROST), Tehran, Iran
3. Dept. of Microbiology, Faculty of Biological Sciences, Islamic Azad University, North of Tehran Branch, Tehran, Iran

Background and Aim: Microalga are simple and free floating photosynthetic microorganisms which have received considerable attention due to the ability of cells to withstand and flourish in saline environment under the effect of osmotic stress. Persian Gulf has typical range of salinity about 35 to 40 ppt. So, salinity is an important factor in culture media of microalgal strains, which were isolated from this region. The main objective of this study was to evaluate the impact of various salinity concentration on the growth of these isolates.

Methods: Six isolated microalga were grown on RM medium with initial density of 10^5 cells mL⁻¹, at different salinities (5, 25, and 35 ppt), separately. The culture condition, including a photoperiod of light: dark regime (16:8), temperature 25°C, in an orbital shaker set to 110 rpm was set for 14 days. Light intensity of 3000 lux was supplied by cold fluorescent tubes. Growth was measured by cell counting, and cell density spectrophotometrically (620 nm). Changes in pH value of culture media were measured during growth.

Results: The growth curve of isolates in standard and different salinities were obtained. The maximum cell densities were obtained in ranges between 1×10^6 - 3.862×10^7 cells mL⁻¹ for 25 ppt, followed by 1×10^6 - 1.716×10^7 cell mL⁻¹ for 35 and 1.4×10^6 - 9.15×10^6 cells mL⁻¹ for 5 ppt, respectively.

Conclusion: Different distinct growth pattern among these microalga under laboratory conditions were observed. With regard to the origin of these strains, now we can manage for pure culture of these isolates on large scale in proper condition.

Keywords: Marine microalgae, salinity, cell growth, Persian Gulf

P854 - 539: EVALUATION OF THE EFFECT OF ORTHO-KIN MOUTHWASH ON DENTAL PLAQUE AROUND DIFFERENT ELASTOMERIC LIGATURES IN ORTHODONTIC PATIENTS

Surur Samie¹, Mehrnaz Moradinejad², Mansour Amin³, Mina Moradi⁴, Mehrandokht Sirous⁵

1. School of Dentistry, Ahvaz Jundishashapur University of Medical Sciences, Ahvaz, Iran
2. Department of Orthodontics, School of Dentistry, Ahvaz Jundishashapur University of Medical Sciences, Ahvaz, Iran
3. Health research institute, Infectious and Tropical Disease Research Center, Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of medical sciences, Ahvaz, Iran
4. Department of Orthodontics, School of Dentistry, Ahvaz Jundishashapur University of Medical Sciences, Ahvaz, Iran
5. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of medical sciences, Ahvaz, Iran

Background and Aim:: Bacterial plaque control is a major concern during orthodontic treatment in order to prevent the occurrence of caries and periodontal inflammation. The aim of this study was to assess the effect of Ortho-kin mouthwash on microbial plaque around different orthodontic elastomeric ligatures.

Methods: Four different types of ligatures were placed on the four premolar teeth in Seventeen patients. Ligatures were removed after 21 days and placed in 5 ml normal saline. Using 10 µl of every sample was streaked on Blood agar and Mitis salivarius agar to count total microbial and viridans streptococci. Identification of viridans streptococci species reached through traditional biochemical tests. In the second stage ligatures were placed on the premolar teeth to use Ortho-kin Mouthwash. Ligatures were removed After 21 days, the number of colonies was counted in the culture medium. GEE and Pairwise comparison test was used to compare the plaque mouthwash use within and between the groups, respectively.

Results: Mouthwash consumption reduced total microbial count around elastomeric ligatures. No significant difference in colony count was detected between the groups. In viridians streptococci count including *S. Salivarius*, *S. Sanguis* and *S. Sobrinus*, there was significant difference between Ortho-technology and other types of elastomeric rings, but no difference among other groups.

Conclusion: Orthokin mouthwash reduces microbial plaque accumulation around all four types of the ligatures. Ortho-technology show more viridans streptococci around itself Compared to the other three types. *Streptococcus Salivarius* was the most frequent on the microbial plaque.

Keywords:: Mouthwash, Microbial plaque, Viridans Streptococci

**P855 - 546: EXPRESSION AND PURIFICATION OF SOLUBLE RECOMBINANT HUMAN
PARATHYROID HORMONE (RHPH1-34) BY TRX TAG IN TWO STRAINS OF
ESCHERICHIA COLI**

Sanaz Yari¹, Farida Behzadian², Hamideh Rouhani Nejad³

1. Research Center for Biosciences and Biotechnology, Malek-Ashtar University, Tehran, Iran.
2. Research Center for Biosciences and Biotechnology, Malek-Ashtar University, Tehran, Iran.
3. Research Center for Biosciences and Biotechnology, Malek-Ashtar University, Tehran, Iran.

Background and Aim: Parathyroid Hormone secreted by parathyroid glands and controls the value of calcium in bones and kidney. PTH is small polypeptide by 84 amino acids, but first 34 amino acids is enough for hormone's biological activity and can be used for treatment of osteoporosis. recombinant protein expression in E.coli is fast and inexpensive, also the rapidity of bacterial protein expression often results in unfolded protein. for fix this problem, fused target protein with special tag that increase solubility and level of expression. In this study Trx tag is used for expression of PTH(1-34).

Methods: rhPTH cassette designed. From 5' to 3', the cassette consisted of; Trx tag, His tag, enterokinase site to cleavage all fusion moieties, and the open reading frame encodes for PTH. This cassette cloned into the pET32a vector, then transferred into each strains of E.coli; BL21 and Rossetagami. Early expression confirmed by SDS-PAGE and western Blotting. crucial expression parameters including IPTG concentration, induction time, temperature, medium and ethanol were optimized. The soluble fusion protein purified by affinity chromatography using Ni-NTA column.

Results: SDS-PAGE analysis showed that the efficiency of expression in Rossetagami is higher than BL21. The optimum expression occurred at Terrific Broth with glycerol 1x, ethanol 1% and IPTG 0.1mM at 30°C after 4 hours. Recombinant protein was highly purified with Ni-NTA column.

Conclusion: we are planning to digest the fused form of PTH, with enterokinase then purify it. This purified form of PTH needs to be assessed in terms of biological activity and safety.

Keywords: PTH, enterokinase, Trx tag

**P856 - 614: UREASE INHIBITORY ACTIVITY OF AERIAL PARTS OF VERONICA
CYMBALARIA BODARAD.**

Javad Sharifi Rad¹, Fatemeh Fallah², Abdolhossein Miri³

1. Zabol Medicinal Plants Research Center, Zabol University of Medical Sciences, Zabol, Iran
2. Pediatric Infections Research Center, Mofid Children Hospital, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. Department of Pharmacognosy, Faculty of Pharmacy, Zabol University of Medical Sciences, Zabol, Iran

Background and Aim: Urease is usually found in different bacteria, fungi, algae, and plants. It is an enzyme that catalyzes the hydrolysis of urea to ammonia and carbamate, which is the final step of nitrogen metabolism in living organisms. The current study was designed to investigate the aerial parts of *Veronica cymbalaria* Bodarad has been used in (crude extract, total sterol and flavonoidal contents, and aqueous fraction) for its urease inhibitory potential.

Methods: The various extracts evaluated separately on enzyme (Jack Bean Urease) solution.

Results: The crude of the plant evoked marked attenuation on urease activity, when tested in various concentrations with IC₅₀ values of 7.08 mg/mL. The inhibitory potential was further augmented in the aqueous fraction (IC₅₀: 4.22 mg/mL) of the plant. When the total sterol and flavonoidal contents were challenged against urease, both showed concentration dependent activity; the latter showed maximum potency with IC₅₀ values of 10.32 and 3.44 mg/mL, respectively.

Conclusion: In conclusion, the aerial parts of the plant demonstrated marked antagonism on urease and thus our study validated use of *V. cymbalaria* for treatment of infections produced by the bacteria such as *Helicobacter pylori* and *Proteus mirabilis* usually with a high urease activity.

Keywords: Urease inhibitory activity, *Veronica cymbalaria* Bodarad.

**P857 - 628: STUDY OF PMMA AS ADJUVANT FOR PRODUCTION OF ANTI DIPHTHERIA
SERUM ALONG WITH ALUMINUM PHOSPHATE**

Ebrahim Abbasi¹, Vafa maljaei²

1. Human bacterial vaccine Department, Razi Vaccine and Serum Research Institute, Karaj, Iran
2. Department of Human Bacterial Vaccine Quality Control. Razi Vaccine and Serum Research Institute, Karaj, Iran

Background and Aim: Nano- particles are solids and having assize ranging from 1-100 nm and we can use these products in treatment and prevention of diseases. Adjuvant or helpers as carriers of drug substances that are associated with drug or vaccines are used. component of the active form (dissolve, entrapped, encapsulated or surface adsorption and chemical binding (11). Most used method for preparation of nanoparticles is Polymethilation of emulsion. The polymers that used for this methods are PMMA, PAA and PACA. The best nanoparticles is PMMA. defect of nanoparticles made of AA and PACA is that produce large amount of organic solvents and active substances. in contrast nanoparticles of PMMA significant amount of antigens in exposed and process their products easily and without difficulty can scale increased and the PMMA of toxicity study and experience are in good and is slowly biodegradable in nature (1,2).

Methods: The methods base on the following general principals. 1-2-preparation of PMMA and aluminum Phosphate. 2-2-formulation of antigen associated with PMMA and aluminum Phosphate. 3-2-Horse and blood transfusion. 4-2-Titration and SN test.

Results: in the titration sera we shown that the PMMA sera titer not being very lower than Phosphate aluminum (600,1040,360 Lf/ml).

Conclusion: Researchers shown that PMMA nano-particles can be used in two forms: the vaccine antigen can either be incorporated in to the nano-particles or it can be adsorbed to previously formed particles. Otherwise the capsulation of Influenza virus in comparison with adsorbed to previously formed particles cans more product of antibody titre, because the antigen protect about the degradation.

Keywords: Nanoparticles, adjuvant, aluminum phosphate, PMMA

**P858 - 665: ISOLATION AND IDENTIFICATION OF BDELLOVIBRIO SP. FROM
ENVIRONMENTAL SAMPLES**

Hajar Valizadeh¹, Gholamreza Zarrini²

1. Department of biology, Faculty of natural sciences, University of Tabriz, Tabriz, Iran
2. Department of biology, Faculty of natural sciences, University of Tabriz, Tabriz, Iran

Background and Aim: Bdellovibrios are gram negative, small, fast swimming and obligate predators of other gram negative bacteria. They have two phases life cycle: attack phase and growth or divide phase. Attack phase cells attach the prey, penetrate into their periplasmic space, multiplying inside the hosts, and causing lysis of the infected cells. The progeny cells escape from the prey and start a new cycle. In this study we're going to isolate these bacteria and identify them.

Methods: Soil samples suspended in water or aquatic samples centrifuged for 5 min at 2000 g, and the supernatant is passed through membrane filters (1 and 0.45 μ m). The final filtrate are plated using the double-layer agar technique. In this method suspension of washed prey cells and the filtrate sample are added to the top molten layer respectively and mixed. Then quickly poured onto the bottom layer plates. The plates incubated for 3 to 8 days at 28°C. The lytic plaques that contain Bdellovibrios will appear on the background of the prey lawn. Identification of Bdellovibrios is performed by PCR technique with specific primers.

Results: With this method we could see plaques in four samples between many aquatic and soil samples. Results of PCR technique confirmed that two of them belong to Bdellovibrio genus.

Conclusion: Bdellovibrios concentration in soil is more than aquatic samples. They prey on various gram negative bacteria, so they could be used against humans, animals and plant pathogens or other harmful bacteria in industry.

Keywords: Bdellovibrio, predator, isolation, prey

**P859 - 713: EVALUATION OF NATURALLY ISOLATED BACTERIOPHAGE EFFECT, MGY2,
AGAINST B-LACTAM RESISTANT ESCHERICHIA COLI O157**

Robab Yousefi¹, Zahra Moradpour², Abdollah Ghasemian³

1. Urmia university of medical sciences, Faculty of pharmacy, Department of pharmaceutical Biotechnology, Urmia, Iran
2. Urmia university of medical sciences, Faculty of pharmacy, Department of pharmaceutical Biotechnology, Urmia, Iran
3. Urmia university of medical sciences, Faculty of pharmacy, Department of pharmaceutical Biotechnology, Urmia, Iran

Background and Aim: *E. coli* is a Gram-negative bacterium that exists in the intestine as normal flora. Infection with this pathogen has been implicated in several clinical cases such as hemolytic uremic syndrome, neonatal meningitis, urinary tract infections, septicemia, traveler's diarrhea and bloody diarrhea. Due to the emergence of antibiotic-resistant bacteria, searching for other antibacterial agents particularly from natural sources is very important. Bacteriophages have been investigated for biocontrol of human pathogens.

Methods: After enrichment and purification, the efficacy of isolated phages was determined by top overlay agar, spot-test method, and liquid lysis test. The morphology of phage was determined based upon the electron microscopy image. The profile of proteins was obtained by the SDS-page method.

Results: In this study, we isolated a potent lytic phage (MGY2) against *E. coli* O157 that was resistant to antibiotics. Isolated phage lysed *E. coli* O157 efficiently. The plaques were observed as clear zones on the bacterial lawn. Also, the spot test revealed clear areas in the site of phage drop. The optical density of the test cultures containing bacteria and bacteriophage declined very rapidly in comparison to control culture including the bacteria without bacteriophage. The bacteriophage belongs to corticoviridae family. The SDS-PAGE analysis indicated 6 major capsid proteins.

Conclusion: Considering the increase in bacterial drug resistance, and the relatively quick and easy production of bacteriophages, phage therapy might be as a way to prevent treatment failure.

Keywords: Bacteriophages, Antibiotic resistance, Antibacterial effect, *Escherichia coli*

**P860 - 743: AN EPIDEMIOLOGICAL SURVEY ON THE PREVALENCE OF ANTHRAX IN
HAMEDAN PROVINCE**

Abdolmajid Mohammadzadeh¹, Pezhman Mahmoodi², Reza Hakimi Alni³, Elaheh Ghytas ranjbar⁴,
Solmaz Kheirandish⁵

1. Department of Pathobiology, Faculty of Veterinary Science, Bu-Ali Sina University, Hamedan, Iran
2. Department of Pathobiology, Faculty of Veterinary Science, Bu-Ali Sina University, Hamedan, Iran
3. Department of Pathobiology, Faculty of Veterinary Science, Bu-Ali Sina University, Hamedan, Iran
4. Department of Pathobiology, Faculty of Veterinary Science, Bu-Ali Sina University, Hamedan, Iran
5. Department of Pathobiology, Faculty of Veterinary Science, Bu-Ali Sina University, Hamedan, Iran

Background and Aim: Anthrax is an infectious zoonotic disease caused by a Gram-positive, spore-forming bacterium named *Bacillus anthracis*. Despite that the disease is controlled in developed countries, it is still a major problem in developing countries. Iran is an endemic area of anthrax which is ranked third among the affected countries in 2012. As Hamadan is one of the contaminated regions in our country, the present study was conducted to investigate the prevalence of anthrax disease in animals in Hamedan province of Iran.

Methods: This study was a retrospective study to describe the prevalence of anthrax during the past decade (1382 to 1392) among animal cases from different regions of Hamedan province.

Results: According to the statistics retrieved from the veterinary office, 11 cases of anthrax were reported in animals over the past decade. There were two centers of the disease. One case occurred in the village Akhtachy, while the other ten cases were reported from Bahar town. Sheep was the only infected species in all of the cases.

Conclusion: The results showed that the disease has occurred in Hamedan province of Iran. Moreover, it seems that Bahar town should be considered as a potential focus of Anthrax. Given that this disease is a lethal infection in humans which is related to animal cases, more information should be provided and applied to take appropriate vaccination programs to battle against the disease.

Keywords: Anthrax, Epidemiology, *Bacillus anthracis*, Hamedan

**P861 - 756: ONE-STEP AND NON-CHROMATOGRAPHIC PURIFICATION OF V ANTIGEN
USING ELASTIN-LIKE PROTEIN**

Maryam Molaei¹, mehdi Zeinoddini ², Saeedinia Ali Reza³

1. Department of Bioscience and Biotechnology, Malek Ashtar University of Technology, Tehran, Iran
2. Department of Bioscience and Biotechnology, Malek Ashtar University of Technology, Tehran, Iran
3. Department of Bioscience and Biotechnology, Malek Ashtar University of Technology, Tehran, Iran

Background and Aim:Elastin like protein (ELP) is a synthetic biopolymer consisting the pentapeptide repeats of VPGXG (X is any amino acid except Pro). This protein is the thermal responsive polypeptide that undergoes a reversible phase transition. At a temperature below the transition temperature (T_t), ELP molecules assume an extended conformation and thus are soluble in aqueous solution. Upon the temperature shift higher than the T_t, however, ELPs become insoluble and form the segregated phase prone to 'rigid' form. The aim of this work is designing of ELP-fused INT and V antigen sequence for simple purification of this protein model

Methods:In this work, ELP10 (150 bp) was synthesized and cloned into pBluescript. Elp oligomerization, was carried out using recursive directional ligation (RDL) for Elp60 (900 bp) production. Then, ELP60 was subcloned into pTXB1 (pTX-INT-ELP) and finally V antigen sequence subcloned into created new plasmid for production of pTX-V-INT-ELP. ELP60 expression fused to INT and V antigen was confirmed using SDS-PAGE method. Also, this protein was purified using sequential steps of inverse transition cycle (ITC).

Results:Data was shown V-INT-ELP expressed and it's successfully purified in one step and non-chromatographic method. Also, The fusion protein is then cleaved by activating the self-cleaving intein and V antigen detaches from ELP

Conclusion:In conclusion, we propose that this method can be used for simple and easy purification of the recombinant proteins

Keywords:Elastin like protein, expression, inverse transition cycle, purification

P862 - 781: MICROBIAL DIVERSITY ASSESSMENT OF THE OIL LAGOONS OF KHARK ISLAND USING CULTURE DEPENDENT AND CULTURE INDEPENDENT APPROACHES

Elham Ahmadi¹, Mahdis Zolfaghar², Maliheh Mehrshad³, Seyed Abolhassan Shahzadeh Fazeli⁴,
Mohammad Ali Amoozegar⁵

1. 1:Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran. 2:Microorganisms Bank, Iranian Biological Resource Centre (IBRC), ACECR Tehran-Iran
2. 1:Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran. 2:Microorganisms Bank, Iranian Biological Resource Centre (IBRC), ACECR Tehran-Iran
3. 1:Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran. 2:Microorganisms Bank, Iranian Biological Resource Centre (IBRC), ACECR Tehran-Iran
4. 1:Microorganisms Bank, Iranian Biological Resource Centre (IBRC), ACECR Tehran-Iran 2: Department of Molecular and Cellular Biology, Faculty of Basic Sciences and Advanced Technologies in Biology, University of Science and Culture, Tehran, Iran
5. 1:Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran. 2:Microorganisms Bank, Iranian Biological Resource Centre (IBRC), ACECR Tehran-Iran

Background and Aim:Khark Island is a continental island located in the Persian Gulf and is considered as an important center in the world regarding oil export. In this research the biodiversity of halophilic and halotolerant microorganisms of the island's oil lagoons have been examined by culture dependent and culture independent methods in order to determine their bacterial population and preserve the isolates for further studies regarding their potential in oil decontamination.

Methods:Samples were taken from oil lagoons and transferred to the lab and analyzed physically and chemically. Serial dilutions of samples were cultured on appropriate media designed in accordance to biochemical characteristics of the samples and incubated at 34°C. In the culture independent methods, the DNA content of the samples were extracted and the PCR amplified 16s rRNA genes were cloned in appropriate vector. The extracted plasmids were sequenced and phylogenetically analyzed.

Results:of the 40 selected isolates, 7.5% of them were gram positive, 92.5% were gram negative. The phylogenetic analysis based on 16s rDNA sequencing of pure isolates showed that predominant groups of microbes are Marinobacter and Halomonas genera with 40 and 35 percent of sequenced isolates respectively. Eighteen of recombinant clones retrieved via culture independent methods were selected and 28% of sequenced clones show similarity to Sulfurovum genus.

Conclusion:This work illustrates the importance of evaluating biodiversity of the polluted areas in order to use biotechnological potential of the microorganisms in bioremediation and other sectors of industry and also have the potential to monitor the changes in the environment in order to protect the environment.

Keywords:Biodiversity, Culture dependent techniques , Culture independent methods, Khark island.

**P863 - 797: NASAL CARRIAGE OF UNCOMMON COAGULASE-NEGATIVE
STAPHYLOCOCCI IN NURSES AND PHYSICIANS OF TEHRAN UNIVERSITY HOSPITALS**

Elaheh Salimi¹, Zahra Pakbaz², Mohammad Reza Pourmand³, Sanaz Dehbashi⁴

1. Urology Research Center, Tehran University of Medical Sciences, Tehran, Iran
2. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
3. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
4. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: Coagulase-negative staphylococci (CoNS) have been identified as a major cause of nosocomial infections. Nasal carriage of CoNS in nurses and physicians is known to be an important risk factor for potential hospital infections. This study was carried out to investigate the prevalence of nasal carriage of uncommon coagulase-negative staphylococci among nurse and physician staffs of Tehran University Hospitals.

Methods: A total of 116 CoNS were isolated from anterior nares of the study participants working in different wards of the hospitals. Thirteen uncommon CoNS were identified using phenotypic and biochemical methods, were subsequently confirmed by API kits.

Results: *Staphylococcus xylosum*, *Staphylococcus haemolyticus*, and *Staphylococcus capitis* species accounted for 53.85%, 30.77%, and 15.38% from the isolates, respectively. Six isolates (46.15%) were found to be resistant to methicillin.

Conclusion: In conclusion, screening of healthcare workers for uncommon CoNS colonization along with identification and testing for susceptibility of cultured isolates is of paramount importance in strengthening effective nosocomial infection control and prevention measures.

Keywords: Healthcare workers; Nasal carriage; Coagulase negative staphylococci

P864 - 808: EFFECT OF ESSENTIAL OIL OF ANETHUM GRAVEOLENS ON INTESTINAL E. COLI ISOLATES IN BROILER CHICKENS

HAMED DEHGHAN¹, azadeh hadad sabzevar², navid ghanad³, saeid rahim⁴

1. Islamic Azad University, Mashhad Branch, Department of Biology, Mashhad, Iran
2. Phd, Ferdowsi University of Mashhad, School of Veterinary Medicine, Department of Pathobiology, Mashhad, Iran
3. Islamic Azad University, Mashhad Branch, Department of Biology, Mashhad, Iran
4. Islamic Azad University, Mashhad Branch, Department of Biology, Mashhad, Iran

Background and Aim:Background and goal: This study was conducted to investigate the effects of diets containing different levels of Anethum graveolens essential oil on Fecal and illum microflora of broiler chicks, resistance antibiotic and invitro assay activity Anethum essential oil against E.coli isolates.

Methods:Materials and Method: Sixty four one-day old male broiler chicks (Ross-308 strain) were used in a completely randomized design with 4 treatments, and 4 replicates were allocated to each treatment.

Results:Results: Sixty four one-day old male broiler chicks (Ross-308 strain) were used in a completely randomized design with 4 treatments, and 4 replicates were allocated to each treatment. Different levels of Anethum essential oil in diets had not significant effects on total bacterial count and E.coli/coliform population in faecal material at 32 days old and illum at 42 days of age ($p>0.05$). Also in this survey Dietary treatment had no effect on the anti-bacterial valus of thirteen antibiotics against E.coli isolates by Disc diffusion method ($p>0.05$). Most of the E.coli isolates were resistant to antibiotics, the most efficient being Penicillin, Vancomycin and sulfamethonazole trimethoprime. Chemical analysis of this oil by capillary GC showed as the main constituent lyhtemid-enarobacedabraciD (%54.56). An invitro assay measuring the antimicrobial activity of Anethum essential oil in disc diffusion method, the highest inhibition areas were observed for the amount of 5 μ l essential extract. The results of MIC and MBC showed the high antimicrobial effect of Anethum essential oil.

Conclusion:Discussion: It seems the presence of lyhtemid-enarobacedabraciD caused the strong anti microbial effect of this oil.

Keywords:Anethum essential oil, antimicrobial effect, Broiler chicks, Micro flora, E.coli

P865 - 837: INFLUENCE OF THE ESCHERICHIA COLI'S HOST ON THE SOLUBILITY OF RECOMBINANT PROTEINS

Farzaneh Farshdari¹, Elham Mohit², Maryam Ahmadzadeh³, Leila Nematollahi⁴, Hoda Jahandar⁵

1. Department of Biotechnology, Faculty of Advanced Sciences & Technology, Pharmaceutical Sciences Branch, Islamic azad University, Tehran- Iran (IAUPS)
2. Department of Pharmaceutical Biotechnology, School of Pharmacy, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. Department of Pharmaceutical Biotechnology, School of Pharmacy, Shahid Beheshti University of Medical Sciences, Tehran, Iran
4. Department of Medical Biotechnology, Biotechnology Research Center, Pasteur Institute of Iran, Tehran, Iran
5. Department of Biotechnology, Pharmaceutical Science Branch, Islamic Azad University, Tehran, Iran

Background and Aim: Expression of recombinant proteins containing disulphide bonds in *Escherichia coli* often results in insoluble and/or non-functional proteins accumulation in the cytoplasm as inclusion body. Cysteines in the *E. coli* cytoplasm are actively kept reduced by pathways involving thioredoxin (trxB) and glutaredoxin reductase (gor). Origami strains have mutations in gor and trxB, facilitating proper disulfide bond formation in the *E. coli* cytoplasm. The aim of this study is to evaluate the influence of *E. coli*'s host on the solubility of recombinant proteins produced in it. Accordingly, anti-HER2 single-chain Fv (scFv), with two disulphide bonds, was selected as the pattern molecules and the solubility of the expressed scFv was compared in BL21 (DE3) and Origami strains.

Methods: Anti HER2-scFv was cloned in the pET22b(+) vector and transformed in BL21(DE3) and Origami strains of *E. coli*. The expression was induced using 1mM isopropyl β -D-1 thiogalactopyranoside (IPTG) at 37°C. Then, the solubility of the expressed Anti HER2-scFv was determined. Briefly, harvested cells was resuspended in lysis buffer and the soluble and insoluble fractions were separated after sonication. Finally, soluble and insoluble fractions were analysed by SDS-PAGE.

Results: Anti-HER2 scFv was expressed in both BL21(DE3) and Origami *E. coli* strain. The results of this study demonstrated that higher soluble protein is produced in *E. coli* Origami than in BL21 (DE3) cells.

Conclusion: High-level expression of the functional anti-HER2 scFv can be obtained in Origami strain, which has an oxidative cytoplasm.

Keywords: *E. coli*, Origami, scFv

**P866 - 850: BIOFILM FORMATION IN METHICILLIN RESISTANT STAPHYLOCOCCUS
AUREUS CLINICAL ISOLATES IN ILAM HOSPITALS, IRAN**

Lida Bimanand¹, Iraj Pakzad², Reza Azizian³

1. 1. Department of Microbiology, Faculty of Medicine and Students Research Committee, Ilam University of Medical Sciences, Ilam, Iran
2. 1. Department of Microbiology, Faculty of Medicine and Students Research Committee, Ilam University of Medical Sciences, Ilam, Iran 2. Clinical Microbiology Research Center, Ilam University of Medical Sciences, Ilam
3. 1. Department of Microbiology, Faculty of Medicine and Students Research Committee, Ilam University of Medical Sciences, Ilam, Iran

Background and Aim: biofilm production capacity, adhesions factors and antibiotic resistance contribute to the success of *Staphylococcus aureus* as a human pathogen in both hospital and community acquired infections. This study aims to evaluate ability biofilm formation in methicillin resistant *Staphylococcus aureus*

Methods: ninthly six isolates of methicillin resistant *Staphylococcus aureus* were collected from hospitals of Iran's western provinces during 2012 to 2013. MRSA clinical isolates were isolated from lesion, sputum, blood stream and urine infections. The presence of Biofilm formation were investigated by microtiter plate assay.

Results: from all isolates, 96 % were produced biofilm. According to degree of biofilm formation 4.2%, 54.2%, 35.4% isolates were high, moderate and weak. The highest biofilm production were seen in bacteria were isolated from blood and Septum isolates is greater moderate biofilm producer.

Conclusion: Our results suggest different biofilm formation ability in clinical isolates of *Staphylococcus aureus*. Biofilm formation on devices such as intravascular catheters can increase the risk of infection. Moreover, bacterial biofilms show increased tolerance to antibiotics. This is a serious problem in medical centers specially, in intensive care units.

Keywords: Biofilm, MRSA, clinical isolates, Ilam hospitals, Iran

**P867 - 851: DETECTION OF SOME VIRULENCE FACTORS OF ESCHERICHIA COLI
ISOLATED FROM URINARY TRACT INFECTION ISOLATED FROM HOSPITALIZED
PATIENTS IN QAZVIN AND KARAJ HOSPITALS**

Mahsa Mahdikhani¹

1. A. Peymani

Background and Aim: Escherichia coli (E. coli) is the most important cause of urinary tract infections in hospitalized patients especially in intensive care unit (ICU). Colonization of E. coli and its attachment to uroepithelium are mediated by adhesins such as type 1 (fimH) and P (papC) fimbriae. The aim of this study was to determine the frequency of type 1 and P fimbriae-encoding genes among uropathogenic E.coli in ICUs.

Methods: In this descriptive study, 120 clinical isolates of uropathogenic E.coli were collected from patients with urinary tract infection in ICUs of Qazvin and Karaj hospitals during 2013 and 2014. All bacterial isolates were identified by standard laboratory methods and the fimH and papC genes were detected using the PCR method.

Results: Forty (33.3%) isolates were positive for fimH gene and 5 (4.2%) isolates were positive for papC gene. Sixty six (55%) isolates were positive for both genes, and 9 (7.5%) isolates were negative for them.

Conclusion: The findings of this study showed the high frequency of type 1 and P fimbriae among uropathogenic E.coli isolates from ICU patients in the studied hospitals.

Keywords: Protein, PapC Protein, Urinary Tract Infections, Intensive Care Units Escherichia coli, FimH

**P868 - 858: INTRODUCTION AND FUNCTIONAL PRESENTATION OF TEHRAN REGIONAL
REFERENCE LABORATORY OF TUBERCULOSIS**

Afsaneh Khoshkhoo¹, Gholam Reza Hamzehloo², Sirus Amini³, Mohammad Reza Allahyar⁴

1. Tehran Regional Reference of Tuberculosis, Health Deputy, Tehran University of Medical Sciences
2. Tehran Regional Reference of Tuberculosis, Health Deputy, Tehran University of Medical Sciences
3. Tehran Regional Reference of Tuberculosis, Health Deputy, Tehran University of Medical Sciences
4. Tehran Regional Reference of Tuberculosis, Health Deputy, Tehran University of Medical Sciences

Background and Aim: Regional reference laboratory has been validated based on reliable international criteria approved by health reference laboratory and it has been assigned some roles including diagnosis, surveillance, quality assurance and educational and investigational activities in the field of Tuberculosis (TB) disease. One national reference, 9 regional reference, 50 culture and 401 direct smear labs are currently active over the network of Tuberculosis diagnosis in the country.

Methods: Tehran regional reference of tuberculosis has been started since February 2014 under support of UNDP and health authorities of the country. The lab contributes in clinical diagnosis of referred samples from health and treatment deputy centers by proportional and molecular diagnosis approaches. It also participates in surveillance over direct smear labs by monitoring in place, distributing external quality control samples and monthly recheck of 10% of negative and positive smears

Results: The lab participated in the external quality assessment of the WHO/GLI TB supernational reference laboratory Network (SRLN) for first line drug susceptibility test and demonstrated excellent proficiency. The lab also has been involved in some approved research studies in collaboration with clinical Microbiology department of Tehran University of Medical Sciences in clinical diagnosis and drug susceptibility tests.

Conclusion: In molecular section, the lab performs rapid diagnosis of TB with the Xpert MTB/RIF assay and PCR. Among 4231 and 945 samples from treatment and health deputy, 176 (4.2%) and 126 (13%) samples had been diagnosed as TB positive, respectively. We also detected 6 cases of Rifampin-resistant samples (0.6%) from health deputy specimens.

Keywords: Regional Reference laboratory, Mycobacterium Tuberculosis, Proportional, Molecular

P869 - 974: IN VITRO SCREENING OF PHOSPHATE AND ZINC SOLUBILIZING STRAINS OF PSEUDOMONAS SPP. FROM RHIZOSPHERIC SOILS OF A FIELD IN KERMAN, IRAN.

Shirin Javadi¹, Farokh Rokhbakhsh-Zamin², Seyed Mohamadreza Khoshroo³

1. M.Sc. student, Microbiology Department Of Kerman Islamic Azad University
2. Affiliation: Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
3. Affiliation: Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.

Background and Aim: Plants need several macro and micro nutrients for their growth and reproduction. Bacteria also play an important role in mobilizing nutrients requisite by the plants to some extent. Phosphorus and zinc is a major nutrient after nitrogen that limits plant growth despite being abundant in soils in both organic and inorganic forms.

Methods: this research, The plant roots and rhizospheric soils were kept in sterile plastic cover, stored on ice bag and transported to the laboratory. 5 g soils were added to 45 ml sterile normal saline. Serially diluted samples were used for pure culture methods.

Results: Identification tests were performed by using characteristics features described in Bergey's manual of systematic bacteriology. Screening of phosphate and zinc solubilizing rhizobacteria were performed by spot inoculation of isolates at the centre Pikovskayas and Zno plates and incubated at 28°C. Diameter of clearance zones were measured during 7 days. Out of 15 strains of pseudomonas sp., 14 isolates could solubilize phosphate and 1 isolate showed zinc solubilization trait.

Conclusion: It can be concluded that Pseudomonas sp. can be considered as an efficient rhizospheric agent possessing various plant growth promoting properties. These activities of Pseudomonas sp. authenticate that it may be as a good bioinoculant agent for the sustainable agro-productivity of common plants with approval with further In vivo tests.

Keywords: Rhizobacteria, pseudomonas , Phosphate and zinc solubilization

**P870 - 979: ISOLATION OF HEAVY METAL RESISTANT PSEUDOMONAS SPP. AND THEIR
PLANT GROWTH PROMOTING ACTIVITIES**

Shirin Javadi¹, Farokh Rokhbakhsh-Zamin², Seyed Mohamadreza Khoshroo³

1. M.Sc. student, Microbiology Department Of Kerman Islamic Azad University
2. Affiliation: Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.
3. Affiliation: Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran.

Background and Aim: Rhizosphere represents a thin layer of soil surrounding plant roots and the soil occupied by the roots and it supports large active groups of bacteria known as plant growth promoting rhizobacteria. Interactions between plants and rhizobacteria can enhance biomass production and tolerance of the plants to heavy metals, making these microorganisms as important components used in bioremediation technology.

Methods: In order to isolate of *Pseudomonas* spp., 1g of soil sample was serially diluted in sterile distilled water and 0.1 ml of soil suspension from 10⁻¹ to 10⁻⁵ was spreaded on the *Pseudomonas* isolation agar medium. plates were incubated at 35°C for 2-4 days in inverted position. The bacterial isolates were identified by different tests according to the Bergey's manual of systematic bacteriology. Freshly prepared agar plates were amended with various soluble heavy metal salts namely Pb, Mn, Ni and Cu, at various concentrations ranging from 25 to 400 µg ml⁻¹ and they were inoculated with bacterial cultures. Heavy metal tolerance was determined by the appearance of bacterial growth after incubating the plates at room temperature for 24-48h.

Results: All of 15 the *Pseudomonas* spp isolates showed tolerance in all tested concentrations (25µg/ml, 50µg/ml, 100µg/ml, 200µg/ml, 400µg/ml).

Conclusion: Some rhizobacteria such as all tested isolates have developed the mechanisms to cope with a variety of toxic metals for their survival in the environment containing heavy metals. Accordingly, these isolates have a good potential to decrease the heavy metal toxicity, as well as increasing the growth of plants.

Keywords: *Pseudomonas* spp. , Heavy metals, Plant Growth Promotion

**P871 - 1024: ANTIBIOTIC RESISTANCE OF GRAM-NEGATIVE BACTERIA ISOLATED
FROM URINARY TRACT INFECTIONS IN PREGNANT WOMEN**

Somaye Amiri danduski¹, Nadia Kazemi-Pour²

1. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran
2. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran

Background and Aim: Recently, increasing in the antibiotic resistance of pathogenic bacteria is a big problem facing to the medical sciences especially about pregnant patients. To have sufficient information about the patterns of bacterial resistance to different antibiotics are very helpful for proper treatments.

Methods: This research is a descriptive cross-sectional study in the laboratory over a period of six months and it was conducted on 50 pregnant women with UTI. Sampling was performed from the central laboratory of south Roodbar from pregnant women. Accordingly, Gram-negative bacteria were isolated and identified by using staining, biochemical tests and using differential and selective media. Antimicrobial susceptibility pattern of isolate related to gentamicin, vancomycin, tetracycline, ciprofloxacin, nitrofurantoin, nalidixic acid was evaluated using disk diffusion method and minimum inhibitory concentration was determined by agar dilution method.

Results: In this study, 150 pregnant women were checked and 26.6% of them had UTI by gram-negative bacteria. This quantity of gram negative bacteria were divided as 50% *Escherichia coli*, 27.5% *Klebsiella*, 17.5% *Enterobacter* and 5% *Pseudomonas* spp. Isolated gram-negative bacteria from pregnant women urine with UTI were sensitive to different antibiotics as gentamicin (97.5%), ciprofloxacin (85%), nitrofurantoin (82.5%), tetracycline (25.5%), Nalidyksyk acid (47.5%), amoxicillin (5%) and were sensitive to vancomycin (2.5%).

Conclusion: The antibiotics gentamicin and ciprofloxacin as the most effective medication for the treatment of pregnant women with UTI were the majority. However, due to the results of the antibiogram in this research.

Keywords: Gram-negative bacteria, antibiotic-resistance, UTI, pregnant women

**P872 - 1150: AUTOMATED TELLER MACHINE (ATM) AS A POTENTIAL SOURCE OF
BACTERIAL CONTAMINATION**

Fatemeh Tarbiyat farsad¹

1. .Department of microbiology, Faculty of basic science, Lahijan Branch, Islamic Azad University, Lahijan ,
Iran

Background and Aim: Automated Teller Machine (ATM) are the most widely used form of computer driven public technology. ATMs are scattered through out cities, and they tend to harbor various microorganisms on their surfaces .The aim of this study was to determine bacterial contamination on keypads of ATMs in Tehran.

Methods:: Collection of samples was done by using cotton swabs, swabs were cultured on different media such as blood agar and Mac Conkey agar , and incubated at 37 C for 24-48 h. Colonies were identified based on standard biochemical tests.

Results: The results of this study revealed that , ATMs are potential areas for pathogens .Seven different organisms were isolated which include : *S. aureus* (20.1%), *E. coli* (24.3%), *Pseudomonas aeruginosa* (16.3%), *Klebsiella* (15.4%) , *Streptococcus* spp (12.2%), *Bacillus* spp (8.6%), *Micrococcus* spp(3.1%).

Conclusion:: Results of study indicate that , ATMs are as a potential source of bacterial contamination ,we should be aware that hand borne transmission through ATM is one of the most important issue for spreading infectious agents in the world.

Keywords:: Automated Teller Machine (ATM), Bacterial contamination, keypads.

P873 - 1160: BIOINFORMATICS STUDY OF PAL ENZYME INVOLVED IN 6-GINGEROL BIOSYNTHESIS WHICH REDUCES PSEUDOMONAS AERUGINOSA BIOFILM FORMATION

Farzaneh Rezamasouleh¹, mehdi moheimani²

1. M.Sc Microbiology graduated, Microbiology department, Islamic Azad University of Rasht, Rasht, Iran
2. M.Sc Biotechnology graduated, Biotechnology department, Imam khomeini International University, Qazvin, Iran

Background and Aim: Phenylalanine ammonia lyase (PAL) is an enzyme that catalyzes the first step of [6]-gingerol biosynthesis pathway. Gingerol have been reported to possess antimicrobial and antifungal properties, as well as several pharmaceutical properties. However, the effective ginger constituents that inhibit the growth of oral bacteria associated with periodontitis in the human oral cavity have not been elucidated. Based on researches 6-Gingerol reduces *Pseudomonas aeruginosa* biofilm formation and virulence via quorum sensing inhibition.

Methods: In this research we achieved protein sequence of PAL by tool uniprot database (www.uniprot.org) and for following procedures we used some online software like ProtParam, TargetP, PSIPred and other online softwares.

Results: According to the result of the Targetp the PAL enzyme was neither mitochondrial nor secretory. In respect of amino acids composition, alanin is the most amino acid in its composition. By using the PSIPred software, it is predicted that PAL possese 5 alpha-helixes and 2 beta-sheets.

Conclusion: Since gingerols are one of the major bioactive compounds present in *Zingiber officinale* by antibacterial activities, their molecular mechanisms of actions and the relationship between their structural features and the activity have not been well studied. So, it seems that the bioinformatics study of this important protein is necessary.

Keywords: Antibacterial activities, Bioinformatics, PAL, *Pseudomonas aeruginosa*

P874 - 1163: LEGAL ISSUES BIOTERRORISM

Tina Jamooli¹, Iraj Goldoziyan², Morteza Rahbar Taremsari³

1. Islamic Azad University, Bandar e Anzali International Branch, Anzali, Iran.
2. Faculty of law and political science, University Tehran, Tehra, iran
3. Departement of Forensic Medicine and Ethics, Guilan University of Medical Sciences, Rasht, Iran

Background and Aim: Biological weapons are considered one of the terrifying means of armed conflicts in the past and a serious threat for future conflicts. The use of biotechnology in development of countries has turned this technology into a weapon against some governments. Hence, the study of bioterrorism is important. Bioterrorism is defined as a terrorist act involving deliberate release of biological agents, which are usually found in nature, and can be used as terrorist weapons if their structure is changed to increase their resistance to treatment and they are sent to specific people, regions, or locations in different ways.

Methods: Bioterrorism has been stressed in the introduction, Article 1, and 17 of the Rome Statute and the Tokyo Tribunal. The theory of parallel litigation in Clause 1, Article 9 of the Yugoslavia and Rwanda Statute of the International Criminal Court was confirmed with the superior authority of the Yugoslav Tribunal. Likewise, in Iranian law, the biological weapons convention, the state comprehensive microbial plan, the fifth five-year development plan, the state policies for the passive defense, the biosafety law, the act of accession of Islamic Republic of Iran to Cartagena protocol on biosafety, the act for fighting against financing of terrorism, and the Procedure have adopted strategies for dealing with bioterrorism.

Results: Much effort has been made to deal with chemical and microbial weapons so far.

Conclusion: The reasons for the attractiveness of this branch of terrorism are its rather low costs, easy preparation, immediate effect, and rapid and terrifying expansion among people.

Keywords: bioterrorism, International Criminal Court, terrorism, genocide, Iranian law

P875 - 1164: BIOINFORMATICS STUDY OF LETHAL FACTOR PROTEIN IN BACILLUS ANTHRACIS

Farzaneh Rezamasouleh¹, hamed Hosseinzadeh Morshedi Dogahe²

1. M.Sc Microbiology graduated, Microbiology department, Islamic Azad University of Rasht, Rasht, Iran
2. M.Sc Biotechnology student, Biotechnology department, Imam Khomeini International University, Qazvin, Iran

Background and Aim: *Bacillus anthracis* is a gram-positive and spore-forming bacterium that causes the disease anthrax. The anthrax toxin contains three components, including the Edema Factor (EF) 89 kDa, Lethal Factor (LF) 90 kDa and protective antigen (PA) 83 kDa. Inhalational *Bacillus anthracis* is a serious bioterrorism-related health threat today. The pathology of anthrax is almost entirely mediated by expression of two secreted toxins, lethal toxin (LeTx) and edema toxin (EdTx).

Methods: In this research we achieved protein sequence of LF by tool uniprot database (www.uniprot.org) and for following procedure we used some online software like ProtParam, SWISS-MODEL, TargetP, SignalP, PSIPred and other online software.

Results: ProtParam software predicts that the LF protein (length 809 amino acids) has a molecular mass of 93770.3 Da with theoretical isoelectric point of 5.6. According to the prediction of TargetP software the LF protein is classified as a secretion protein. Finally PSIPred predicts that this protein possesses 28 alpha-helices and 17 beta-sheets.

Conclusion: Study of LF protein in *B. anthracis*, the bacterium that causes anthrax disease can give more molecular recognition and maybe a new way to control these bacteria. As results declare this protein classified as an unsatable protein and has no N-terminal signal peptide for probable localization in chloroplast, mitochondria and Golgi.

Keywords: *B. anthracis*, Bioinformatic, Lethal Factor

P876 - 1174: ISOLATION LACCASE PRODUCER-YEAST FROM FROM BARK

Fatemeh Sheikh¹, Mohammad Roayaei Ardakani²

1. Res Institute of Khuzestan
2. Department of Biology , Faculty of Science, University of Shahid Chamran, Ahvaz

Background and Aim: Laccases (EC 1.10.3.2) are multicopper enzymes belonging to the group of blue oxidases which exist widely in nature and are defined in the Enzyme Commission (EC) nomenclature as oxidoreductases which oxidize diphenols and allied substances and use molecular oxygen as an electron acceptor

Methods: Isolation and purification of yeast from collected samples was done on malt extract agar medium (MEA). In order to screen Laccase producing strains MEA containing 0.3 g l-1 ABTS [2, 2-azino-bis (3-ethylbenzothiazoline-6-sulfonic acid)] was used.. For laccase activity detection, the isolated fungi were grown at 30°C for 15 days on a rotary shaker (110 rpm) in 250-ml baffled Erlenmeyer flasks. Laccase activity was determined using the oxidation rate of 0.5 mM ABTS ($\epsilon = 29,300 \text{ M}^{-1} \text{ cm}^{-1}$ $\lambda_{\text{max}} = 436 \text{ nm}$) buffered with 50 mM succinate buffer, pH=4.5. Increase in absorption at 436 nm was measured by Niku-Paavola method .One activity unit (U) was defined as the amount of enzyme that oxidised 1 μmol of ABTS per min. Catalase (1000 U/mL) was added to the assay solution and incubated for 30 min at 30°C to remove H₂O₂ from the solution and, thus prevent the possible peroxidase enzyme activity in the experiments.

Results: 4 yeast were selected by primary screening on plate for activity assay in liquid culture, one of them selected as a best producer

Conclusion: The highest level of laccase production was obtained by one of the strains 24 U ml⁻¹ within 12 days of incubation.

Keywords: Laccase, Yeast, Isolation

P877 - 1196: BIOINFORMATICS STUDY OF PA20 IN BACILLUS ANTHRACIS

Raheem Haddad¹, hossein honari ², Hamed hossein zadeh ³

1. Associated professor, biotechnology department, Imam khomeini International University, Qazvin, Iran
2. Associated professor, Imam hossein University, Tehran, Iran
3. M,sc biotechnology student, biotechnology department, Imam khomeini International University, Qazvin, Iran

Background and Aim: Anthrax is caused by *Bacillus anthracis* that produce two exotoxins, lethal toxin and edema toxin. The lethal toxin is composed of the lethal factor (LF) complexed with the cell binding protective antigen (PA83, 83 kDa). Likewise, the edema factor (EF) binds to the PA83 to form the edema toxin. Once PA83 is bound to the host cell surface, a furin-like protease cleaves the fulllength, inactive protein into 63 kDa and 20 kDa antigens (PA63 and PA20).

Methods: In this research we achieved protein sequence of PA20 from uniprot database (www.uniprot.org) and for following procedures we used some online software like ProtParam for prediction of protein characteristics, SWISS-MODEL for prediction of protein 3d structure and finally PSIPred for prediction of protein second structure.

Results: According to the result of the ProtParam the PA20 protein classified as a stable protein with molecular mass of 18831.8 Da and its theoretical isoelectric point is 5.13. based on the PSIPred this protein has no alpha-helix and has 12 beta-sheets.

Conclusion: Anthrax toxin is composed of a cell-binding protein, known as protective antigen (PA), and two enzyme components, called edema factor (EF) and lethal factor (LF). These three proteins components act together to impart their physiological effects. Since Anthrax toxin can be applied as a bioterrorism weapon the molecular and bioinformatics studies can help us have a better understanding of this protein.

Keywords: *Bacillus anthracis*, Bioinformatics, PA20

**P878 - 1252: ANTIBIOTIC RESISTANT PATTERNS OF ACINETOBACTER SPP. STRAINS
ISOLATED FROM PATIENTS WITH PULMONARY INFECTIONS IN TWO HOSPITALS OF
KERMAN, IRAN.**

Rezvan Nikbakht¹, Nadia Kazemi-Pour²

1. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran
2. Department of Microbiology, Islamic Azad University, Kerman Branch, Kerman, Iran

Background and Aim: Acinetobacter spp. strains are coccobacilli found in natural environment and it has an important role in pulmonary infections and pneumoniae. These bacteria have developed resistance to different antibiotics. So, management of related infections by multidrug resistant Acinetobacter spp. are ongoing challenge. We report antibiotic susceptibility pattern of Acinetobacter strains isolated from patients with pulmonary infections

Methods: Eighty samples collected from pulmonary infections. Detection and identification of Acinetobacter spp. strains was performed by biochemical tests. MIC of 13 antibiotics was checked too. Cell surface hydrophobicity of 21 strains of Acinetobacters were evaluated using xylene. Those with hydrophobicity indices less than 30% and more than 70% were selected for biofilm tests. Biofilm tests were performed on the surfaces of glass, plastic and catheter.

Results: 21 isolated Acinetobacters were sensitive to Imipenem, Rifampin, Colistin, Mropenem Sulbactam_Ampicillin and Sulbactam_Cefoprazon. Biofilm production on plastic was more than glass surface. Biofilm production in shaking state was more than static one. Quantity of total bacteria was reduced from 5000 to 2950 in 0.5 MIC of colistin on pulmonary catheter

Conclusion: In this study, Biofilm formation on different surfaces was known to be very important point in spreading of nosocomial infections. So, finding and using medical devices with less adhesion potential to bacteria should be developed. **Keywords:** Acinetobacter, Biofilm, Antibiotic resistance

Keywords: Acinetobacter, antibiotic

**P879 - 1262: ANTIMICROBIAL EFFECTS OF SILVER NANOPARTICLES
FUNCTIONALIZED WITH IMIPENEM ON ACINETOBACTER BAUMANNII**

ELHAM Zendegani¹, Samane Dolatabadi²

1. Department of Microbiology, Islamic Azad University, Neyshabour Branch, Neyshabour, Iran
2. Department of Microbiology, Islamic Azad University, Neyshabour Branch, Neyshabour, Iran

Background and Aim: *Acinetobacter baumannii* is an emerging gram-negative bacteria that can cause nosocomial infections among patients. Treatment is complicated for cases of healthcare-acquired infection with *A. baumannii* resistant to imipenem. This study was conducted to evaluate the antimicrobial effect of silver nanoparticles alone and functionalized with imipenem on *A. baumannii* resistant to imipenem.

Methods: This cross-sectional study was isolated *A. baumannii* by common microbiological and chemical test. A disk diffusion method was used to isolate *A. baumannii* resistant to imipenem. Synthesis of uniform 20-nm silver nanoparticles was performed by reduction of AgNO₃ using sodium borohydride (NaBH₄). The minimum inhibitory concentration of silver nanoparticles and imipenem were calculated against the bacteria. The antimicrobial effect of silver nanoparticles functionalized with the imipenem was determined. Standard strain of *A. baumannii* ATCC 25922 was used as control.

Results: From 430 samples, 146 isolates were *Acinetobacter* spp. 100 isolate reported as *A. baumannii*. Ten clinical sample were resistant to imipenem (up to 28 mg.mL⁻¹). MIC of the silver nanoparticles against the isolate was 160 mg.mL⁻¹. The combination of 16 pg.mL⁻¹ of antibiotic with 80 mg.mL⁻¹ of silver nanoparticles were able to inhibit the growth of the isolate. Silver nanoparticles have been functionalized by thioether moiety present in the structure of imipenem.

Conclusion: Silver nanoparticles functionalized with imipenem was effective broad-spectrum bactericides against Gram-negative bacteria. Silver nanoparticles functionalized with imipenem can impair antibiotic resistance mechanisms of bacteria as it can make the imipenem resistant the aforementioned bacterium more susceptible to weaker concentrations of antibiotic

Keywords:-

**P880 - 1265: A SEARCH FOR TRACES OF AFRICAN 1 CLONAL COMPLEX OF
MYCOBACTERIUM BOVIS ON THE IRANIAN SOIL**

Sara Kazemnia¹, Keyvan Tadayon², Fahime Nemati³

1. Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, Iran
2. Razi Vaccine & Serum Research Institute, Karaj, Iran
3. Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, Iran

Background and Aim: Until present four clonal complexes of *Mycobacterium bovis* have been globally described with their origins found in Africa (AF1 and AF2) or Europe (EU1 and EU2). Iran was a systematic live-cattle importing country in the 20th century, it was also a major player in domestication of cattle in the history. These are therefore convincing reasons to expect circulation of both modern and old (in evolutionary sense) strains of *M. bovis* on the Iranian soil.

Methods: The present work describes recently-found evidences on likely presence of African 1 clonal complex isolates in Iran.

Results: PCR-based amplification and sequencing have been used to trace the Af1 specific marker in the genome of a local collection of *M. bovis* isolates representing majority of the Iranian provinces. All the examined Iranian *M. bovis* isolates produced a 608 bp long amplicon in the AF1-PCR while this locus is 350 bp in the genome of *M. bovis* BCG and *M. bovis* 212297. This is an indication of belonging IR *M. bovis* isolates to the African1 clonal complex.

Conclusion: The epidemiological meaning of this finding merits further analysis.

Keywords:-

**P881 - 1266: A COMPARATIVE STUDY OF THE PRODUCTION OF α -AMYLASE ENZYME
IN STRAINS OF ASPERGILLUS ORYZAE ON WASTE STARCH AND MOLECULAR
IDENTIFICATION OF TOP ENZYME-PRODUCING STRAINS**

Mohadese Radmehr¹, Vahid Hasani²

1. Department of Microbiology, Damghan Branch, Islamic Azad University, -Damghan, Iran
2. Department of Microbiology, Tonekabon Branch, Islamic Azad University - Tonekabon,

Background and Aim: *Aspergillus oryzae* is one the useful species to create the α -Amylase. Study of the production of α -Amylase from strains of *A. oryzae* in starch waste and molecular identification of the best producing strain the enzyme has been paid.

Methods: Samples of rice, moldy bread, mucky soil and mucky soil containing potato were cultured on PDA media. Samples containing enzyme characteristics by a factor of stability at different temperatures and sustainability buffers pH with sodium acetate, citrate, phosphate, Tris and glycine were examined. Samples were sequenced to determine species also.

Results: α -Amylase in the presence of Tris, glycine, citrate phosphate and sodium acetate at pH 6 has most activity and at pH 5 has lowest. Sequencing analysis of 16S rRNA gene showed 99% sequence similarity with the standard strain of *A. oryzae* PTCC 5164.

Conclusion: Amylase enzyme production during fermentation immersed in the present study showed that the main environments and mucky soil environments are suitable for production and stability of the enzyme amylase and also buffers Tris and glycine to do so will have a better result

Keywords: enzyme α -Amylase, *Aspergillus oryzae*, the PCR

P882 - 1267: PRODUCTION OF FUNGAL PECTINASE ENZYME BY ASPERGILLUS NIGER SPECIES BY WASTE PLANTS JUICER AND MOLECULAR IDENTIFICATION OF THEM

NOSHIN NEMATI¹, Vahid hasani²

1. Department of Microbiology, Damghan Branch, Islamic Azad University, -Damghan, Iran
2. Department of Microbiology, Tonekabon Branch, Islamic Azad University - Tonekabon, Iran

Background and Aim: Pectinase is a natural enzyme that impacted on Pectin and making transparent juice that in order to physical properties, stability, taste and texture changes are created. In this study, has been paid to the fungal pectinase produced or isolated by *Aspergillus* species of waste of plants juicer and molecular identification of them.

Methods: Pomegranate concentrate samples prepared from plants with fungal samples taken from the collection of fungi were cultured in the YGC environment. The effects of incubation time, temperature, pH, carbon in enzyme activity were examined. PCR sequencing was performed.

Results: Production of enzyme between 20 °C to 30 °C was increasing. Production of enzyme was increased in pH 3 to 7. Activity of pectinase in the temperature between 20 °C to 50 °C has been increasing. Starch (As carbon sources) is the most stimulating the production of pectinase and then glucose, lactose and sucrose, respectively. The results of sequencing of the 2 isolates related to *A. niger*.

Conclusion: The results obtained in this study concluded that for the production of pectinase in different fungal species need to optimize conditions for any specific species.

Keywords: Pectinase, *Aspergillus niger*, waste of juicer, PCR

**P883 - 1268: DIFFERENTIATION OF MYCOBACTERIUM BOVIS STRAINS ISOLATED
FROM TB INFECTED CATTLE IN WEST AZERBAIJAN PROVINCE OF IRAN BY RFLP
TYPING**

Shima Rezaee¹, Naheed Mojgani², Nader Mosavari ³, Mehrdad Hashmi⁴

1. Islamic Azad University
2. Tehran Tuberculin and Mallein Research and Production Department
3. Razi Vaccine and Serum research Institute, Karaj, IR Iran
4. Razi Vaccine and Serum research Institute, Karaj, IR Iran

Background and Aim: *Mycobacterium bovis*, a member of *M. tuberculosis* complex is most commonly found in cattle and other animals such as bison, elk and deer. In developing countries, bovine tuberculosis also represents a significant zoonosis and is also responsible for TB disease in human. In order to eradicate the disease the exact identification of the strains, the source of infection and route of transmission should be accurately identified. One of the successful approaches and most widely used method for DNA typing of *M. bovis* strains is Restriction fragment Length Polymorphism (RFLP). The most commonly applied RFLP probes for *M. bovis* typing are IS6110, PGRS, and DR. The RFLP patterns obtained are reliable indicators of strain identity. In this study, thirteen *M. bovis* samples collected from infected cattle in West Azerbaijan province were analyzed and their DNA finger prints recorded. Initially the isolates cultured on Lowenstein Jensen (LJ) media containing pyruvate (pyruvic acid) were identified according to OIE recommendations. The genomic DNA of the samples were extracted by WHO standard protocols and subjected to TB complex specific insertion sequences IS6110 primers. The DNA was then digested with restriction enzyme PvuII, and hybridized by Oligonucleotide probes PGRS and DR. Polymorphic banding patterns obtained after hybridization discriminated the *M. bovis* strains. According to the results, the 13 isolates showed 5 different DNA patterns with PGRS probe and similarly 5 patterns were obtained with the DR probe. PP-1 pattern was found almost among all the isolates while a distinct DNA pattern PP-3 was seen specifically from the West Azerbaijan Province

Methods:-

Results:-

Conclusion:-

Keywords: *Mycobacterium bovis*, IS6110, Restriction Fragment Length Polymorphism (RFLP), PGRS, DR

**P884 - 1269: CHARACTERIZATION OF BLATEM GENE IN KLEBSIELLA SPP. ISOLATED
FROM URINARY TRACT INFECTIONS (UTIS)**

Zahra Kargar jahromi¹, Solhjoui Kavous², Amozagaran Sorraya³, Rezaeian Abbasali⁴, Dehghani
Aliakbar⁵, Saadat Sare⁶, Jalal Mardaneh⁷

1. Zoonosis Research Center, Jahrom University of Medical Sciences, Jahrom, Iran
2. Zoonosis Research Center, Jahrom University of Medical Sciences, Jahrom, Iran
3. Student Research Committee, Jahrom University of Medical Sciences, jahrom, Iran
4. Department of Microbiology, Professor in Islamic Azad University, Jahrom, Iran
5. Department of Microbiology, Student in Islamic Azad University, Jahrom, Iran
6. Microbiology Department, Islamic Azad University, Jahrom Branch (the member of young scientific research club of Islamic azad university of jahrom), Jahrom, Iran
7. Department of Microbiology, School of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran

Background and Aim: Klebsiella presents a serious virulence bacterium in both community and nosocomial environments. Unfortunately, selection of the most appropriate antibiotic is complicated by the ability of Klebsiella develop resistance to multiple classes of antibacterial agents, even during the course of treating an infection. This study aimed to assess the molecular basis of the resistance to beta-lactams drugs in clinical isolates of Klebsiella spp. recovered from urinary tract infections (UTIs).

Methods: In this cross-sectional study, Klebsiella spp. were isolated from urinary tract infections (UTIs) in Jahrom (IRAN). Urine specimens were cultured on microbiological media. The isolates were identified as Klebsiella spp. using manual morphological and biochemical assays. Respectively, Disc diffusion and combined disk test was done for antibiotic susceptibility testing and ESBL detection with attention to CLSI (2014) recommendations. The blaTEM gene was detected in the isolates by PCR method.

Results: In the current study, a total 216 isolates of Klebsiella spp. were recovered from urine samples. Among investigated isolates 50.46% were ESBL-positive by phenotypic test. AST results showed, sensitivity of ESBL-positive isolates to ciprofloxacin and nalidixic acid is 10.64% and 3.70%, respectively. Molecular survey of blaCTX-M gene in isolates showed that 19.26% (21 strains) of them harboring this gene. Conclusion: In conclusion, we describe the predominance of ESBL-producing Klebsiella spp. in UTIs. Our isolates exhibited high percentages of resistance to fluoroquinolones (ciprofloxacin), and community-acquired infections as well as inter-hospital dissemination can occur.

Conclusion:-

Keywords: Children, urinary tract infections, Klebsiella spp., blaTEM gene.

**P885 - 1270: PHENOTYPIC AND GENOTYPIC DETECTION OF ESBLs IN KLEBSIELLA SPP.
ISOLATES**

Solhjou Kavous¹, Zahra Kargar jahromi², Amozagaran Sorraya³, Rezaeian Abbasali⁴, Dehghani Aliakbar⁵, Saadat Sare⁶, Jalal Mardaneh⁷

1. Zoonosis Research Center, Jahrom University of Medical Sciences, Jahrom, Iran
2. Zoonosis Research Center, Jahrom University of Medical Sciences, Jahrom, Iran
3. Student Research Committee, Jahrom University of Medical Sciences, jahrom, Iran
4. Department of Microbiology, Professor in Islamic Azad University, Jahrom, Iran
5. Department of Microbiology, Student in Islamic Azad University, Jahrom, Iran
6. Microbiology Department, Islamic Azad University, Jahrom Branch (the member of young scientific research club of Islamic azad university of jahrom), Jahrom, Iran
7. Department of Microbiology, School of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran

Background and Aim: Infectious diseases caused by bacteria have been an important cause of morbidity and mortality throughout our history. Klebsiella is one of the most common pathogen associated with urinary tract complications, and drug-resistance in this pathogen is problematic. The aims of the present study were isolation of Klebsiella spp. from urine specimens, determination antimicrobial susceptibility patterns and phenotypic and genotypic detection of ESBLs isolates.

Methods: Urine samples of patients suspected to UTIs, were collected and culture was done on clinical microbiology media. Conventional biochemical tests were used for identification of Klebsiella spp. Antibiotic susceptibility test (AST), and ESBL detection was performed according clinical and laboratory standards institute (CLSI, 2014) procedures. PCR molecular method was used for detection of ESBL-encoding genes.

Results: In the current study, a total of 585 children suspected to UTI patients were investigated. Klebsiella spp. strains were isolated from 216 specimens. 37.03 isolates were recovered from aged between 4-6 years (7.87% males vs 29.16% females). Nitrofurantoin and ceftazidim were effective on 86.57% and 32.87% of cases, respectively. A total 50.46% of strains were ESBL(+). Thirty-one (14.35%) ESBL(+)-isolates showed resistance to gentamicin. ESBL(+) Klebsiella spp. carrying blaCTX-M gene were detected in 18 (16.51%)

Conclusion: Because of the variation of antibiotic resistance profile in Klebsiella isolates in each region it is important for each area to formulate their antibiotic policy according to their local resistance patterns. It seems that Klebsiella isolated from UTIs harbored different ESBLs genes, but further studies must be done to prove these findings.

Keywords: Klebsiella spp., antibiotic sensitivity, ESBL-producers, blaCTX-M gene.

P886 - 1271: EXPLORING THE POSSIBILITY OF ATTACHING GOLD NANOPARTICLES BY OXYSPORUM FUSARIUM TO BETA-LACTAM ANTIBIOTICS PRODUCED AND REVIEW EXERTED BY ITS TOXICITY IN CULTURED FIBROBLAST CELL LINES

Farzane Ahmadi¹, Behrouz Yahyaei², Parastoo PourAli³

1. Department of Microbiology, Damghan Branch, Islamic Azad University, -Damghan, Iran
2. Department of Microbiology, Damghan Branch, Islamic Azad University, -Damghan, Iran
3. Department of Microbiology, Damghan Branch, Islamic Azad University, -Damghan, Iran

Background and Aim: The fungus *Fusarium oxysporum* showed the synthesis of gold nanoparticles. Furthermore, the number of new antibiotics didn't have a good activity against multi-drug resistant fungi. On the basis of this study, was paid to investigate the possibility of attaching gold nanoparticles produced by *Fusarium oxysporum* beta-lactam antibiotics.

Methods: The fungus *Fusarium oxysporum* was cultured in the Sabouraud - Dextrose broth. Approval for production of nanoparticles, from Spectrophotometric methods, TEM and FTIR and Haypny penicillin G and ceftriaxone antibiotic binding to nanoparticles and confirmed by connecting them through, drop nano spectrophotometer, TEM and FTIR was performed. The cytotoxicity test was conducted by MTT test

Results: absorption peak was 500 nm. TEM images were spherical shape. Confirmed the antibiotic binding to nanoparticles has similar absorption peaks. In FTIR the binding process was carried out. The results of TEM images to connect antibiotics, showed changes in particle size from nano to micro particles. In the MTT test cytotoxicity reduced.

Conclusion: Antibiotics penicillin G and ceftriaxone connection to nanoparticles would be done without any intermediaries

Keywords: Gold nanoparticles, penicillin G antibiotics, ceftriaxone, MTT, *Fusarium oxysporum*

**P887 - 1272: SURVEY OF ATOPOBIUM VAGINA IN VAGINAL SAMPLES OF
SYMPTOMATIC NON-PREGNANT WOMEN BY PCR**

Hamideh Maftoon¹, Nour Amirmozafari², Maryam Kashanian³

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Background and Aim: Bacterial vaginosis is not a mono-factorial infection. A synergism of microaerophilic bacteria, *Mycoplasma* spp., and anaerobic bacteria such as *Atopobium vaginae*, *Porphyromonas* spp., *Bacteroides* spp., *Prevotella* spp., and others are involved in these infections. The aim of present study was to determine the prevalence of *Atopobium vaginae* in non-pregnant women suffering from bacterial vaginosis.

Methods: A total of 102 non-pregnant women who referred to Shahid Akbarabadi hospital in Tehran were tested for bacterial vaginosis. Bacterial culture was performed on Columbia agar containing 2mg/ml Amphotericin B, 30mg/ml Nalidixic acid and 4mg/ml Colistin. Additionally, they were simultaneously cultured on blood agar plates containing fresh human blood and Amphotericin B under anaerobic conditions. Finally, PCR using *Atopobium vaginae* specific primers were also carried out on extracted DNA from grown colonies as well as from vaginal specimens.

Results: From a total of 102 symptomatic women who referred to the hospital, 37% (38/102) were classified as bacterial vaginosis, 43% (44/102) were classified as intermediate status and 20% (20/102) women were asymptomatic. Sixty urine samples were collected. *Atopobium vaginae* were detected in 66% (25/38) of bacterial vaginosis cases and in 10% (4/44) samples with intermediate vaginal flora. It was not detected in asymptomatic women. The bacterium was seen in 10% (3/30) women with urinary tract infection and none in pregnant women.

Conclusion: This is the first report of *Atopobium vaginae* isolation in Iran. The results of this investigation points to a clear association of *Atopobium vaginae* with bacterial vaginosis. It should therefore be considered as a probable etiological agent.

Keywords: Bacterial vaginosis, *Atopobium vaginae*, Culture, PCR

**P888 - 1273: EVALUATION OF DIAGNOSTIC AND PREDICTIVE VALUES OF
HELICOBACTER PYLORI TOOL ANTIGEN TEST FOR HP INFECTION IN IRANIAN
DYSPEPTIC PATIENTS**

Fahimeh Safarnezhad Tameshkel¹, Mohammad Hadi Karbalaie Niya², Zahedin Kheyri³, Davood Azizi⁴,
Samaneh Khorrami⁵

1. Gastrointestinal & Liver Disease Research Center (GILDRC), Iran University of Medical Sciences, Tehran, Iran.
2. Department of Virology, Faculty of Medicine, Iran University of Medical Sciences, Tehran, Iran.
3. Department of Internal Medicine, Amiralmomenin hospital, Arak University of Medical Sciences, Arak, Iran.
4. Department of Pathology, Amiralmomenin hospital, Arak University of Medical Sciences, Arak, Iran
5. Immunology Research Center, Iran University of Medical Sciences, Tehran, Iran.

Background and Aim: Considering aging population, Iran, as a low and middle income and developing country, is experiencing high burdens of Helicobacter pylori (HP) associated non-communicable diseases. HP stool antigen test (HPSA) is widely used as an inexpensive and feasible noninvasive method for diagnosis of HP infection, alternatively to invasive approaches. We designed a study to evaluate the diagnostic and predictive values of HPSA test for HP infection in Iranian dyspeptic patients.

Methods: It's a cross sectional study of 100 dyspeptic patients. Gastric mucosal specimens were taken, processed and examined according to standard protocols. Simultaneous stool samples were obtained and sent to laboratory. We assessed HP stool antigen titers using ELISA method. Receiver operating curve was drawn and statistical analysis was performed using IBM SPSS v.22.

Results: Stool antigen titers was found not associated with sex (p -value=0.279), but correlated to age (Pearson correlation=0.213, p -value=0.034). Considering 0.385 as cut-off point, the HPSA test had 80.4% sensitivity and 85.7% specificity.

Conclusion: Regarding rising trend of HP associated non-communicable diseases in Iran and the cost-effectiveness of HPSA test, our findings endorse the use of HPSA test to detect and follow HP infected Iranians, as an alternative to the invasive procedures.

Keywords: Helicobacter pylori, stool antigen test, sensitivity, specificity

**P889 - 1274: SENSITIVE HIGH-RESOLUTION MELTING (HRM) ANALYSIS FOR
SCREENING OF KRAS AND BRAF MUTATIONS, IN IRANIAN HUMAN METASTATIC
COLORECTAL CANCER (MCRC)**

Mohammad Hadi Karbalaie Niya¹, Fahimeh Safarnezhad Tameshkel², Nasser Rakhshani³, masoudreza
sohrabi⁴

1. Department of Virology, Faculty of Medicine, Iran University of Medical Sciences, Tehran, Iran.
2. Gastrointestinal & Liver Disease Research Center (GILDRC), Iran University of Medical Sciences, Tehran, Iran.
3. Gastrointestinal & Liver Disease Research Center (GILDRC), Iran University of Medical Sciences, Tehran, Iran.
4. Gastrointestinal & Liver Disease Research Center (GILDRC), Iran University of Medical Sciences, Tehran, Iran.

Background and Aim: investigations in the methods of mutation detection uncovered the major weaknesses of direct sequencing and pyrosequencing that were high costs and low sensitivity, though they are described as the “golden standard” for screening of known or unknown mutations. High resolution melting (HRM) analysis seems to be an alternative tool for the rapid detection of mutations. Here we describe the accuracy of HRM in screening KRAS and BRAF mutations in metastatic colorectal cancer (mCRCs) samples.

Methods: In this regard, we examined 1000 mCRC patients of Mehr Hospital, Tehran, Iran, from Feb 2008 to May 2012 for KRAS mutations and 242 of them for BRAF mutations by HRM analysis. In order to calculate the sensitivity and specificity, HRM results were checked by pyrosequencing as the golden standard and Dxs Therascreen as another method

Results: of 1000 participants we found there were 664 (66.4%) wild types and 336 (33.6%) mutants of KRAS gene in codon 12 and 13. Of 242 samples that randomly checked for BRAF gene, all were detected wild type by HRM. Pyrosequencing and Dxs Therascreen results confirm HRM results. In this regards, the sensitivity and specificity of HRM evaluated 100%.

Conclusion: The findings suggest that the HRM, in comparison with DNA sequencing, is a more appropriate method for precise scanning of KRAS and BRAF mutations. It is also possible to state that HRM may be a more attractive technique for detection of known or unknown somatic mutations of other genes.

Keywords: High-Resolution Melting (HRM), Mutation Analysis, KRAS, BRAF, metastatic colorectal cancer (mCRC), pyrosequencing, Dxs Therascreen

**P890 - 1275: TREATMENT OF XANTHOMONAS CITRI SUBSP. CITRI BY NITROUS ACID
AND SELECTION OF A POTENT MUTANT WITH CAPABILITY TO PRODUCE MORE
XANTHAN GUM**

Safoora Cheraghalikhani¹, Fahimeh Baghbani-Arani², Mehrdad Azin³

1. Department of Microbiology, Varamin-Pishva Branch , Islamic Azad University, Varamin, Iran
2. Department of Genetics and Biotechnology, Varamin- Pishva branch, Islamic Azad University, Varamin, Iran
3. Department of Biotechnology, Iranian Research Organization for Science and Technology, Tehran,Iran

Background and Aim:Xanthomonas citri subsp. Citri is a gram negative bacterium, which is the causal agent of citrus canker disease. The bacterium also produces acidic heteropolysaccharide called xanthan. Xanthan gum is one of the most popular biochemical agents, widely used as stabilizer, emulsifier and suspender in many industries including cosmetics food, textiles, drug and petroleum etc. This is mainly because of high viscosity characteristic of xanthan. Bacteria belonging to Xanthomonas genus are capable to produce this exopolysaccharide in glucose and sucrose containing media. Although xanthomonads are not capable to consume lactose, Xanthomonas citri has a specific ability to consume this sugar in culture medium containing whey. The purpose of this investigation is using mutation and selection technic to create Xanthomonas citri subsp. citri (Xcc) mutants with capability to producing more xanthan gum.

Methods:In this study, a series of mutants were isolated from Xanthomonas citri K37 by classical mutagenesis, by using nitrous acid. Initial screening was based on the enhanced diameter of the colonies in comparison with that of the wild strain on lactose containing agar medium. Second step screening was based on production of xanthan in liquid medium.

Results:Among numerous screened colonies, twenty mutants with colony diameter bigger than the parental strain were isolated. At the next step, the amount of produced xanthan and the viscosity of mutants was compared with that of the parental strain in production medium. As a result, while the native strain produced 27.9 g/L of xanthan, mutant NA-8, which produced 33.46 g/L xanthan was isolated

Conclusion:-

Keywords:Xanthomonas Citri, Xanthan Gum, Mutation and Selection, Nitrous Acid, Viscosity

P891 - 1276: THE CORRELATION OF BETWEEN MAZEF, RELBE AND HIGBA TOXIN-ANTITOXIN SYSTEM AND BIOFILM FORMATION

Hassan Valadbeigi¹, Majid Baseri Salehi², Nourkhoda Sadeghifard³

1. Department of Microbiology College of Science, Agriculture and Modern Technology, Shiraz Branch, Islamic Azad University, Shiraz, Iran
2. Department of Microbiology, Kazeroun Branch , Islamic Azad University, kazeroun, Iran
3. Clinical Microbiology Research Center, Ilam University of Medical Sciences, Ilam, Iran

Background and Aim: Toxin-antitoxin (TA) system are composed of toxin and antitoxin loci on an operon, which stable toxin inhibited by unstable antitoxin (rapidly degraded by proteases). TA system plays a major role in biofilm formation. Therefore, to evaluate prevalence two important virulence factors in biofilm formation , pilA and algD genes , as well as mazEF, relBE and higBA genes of type II TA system in *P. aeruginosa*. Also, correlation between biofilm formation in normal condition and temperature stress an addition mazEF, relBE and higBA genes of TA system toxin in clinical strains of *P. aeruginosa*.

Methods: PCR for identification of genes and Biofilm formation for detection the correlation were applied.

Results: Our results demonstrated that algD presented in all Urinary tract, Tracheal and burn infections while this was not true story for pilA. The majority of isolates demonstrated mazEF as dominant TA loci, which when these isolates exposure to stress conditions showed stranger biofilm formation in comparison with normal condition.

Conclusion: The results showed there is correlation between biofilm formation and TA loci. Among them mazEF plays crucial role. We recommended doing more experiments in different hospital and also checking the potency of mazEF TA loci. Despite several virulence factors production associated with the bifiofilm formation, the role of many TA loci remains unclear. Therefore, it appears necessary to find new strategies for prevention and eradication of pathogenic bacteria, given that one of them, the pathogenic *P. aeruginosa* is a concern worldwide.

Keywords: Toxin- Antitoxin, biofilm, *Pseudomonas aeruginosa*

**P892 - 1277: THE PREVALENCE OF PILA AND ALGD VIRULENCE GENES IN
PSEUDOMONAS AERUGINOSA URINARY TRACT AND TRACHEAL ISOLATES**

Hassan Valadbeigi¹, Majid Baseri Salehi², Nourkhoda Sadeghifard³

1. 1Department of Microbiology College of Science, Agriculture and Modern Technology, Shiraz Branch, Islamic Azad University, Shiraz, Iran
2. 2Department of Microbiology, Kazeroun Branch , Islamic Azad University, kazeroun, Iran
3. 3Clinical Microbiology Research Center, Ilam University of Medical Sciences, Ilam, Iran

Background and Aim: Nowadays, it is debated about *Pseudomonas aeruginosa* as an opportunistic pathogen and mainly is known as a true pathogen. It causes many infections in urinary tract and lung. It also considered as an important nosocomial infection and responsible for morbidity and mortality. The aim of this study was to evaluate the prevalence of virulence genes including *algD* and *pilA* among *Pseudomonas aeruginosa* clinical isolates.

Methods: For this reasons, after DNA extraction of clinical isolates PCR was performed.

Results: Because of the importance of *algD* and *pilA* in the pathogenicity of *P. aeruginosa*, our study considered the prevalence of indexed virulence factors in *P. aeruginosa* clinical isolates. The results demonstrated that *algD* was predominant in both tracheal and UTI isolates, while *pilA* showed 3.2% and 28.6% frequency in tracheal and UTI isolates, respectively. When *pilA* was highlighted, we found that the prevalence in tracheal isolates was more than in UTI isolates.

Conclusion: We concluded that more pathogenicity may be caused by *algD*, but in isolated UTIs the role of *pilA* is notable. This should be considered for future study, which should be focused on confirming the pathogenicity process found by this study.

Keywords: *Pseudomonas aeruginosa*, virulence genes, *algD*, *pilA*

P893 - 1278: CHARACTERIZATION OF UROPATHOGENS AND THEIR ANTIBIOTIC SUSCEPTIBILITY PATTERNS DERIVED FROM PATIENTS SUFFERING FROM BOTH DIARRHEA AND URINARY TRACT INFECTION IN IRAN

Moein Saleh¹, Fatemeh Mir-Marashi², Shahram Sabeti MD³, Saeid Bouzari PhD⁴, Masoud Mardani MD⁵, Mohammad Pooya MD, PhD⁶

1. Department of Microbiology, Islamic Azad University, Shahr-e Ghods branch
2. Department of Microbiology, Islamic Azad University, Karaj branch
3. Loghman Hakim Hospital, Shahid Beheshti University of Medical Sciences
4. Department of Molecular Biology, Pasteur Institute of Iran
5. Loghman Hakim Hospital, Shahid Beheshti University of Medical Sciences
6. Department of Molecular Biology, Pasteur Institute of Iran

Background and Aim: While the association between urinary tract infection (UTI) and diarrhea has been demonstrated, few investigations have been performed to show any probable differences according to the causative pathogens and their antibiotic susceptibility pattern in Iran. The aim of this study was to evaluate the bacteria responsible for UTI in patients with or without diarrhea and to detect their antibiotic resistance pattern.

Methods: A 6-year study was conducted among the patients having UTI, with or without diarrhea at the same time, referred to the Loghman hospital from March 2008 until September 2014. The isolates were subjected to antibiotic susceptibility test using disk diffusion method. Multi-drug resistance (MDR) was defined based on the latest guidelines

Results: A total number of 123 isolates were recovered from 120 UTI patients divided into two groups (60 with and 60 without diarrhea). *E. coli* were the predominant uropathogens in both groups followed by *Klebsiella pneumonia* in diarrhea group and *Proteus* in non-diarrhea group. The percentage of MDR *Klebsiella* not only was significantly higher in the diarrhea group than the non-diarrhea group, but was 2 times more than MDR *E. coli* in diarrhea group. Noticeably, all of the *Staphylococcus* isolates in non-diarrhea group and none of them in diarrhea group showed MDR pattern. Meanwhile, comparing diarrhea and non-diarrhea groups, each bacterial species showed different and sometimes opposite antibiotic resistance patterns.

Conclusion: It seems that the presence of diarrhea should be considered as an important factor for choosing the appropriate drug for antibiotic treatment of UTI.

Keywords: urinary tract infection, diarrhea, antibiotic susceptibility

**P894 - 1279: EVALUATION OF MICE HUMORAL IMMUNE RESPONSES AFTER
INTRANASAL ADMINISTRATION OF MYCOBACTERIUM TUBERCULOSIS
RECOMBINANT FUSION PROTEINS**

Mozhdeh Namvarpour¹, Majid Tebianian², Reza Mansouri³

1. MSc Students of Immunology, Shahid Sadoughi University of Medical Science, Yazd, Iran
2. Razi Vaccine and Serum Research Institute, Karaj, Iran
3. Immunology Department, Shahid Sadoughi University of Medical Sciences, Yazd, Iran

Background and Aim: A third of the world's population is infected with Mycobacterium tuberculosis, and 2 million people die every year. Even though the BCG vaccine has been available for more than 75 years. The search for a new and improved vaccine against tuberculosis is currently a very active field of research. Secretory antigen of Mycobacterium tuberculosis, culture filtered protein 10 (CFP-10) and early secreted antigenic target 6 kDa protein (ESAT-6) are closely correlated with immunogenicity and virulence of Mycobacterium tuberculosis. Studies demonstrated that the delivery of vaccines through the mucosal route is very practical, non-invasive and efficacious for the induction of mucosal and systemic immune responses. In this study, we have evaluated the relative effect of intranasal (i.n) immunization on the induction of protective humoral immune responses against TB.

Methods: Initially, ESAT-6/CFP-10 complex and a group of 6 to 8 weeks old female BALB/c mice were obtained from Razi Vaccine and Serum Research Institute. The mice were immunized i.n twice at 2-week intervals with recombinant protein of ESAT-6/ CFP-10, formulated with or without adjuvant. Blood was collected from retro-orbital sinus 10 days after each immunization and after separation of sera, they were evaluated for specific antibodies against recombinant proteins by an indirect ELISA method which had set up during the research.

Results: Mice vaccinated against recombinant fusion proteins had high titer of specific antibodies compared to controls. Our results show that we can activate the mucosal and systemic immune responses via i.n administration which has less side effects than other invasive routes of vaccinations.

Conclusion:-

Keywords: Mycobacterium tuberculosis, ESAT-6-CFP10 fusion protein, Intranasal administration

P895 - 1280: STUDY OF THE EFFECT OF THE SILVER NANO PARTICLES ON EXTENDED SPECTRUM B LACTAMASES PRODUCERS OF URINARY ESCHERICHIA COLI

Elaheh Yazdi¹, Teena Dadgar², Hamid Reza Pordeli³

1. MSc of Microbiology, Department of biology, Golestan Science and Research Branch, Islamic Azad University, Gorgan, Iran
2. Assistant professor of Microbiology, Department of biology, Golestan Science and Research Branch, Islamic Azad University, Gorgan, Iran
3. Assistant professor of Microbiology, Department of biology, Golestan Science and Research Branch, Islamic Azad University, Gorgan, Iran

Background and Aim: The aim of this study was identification of urinary *Escherichia coli* resistant to extended-spectrum β -lactamase Enzymes (ESBLs) and determination of the effect of silver nanoparticles on them

Methods: 100 clinical isolates of *E. coli* were studied to recognize ESBLs production. The antimicrobial efficacy of different concentrations of colloidal nanosilver (average size: 30 ± 10 nm, concentration: 4000 $\mu\text{g/ml}$) prepared in Tehran Nano Pars Company were determined by the CLSI methods, and MIC was calculated by micro titer plate method. The MBC was measured by subculturing the bacteria from the wells that showed no apparent growth onto Mueller-Hinton agar. The data was analyzed by SPSS software package

Results: 58% of *E. coli* isolated from urinary tract infections in Gorgan are ESBL producing. All samples are sensitive to the nano silver solution with density of 4000, 200, 1000 and 500 $\mu\text{g/ml}$. The (MIC) and (MBC) values of nano silver solution against ESBL and Non ESBL strains were in the range of 7.8 to 15.62 $\mu\text{g/ml}$. and 7.8 to 62.5 $\mu\text{g/ml}$ respectively

Conclusion: obtained suggested that Nano Colloidal Silver exhibit a good bacteriostatic and bactericidal effect on ESBL and Non ESBL strains of *E. coli*. nanoparticles had bacteriostatic effect at low concentrations and that The ability of silver nanoparticles inhibitory effect was found to be no significant difference against ESBL producing strains of *E. coli* than ESBL non producing strain..

Keywords: ESBLs, silver nanoparticles, antibacterial

Perinatal Microbiology and Infertility

P896 - 20: کلیندامایسین سویه های جدا شده در زنان و الگوی مقاومت فنوتیپی القا شده به B بررسی استریتوکوکوس های گروه 20 - 896
صارم در سالهای ۹۳ تا ۹۴ باردادار مراجعه کننده به بیمارستان

Bizhan Nomanpour¹, Pyman Lashkari ², Farzad Hassani³

1. Microbiology Dept.Sarem special women Hospital-Tehran-Iran
2. Microbiology Dept.Sarem special women Hospital-Tehran-Iran
3. Microbiology Dept.Sarem special women Hospital-Tehran-Iran

Background and Aim:Streptococcus agalactiae strains or group B streptococci (GBS) are the leading cause of bacterial infection in neonatal and post-partum. Additional to prevalence of group B streptococci (GBS) ,The resistance patterns of specimens by phenotypic methods (D-test) in isolated of who referred to Sarem hospital laboratory from October 2013to June 2014, was performed

Methods:After a physical examination on 861 pregnant women by a gynecologist, two vaginal swabs of vaginal discharges were taken in 1 Ml sterile normal saline tube. And two slides for staining. Specimens were cultured on conventional media. By GBS isolation, Antimicrobial susceptibility testing According to CLSI - M24 (2014) and D-Test were done .

Results:From 861 samples, 296 positive cultures that 141 (16.26%) of GBS and the rest of staphylococci, enteric gram-negative bacteria, Candida and others. Nugnet Score revealed 32.29% (278 cases was) detected as vagenit . Resistant pattern to penicillin, cephalexin and ceftazidime was, 98.87, 98.87 and 98.58 %, respectively. Two isolates was resistant to penicillin by disk diffusion .But MIC determination by CLSI guideline did not show resistance. Resiustancy to ampicillin, ceftriaxone, and ciprofloxacin 3.55% (4 cases) . D-test the resistance seen in 21 (14.89%) positive cases of resistance to clindamycin and erythromycin and sensitive to erythromycin alone at 6.38% 67 cases were observed.

Conclusion:Regarded to GBs incidence and Erythromycin- inducible resistances to clindamycin in this study, D-test must be done for achieving appropriate treatment due to GBS.

Keywords:Group B Streptococci, Drug Resistance ,Pregnant women

Probiotics

P897 - 34: THE EFFECT OF ADDING ALLIUM AMPELOPRASUM L. SUBSP. IRANICUM ON SENSORY CHARACTERISTICS AND SURVIVABILITY OF LACTOBACILLUS ACIDOPHILUS IN IRANIAN WHITE CHEESE

Mina Razavi¹, Tooraj Mehdizadeh²

1. Department of Biology, Urmia Branch, Islamic Azad university, Urmia, Iran
2. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Urmia University, Urmia, Iran

Background and Aim: Worldwide trends in production and consumption of functional food ingredients to improve human gastrointestinal health is increasing. Consumption of beneficial probiotic bacteria combined with prebiotics plants may enhance colonic beneficial bacterial. Lactobacillus, the most commonly probiotic used in dairy products have inhibiting effect on the growth of undesirable bacteria. Allium ampeloprasum, which is part of the allium family with the fructan component is a prebiotic plant. In this study the survival of Lactobacillus acidophilus in Iranian white cheese containing prebiotic plant at the levels of 1 % and 2% (dry & fresh) was investigated.

Methods: After production of experimental cheeses, samples were tested for pH, microbial count, as well as sensory evaluation in a 45-day process at 0, 15, 30, 45 days.

Results: The results showed that adding Leek at different concentrations increases the activity of the probiotic bacteria. Cheese samples containing 1% (dry and fresh) and acidophilus bacteria received significantly higher sensory scores ($P < 0.05$).

Conclusion: The final results showed that probiotic acidophilus bacteria can be associated with leak, can be successfully used in fresh white Cheese.

Keywords: Prebiotic, Probiotic, Iranian white cheese, Lactobacillus acidophilus, Allium ampeloprasum

**P898 - 149: ISOLATION AND MOLECULAR IDENTIFICATION OF BIFIDOBACTERIUM
FROM INFANT FECES OF HAFEZ HOSPITAL IN SHIRAZ**

Sepideh Bahmani¹

1. MS.c student, Department of Microbiology, Faculty of Science, Science and research branch, Islamic Azad University, Fars, Iran

Background and Aim: Probiotics are live microorganisms that are useful for human or animal consumption. These bacteria have beneficial effects on human health. Nowadays probiotics are known as a factor for the prevention of many infectious diseases. Probiotic bacteria are usually intestinal flora and Bifidobacterium are normal colon bacteria. The purpose of this study was to isolate Bifidobacterium in fecal samples of infants at Hafez hospital in Shiraz.

Methods: In this study, 45 samples of infant feces from the Hafez hospital were collected. BFM medium agar was used for Bifidobacterium isolation which incubated at 37° C for three days. Identification was done by colony morphology, points and pigments, gram stain, catalase test and biochemical tests (fermentable carbohydrates). While specifically molecular identification was done by specific primers (Bif164 and Bif662).

Results: In this study, 7 strains were isolated by streaking 45 stool samples from Hafez hospital, in enrichment media and gram staining. Shape of Bifidobacterium was seen Y or V-shaped there were also some club shaped. Molecular identification by specific primers achieved a band with 523 bp that was compared with standard Bifidobacterium sample. 5 isolates were identified as Bifidobacterium from infant feces of Hafez hospital in Shiraz.

Conclusion: As a result of the studies, 5 Bifidobacterium strains were isolated from 45 infant feces samples. The frequency of Bifidobacterium is very low in infant stools.

Keywords: Bifidobacterium, Infant feces, Probiotic, Lactic acid bacteria

P899 - 316: ANALYSIS OF BAX AND BCL2 GEN EXPRESSION BY REAL TIME PCR IN COLON CANCER CELL LINE TREATED WITH LACTOBACILLUS RHAMNOSUS AS A PROBIOTIC EXTRACT

Hedieh Oliaei¹, mina ovrang², farzane farokhi³

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Background and Aim: Probiotics such as lactobacilli inhibit cancer cells growth with different mechanisms. In this study, the effect of different concentration of lactobacillus rhamnosus extracts on inhibition of colorectal cancer cells and expression of apoptosis regulatory genes including Bcl2 and Bax is considered.

Methods: Lactobacillus rhamnosus extracts with different concentrations, from 0.01 to 1000 µg/ml, were added to RPMI culture medium containing colorectal cancer cells and then IC50 of bacterial extract was assayed after 24 and 48h using MTT method. After total RNA extraction, cDNA was synthesized and the expression of Bcl2 and Bax genes was evaluated using the Real-time PCR method.

Results: Bacterial extract showed the highest inhibitory effects ($p < 0.001$) on cancer cells at concentration of 1000 µg/ml after 24 and 48h (with a mean cell viability of $23.5 \pm 0.45\%$ and $16 \pm 0.64\%$, respectively), while it demonstrated the lowest inhibitory effects at concentration of 0.01 µg/ml (with a mean cell viability of $94.0 \pm 0.31\%$ and $87.5 \pm 0.29\%$, respectively). The mean IC50 of bacterial extracts after 24 and 48h was 48.5 ± 1.24 µg/ml and 10 ± 0.74 µg/ml, respectively. The expression of Bax and Bcl2 genes in treated cancer cells was significantly ($p < 0.001$) changed by 1.29 ± 0.76 and 0.43 ± 0.83 folds.

Conclusion: Probiotic containing Lactobacillus rhamnosus can be used to prevent and treatment of colorectal cancer.

Keywords: Probiotics, Lactobacillus rhamnosus, colorectal cancer, Bax and Bcl2 genes

**P900 - 321: MOLECULAR IDENTIFICATION OF STREPTOCOCCUS THERMOPHILUS
ISOLATED FROM CHEESES SAMPLES IN FARS AND KERMANSHAH PROVINCE**

Negar Mirzadeh¹

1. 1MS.c student, Department of Microbiology, Faculty of Science, Science and research branch, Islamic Azad University, Fars, Iran Email:negarmirzadeh66@gmail.com

Background and Aim:Today, probiotics are available in a variety of food products and supplements and have got wide applications in the control of cholesterol, cancer, allergies, etc. In the present study, the isolation and identification of “*Streptococcus thermophilus*” as a probiotic and the starter-culture in the dairy products were evaluated.

Methods:20 samples of local and pasteurized cheeses were collected from pristine areas in Fars and Kermanshah provinces. The bacteria were isolated based on the International Standard Methods. They were cultured on the specific mediums (Agar M17 &Agar ST) with the temperature 42 °C in the Microaerophilic conditions during 48 hours. When the typical colonies were acquired, they were observed on the microscope and identified by biochemical tests and PCR.

Results:In the present study, 10 strains were isolated from 20 samples of local and pasteurized cheeses by the specific mediums (Agar M17 &Agar ST). All of them were in the forms of micro-chain Coccus and the gram stain positive. In order to perform the molecular identification via the specific primers and PCR technique, the 960 bp bands were searched and they were compared with the standard sample of *Streptococcus thermophilus* prepared by PTCC. From 10 initial isolated samples, 7 samples were our specific bacteria, *Streptococcus Thermophilus*.

Conclusion:The amount of *Streptococcus thermophilus* was varied in different local and pasteurized cheeses. With regard to the findings of this study, it was found that the amount of *Streptococcus thermophilus* bacteria had been considerably more in the local cheeses.

Keywords:Probiotic, *Streptococcus Thermophilus*, Cheese, Molecular identification

P901 - 366: LACTOBACILLUS ACIDOPHILUS EFFECT ON THE ESCHERICHIA COLI AND SHIGELLA SONNEI BACTERIA

Behboud Jafari¹, Mahsa hamdollahi², Akbar nazari³

1. Department of Microbiology, Ahar Branch, Islamic Azad University, Ahar, Iran
2. Department of Microbiology, Ahar Branch, Islamic Azad University, Ahar, Iran
3. Department of Biochemistry, Ahar Branch, Islamic Azad University, Ahar, Iran

Background and Aim: The treatment of many gastrointestinal diseases mediated by microbial agents is an obvious and growing issue. In this regard, probiotics, particularly lactobacillus play an important role. The aim of this study was to examine the antimicrobial effect of lactobacillus on two common gastrointestinal tract pathogens.

Methods: In this study, lactobacillus strains, belonging to the standard species lactobacillus acid and Philos (ATCC4356) were used to examine the antimicrobial properties against two gastrointestinal tract pathogens, including Escherichia coli (ATCC25922) and Shigella Sonnei (ATCC9290) and Agar spot test was carried out to examine the probiotic antimicrobial activity. In this method, 2 micro-liters of the probiotic strains were placed on the pathogenic E. coli and Shigella Sonnei purplate culture and were examined after 24 hours for halo of growth and halo of inhibition. In order to minimize errors, each experiment was repeated three times and finally the size of the average growth halo and halo of inhibition was determined and the sizes of these two pathogens were compared with each other.

Results: The results of this test showed inhibitory effect of two pathogens by lactobacillus acidophilus where most inhibition was seen in Shigella Sonnei and Escherichia coli was in second rang.

Conclusion: According to the results, it can be concluded that Lactobacillus acidophilus strains have a significant effect on prevention and treatment of gastrointestinal infections.

Keywords: probiotics, pathogens, antibacterial, Shigella Sonnei

P902 - 368: ISOLATION AND MOLECULAR IDENTIFICATION OF LACTIC ACID BACTERIA FROM TRADITIONAL AND PASTEURIZED YOGURT AND CHEESE

Roya Shafaeian¹, Elham Moazamian², Negar Azarpira³

1. MS.c Student Department of Microbiology, Faculty of Science, Science and Research Branch, Islamic Azad University, Shiraz, Fars, Iran Email: roya.sh.kh@gmail.com
2. Professor, Department of Microbiology, Faculty of Science, Agriculture and New Technology, Shiraz Branch, Islamic Azad University, Shiraz, Fars, Iran. Email: elhammoazamian@gmail.com
3. Assistant Professor, Organ Transplant Research Center, Shiraz University of Medical Science, Shiraz, Fars, Iran. Email: negarazarpira@yahoo.com

Background and Aim: Probiotics have become a major focus of lactic acid bacteria (LAB) research over the past decade. They cause reduction serum cholesterol, stabilization of gut microflora and prevention of cancer cell growth. The purpose of this study was to isolate LAB from traditional and pasteurized yogurt and cheese in Fars province.

Methods: A total 30 samples of cheese and yogurt collected from Fars province. Isolation serially diluted and plated on MRS agar and incubated at 37°C and 42°C for three days in anaerobic toward CO₂. All stains were initially subjected to Gram staining, catalase and oxidase test, growth at 15°C, 30°C, 45°C in MRS agar, gas production from glucose, growth in presence of 2% and 4% of NaCl. The fermentation of carbohydrates (Lactose, Glucose, Maltose, Galactose, sucrose) was performed in phenol red. Designing PCR assays for the identification of lactobacillus species by specific primers (LB1 and LB2).

Results: Colonies of LAB were very small, opaque, glossy and round on the surface of MRS plates. Out of 30 positive colonies picked from MRS agar, only 19 were identified as LAB by biochemical and molecular test.

Conclusion: As far as we know, LAB distribution showed a high diversity of species that are dominate and frequently described in various dairy products. Indeed, the amount of LAB in traditional cheese and yogurt were more than pasteurized products.

Keywords: Lactic acid bacteria, Traditional, pasteurized products, Molecular identification

**P903 - 399: EFFECT OF LACTOBACILLUS DELBRUECKII ON OXIDATIVE STRESS IN
DIABETIC MICE**

Reza Dolatyari eslami¹, Asghar Tanomand², Jamal Hallajzadeh³, Sajjad Hosseinzadeh⁴

1. Higher Education Institute of Rabe Rashid
2. Maragheh Faculty of Medical Sciences
3. Maragheh Faculty of Medical Sciences
4. Higher Education Institute of Rabe Rashid

Background and Aim: Probiotics are living organisms that are useful for human health. Oxidative stress have essential mediatory roles in the development of diabetes. The aim of this study is an investigation of the anti-diabetic effect of lactobacillus delbrueckii (PTCC 1057) on diabetic mice oxidative stress.

Methods: 24 female mice ranging from 6 to 8 weeks old weighting 20 to 25 grams were selected. Then, at 12 of them 180 mg/kg streptozotocin was administered as intra peritoneal injection. After ten days, level of their blood sugar was measured and the mice whose blood sugar level was over 200 mg/dl were considered to be diabetic. Then the mice were orally administered 0.1 ml of PBS (control group) or Lactobacillus delbrueckii PTCC 1057 (3x10⁶ CFU) (experimental group) one time a day for 4 weeks. Finally, their serum was extracted and ELISA test was administered to these serums with ELISA test kits for malondialdehyde and total antioxidant.

Results: Total antioxidant in diabetic control group had a significant increase in comparison with non-diabetic groups and its insignificant decrease was observed in diabetic experimental group compared to diabetic control group. Moreover, in comparison with non-diabetic control group, malondialdehyde in diabetic control group insignificant increased and it insignificant decreased in diabetic experimental group in comparison with diabetic control group.

Conclusion: The results obtained from this study suggest that applying Lactobacillus delbrueckii can have anti-diabetics effects. However, clinical studies are required to prove these effects.

Keywords: Lactobacillus delbrueckii, Diabetes, Anti diabetic, Probiotics, Streptozotocin, Oxidative Stress.

P904 - 400: EFFECT OF LACTOBACILLUS DELBRUECKII ON GAS6 IN DIABETIC MICE

Reza Dolatyari eslami¹, Asghar Tanomand², Jamal Hallajzadeh³, Sajjad Hosseinzadeh⁴

1. Higher Education Institute of Rabe Rashid
2. Maragheh Faculty of Medical Sciences
3. Maragheh Faculty of Medical Sciences
4. Higher Education Institute of Rabe Rashid

Background and Aim: Probiotics have a significant role in diabetes type 1, 2 treatment. Among the variety of lactic acid bacteria, lactobacillus strains are well known in probiotics for their different properties. Recent research shows that plasma GAS6 concentrations were significantly lower among patients with type 2 diabetes compared to subjects with impaired glucose tolerance and normal glucose tolerance. The aim of this study is an investigation of the anti-diabetic effect of *Lactobacillus delbrueckii* (PTCC 1057) on diabetic mice GAS6.

Methods: 24 female mice ranging from 6 to 8 weeks old weighting 20 to 25 grams were selected. Then, at 12 of them 180 mg/kg streptozotocin was administered as intra peritoneal injection. After ten days, level of their blood sugar was measured and the mice whose blood sugar level was over 200 mg/dl were considered to be diabetic. Then the mice were orally administered 0.1 ml of PBS (control group) or *Lactobacillus delbrueckii* PTCC 1057 (3x10⁶ CFU) (experimental group) one time a day for 4 weeks. Finally, their serum was extracted and ELISA test was administered to these serums with ELISA test kit for GAS6.

Results: In addition to this, in comparison with non-diabetic control group, GAS6 insignificantly decreased in diabetic control group and it insignificantly increased in diabetic experimental group compared with diabetic control group.

Conclusion: The result of this study suggest that *Lactobacillus delbrueckii* can be impressive in diabetes treatment. However, another clinical study is needed for proving the exact effect of this probiotic on diabetes.

Keywords: *Lactobacillus delbrueckii*, Diabetes, Anti diabetic, Probiotics, Streptozotocin, GAS6.

**P905 - 402: IN VIVO STUDY OF ANTIBACTERIAL EFFECTS OF LACTOBACILLUS CASEI
PTCC 1608 ON PSEUDOMONAS AERUGINOSA PAO1**

Sajad Hosseinzadeh¹, Asghar Tanomand², Alireza Dehnad³, Reza Dolatyari eslami⁴

1. Higher Education Institute of Rabe Rashid
2. Maragheh Faculty of Medical Sciences
3. Higher Education Institute of Rabe Rashid
4. Higher Education Institute of Rabe Rashid

Background and Aim: Probiotics are microbial nutritional supplements that have beneficial effects on human health through keeping microbial balance in intestines. The present study was done with the prospect of studying anti-microbial effects of lactobacillus casei PTCC 1608 on *P. aeruginosa* PAO1 under in vivo culture conditions.

Methods: Antibacterial effects of lactobacillus casei on *p. aeruginosa* were investigated in four mouse groups. The first group as control group was fed with carrot juice for a month. After wards, mortality rate was considered through injecting 2xLD50 pseudomonas aeruginosa. The second group as prevention group was fed with carrot juice and lactobacillus casei for one month. After a month, through injecting 2xLD50 pseudomonas aeruginosa mortality rate was investigated. To the third group as treatment group, first, 2xLD50 pseudomonas aeruginosa injection was administered and after feeding with lactobacillus casei and carrot juice, mortality rate was considered. Finally, in the fourth group as aided treatment, at first 2xLD50 pseudomonas aeruginosa injection was administered and then the group was fed with lactobacillus casei and carrot juice and the treatment was done with gentamicin and finally mortality rate was measured and recorded.

Results: The results obtained from in vivo experiments showed that the highest mortality rate was for the control and treatment groups in which 100% and 83% of the mice died, respectively. The lowest mortality rate was for aided treatment and prevention groups in which 100% and 63% of the mice survived, respectively.

Conclusion: Lactobacillus casei proved to have a preventive effect on *P. pseudomonas aeruginosa*.

Keywords: *P. aeruginosa* , lactobacillus casei, Probiotic, In vivo

**P906 - 403: IN VITRO STUDY OF ANTIBACTERIAL EFFECTS OF LACTOBACILLUS CASEI
PTCC 1608 ON PSEUDOMONAS AERUGINOSA PAO1**

Sajad Hosseinzadeh¹, Asghar Tanomand², Alireza Dehnad³, Reza Dolatyari eslami⁴

1. Higher Education Institute of Rabe Rashid
2. Maragheh Faculty of Medical Sciences
3. Higher Education Institute of Rabe Rashid
4. Higher Education Institute of Rabe Rashid

Background and Aim: Probiotics are microbial nutritional supplements that have beneficial effects on human health through keeping microbial balance in intestines. They play an important role in producing and supplying probiotic products. The present study was done with the prospect of studying anti-microbial effects of lactobacillus casei PTCC 1608 on pseudomonas aeruginosa PAO1 under in vitro culture conditions.

Methods: In the present study, antibacterial effects of lactobacillus casei on pseudomonas aeruginosa under in vitro culture condition through well diffusion method and from 4-hour, 24-hour, and 48-hour cultures by using pure microbe, solution application and filtered solution application of the microbe provided from bacteria culture environment were considered. Diameter of the zone of growth inhibition halo around the well was measured and so as to decrease the likelihood of error, each test was repeated at least for three times. Next, the mean of the zone of growth inhibition halo on Mueller Hinton agar was measured and recorded.

Results: The most preventive effect in well diffusion method was for 48-hour culture and pure microbe injected to the well whose zone of growth inhibition halo was measured as 18.33 millimeters.

Conclusion: Lactobacillus casei proved to have a preventive effect on pseudomonas aeruginosa. This preventive effect is obvious in different bacteria cultures under in vitro culture conditions .

Keywords: P.aeruginosa, lactobacillus casei, Probiotic, In vitro

**P907 - 410: EVALUATION ANTIMICROBIAL EFFECTS SUPERNATANT OF L.
ACIDOPHILUS AND ANTIBIOTIC ON SALMONELLA TYPHIATCC14028 WITH AGAR
WELL DIFFUSION METHOD**

Nima Porfazlali¹, Nima Pourfazlali asle Miandoab², Zahra Hojjati Bonab^{2,3}, Somayyeh Taghizadeh^{3,4}

1. Student in Department of Microbiology, Islamic Azad University of Bonab, Bonab, Iran
2. . Department of Microbiology, Islamic Azad University of Bonab, Bonab, Iran 3. PhD student in Department of Microbiology, Alzahra University of Tehran, Tehran, Iran
3. PhD student in Department of Microbiology, Alzahra University of Tehran, Tehran, Iran

Background and Aim: Indiscriminate use of antibiotics, regardless of the resistance of these bacteria can cause the emergence of strains that are resistant even to new treatments. Lactobacillus bacteria are non pathogenic bacteria that by reduction of environment PH and production materials such as Bacteriocin, Fatty acids, etc. The inhibitory effects on the growth of many microorganisms. Probiotics as microorganisms that in the live environment can cope with pathogenic bacteria, can protect the body against pathogens.

Methods: For this purpose, bacterial suspension at 5.0 Mc Farland turbidity tube provided then balance on the plates containing Mueller Hinton agar. In order to synergistic effects an equal amount of supernatant of L. acidophilus ATCC4356 and antibiotic with agar well diffusion method. Cultures were incubated for 24 hours.

Results: The results of this study represent well a simultaneous antimicrobial effect of supernatant of L. acidophilus and antibiotic, which is characterized by the formation of inhibition on Salmonella typhi ATCC14028

Conclusion: In a study designed to demonstrate inhibition of L. acidophilus against intestinal infection caused by pathogens carried out, the results indicate a positive effect of probiotics against intestinal pathogens. The clay has been shown that antibiotic resistance in salmonella typhi were sensitive to Aflaksasin, Tetracycline, Kanamycin, Neomycin and Furazolidone.

Keywords: L. acidophilus . Salmonella typhi . supernatant . antibiotic

**P908 - 413: ANTIBACTERIAL EFFECT OF SUPERNATANT LACTOBACILLUS
ACIDOPHILUS ON SALMONELLA TYPHI**

Nima Porfazlali¹, Nima Pourfazlali asle Miandoab², Zahra Hojjati Bonab^{2,3}, Somayyeh Taghizadeh^{3,4}

1. Student in Department of Microbiology, Islamic Azad University of Bonab, Bonab, Iran
2. Department of Microbiology, Islamic Azad University of Bonab, Bonab, Iran 3. PhD student in Department of Microbiology, Alzahra University of Tehran, Tehran, Iran
3. PhD student in Department of Microbiology, Alzahra University of Tehran, Tehran, Iran

Background and Aim: Probiotics are defined as non-pathogenic microorganisms, which when ingested, exert a positive influence on the host health or physiology. The most probiotics include lactobacillus species that are non-pathogenic bacteria and have an inhibitory effect on the growth of many microorganisms. Enteropathogenic bacterial species are common infectious agents, among salmonella typhi is infectious bacterial.

Methods: *L. acidophilus* ATCC4356 were grown in MRS broth under microaerophilic conditions. 48 hour culture bacteria were centrifuged at 10000 g for 30min at 40c. The resulting supernatants were filtered. Supernatant Antimicrobial activity on *Salmonella* ATCC14028 was evaluated by well diffusion Agar.

Results: The results indicate that supernatant of *L. acidophilus* inhibit the growth of *salmonella typhi*

Conclusion: suggesting that antimicrobial compounds production, such as hydrogen peroxide or bacteriocins may be responsible by bacterial inhibitor.

Keywords: *Lactobacillus acidophilus*, *Salmonella typhi*, Supernatant

P909 - 419: EFFECT OF ORAL ADMINISTRATION OF LACTOBACILLUS ACIDOPHILUS AND BIFIDOBACTERIUM BIFIDUM CAN INDUCE IMMUNE RESPONSE IN BALB/C MICE BEARING TRANSPLANTED BREAST TUMOR.

Marjan Keypour¹, Marjan keypour², Fatemeh Hajari Taheri³, Mehdi Mahdavi⁴, Mohsen Abolhassani⁵

1. -
2. Hybridoma Lab., Immunology Department, Pasteur Institute of Iran -Islamic Azad University ,
Pharmaceutical Sciences Branch
3. Hybridoma Lab., Immunology Department, Pasteur Institute of Iran,
4. Hybridoma Lab., Immunology Department, Pasteur Institute of Iran
5. Hybridoma Lab., Immunology Department, Pasteur Institute of Iran

Background and Aim:Breast cancer is a global problem . Probiotics are defined as useful microorganisms that if consumed sufficient amount in foods will have beneficial effects on the host. Probiotics including lactobacillus and bifidobacterium stimulate host immune system through a diverse mechanism.

Methods: Lactobacillus acidophilus ATCC 43121 and Bifidobacterium bifidum ATCC 29521 were anaerobically grown in MRS agar. One group of female (6-7 weeks old) BALB/c mice was fed orally with 100 µl (5x10⁸cells) containing Lactobacillus acidophilus and Bifidobacterium bifidum daily for one month before tumor transplantation. The control group received equal volume of PBS without bacteria. The breast tumor was transplanted subcutaneously into the right flank and the administration of probiotic was continued for 14 days after tumor transplant with 7days intervals .Three mice were sacrificed from treatment and control groups, and the spleen cells were isolated. Splenocyte (4x10⁵ cell/ml) were counted and added to each well 100µl of ninety-six plate. The plate incubated 72h in humidified with 5% CO₂ at 37°C. The supernatant to each well was used for cytokine determinations. IL-4, IL-17, IL-12 and IFN-γ levels were measured in the spleen cell culture supernatants using sandwich ELISA.

Results:the level of IL-4, IL-17 and IFN-γ were significantly higher in Lactobacillus acidophilus and Bifidobacterium bifidum group when compared with control group (P<0.0001). IL-12 level did not show any differences between the experiment groups and the control.

Conclusion:Our research showed potential advantages of the probiotics to stimulate the immune system against breast cancer

Keywords:Probiotic, breast cancer, Lactobacillus

پروبیوتیک بومی ایران در مقیاس JQ61819 بهینه سازی شرایط رشد باکتری باسیلوس سابتیلیس با کد شناسایی: P910 - 434
ارلن آزمایشگاهی

Mahbubeh Abdoli Senejani¹, ²پروانه جعفری

1. دانشجویی کارشناسی ارشد میکروب شناسی، دانشکده علوم پایه، دانشگاه آزاد اسلامی واحد علوم و تحقیقات ساوه، ایران
2. استادیار میکروب شناسی، دانشکده علوم پایه، دانشگاه آزاد اسلامی واحد اراک، ایران

Background and Aim: انسان و ها میکروارگانیسم های زنده ای هستند که مصرف آن ها، اثرات مفیدی روی سلامت پروبیوتیک: محصولات پروبیوتیکی برای باکتری باسیلوس سوبتیلیس در درمان اختلالات گوارش کاربرد دارد. امروزه رشد دام و طیور می گذارند شرایط در این مطالعه با هدف بدست آوردن بیش ترین باکتری پروبیوتیکی، بهینه سازی دام، برپایه باسیلوس سوبتیلیس تهیه می شود محیط کشت، شرایط و مقادیر مناسب آن به اجزای مناسب شد که برای رسیدن به محصول مورد نیاز ابتدا لازم است محیط کشت انجام دست یافت.

Methods: تعیین بومی از شرکت تک ژن تهیه و استفاده شد. مرحله بعد از انجام تست های تشخیصی در این پژوهش، سویه های pH در رشد و pH بود که عواملی چون منبع کربن، ازت و محیط کشت 50 ml که حاوی 100 ml ترکیب بهینه محیط کشت در ارلن های میزان رشد باکتری در محیط کشت های مختلف پس از انجام محیط کشت مد نظر قرار گرفتند تولید محصول در بهینه سازی و میانگین و انحراف معیار مشخص شد 600 nm میزان جذب نوری در طول موج آزمایش ها با تعیین

Results: PH بود. باکتری در کربن بیش از سایر مقادیر 30 gr/ml مشخص شد که رشد باکتری در مقدار در بررسی نتایج حاصل ازت اختلاف معناداری 2.2، 1.7، 1.2 gr/ml باکتری در غلظت های خنثی و قلیایی بهتر رشد کرده است. همچنین میزان رشد ندارد.

Conclusion: نتیجه را گرفت که از منابع طبیعی موثر در رشد باکتری باعث افزایش تولید آنزیم باکتری شده و می توان این عوامل باشند، در محیط کشت صنعتی برای رشد این باکتری می توان استفاده نمود که دارای درصد بالایی از این ترکیبات می

Keywords: پروبیوتیک، باسیلوس سابتیلیس، بهینه سازی

**P911 - 511: EVALUATION OF PROBIOTIC POTENTIAL OF METHYLOTROPHIC YEASTS
ISOLATED FROM PLANT MATERIALS**

Marzieh Geranpayeh Vaghei¹, Shaghayegh Nasr², Mohammad Reza Soudi³

1. Microbiology Department, Faculty of Science and Novel Technologies, Islamic Azad University, Tehran, Iran
2. Microorganisms Bank, Iranian Biological Resource Center (IBRC), ACECR, Tehran, Iran, Department of Microbial Biotechnology, Faculty of Basic Sciences and Advanced Technologies in Biology, University of Science and Culture, Tehran, Iran
3. Department of Microbiology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran

Background and Aim: Probiotics provide numerous benefits for the gastrointestinal system of the consumers. Methylophils are a heterogeneous group of microorganisms which can use reduced compounds such as methanol as their sole carbon and energy source. Since methane is an abundant natural gas and methanol is a cheap carbon source, methylophils are particularly interested in probiotics production.

Methods: Sampling, enrichment, screening and isolation of the plant materials were conducted to obtain methylophilic yeasts. The isolates have been identified by morphological and biochemical characterization. Molecular identification was carried out by sequencing of D1/D2 region of the large subunit of the 26S rDNA using NL1 and NL4 primers. Probiotic potential of methylophilic isolates were evaluated by investigation of their survival in chemically-simulated gastrointestinal conditions, bile salt tolerance, antimicrobial activity, resistance to trypsin, and hemolytic activity.

Results: A total of 16 different morphotypes of yeasts were isolated from plant materials. Our enrichment and screening strategy resulted in the selection of three isolates. The molecular analysis indicated that the isolates had the closest similarity to: *Meyerozyma caribbica*, *Trichosporon asahii*, and *Rhodotorula benthica*. The study of probiotic characteristics revealed that, *M. caribbica* was the most resistant to low pH of 2.5, bile (0.3% w/v), and trypsin. It doesn't show any sign of hemolytic activity. It shows antimicrobial effect towards *Staphylococcus aureus* as an indicator of gram positive bacteria.

Conclusion: Our experiments indicate that *M. caribbica* can be considered as a potential probiotic.

Keywords: In vitro characteristics, Methylophilic yeasts, *Meyerozyma caribbica*, Probiotics

P912 - 603: EXTRACTION, BIOCHEMICAL AND MOLECULAR DETECTION OF YOGHURT PROBIOTIC SPECIES AND OPTIMIZATION OF MAXIMUM GROWTH CONDITIONS

Zahra Ghaffarian¹, Nafiseh Naghavi²

1. Department of Microbiology, Islamic Azad University Falavarjan Branch, Isfahan
2. Department of Microbiology, Islamic Azad University Falavarjan Branch, Isfahan

Background and Aim: The consumption of probiotic products is helpful in maintaining good health, since probiotic bacterias, are ideal microorganisms which re-establish the intestinal microflora balance. Yogurt has long been recognized as product by which consumers can take in large amounts of probiotic cells for the therapeutic effect. Therefore, the aim of this study was extraction, biochemical and molecular detection of probiotic species from yoghurt and optimization of maximum growth conditions.

Methods: Extractions were carried out based on international standards from yoghurt samples. Following several culturing on specific mediums including MRS, broth agar, M17, SIM, TSB, TSI and ADH broth by obtaining typical colonies and microscopic observations, some bacterias were extracted for further investigations. In order to carry out biochemical detections, experimentations such as fermentation of 19 sugars, growth in 10, 15, 40 and 45°C, nitrate reduction, gelatin melting, arginine hydrolysis, Mupirocin antibiotic resistance, growth in a concentration range of salt and finally Esculin response were done. They were also cultured in presence of glucose as the best source of carbon. The molecular analysis of PCR was carried out to approve the biochemical results.

Results: The experimentations detected the extracted bacterias as follow: *Lactobacillus delbrueckii*, *Lactobacillus acidophilus*, *bifidobacterium* and *streptococcus thermophiles*. This bacteria in the presence of glucose as the carbon source and pH of 6.2 had the best growth conditions.

Conclusion: The results of this study suggests the introduction of probiotic bacterias not only in dairy products but also in many other food products such as probiotic cakes, juices and etc. for maintaining the good health.

Keywords: Probiotics, Yoghurt, Growth Condition, Biochemical and molecular detection, Optimization.

**P913 - 604: OPTIMIZATION OF GROWTH CONDITIONS AND LACTIC ACID PRODUCTION
OF LACTOBACILLUS DELBRUECKII SPP. BULGARICUS ISOLATED FROM YOGURT
USING TAGUCHI METHOD**

Zahra Ghaffarian¹, Nafiseh Naghavi²

1. Department of Microbiology, Islamic Azad University Falavarjan Branch, Isfahan
2. Department of Microbiology, Islamic Azad University Falavarjan Branch, Isfahan

Background and Aim: *Lactobacillus delbrueckii* ssp. *bulgaricus* is widely used as a starter culture to convert milk into yogurt. Fast acidification during fermentation is regarded as a useful property of *L. bulgaricus* in industrial applications. Hence, the aim of this study was optimization of growth conditions and acid lactic production by *L. bulgaricus* isolated from yogurt.

Methods: Herein, initially bacteria using specific MRS medium was isolated from yogurt. Following purification, biochemical and molecular tests were carried out to identify the isolated bacteria. Optimization process was done utilizing one factor at a time and Taguchi statistical analysis based on pH, temperature and bacteria number in order to find the best effective factor.

Results: Based on one factor at a time tests, the activity range of isolated bacteria for lactose fermentation and pH reduction in MRS culture medium was following values: temperatures of 40, 41 and 42 °C, pH values of 6, 6.2 and 6.4 and bacteria number of 5000, 10000 and 15000 per one ml culture medium. The results obtained by Taguchi investigations showed that bacteria factor number with 34.8% effectiveness, has the highest effect of pH reduction via isolated bacteria. Besides Taguchi, suggested the pH value of 6.2 and temperature of 40 °C and the bacteria number of 10000 cfu/ml as the best conditions of bacteria activity.

Conclusion: In conclusion, regarding the results of present study, optimization of bacteria number and growth conditions in addition to a favorable taste and odor in yogurt would provide a giant leap in dairy industry and starters in Iran.

Keywords: *Lactobacillus delbrueckii* subsp. *bulgaricus*, Yogurt, Lactic acid producing bacteria, Starter, Optimization, Taguchi.

**P914 - 635: ISOLATION , IDENTIFICATION AND OPTIMIZATION OF LIPASE
PRODUCTION USING A NOVEL LACTOBACILLUS FERMENTUM BY RESPONSE
SURFACE METHODOLOGY (RSM)**

Foruzan Fathi gelekolaee¹, Ruha Kasra Kermanshahi², Seyedeh Zahra Moosavi-Nejad ³, Elaheh Mobarak Ghamsari ⁴

1. M.Sc student of microbial biotechnology at Alzahra university Tehran , Iran
2. Faculty member of Microbiology at Alzahra university Tehran , Iran
3. Faculty member of biotechnology at Alzahra university Tehran , Iran
4. PHD student of Microbiology at Alzahra university , Tehran , Iran

Background and Aim: Lipids constitute a large part of the earth's biomass, and lipolytic enzymes play an important role in the turnover of these water-insoluble compounds. Response surface methodology (RSM) was employed to optimize the extracellular lipase production by *Lactobacillus fermentum*.

Methods: In this project , 18 strains of probiotic bacteria isolated from indigenous dairy products were studied. Qualitative assessment of lipolytic activity was done by Using different pour plates cultures containing olive oil and strains with lipolytic activity were selected. The activity of lipolytic enzymes was measured by following decrease in A410 of the substrate para-nitro phenyl acetate. Nine process variables were screened using Plackett–Burman design and were further optimized by central composite design of response surface methodology for lipase production in submerged fermentation.

Results: Results showed, 5 samples (6a, 6b, 6c, 5a, 5c) have both qualitatively and quantitatively lipolytic activity and the 5c named *Lactobacillus fermentum*, exhibited a greater clear zone and the highest lipolytic enzyme activity (65.54 U/ml). Therefore, 5c was selected for media optimization studies. Maximum lipase production of 75.71 U/ml were predicted in medium containing olive oil (40 g/L), Egg yolk (0.25 g/L), NH₄Cl (4.23 g/L) and Other compounds with previous extent at 37.69° and pH 7. A mean value of 78.16 ± 1.76 U/ml of lipase was acquired from real experiments.

Conclusion: The analysis of variance revealed that the established model was significant ($p < 0.01$).

Keywords: *Lactobacillus fermentum* , extracellular lipase, Plackett– Burman design, response surface methodology

P915 - 652: ANTI-INFLAMMATORY MECHANISM OF TWO SPORE PROBIOTICS IN LPS-STIMULATED HT-29 CELL LINE

Masoumeh Azimirad¹, Masood Alebouyeh ², Tahereh Naji³

1. 2- Cell and Molecular Department, Pharmaceutical sciences Branch, Islamic Azad University, Tehran, Iran
2. 1- Foodborne and Waterborne Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran. 2. Gastroenterology and Liver Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
3. Cell and Molecular Department, Pharmaceutical sciences Branch, Islamic Azad University, Tehran, Iran

Background and Aim: Since the use of spore forming bacteria as a probiotic may offer interesting advantages in modulation of immune system, this study was aimed to investigate anti-inflammatory potential of two *Bacillus* spp. in LPS-HT-29 cell line.

Methods: Differentiated HT-29 cell line was stimulated with LPS (10 µg/mL) and fold changes of inflammatory cytokines interleukin -8, tumor necrosis factor (TNF)-α, and Toll-like receptor 4 (TLR-4) were measured in the pre-treated and post-treated cells with of two *Bacillus* spores (*B. subtilis* and *B. coagulans*; MOI: 100). Changes of the pro-inflammatory genes expression levels was determined by ELISA (IL-8) and quantitative-relative real time PCR (IL-8, TNF- α, TLR-4).

Results: High concentration of IL-8 and its mRNA were determined in the LPS induced HT-29 cells. A significant decrease on IL-8 levels was measured in the pre-treated cells with *B. coagulans* spores at t5, which was higher than those detected for *B. subtilis*. Both spore probiotics also down-regulated the LPS induced TNF-α, the levels of TLR4 induced by LPS for *B. natto* were higher than those induced by *B. coagulans*.

Conclusion: *B. coagulans* spores were able to attenuate LPS induced IL-8 and TNF-α. Down regulation of the inflammatory cytokines by *B. subtilis* treated cell at later incubation times proposed possible involvement of vegetative form of *B. subtilis* in inhibition of the induced pro-inflammatory cytokines through blocking of TLR-4 signaling pathway

Keywords: Anti-inflammatory mechanism, *B. subtilis*, *B. coagulans*, TNF-α, TLR-4

**P916 - 657: COMPARATIVE SURVIVAL STUDY OF ENCAPSULATED BIFIDOBACTERIUM
BIFIDUM IN THE PRESENCE OF BETA-CAROTENE**

AZAM POURSEYFOLLAH¹, Davood Zare²

1. Shahr-e-Qods, Islamic Azad University, Tehran, Iran
2. Iranian Research Organization for Science and Technology, Department of Biotechnology

Background and Aim: Bifidobacterium bifidum is a beneficial probiotic that usually utilized as supplement in food products. Probiotics has beneficial effects on function and human health. Beta-carotene is also a food supplement with an antioxidant activity. β -carotene as an antioxidant may increase the viability of B.bifidum during preservation. The aim of this study was to evaluate the viability of B.bifidum after encapsulation and in the presence of β -carotene

Methods: Samples of emulsified β -carotene (0.03%) in a solution of sodium caseinate (2,4,6%) and carrageenan (0.03%) were prepared and then were mixed with a dense suspension of B. bifidum (PTCC 1644). Samples with the same conditions without β -carotene were prepared as control. The final number of bacteria in resulting solution was $(6.7 \pm 0.18) \times 10^7$ cfu/ml. Then, the solutions were processed with ultrasonic and freeze dryer devises, the viability of bacteria was determined using colony forming unit (CFU) method.

Results: The existence of β -carotene could increase the viability of encapsulated bifidobacteria, significantly. The viability of encapsulated bifidobacteria decreased $(5.1 \pm 0.29) \times 10^6$ cfu/g in the presence of β -carotene while it decreased $(8.7 \pm 0.16) \times 10^2$ cfu/g when bacteria encapsulated without β -carotene. This could be due to the antioxidant activity of β -carotene which is possible through several mechanisms including trapping oxygen and etc.

Conclusion: β -carotene causes a delay in initiation reaction successive radical activities and thus, enhances the viability of anaerobic bacteria. Further investigation was accomplished to estimate the effect of different concentrations (0.01,0.03,0.05) of β -carotene on the viability of bifidobacteria. A concentration of 0.03% was the most effective concentration on the viability of bacteria.

Keywords: β -carotene, B.bifidum, Microencapsulation.

**P917 - 745: ISOLATION AND IDENTIFICATION OF LACTIC ACID BACTERIA OF SOME
IRANIAN TRADITIONAL SOURDOUGH**

Saeed Shalbaf¹, Safoura Salahi², Maryam Tajabadi Ebrahimi³

1. Young Researchers and Elite club, Central Tehran Branch, Islamic Azad University, Tehran, Iran
2. Young Researchers and Elites Club ,Saveh branch ,Islamic azad university ,Saveh ,iran
3. Associate Professor of Microbiology at Islamic Azad University, Central Tehran Branch

Background and Aim:Bread is an important food. However, the Iranians consume bread about 6 times the world's population, but unfortunately, the amount of calories and protein intake from bread is far below world standards. One of the significant reasons for this is poor quality of sourdough and the use of harmful substances, such as baking soda, Sodium dithionite and The purpose of this study is isolation and identification of lactic acid bacteria in traditional sourdough to improve the quality of industrial bread.

Methods:After dilution, the suspension obtained in MRS agar plate which was incubated under anaerobic conditions at 30 ° C for 48 hours, was cultured. Following incubation, colonies were isolated which were under gram staining and catalase test. Isolated colonies of Lactobacillus (G + and Basil Catalase -) were selected for further identification. This growth of these isolated samples was tested at 15 and 45 ° C in MRS broth for 7 days and 48 hours. Sourdough is consists essentially of LAB and yeast.

Results:Sourdough is consists essentially of LAB and yeast. The presence of lactic acid bacteria in sourdough is well known and many of these bacteria belong to the Lactobacillus genus. Such as lactobacillus sanfranciscensis strains, Lactobacillus Pentosus, Lactobacillus brevis, Lactobacillus plantarum, Lactobacillus acidophilus and Lactobacillus rossiae.

Conclusion:Finally, lactic acid bacteria, especially Lactobacilli play an important role in the process of preparing sourdough. They also improve the quality of wheat bread, therefore, the use of appropriate Sourdough can be considered as a useful product to improve the quality of flavor in bread.

Keywords:lactic acid bacteria, sourdough, traditional

**P918 - 784: THE EFFECT OF PREBIOTICS ON THE ANTIMICROBIAL ACTIVITY OF
LACTOBACILLUS FERMENTUM ATCC 9338 AND ISOLATE OF THIS STRAIN.**

Elahe Rezaie¹, Rouha kasma kermanshahi ², Jamshid fooladi³, Elahe mobarak-qamsari⁴

1. microbiology master of sciences student ,alzahra university, faculty of biological sciences,Iran.
2. microbiology professor, alzahra university, faculty of biological sciences,Iran.
3. microbiology professor,,alzahra university, faculty of biological sciences,Iran.
4. microbiology Ph.D student, alzahra university, faculty of biological sciences,Iran.

Background and Aim:probiotics are live microorganisms that cause health improvement in host. prebiotics are non digestible food ingredients that by selectively stimulating that growth or activity of one or limited number of bacteria in colon have beneficially affect in host health. aim of this study effect of prebiotic on production of antimicrobial properties of Lactobacillus fermentum ATCC 9338 bacteria and isolated bacteria.

Methods: in this study used of strain Lactobacillus fermentum ATCC 9338 and isolated this strain (Lactobacillus fermentum6B , Lactobacillus fermentum5C) growth in MRS broth as basic media(lacking prebiotic) and 2% prebiotics (trehalose ,inulin ,sorbitol)as test media on microaerophile qualification and 37 C° temperature .antimicrobial activity of bacterial culture supernatant was tested using of well diffusion method against strains Escherichia ATCC 25922, Staphylococcus aureus ATCC 25923 , Pseudomonas aeruginosa ATCC27853.

Results: according to data maximum antimicrobial activity showed in L. fermentum5C against E.coli ATCC 25922 basic media and L. fermentum ATCC 9338 against E.coli ATCC 25922 in media with 2% sorbitol. L. fermentum6B had not activity against said pathogenic bacteria.

Conclusion:this study has demonstrated that can prebiotics cause increase and decrease antimicrobial activity that indicate any prebiotic has specific for a probiotic and according to strain type different effects.

Keywords:probiotic, prebiotic , antimicrobial activity , Lactobacillus fermentum

P919 - 785: THE EFFECT OF PREBIOTICS ON THE LYPOLYTIC ENZYMES ACTIVITY OF LACTOBACILLUS FERMENTUM ATCC9338 AND ISOLATE OF THIS STRAIN.

Elahe Rezaie¹, Rouha kasra kermanshahi ², Jamshid fooladi³, Zahra moosavi-nejad⁴, foruzan fathi⁵

1. microbiology master of sciences student ,alzahra university, faculty of biological sciences, Iran.
2. microbiology professor, alzahra university, faculty of biological sciences, Iran.
3. microbiology professor, alzahra university, faculty of biological sciences, Iran.
4. microbiology professor, alzahra university, faculty of biological sciences, Iran.
5. microbiology master of sciences student ,alzahra university, faculty of biological sciences, Iran.

Background and Aim:: Probiotics are live microorganisms, which when administered in adequate amount give a health benefit to the host. Prebiotics are short-chain carbohydrates (SCCs) that are metabolized by lactic acid bacteria and have beneficial effects on the host. Lypolytic enzymes are most pliable biocatalysts and bring a wide range of bioconversion reactions.

Methods:: In this study, we used the strain *Lactobacillus fermentum* ATCC 9338 and isolated this strain (*Lactobacillus fermentum* 6B, *Lactobacillus fermentum* 5C) growth in assay enzyme media with 2% olive oil and 2% prebiotics (trehalose, inulin, sorbitol). Enzyme activity was assayed by p-nitrophenol acetate (pNPA) as enzyme substrate and performed by spectrophotometrically method at λ :420nm.

Results: Data in the study showed that *L. fermentum* ATCC 9338 have enzyme activity maximum in the 2% sorbitol and 2% inulin media and then in basic media (lacking prebiotic) and *L. fermentum* 6B with 2% sorbitol and 2% trehalose in media respectively. *L. fermentum* 5C have enzyme activity lower than two said strains and prebiotics had low decrease in enzyme activity in this strain.

Conclusion: Based on the finding in this study, any prebiotic effect on specific probiotic strain and according to the probiotic strain have different effect on them.

Keywords: Probiotic, Prebiotic, *Lactobacillus fermentum*, Lypolytic enzyme

**P920 - 833: EVALUATION OF PROBIOTIC LACTOBACILLUS SPP IN WHITE FISH (
RUTILUS FRISII KUTUM)**

Monireh Faeed¹, Rouha Kasra Kermanshahi²

1. Iranian Fisheries Science Research Institute (IFSRI), in land waters Aquaculture research center, Agriculture Research Education and Extension Organization (AREEO) Anzali, Iran
.Email:m_faeed@yahoo.com
2. Department of Microbiology, Faculty of biological Sciences, AlzahraUniversity, Tehran, Iran.Email:rkasra@yahoo.com

Background and Aim: Lactic acid bacteria are beneficial bacteria in the intestinal tract of humans and animals. LAB improve the intestinal microflora and increase the growth and health of animal, lactobacillus is a genus of Lactic acid bacteria which are positive gram, rod shaped, none spore forming, non motile bacteria and non catalas enzyme in this study, our aim were to isolate Lactobacillus sp form intestinal tract of Rutilus frisii kutum. Rutilus frisii kutum is one of the economically important fish of the Caspian sea.

Methods: Identification was based on biochemical and molecular (16 SrDNA) methods. They evaluated to tests as tolerance to salt and acid, sustainability and resistance antibiotics, The effects antagonistic in different degree and times.

Results: Bacteria were detected L. brevis and L. Plantarum. They had positive effects in vitro tests. But L. brevis had probiotic effects better than L. Plantarum.

Conclusion: The result showed this probiotics can be used for different industries.

Keywords: probiotic, Rutilus frisii kutum, L. brevis, L. Plantarum

P921 - 934: EFFECT OF LACTOBACILLUS CASEI STRAIN TD3 ON EXPRESSION OF 3-HYDROXY-3-METHYLGLUTARYL GENE IN HYPERCHOLESTEROLEMIC RATS

Abolfazl Dehkohneh¹, hossein fahimi², parvaneh jafari³

1. Active Pharmaceutical Ingredient Research Center, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran-Iran (IAUPS)
2. Department of Molecular and Cellular Sciences, Faculty of Advanced Sciences & Technology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran-Iran (IAUPS)
3. Department of Microbiology, Science Faculty, IAU, Arach Branch, Arak-Iran

Background and Aim:Hypercholesterolemia is a major risk factor for cardiovascular disease. Not all patients respond well to traditional cholesterol lowering medications. The microbiome plays an important role in lipid metabolism but how the introduction of probiotic communities affects host lipid metabolism is poorly understood. This study was performed to evaluate the efficacy of L.casei strain TD3 in expression of 3-hydroxy-3-methylglutaryl(HMG) gene in hypercholesterolemicrats.

Methods:Twenty-one wistar male rats were divided into three group randomly (n=7) in following: negative control with normal regime; positive control with high-cholesterol diet added of 0.1 ml PBS; Trial group with high cholesterol diet plus 0.1ml of probiotic bacterium (Lactobacillus casei, TD3 strain). In 21th day the rats were killed and then their Adipose tissue were separated and storage in -80 C. then isolate RNA from adipose tissue and cDNA synthesized. Eventually real time PCR technique was used to evaluate expression of HMG gene

Results:our results indicated that lactobacillus casei strain TD3 can affect on expression of HMG gene. HMG expression level in trial group was already one third of control group and delta - delta ct values were 1.1 and 3.2, respectively.

Conclusion:The finding indicated that using probiotic can be effective approach for cholesterol lowering and cardiovascular disease can used probiotic products to reduce their serum cholesterol

Keywords:lactobacillus casei, probiotic, hypercholesterolemic

**P922 - 935: THE EFFECT OF LACTOBACILLUS CASEI , STRAIN TD3, ON WOUND
HEALING IN MALE WISTAR RATS ON DAYS 3,7,14 AND 21**

Abolfazl Dehkohneh¹, ahmad jiriaie², ahmad sarikhani³, parvaneh jafari⁴, kambiz kamyab Hesari⁵

1. Active Pharmaceutical Ingredient Research Center, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran-Iran (IAUPS)
2. graduated in cellular and molecular biology, biotechnology, IAU, Arach Branch, Arak-Iran
3. graduated in cellular and molecular biology, biotechnology, IAU, Arach Branch, Arak-Iran
4. Department of Microbiology, Science Faculty, IAU, Arach Branch, Arak-Iran
5. associated proffessor pathology department fellowship in dermatopathology, Tehran university of medical science

Background and Aim:Probiotics are microorganisms in the gastrointestinal tract that can improve immunity and reduce inflammation. The beneficial effects of these bacteria on ulcer healing have been proved but little research has been done in the field of cutaneous wound healing. In this study we have examined the effect of Lactobacillus casei strain TD3 on cutaneous wound healing.

Methods:Lyophilized L.casei Strain TD3 was purchased from Takgen zist company. Wistar male rats divided into 3 groups; negative control, positive control and trial (n = 12) and a full-thickness wound (1.5 × 1.5 cm) was made on the back of each rat. After 24 h of injury, two groups, positive control and trial, were treated by eucerin, and eucerin contained L. casei strain TD3, respectively. but the negative-control group did not receive anything. On days 1, 3, 7, 14 and 21, rats were killed and wound samples were collected for histological and statistical analysis.

Results:L. Casei strain TD3 significantly decreased wound area as compared to other groups and increased wound healing. Histological study on day 3 showed significant increase in the number of monocytes. Edema and the number of lymphocytes were decreased in day 21 but were not significant

Conclusion:In conclusion, our study demonstrated that L.casai strain TD3 have the potential to improve wounds and using probiotics can be useful method for treatment of wound.

Keywords:lactobacillus casei, probiotic, wound healing

P923 - 939: SCREENING OF LACTOBACILLI ISOLATES FROM IRANIAN LOCAL DAIRY PRODUCTS FOR EXTRACELLULAR EXOPOLYSACCHARIDE PRODUCTION

Amir Mortezaeifar¹, Maryam Ghobadi Dana²

1. Damghan Azad University
2. standard research institute of Iran Microbiology Department

Background and Aim: Exopolysaccharides from lactic acid bacteria contribute to specific rheology and texture of fermented milk products. In addition exopolysaccharides have benefits in human health and have an important role against gastrointestinal diseases as they act as a no digestible food fraction the synthesis of lactic acid, there are several LAB traits that could confer desirable attributes to specific fermented products; this is the case of exopolysaccharide production in dairy fermentations. The aim of this study was screening of seventy lactobacilli strain isolated from traditional dairy products for Extracellular exopolysaccharide production and selecting superior strains for introducing to food industries

Methods: Seventy strains of *Lactobacillus* were cultured in MRS medium and incubated at 37°C for 48 hours in anaerobic conditions. The amount of Extracellular EPS was found by phenol sulphuric acid method. The absorbance was read at 490 nm and Extracellular exopolysaccharides production was expressed as mg / lit.

Results: Among Seventy strains, all of them have potential to produce Extracellular EPS, The Extracellular EPS production ranged between 11-410mg l⁻¹. Thirteen strains have low Extracellular EPS production (up to 100 mg l⁻¹), twelve strains such as L78 and L138 *L.paracasei*, L90 and L125 *L.crustorum*, have high Extracellular EPS production (300 to 410 mg l⁻¹).

Conclusion: The selected strains from this study can be used as starter for production of fermented dairy products for improving the rheological properties of dairy products

Keywords: Extracellular Exopolysaccharide, Isolation, Screening, microbiology, probiotic

P924 - 941: SCREENING OF LACTOBACILLI ISOLATES FROM IRANIAN LOCAL DAIRY PRODUCTS FOR CONNECTED EXOPOLYSACCHARIDE PRODUCTION

Amir Mortezaeifar¹, Maryam Ghobadi Dana²

1. Damghan Azad University
2. Standard Research Institute of Iran Microbiology Department

Background and Aim: Microbial exopolysaccharides are considered as natural bio-thickeners abundantly used in dairy and fermented food industries for quality improvement. Exopolysaccharides produced by Lactic acid bacteria possess the possibility of replacing stabilizer and thickeners currently produced commercially by non-food culture grade bacteria. Currently, much attention is being paid for improving the texture of food by screening the new exopolysaccharides producing strains. The aim of the present work was to screen connected EPS producing Lactobacilli strains

Methods: Seventy strains of Lactobacillus were cultured in MRS medium and incubated at 37°C for 48 hours in anaerobic conditions. The amount of connected EPS was found by phenol sulphuric acid method. The absorbance was read at 490 nm and exopolysaccharides production was expressed as mg / lit

Results: Among Seventy strains, all of them have potential to produce connected EPS. The connected EPS production ranged between 6-144mg l⁻¹. Twenty four strains have very low connected EPS production (up to 10mg l⁻¹) such as L147 and L17. Six strains have medium connected EPS production (100 to 144 mg l⁻¹) such as L200 and L66 .

Conclusion: The selected strains from this study can be used as starter for production of fermented dairy products for improving the health and rheological properties of food.

Keywords: connected Exopolysaccharide, Isolation, Screening, microbiology, probiotic

**P925 - 984: AN IN-SILICO SCREENING ON THERMAL STABILITY OF A SERIES OF
BACTERIA DIOXYGENASE FOR PROBIOTIC DEVELOPMENT**

Safoora Shahreki mojahed¹, Safoora Shahreki-mojahed², Aliakbar Haddad-Mashadrizesh³, Jafar Saeidi⁴

1. Department of Biology, Science and Research branch, Islamic Azad University, Khorasan Razavi, Neyshabur, Iran
2. Cell and Molecular Research Group, Institute of Biotechnology, Ferdowsi University of Mashhad, Mashhad, Iran
3. Department of Biology, Islamic Azad University, Khorasan Razavi, Neyshabur, Iran

Background and Aim:Industrialization of the societies leads to critical change in diet and environment. This transition led to appearance new compounds such as polycyclic aromatic hydrocarbons (RAH) in the human environments that are the essential causes of many diseases such as cancers. So, removal such pollutants from the environment and diet provide promising approaches for cancer prevention which are considered in this study through protein screening in order to probiotic development.

Methods:In this regard, a profile of the bacterial dioxygenases was collected based on literature. Corresponding nucleotide and protein sequences of the selected enzyme were retrieved from NCBI and UNIPROT databases. CD Search, Motif Scan, Blast, MEGA6, Hex and ClusPro2.0 programs were performed to evaluate data from literature. The thermal stability of the selected enzymes and domains were carried out using GROMACS5.07 under the OPLS force field at during 500ps for the NVT and NPT, and 20ns for MD stage.

Results:The results of this study provide a series of catalytic domains that have already mentioned in the literature with degradation capacity of RAH. Moreover, the assessment of thermal stability of the selected domains and enzyme led to reveal a range of stability of them in different temperature.

Conclusion:In general, this analysis led to present a series of temperature resistance enzyme, with the ability to RAH degradation, which could be applying for probiotic development based on genetic engineering.

Keywords:Industrialization, RAH, Cancer, Probiotic, GROMACS5.07

P926 - 1048: SCREENING OF COCCI ISOLATES FROM IRANIAN LOCAL DAIRY PRODUCTS FOR EXTRACELLULAR EXOPOLYSACCHARIDE PRODUCTION

Sevda Ameli¹, maryam ghobadie dana²

1. azad university of damghan
2. microbiology research group standard institute of iran

Background and Aim:Exopolysaccharide are exocellular polysaccharides which produced by Streptococcus, Lactobacillus, Lactococcus, Leuconostoc, and Pediococcus. They used as thickeners, stabilizers and gelling agents in food industry. In addition, they have beneficial effects on human health such as cholesterol-lowering ability, immunomodulating, and antitumoral activities and prebiotic effects. The aim of this study was Screening of 45strains of cocci isolates from local dairy products for extracellular exopolysaccharide production and selecting superior strains for introducing to food industries.

Methods:Forty five strains of cocci isolates from local dairy products were cultured in M17 medium containing 2% glucose and incubate in Microaerobic conditions at 37 ° C for 24-48 hours. Then they were screened for EPS producing activity so abandoned exopolysaccharide were extracted by phenol sulphuric acid method. The absorbance was read at 490 nm and exopolysaccharides production was expressed as mg l⁻¹.

Results:Among forty five strains, all of the strains have ability to produce extracellular exopolysaccharides. The extracellular EPS production ranged between 43-325 mg l⁻¹. Eighteen strains have low Extracellular EPS production (up to 100 mg l⁻¹), Six strains such as C100 and C52, have high Extracellular EPS production (300 to 325 mg l⁻¹).

Conclusion:The selected strains from this study can be used as starter for production of fermented dairy products for improving the organoleptic and textural qualities of fermented dairy products.

Keywords:exopolysaccharides, cocci, Screening, microbiology, probiotic

**P927 - 1087: DETERMINATION OF HEMOLYTIC PROPERTIES OF ISOLATED
LACTOBACILLI FROM TRADITIONAL DAIRY PRODUCTS FOR SELECTION OF
PROBIOTIC STRAINS**

Mahrokh Javidmehr¹, maryam ghobadi dana²

1. Expert
2. Professor

Background and Aim: Nowadays, most probiotic bacteria belong to the genera *Lactobacillus* that has a capacity to interact with the host mucosa and may beneficially modulate the immune system. However rigorous in vitro testing is required prior to progressing to in vivo trials for any probiotic candidate organisms. Therefore, the objective of the present study was, to characterize hemolytic properties of 100 lactobacilli that isolated from traditional dairy products.

Methods: Hemolysis was determined on 5% sheep blood agar plates, streaked with colonies from fresh MRS Agar plates. Reading was taken after incubation at 37°C for 24h in anaerobic conditions. *Staphylococcus aureus* (ATCC 25923) was used as a positive control. Clear zone indicates a positive reaction and complete hemolysis considered β and no hemolysis from triplicate assays indicates γ .

Results: Only 19 of the isolates showed complete β -hemolysis and 21 others were only α hemolytic and 79 isolates did not display any hemolytic activity.

Conclusion: 79 percent of strain with gamma hemolytic property and no ability to cause disease and complications in consumers and they can be introduced to the food industry after completing other in vitro and in vivo tests

Keywords: *Lactobacillus*, hemolytic, probiotic, traditional, Dairy product

**P928 - 1093: SELECTION LACTOBACILLI ISOLATED FROM TRADITIONAL DAIRY
PRODUCTS FOR RESISTANCE TO BILE OXALATE**

Mahrokh Javidmehr¹, maryam ghobadi dana²

1. Food Sciences & Technology, , Pharmaceutical Sciences Branch, Islamic Azad University,, Tehran
2. Food Sciences & Technology, institute of standard, Karaj, Iran, Islamic Republic Of

Background and Aim:Over the past few decades, probiotic lactobacillus have been very intensively investigated, The objective of this study was to identify and establish the functional characteristics of potentially probiotic Lactobacillus strains isolated from traditional dairy products, They benefit the host by improving the nutritional and microbial balance in the intestinal tract as well as by systemic immunity,Therefore, the objective of the present study was, to Therefore, the objective of the present study was, to resistance to bile oxalate of 47 lactobacillus that isolated from traditional dairy products.

Methods:The bile salt solutions were prepared using oxgall (Sigma) powder, at the final concentrations of 0.3%, 0.5%, and 1%.Cell suspensions containing were added to each solution 0.3%, 0.5%, 1% and incubated at 37°C for 1, 2/5, 4, 24h in anaerobic conditions. After 1, 2/5, 4, 24 h incubation, 1 mL of each culture was diluted in sterile 9 mL of 0.85% saline blanks. Plates were incubated in the anaerobic chest at 37°C for 24-48h. counting on agar culture and also done by spectrophotometer.

Results:Only 30 strains generally resisted bile salts and were selected for further analyzing their probiotic properties.

Conclusion:Stringent selection criteria for the identification of probiotic strains are now being considered essential. There was considerable variability in resistance to bile salts among the different species of Lactobacillus, supporting the importance of assessing the bile tolerance of isolates in selecting potential probiotics.

Keywords:Lactobacillus, oxgall bile, probiotic, traditional, Dairy product

**P929 - 1170: THE INTERACTION BETWEEN THE BRAIN AND THE GUT MICROFLORA
AND THEIR ROLE IN BEHAVIORAL CHANGES**

Seyed omidreza Mousavi¹, Saeed Enayatollahi², Ehsan Dehghanpour Farasha³, Behnam Behnouieh^{3,4}

1. Genetic Department, Faculty of Science Trail, medical branch, Islamic Azad University, Tehran, Iran
2. Microbiology Department, Faculty of Science, Islamic Azad University, Science and Research Branch, Tehran, Iran
3. Biotechnology Department, Faculty of Agriculture, Islamic Azad University, Yazd, Iran
4. Biotechnology Department, Faculty of Agriculture, Islamic Azad University, Yazd, Iran

Background and Aim: Gut flora consists of a complex of microorganism species that live in the digestive tracts of animals in a symbiotic relationship with the host. The gut-brain axis refers to the biochemical signaling taking place between the gastrointestinal tract and the nervous system, often involving intestinal microbiota, which have been shown to play an important role in healthy brain function.

Methods: Poor diet, infections, aging and antibiotic consumption change the structure of microbiota, that is malicious for creatures. Microflora associated with the central nervous system (CNS) through neural pathways (vagal nervous system), immunity (cytokines) and endocrine (cortisol). Moreover gut bacteria produce amino acids, such as GABA and tryptophan, and monoamines, such as serotonin, histamine and dopamine, that play important roles in the brain as neurotransmitters.

Results: The discovery that differential microbial composition is associated with alterations in behavior and cognition has significantly contributed to establishing the concept of gut-brain axis. Research has shown that microflora affects widely on the physiology of brain function and behavior.

Conclusion: Because probiotics are proven to reduce anxiety and stress, and improvement of patients with IBS, so we conclude that changes in gut microflora, for example, by using probiotics can be effective in treating some neurological diseases.

Keywords: microflora, signaling, behavior, cytokine

**P930 - 1239: ISOLATION AND EXAMINED THE ANTIMICROBIAL EFFECT OF THE
INDUSTRIAL AND LOCAL PROBIOTICS ON SEVERAL SPECIES OF ANTIBIOTIC
RESISTANT PATHOGENIC BACTERIA**

Elnaz Ahmadnejad¹

1. Elnaz Ahmadnejad

Background and Aim: probiotic bacterial are microbial food supplement with beneficial properties on human health. the aim of the study was to isolate lactobacillus dairy products (yogurt, cheese) local, industrial in rural area of Neyshabour and also antimicrobial activity against pathogenic bacteria (staphylococcus aureus, clostridium perfringens)

Methods: in this study, our sample cheese, yogurt local, industrial city of Neyshabour prepared and lactobacilli were isolated by culture in specific media, then using tests such as catalase test and biochemical test such as determining optimum growth in pH, NaCl tolerance assay, bile salt tolerance assay, quantification of organic acid was used for isolation of probiotic lactobacilli. probiotics antimicrobial activity against pathogenic bacteria staphylococcus aureus, clostridium perfringens were examined by disc diffusion method, well method. each test was repeated three times to reduce the error. diameter inhibition zone was then able to compare their antimicrobial and by using minimum inhibitory MIC, MBC probiotic bacteria after certain antibiotics were compared with control.

Results: lactobacilli from local dairy product Neyshabour have growth inhibitory effect against pathogenic bacteria were staphylococcus aureus, clostridium perfringens. the highest inhibitory effect against clostridium perfringens in the wells with an average diameter of inhibition zone of 12mm, also compared two methods of disc and well, well methods much more sensitive way is the disc way

Conclusion: according to this study, some lactobacillus strain isolated from dairy products useful in the management of diarrhea, other gastrointestinal disease. the use of can be useful for prevention and treatment.

Keywords: lactobacilli, probiotic, antimicrobial effect, yogurt and local cheeses and industrial

Sexually Transmitted Disease

P931 - 362: FREQUENCY OF GROUP B STREPTOCOCCUS AND TRICHOMONAS VAGINALIS GENITAL INFECTIONS IN PREGNANT WOMEN AND WOMEN WITH SPONTANEOUS ABORTION BY THE PCR METHOD

Amjad Ahmadi¹, Rashid ramazanzadeh ², Fariba Farhadifar ³, Daem Roshani ⁴, Mozhdeh Zarei⁵, Masoome Rezaii ⁶, Sholeh Shahghaibi⁷

1. Department of Microbiology, Faculty of Medicine, Kurdistan University of Medical Sciences, Sanandaj, Iran.
2. Cellular and Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran.
3. Social Determinants of Health Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran
4. Social Determinants of Health Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran
5. Master of Midwifery.Mph of Reproductive health, Deputy of Research and Technology, , Kurdistan University of Medical Sciences, Sanandaj, Iran
6. Department of Gynecology, Faculty of Medicine , Kurdistan University of Medical Sciences , Sanandaj, Iran
7. Department of Gynecology, Faculty of Medicine , Kurdistan University of Medical Sciences , Sanandaj, Iran

Background and Aim:Group B Streptococcal is one of the important factors of death in newborns in both developed and developing countries. Trichomoniasis is considered as one of the most prevalent sexually transmitted diseases (STDs) in the world, which is caused by Protozoan Trichomonas Vaginalis

Methods:In this case-control study 109 women were included with spontaneous abortion with gestational ages between 11-20 weeks (Cases), and 109 pregnant women with gestational ages between 35-37 weeks (Controls) in Sanandaj, Iran. Specific primers were used and DNAs were extracted by endocervical swabs, and the PCR test was used for detecting, in both women groups

Results:The rate of prevalence of Group B Streptococcal infection in the control group was four persons (3.6%) and, in the patient group, it was eight persons (7.2%), and the rate of prevalence of Trichomonas Vaginalis in both groups, was zero

Conclusion:The present study, showed that there is no relationship between Group B Streptococcus infections (Pvalue:0.235) and Trichomonas Vaginalis.

Keywords:Group B Streptococcal, Trichomonas Vaginalis, spontaneous abortion

**P932 - 875: THE INFORMATION SOURCE OF STUDENTS OF ZABOL UNIVERSITIES
ABOUT HIV/AIDS**

Mohammad Ali Kavosi¹, Saeed Salari², Mehrdad PoyanMehr³

1. Department of Pathobiology, Faculty of Veterinary Medicine, University of Zabol, Zabol, Iran
2. Department of Pathobiology, Faculty of Veterinary Medicine, University of Zabol, Zabol, Iran
3. Department of Pathobiology, Microbiology section, Faculty of Veterinary Medicine, University of Razi, Kermanshah, Iran

Background and Aim: Acquired Immune Deficiency Syndrome (AIDS) is a fatal disease. In developing countries, less attention have been paid to how to inform the society. Zabol, as a border and deprived city, and young people also as at risk population require more attention regarding to AIDS. This study was aimed to clarify the source of information (SI) of the 3 student groups in Zabol universities including BSc in non-Medical Sciences (BNMS), Doctor of Veterinary Medicine (DVM) and BSc in Medical Sciences (BMS).

Methods: A questionnaire including questions relating to SI were distributed, as a cross sectional study, among sixty-six fresh students of two universities of Zabol (University of Zabol and Zabol University of Medical Sciences) studying in BMS, DVM and BNMS. χ^2 and one way ANOVA tests and P value < 0.05 were applied for statistical analysis.

Results: The majority of study population (47%) mentioned television as their main source of information, while only one person (1.5%) obtained information from newspapers. A significant correlation between field of study and source type of information were observed ($P < 0.05$).

Conclusion: Our results indicated that modification of the red lines existed in strategical sights and the media, especially for TV, will reduce the risk of HIV and revision and improvement of SI should be a priority for all institutions and universities especially in study area.

Keywords: AIDS, Information source, Students, Zabol

Tuberculosis and Mycobacteria

P933 - 72: IMPROVEMENT OF HEAT STABILITY OF MYCOBACTERIUM BOVIS IN LYOPHILIZED BCG VACCINE

Fatemeh Jahanbakhsh sefidi¹, Fatemeh Jahanbakhsh sefidi. M.Sc², Mehdi Hassanzadeh ph.D³, Gholamali Moradli ph.D⁴, Homan Kaghazian ph.D⁵

1. -
2. Department of Biology, Faculty of Basic science, ISLAMIC AZAD UNIVERSITY Savah Branch
3. Pasture Institute of Iran
4. Department of Biology, Faculty of Basic science, ISLAMIC AZAD UNIVERSITY Savah Branch
5. Pasture Institute of Iran

Background and Aim: BCG vaccine contains bacillus Mycobacterium bovis BCG strain 1173P2. The amount of this in BCG vaccine is about $1.5-6 \times 10^6$ cfu / mg. Important indicator is thermal stability of the vaccine (HST). The ratio of the mass of the live vaccine after 28 days of incubation at 37°C to live mass vaccination after 28 days of storage at 5°C shall not be less than 20% or the ratio should not be less than 0.3×10^6 cfu / mg. Heat index is the indicator for vaccine uniform production conditions. Now HST vaccine is variable and generally at zero.

Methods: The aim of this study is to evaluate different factors affecting HST and going to improve it. In this regard, the impact of culture medium for bacteria, bacterial incubation time (5 and 9 days) before harvesting conditions, lyophilized bacteria vaccine in the final stages (three different conditions) and The final formulation of the bulk of vaccine prior to lyophilization (addition of moist absorbent material to final bulk of vaccine) was examined on the HST.

Results: The results showed that only a formulation change is effective for improvement of HST. Moist absorbent material such as lactose, dextran and glucose in concentration of less than 1%, increased thermal resistance compared with the vaccines without this substance (HST = 0).

Conclusion: In the best condition HST = 0.75 was considered a great success. Other quality control tests of new vaccine (with different formulations) also yielded good results.

Keywords:: BCG vaccine, HST, Mycobacterium bovis

P934 - 87: PARATUBERCULOSIS IN THE ISLAMIC REPUBLIC OF IRAN

Masoud Hassani¹

1. Graduated from the Faculty of Veterinary medicine, Tehran University, Iran

Background and Aim: This article attempts to review the epidemiological status of paratuberculosis in Islamic republic of Iran.

Methods: Literature was obtained by searching various databases including PubMed, Google scholar, SID, MAGIRAN and library searching.

Results: *Mycobacterium avium* subspecies paratuberculosis (*M. paratuberculosis*) is an organism causes paratuberculosis or Johne's disease, an intestinal granulomatous in most often among domestic and wild ruminants and possibly human with a global distribution. The disease was first recognized in 1960, which is now endemic in the entire country. Paratuberculosis has been found in cattle, sheep, goats, camels, buffaloes and wildlife in Iran. The prevalence of paratuberculosis is different between species but estimated 4.1-12% infection rate in cattle by faecal culture as the gold-standard test.

Conclusion: In Iran, the current strategy for the control of paratuberculosis is voluntary by herd owners but a well-designed program by the quality and organization of the veterinary service is required to control the disease.

Keywords: Iran, Paratuberculosis, ruminants

**P935 - 159: EXTRACTION AND BIOLOGICAL EVALUATION OF MYCOBACTERIUM
KANSASII MEMBRANE VESICLES**

Zahra Hoseini Tavassol¹, Farzam Vaziri², Mohammad Kamran Sarkandi³, Morteza Ghazanfari⁴, Ava Behrouzi⁵, Morteza Masoumi⁶, Seyyed Davar Siadat⁷

1. Department of Biology, Faculty of Basic Science, Science and Research Branch Islamic Azad University, Tehran, IR Iran
2. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, IR Iran
3. Department of Biology, Faculty of Basic Science, Science and Research Branch Islamic Azad University, Tehran, IR Iran
4. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, IR Iran
5. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, IR Iran
6. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, IR Iran
7. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, IR Iran

Background and Aim: *Mycobacterium kansasii* is a bacterium in the Nontuberculous Mycobacteria (NTM) family that is generally the second most common cause of NTM infections. Like many microorganisms, *Mycobacterium kansasii* naturally release Membrane Vesicles (MVs) in a variety of growth mediums with diverse biological roles that probably made MVs one of the bacterial evolution factors. Also MVs can be considered as a non-classical secretory system. Interaction with environment and role in microbial physiology and pathogenesis are the available features of MVs. The aim of this study was the extraction and biological evaluation of *Mycobacterium kansasii* MVs.

Methods: Culturation of *Mycobacterium kansasii* have been done in Lowenstein-Jensen and 7H9 Medium. The MVs extraction have been done by density gradient ultra-centrifugation (Claassen's modified method). Biological evaluation of MVs have been performed by Nanodrop technique, Bradford protein assay, SDS-PAGE and electron microscopy. Safety test have been evaluated by LAL test.

Results: Nanodrop technique and the Bradford protein assay revealed the extracted protein concentration about 1.4 mg/ml. SDS-PAGE result showed more than five strong protein bands (between 60-180 kDa). The intactness of vesicles have been checked with electron microscope that we could see the configuration of MVs with diameter of 200-300 nm. The amount of lipopolysaccharide existing in MVs was in the usage limit range of biological products.

Conclusion: In this study, MVs were prepared in high quality composition and the conformational structure of MVs have been intactness throughout the extraction procedure. Extracted MVs have early sufficient efficiency property as a vaccine candidate. Features such as safety, stability, and having required antigens.

Keywords: Nontuberculous Mycobacteria, *Mycobacterium kansasii*, membrane Vesicle

P936 - 167: GENETIC LINEAGES OF MYCOBACTERIUM TUBERCULOSIS ISOLATES IN ISFAHAN, IRAN

Fatemeh Riyahi zaniani¹, Bahram Nasr Esfahani², Sharareh Moghim³

1. Department of Microbiology, Faculty of Medicine, Isfahan University of Medical Sciences
2. Department of Microbiology, Faculty of Medicine, Isfahan University of Medical Sciences
3. Department of Microbiology, Faculty of Medicine, Isfahan University of Medical Sciences

Background and Aim: In this study we aimed to identify the genetic lineages of Mycobacterium tuberculosis isolates in Isfahan via the mycobacterial interspersed repetitive-unit-variable number tandem repeat typing method based on 15 loci.

Methods: Forty nine M. tuberculosis isolates were collected between 2013 and 2015 from Tuberculosis patients in Mollahadi Sabzevari Tuberculosis Center in Isfahan. All isolates were typed by 15-locus MIRU-VNTR typing.

Results: The highest percentage of isolates, 44.89% (22/49), belonged to the Euro-American lineage, while the frequency of the East-African-Indian, East-Asian and Indo-Oceanic lineages were 28.57% (14/49), 24.4% (12/49) and 2.04% (1/49) respectively. Among the 22 isolates of the Euro-American lineage, those belonging to the NEW-1 sub-lineage was most prevalent (24.4%). Approximately, the same proportion of isolates belonging to the Delhi/CAS, Beijing and NEW-1 sub-lineages were identified in Iranian and Afghan immigrant patients. The Delhi/CAS and Beijing sub-lineage isolates were prevalent among patients who had been previously treated for TB. Results showed that all of the 49 MIRU-VNTR patterns were unique and the clustering rate of the 15-locus MIRU-VNTR was 0.0 (minimum recent transmission).

Conclusion: The results of this study show that the lineages of M. tuberculosis isolates in Isfahan are similar to those reported in the Eastern Mediterranean region (indicative of the epidemiological relationship between the countries in the region). The low clustering rate in our results reveals that transmission of tuberculosis in Isfahan is, in most cases, a reactivation of previous tuberculosis infection and the role of recently transmitted disease is minor.

Keywords: Mycobacterium tuberculosis, mycobacterial interspersed repetitive unit-variable number tandem repeat, typing

**P937 - 174: DEVELOPMENT OF A CULTURE-COLORIMETRIC METHOD FOR RAPID
DETERMINATION OF CFU OF MYCOBACTERIUM BOVIS B.C.G**

Fatemeh Jahanbakhsh sefidi¹, Fatemeh Jahanbakhsh sefidi- Zahra Jalali², S.Mehdi Hassanzadeh³,
Maryam Shahali⁴, Parvaneh Keshavarzi⁵, Tayebah Seifi⁶, Samira Khodamrezaei⁷, Fatemeh zahedi⁸,
Robab Mehralizadeh⁹, Zahra Barghi¹⁰

1. -
2. QC lab, Research & Production Complex of Pasteur Institute of Iran
3. Production unit, Research and Production Complex of Pasteur Institute of Iran
4. QC lab, Research & Production Complex of Pasteur Institute of Iran
5. QC lab, Research & Production Complex of Pasteur Institute of Iran
6. QC lab, Research & Production Complex of Pasteur Institute of Iran
7. QC lab, Research & Production Complex of Pasteur Institute of Iran
8. QC lab, Research & Production Complex of Pasteur Institute of Iran
9. QC lab, Research & Production Complex of Pasteur Institute of Iran
10. QC lab, Research & Production Complex of Pasteur Institute of Iran

Background and Aim: Tuberculosis (TB) remains a major public health problem around the world. The best way to prevent infection of progressive TB is vaccination by BCG vaccine. The estimation of vaccine potency is based on number of viable particles. The current method recommended by WHO is performed by cultivation on solid medium (Lowenstein-Jensen medium). This method takes 35 days, and may give variable results. Preliminary studies on performing a tetrazolium salt test has been developed and evaluated as a potential additional or replacement method for determination of BCG viability.

Methods: The tetrazolium salt (XTT) used as alternative substrate in the assay gave more rapid and reproducible result than the conventional viable count. The XTT assay was effective for viability estimation of suspensions prepared from several BCG vaccine batches covering a range of viable units. The method is easily performed and takes between 24 and 48 hours to estimate and analyze viable cells content compared with 35 day's for the conventional method. We also modified the composition of culture media (LWJ), and solvent of vaccine (diluted Sauton) to increase the recovering of BCG bacilli. Tween 80, FBS, and PG had the most significant effect to reach this aim.

Results: Results were accurate and reproducible, thus we suggest working more on this test to make it as an alternative or main test for counting and potency of BCG vaccine.

Conclusion: We modified a new method base on culturing and reduction assay "XTT-Culture" to improve counting the real number of BCG unit in the BCG vaccine.

Keywords: BCG vaccine , Lowenstein-Jensen medium, Tetrazolium salt (XTT)

**P938 - 226: BIAS IN DETECTION OF MYCOBACTERIUM TUBERCULOSIS POLYCLONAL
INFECTION**

Ghazaleh Farmanfarmaei¹, Mansour Kargarpour Kamakoli², HamidReza Sadegh³, Morteza Masoumi⁴,
Farid Abdolrahimi⁵, Abolfazl Fateh⁶, Nayereh Ebrahimzadeh⁷, Gholamreza Javadi⁸, Farzam Vaziri*⁹,
Seyed Davar Siadat¹⁰

1. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran
3. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran
4. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
5. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
6. 1. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran 2. Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
7. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
8. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran
9. 1. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran 2. Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
10. 1. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran 2. Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran

Background and Aim: The application of genotyping tools has unveiled that infection by Mycobacterium tuberculosis (MTB) can be polyclonal. Genotyping methods is generally carried out on cultures. However, there is a paucity of data which shows the differences in detecting mixed genotypes between direct genotyping on clinical samples and cultures.

Methods: The DNA extracted from the thirty-eight clinical samples and their respective cultures was genotyped using 24 loci mycobacterial interspersed repetitive unit-variable number tandem repeat analysis (MIRU-VNTR) to detect the mixed infection.

Results: According to 24 loci MIRU-VNTR analysis, 21/38 of the clinical samples were infected with multiple strain of M. tuberculosis and the estimated rate of mixed infection was 55.3%. On the other hand, the rate of the poly clonal infection in their respective cultures was 3/38(7.8%).

Conclusion: In conclusion, our comparative study demonstrated that based on the studied samples (clinical specimen or culture) detection of polyclonal M. tuberculosis infection can be significantly different. The results of our comparative study showed that clonal composition changed significantly ($P=0.001$) after culture.

Keywords: 24 loci MIRU-VNTR; comparative study; Mycobacterium tuberculosis; polyclonal infection

**P939 - 265: ISOLATION & IDENTIFICATION OF MYCOBACTERIUM TUBERCULOSIS
COMPLEX BACTERIA FROM TUBERCULIN POSITIVE CATTLE AND RODENTS FROM
INFECTED CATTLE FARMS IN SEMNAN PROVINCE**

Mohammad Rafiee Barzoki¹, Nader Mosavari², Rohollah Keshavarz³, Hasan Hashemzadeh⁴

1. Iran, Karaj, Razi Vaccine and Serum Research Institute
2. Iran, Karaj, Razi Vaccine and Serum Research Institute
3. Iran, Karaj, Razi Vaccine and Serum Research Institute
4. Iran, Semnan, Semnan Province Veterinary Office

Background and Aim: Bovine tuberculosis (bT.B) is an infectious disease of cattle caused by *Mycobacterium bovis*, a member of the *Mycobacterium tuberculosis* complex. This chronic disease also affects a wide range of other domestic and wildlife animals and may also cause disease in humans. It is very important to control and prevent the epidemic among human and animals because of zoonotic identity of the pathogen and several cattle flocks in suburb of cities. And it must be done better through more active surveillance.

Methods: 56 samples were collected lymph node positive T.B cases. All samples were referred to laboratory, then cultured in specific Lowenstein-Jensen slant media at 37 ° C for at least 8 weeks.

Results: After at least 8 weeks incubation (at 37°C) DNA was extracted from 17 isolates of 56 lymph nodes to identify the isolates belonging to the *Mycobacterium tuberculosis* complex, by using PCR detection of insertion sequence 6110 (IS6110).. Based on obtained results, 17 isolates of reactor cattle were confirmed as *Mycobacterium bovis*.

Conclusion: The prevalence of *M. bovis* in the human population as an important component of the health of the countries used in the show. To eradicate this disease eradication program should not be limited to industrial and semi-industrial livestock, domestic animals as reservoirs of disease transmission to humans and other animals considered.

Keywords: *Mycobacterium tuberculosis*, Semnan, Cattle

P940 - 346: COMPARISON OF DNA EXTRACTION METHODS FOR DETECTION OF NON-TUBERCULOSIS MYCOBACTERIA BY REAL-TIME PCR

Samira Mohammadi¹, Bahram Nasr Esfahani², Sharareh Moghim³, Hossein Mirhendi⁴, Fatemeh Riyahi Zaniani⁵, Hajieh Ghasemian Safaei⁶, Hossein Fazeli⁷, Mahshid Salehi⁸

1. Department of Microbiology, Faculty of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
2. Department of Microbiology, Faculty of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
3. Department of Microbiology, Faculty of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
4. Department of Medical Parasitology and Mycology, Faculty of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
5. Department of Microbiology, Faculty of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
6. Department of Microbiology, Faculty of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
7. Department of Microbiology, Faculty of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
8. Mollahadi Sabzevari Tuberculosis Center, Isfahan, Iran

Background and Aim: The accurate identification of Mycobacteria isolates is important and it would help to procure the best plan for its treatment. Identification of mycobacteria isolates by conventional methods including biochemical tests, growth rates, colony pigmentation, and presence of acid-fast bacilli is widely used but these methods are time-consuming, labor-intensive, and may sometimes remain inconclusive.

Methods: In order to compare six methods of DNA extraction namely, CTAB, FTA® elute card, Chelex 100, Chelex+ Nonidet, Boiling and Phenol-chloroform, DNA was extracted from NTM culture in different dilutions. The quantity and quality of the DNA extracted via these methods were determined using UV-photometer and Real-time PCR of 16SrRNA. Results of Real-time PCR were analyzed with Ct and melting curve.

Results: Results and Ct analysis showed that Chelex, FTA® elute card and boiling protocols followed by extraction of culture were the most successful extraction protocols in comparison with the others methods.

Conclusion: The major goal in this study was to find DNA extraction protocol that was rapid, simple method and labor intensity beside quantity and quality for the extraction of DNA from mycobacteria. Our results indicate that use of Chelex, FTA® elute card and boiling in terms of time, cost and labor intensity were more appropriate compared to other techniques. We hope that these methods will be used to extract mycobacteria DNA from tissue and sputum.

Keywords: Mycobacteria, Real-Time PCR, DNA extraction methods

P941 - 374: MOLECULAR ANALYSIS OF ETHAMBUTOL RESISTANT M. TUBERCULOSIS STRAINS IN IRAN

NARGES SHAHBAZI¹, Saeed Zaker Bostanabad², Abdolrazagh Hashemi Shahraki³

1. Biology and Microbiology Department, Science Faculty, Islamic Azad University, Research and Science branch, Tehran-Iran
2. Biology and Microbiology Department, Science Faculty, Islamic Azad University, Parand branch, Tehran-Iran
3. Department of Epidemiology, Pasture Institute of Iran

Background and Aim: The aim of this study was to determine the occurrence of embB and embC mutations in EMB-resistant M. tuberculosis strains from different geographical location.

Methods: In total 110 clinical isolates of M. tuberculosis were recovered from three provinces in Iran, Tehran, Isfahan and Khuzestan from January 2014 to January 2016. Drug susceptibility to EMB was determined by conventional proportional method for all of the isolates. From each EMB-resistant isolate, embB and embC gene was amplified and sequenced to detect their point mutations.

Results: Out of 110 clinical isolates, 41 isolates (37.5%) were EMB-resistant by conventional proportional method. Out of 41 EMB-resistant isolates, 34 isolates (83%) had point mutation while 7 isolates (17%) shown wild type embB gene signature. Mutation at codon 306 was dominant (17 isolates, 50%). The second most common was mutation at codon 406 (11 isolates, 32%). Out of 69 EMB-susceptible isolates, 6 isolates (9%) had point mutation in embB gene. In total 8 isolates (19.5%) had embC gene mutations among EMB-resistant isolates.

Conclusion: Although monitoring of point mutation at position 306 of embB gene is a best strategy to detecting EMB resistance, but the significance of other alteration through embB gene should be considered.

Keywords: M. tuberculosis, Iran, EMB-resistant, embB, embC

**P942 - 503: LATENT TUBERCULOSIS INFECTION IN HEALTH CARE WORKERS) HCWS(
IN IRAN- REVIEW ARTICLE**

Davood Mansury¹, Mahdis Ghavidel ², Adel Najafi³, Kiarash Ghazvini⁴

1. PhD student, Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
2. PhD student, Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
3. PhD student, Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
4. Associate Professor, Antimicrobial Resistance Research Center, Buali Research Institute, Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Background and Aim: The members of Mycobacterium tuberculosis complex (MTBC) are known as causative agents of human tuberculosis. In general, there are two types of tuberculosis include, latent infection and active TB. Latent tuberculosis infection (LTBI) means a patient is infected with Mycobacterium tuberculosis but the patient does not have active tuberculosis, clinical symptoms and radiological findings. Since health-care workers (HCWs) are a group that cause of increased risk of LTBI; The aim of this study was to Investigate latent tuberculosis infection in HCWs.

Methods: In this review of the literature related to LTBI in HCWs in Iran from Scientific databases such as, SID, Google Scholar, Scopus, PubMed, Chemical abstract, EBSCO, MedLib, ISI, ISC, Medex Iran were searched and Data analysis was performed for Qualitative.

Results: We identified 22 articles and extracted data on prevalence and risk factors for LTBI among HCWs. The prevalence of LTBI among HCWs were reported as 18% in Khorram abad up to 60.3% in Zahedan. the risk factor acquisition of TB infection was associated with certain hospital wards (lung disease unit, laboratory, etc) , Increasing age and duration of employment.

Conclusion: Briefly, our review indicates that TB is a significant problem among HCWs in Iran. Infection control and personal protective measures with training programs to patients and HCW is required to reduce the occupational risk of TB.

Keywords: Latent tuberculosis (LTBI), health care workers) HCWs (Mycobacterium tuberculosis, Infection

P943 - 566: AN INVESTIGATION OF EPIDEMIOLOGICAL STATUS OF TUBERCULAR (TB) PATIENTS IN ARDABIL PROVINCE, IRAN, IN 2015

Seyyedeh negar Modarres sadrani¹, Dr. Sadegh Hazrati², Dr. Naghmeh Khaligh³, Dariush Emdadi⁴

1. M.Sc in Biochemistry, Ardabil Province Health Center, Ardabil University of Medical Sciences, Ardabil, Iran
2. Occupational Health PhD, Ardabil Province Health Center, Ardabil University of Medical Sciences, Ardabil, Iran
3. M.D, Ardabil province Health Center, Ardabil, Iran
4. M.Sc in entomology Ardabil Province Health Center, Ardabil University of Medical Sciences, Ardabil, Iran

Background and Aim: Nowadays, tuberculosis (TB) is one of the biggest challenges for public health.

Methods: This analytical retrospective study was performed on data recorded from TB patients referred to health centers of the province in 2015. Data were extracted from the software recording of TB patient information of the cities of the province.

Results: 125 patients were diagnosed for tuberculosis in Ardabil province in 2015. The average incidence rate of TB patients was 9.3 and patients with sputum smear-positive pulmonary TB was three per 100,000 people. The patients are suffering from sputum positive pulmonary TB (31.2%), sputum negative pulmonary TB (15.2%), extrapulmonary TB (48.8%), recurrent TB (2.4%), MDR-TB (1.6%) and other types of TB (0.8%). Over the year, 66% urban and 34% rural people. Of the total TB patients, 42% were in the age group of 15 to 35 years and 46% in the age group of 15 to 35 years

Conclusion: Considering the high prevalence of the disease in younger age groups, it is recommended to strengthen the screening and case finding, train and inform the group.

Keywords: Tuberculosis (TB), Tubercular, DOTS, Sputum Positive, Ardabil, Iran

**P944 - 618: DETERMINATION OF POLYMICROBIAL INFECTIONS AND
HETERORESISTANCE IN MYCOBACTERIUM TUBERCULOSIS**

Mansour Kargarpour Kamakoli¹, Hamidreza Sadegh², Ghazaleh Farmanfarmaei³, Morteza Masoumi⁴,
Farid Abdolrahimi⁵, Abolfazl Fateh⁶, Nayereh Ebrahimzadeh⁷, Gholamreza Javadi⁸, Farzam Vaziri^{*9},
Seyed Davar Siadat¹⁰

1. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran
3. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran
4. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
5. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
6. 1. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran 2. Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
7. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
8. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran
9. 1. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran 2. Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
10. 1. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran 2. Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Mixed (poly clonal) infections of Mycobacterium tuberculosis make diagnosis, treatment, and control of tuberculosis (TB) more difficult. This study was aimed to evaluate the relationship between mixed infections and antibiotic resistance.

Methods: One hundred and six clinical samples from TB patients referring to department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran were selected for this study. Genotyping based on 24 loci MIRU-VNTR procedure was performed directly on clinical samples. For mixed samples, Drug Susceptibility Test (DST) was done on three single colonies according to the WHO guidelines.

Results: In the studied samples, 52.83% showed mixed infection. Among loci used in MIRU-VNTR, loci of 2401, 577, 154 and 2996 were more successful in identification of mixed infections. In the mixed samples, 8.93% showed different resistant patterns.

Conclusion: Genotype based on MIRU-VNTR procedure is fast and has strong differentiation for genotyping and determining the mixed infections. The data from DST on different colonies from individual patients will help us in the treatment of TB patients. This study will be continued to detect polyclonal and heteroresistance infections on more TB patients.

Keywords: Tuberculosis; heteroresistance; MIRU-VNTR; mixed infection

P945 - 721: BIOINFORMATIC CHARACTERIZATION, CLONING AND EXPRESSION OF MYCOBACTERIUM TUBERCULOSIS RPF E PROTEIN IN E. COLI

Mitra Ashayeri-panah¹, Mohammad Mehdi Feizabadi², Fereshteh Eftekhari³, Bahram Kazemi⁴, Joan Joseph⁵

1. Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, G.C., Tehran, Iran.
2. Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran
3. Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, G.C., Tehran, Iran.
4. Department of Biotechnology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
5. AIDS Research Group, Hospital Clinic/HIVACAT, School of Medicine, University of Barcelona, Barcelona, Catalonia, Spain

Background and Aim: Resuscitation promoting factor E (RpfE) is one of the five Rpf proteins encoded by *Mycobacterium tuberculosis*. These are induced during reactivation of dormant tubercle bacilli occurring upon suppression of the host's immune protection. RpfE is antigenic, immunogenic and probably secreted which makes it a potential tuberculosis vaccine candidate.

Methods: T- and B-cell epitopes, antigenicity, allergenic potential, signal peptide cleavage site, twin-arginine translocation (Tat) motif, subcellular localization, number of transmembrane helices and some other bioinformatic characteristics of RpfE were predicted. The coding sequence of *rpfE* gene was chemically synthesized, cloned as a BamHI-HindIII fragment in pET-23a(+) and its sequence was verified. The polyhistidine-tagged protein was expressed in *E. coli* strain BL21 (DE3) and analyzed by SDS-PAGE. The protein band was identified by western blot using anti-His tag antibodies and whole serum from tuberculosis patients.

Results: Bioinformatic analyses predict RpfE as a promising vaccine candidate. The cloned recombinant His-tagged RpfE was expressed in *E. coli*. Molecular weight of the protein was between 24 and 31 KDa using SDS-PAGE. Western blot analysis confirmed the expression of the His-tagged protein and the same-sized band was detected by the serum from tuberculosis patients.

Conclusion: RpfE from *M. tuberculosis* was expressed in *E. coli*. This recombinant protein has the potential to be used for designing a multi-stage and/or post-exposure vaccine against tuberculosis.

Keywords: *Mycobacterium tuberculosis*, resuscitation promoting factor E, expression, *E. coli*

P946 - 722: BIOINFORMATIC CHARACTERIZATION, CLONING AND EXPRESSION OF MYCOBACTERIUM TUBERCULOSIS RV1733C PROTEIN IN E. COLI

Mitra Ashayeri-panah¹, Mohammad Mehdi Feizabadi², Fereshteh Eftekhari³, Bahram Kazemi⁴, Joan Joseph⁵

1. Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, G.C., Tehran, Iran.
2. Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran.
3. Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, G.C., Tehran, Iran.
4. Department of Biotechnology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
5. AIDS Research Group, Hospital Clinic/HIVACAT, School of Medicine, University of Barcelona, Barcelona, Catalonia, Spain

Background and Aim: Due to huge population latently infected with Mycobacterium tuberculosis worldwide, vaccines that would prevent the establishment of latent tuberculosis will make a dramatic impact on the global tuberculosis burden. It is proposed that the antigens of M. tuberculosis which are preferentially expressed during latent infection, may be promising candidates for being incorporated into such vaccines. Rv1733c is a latency antigen from M. tuberculosis with antigenic and immunogenic properties in human and animal studies.

Methods: Various bioinformatic characteristics of Rv1733c were predicted. The rv1733c gene from M. tuberculosis H37Rv was chemically synthesized and cloned into pET-23a (+). Sequencing was performed to confirm the identity of the cloned DNA fragment and the recombinant plasmid was transformed into E. coli strain BL21 (DE3). The recombinant protein expression was confirmed using SDS-PAGE followed by western blotting using monoclonal anti-penta-His antibody as well as tuberculosis patients' serum.

Results: Bioinformatic analyses predict Rv1733c as a probable integral-membrane protein with promiscuous T-cell and B-cell epitopes which can be a pertinent vaccine candidate. The recombinant His-tagged Rv1733c was expressed in E. coli. Molecular weight of the protein was between 17 and 24 KDa on SDS-PAGE. Anti-penta His antibody and serum from tuberculosis patients detected bands of the same size in western blot analyses.

Conclusion: The recombinant Rv1733c protein from M. tuberculosis expressed in this research can be considered a promising subunit vaccine or booster in heterologous prime-boost vaccination against tuberculosis.

Keywords: Mycobacterium tuberculosis, latency antigen, Rv1733c, expression, E. coli

P947 - 724: CONSTRUCTION OF A RECOMBINANT BCG OVER-EXPRESSING LATENCY-ASSOCIATED ANTIGEN RV1733C

Mitra Ashayeri-panah¹, Mohammad Mehdi Feizabadi², Fereshteh Eftekhari³, Bahram Kazemi⁴, Joan Joseph⁵

1. Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, G.C., Tehran, Iran.
2. Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran.
3. Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, G.C., Tehran, Iran.
4. Department of Biotechnology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
5. AIDS Research Group, Hospital Clinic/HIVACAT, School of Medicine, University of Barcelona, Barcelona, Catalonia, Spain

Background and Aim: It has been reported that immunization with *Mycobacterium bovis* Bacille Calmette–Guerin (BCG) did not induce adequate Th1 responses to the latency antigen, Rv1733c. Over-expression of this antigen by BCG may increase its immunogenicity and protective efficacy.

Methods: A systematic review and bioinformatic analyses were carried out addressing antigenicity, immunogenicity and protective efficacy of latency antigens from *M. tuberculosis*. Rv1733c was chosen for over-expression in BCG. pJH223 *E. coli*/mycobacterial shuttle vector was used to integrate rv1733c plus HA-tag into BCGΔlys Pasteur strain genome. This shuttle vector employs a lysine auxotrophic-complementation system for plasmid selection. The recombinant strains were analyzed genetically and phenotypically.

Results: Integration of the recombinant plasmid into BCG genome was confirmed by PCR using forward primers on the insert and reverse primers on BCG genome. PCR experiments using specific primers for rv1733c-HA revealed products with the expected size of 705 bp for positive clones. The genetically positive clones were also positive for dot-blotting and western blotting using anti-HA monoclonal antibody while BCG wildtype and BCGΔlys transformed with empty pJH223 were negative. The western blots detected a band with the size between 24 and 31 KDa for the positive clones.

Conclusion: A recombinant BCG over-expressing latency antigen Rv1733c was successfully constructed and characterized in the genomic and proteomic scales. It can be useful for immunogenicity testing in animal models.

Keywords: Recombinant BCG, latency antigen, Rv1733c, over-expression

**P948 - 727: CONSTRUCTION OF A RECOMBINANT BCG OVER-EXPRESSING
RESUSCITATION-PROMOTING FACTOR E**

Mitra Ashayeri-panah¹, Mohammad Mehdi Feizabadi², Fereshteh Eftekhari³, Bahram Kazemi⁴, Joan Joseph⁵

1. Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, G.C., Tehran, Iran.
2. Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran.
3. Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, G.C., Tehran, Iran.
4. Department of Biotechnology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
5. AIDS Research Group, Hospital Clinic/HIVACAT, School of Medicine, University of Barcelona, Barcelona, Catalonia, Spain

Background and Aim: Mycobacterium bovis Bacille Calmette–Guerin (BCG) and most new generation tuberculosis vaccines have been designed as prophylactics which are unable to solve the global problem of latent tuberculosis. It is proposed that vaccines incorporating reactivation antigens of M. tuberculosis can be used as multi-stage and/or post exposure vaccines aiming to prevent reactivation of latent infection.

Methods: The coding sequence of rpfE ended with V5-tag was cloned into the HindIII site of pJH223 E. coli/mycobacterial shuttle vector. This vector is integrative and contains the needed sequence for expression of lysA gene in Mycobacteria. BCG Δ lys Pasteur strain was transformed with the recombinant plasmid. Integration of the fragment into the bacterial genome was detected by PCR. Expression of the recombinant protein was shown by dot-blotting and western blotting using anti-V5 tag monoclonal antibody.

Results: PCR results confirmed the integration of the recombinant construct into the BCG genome. Dot-blotting results revealed positive recombinant clones but wildtype BCG and BCG Δ lys transformed with empty pJH223 were negative. Western blots detected a band with a molecular size between 17 and 24 KDa for positive clones but not for wildtype BCG and BCG Δ lys:pJH223 without the construct.

Conclusion: The recombinant BCG over-expressing RpfE may have the potential to be used as a multi-stage vaccine to test its immunogenicity in animal models.

Keywords: Recombinant BCG, reactivation antigen, resuscitation-promoting factor E, over-expression

**P949 - 775: COMPARISON OF DR AND PGRS PROBES IN RFLP TECHNIQUE TO
DIFFERENTIATION OF MYCOBACTERIUM BOVIS STRAINS IN QOM PROVINCE**

Sina Nimrooz¹, Taghi Zahraei Salehi², Nader mosaveri³

1. Department Microbiology, Saveh Branch, Islamic Azad university, Saveh, IRAN
2. Department of Microbiology and Immunology, University of Tehran, Tehran, IRAN
3. TB Department, Razi Vaccine and Serum Research Institute, Karaj, IRAN

Background and Aim: Bovine tuberculosis is one of the important zoonotic disease in the world. The main agent of disease is *Mycobacterium bovis*. Control and eradication scheme of bovine tuberculosis held on 1973 by test and slaughter program and incidence rate decreased from 5% to 0.14%. Aim of this study was isolation, identification and differentiation of *Mycobacterial* isolates of tuberculin positive cattle from Qom province by RFLP with DR and PGRS probes.

Methods: Out of 30 lymph nodes which submitted to reference "Animal tuberculosis laboratory of Razi Vaccine & Serum Research Institute" since June 2013 to January 2014, 21 *Mycobacterium*, isolated by culture, and identified as *Mycobacterium tuberculosis* complex by PCR-IS6110. Then differentiation of strains performed by DR-RFLP and PGRS-RFLP.

Results: Three- and four different patterns obtained by PvuII-PGRS and PvuII-DR, RFLP respectively. BCG like pattern was the most frequent pattern in this province.

Conclusion: This research is a part of "National Control and Eradication Programme" for "Bovine Tuberculosis" in IRAN. According to the results which obtained from patterns, PvuII-PGRS made a better differentiation between the strains than PvuII-DR by RFLP technique.

Keywords: TB, PGRS, DR, RFLP, IRAN, *Mycobacterium bovis*

**P950 - 792: MOLECULAR IDENTIFICATION OF MYCOBACTERIUM TUBERCULOSIS
COMPLEX BY RD-TYPING AND PCR-RFLP METHOD**

noosh afarin Torabi¹, nader mosavari², razie nazari³

1. department of microbiology,qom branch,islamic azad university,qom,iran
2. Razi Vaccine and Serum Research Institute Karaj, Iran
3. department of microbiology,qom branch,islamic azad universiy,qom,iran

Background and Aim: Tuberculosis is still considered one of the most important zoonotic diseases and the second cause of infectious death that causes human casualties. Successful treatment of diseases related to the rapid identification of appropriate treatment. The main purpose of this study was to set up and identify of Mycobacterium tuberculosis complex isolates in FARS province patients by RD typing.

Methods: In this study, DNA from 50 isolates and two standard strains of M. tb and M.bovis as standard were extracted by boiling method. To identification of isolates 16srRNA, IS6110 and RD typing PCRs performed respectively. Then PCR-RFLP technique for oxyR pseudogene performed for confirmation of results.

Results:All isolates showed 543, 245, 146, 172, 235 and 369 bp bands in 16srRNA, IS6110, RD1, RD4, RD9 and RD 12 PCRs respectively, so all isolates were identified as Mycobacterium tuberculosis and PCR-RFLP of oxyR pseudogene confirmed the results

Conclusion:In this research all isolate which submitted from Fars province were Mycobacterium tuberculosis. Absence of other Mycobacteria like as Mycobacterium bovis represents as a good hygiene and consumption of pasteurized milk in this province or may be for proper control and eradication scheme for bovine tuberculosis. In the other hand, biochemical identification of mycobacteria is a time-consuming and dangerous method for laboratory staff, but RD typing is a high precision, fast, and low risk technique.

Keywords:Mycobacterium tuberculosis complex, RD-Typing, PCR 16srRNA, IS6110

**P951 - 861: EVALUATION THE OCCURRENCE AND THE DRUG-RESISTANCE OF
PULMONARY TUBERCULOSIS IN THE SISTAN REGION DURING1389-1394(2010-2016)**

Reza Shirazinia¹, abolfazl panahi mishkar², zohreh khalili³, salia amini pooya⁴

1. student of Veterinary Medicine - Department of Basic Sciences, Faculty of Veterinary Medicine, University zabol,Iran,
2. human ecology MSc student,kerman university of medical science,kerman,iran
3. human ecology MSc student,kerman university of medical science,kerman,iran
4. Student of zabol University of Medical Sciences, Zabol, Iran

Background and Aim:purpose of the study was evaluating occurrence of pulmonary Tuberculosis and drug resistance in the city of Zabol and suburban in the years89-93(march 21, 2010-march,19 2016)

Methods:: the data was provided by the Center for Combating Tuberculosis Zabol University of Medical Sciences and Data analysis was using spss software version14.

Results:incidence of smear positive patients in this region for year89 was61.2and smear negative for this year was18.3and all tuberculosis rate for this year was97.7this values for the year90 were65,17,106 respectively this rate for year91 were63.4,17.8,100.9 respectively this values for92 were 54.1,10.6,81.8 respectively this values for93 were 45.2,17,79.8 respectively this values for 94 were 44.4,23.9and88.8 respectively.The usual ways to diagnose patients were: smear preparation, antibiogram, molecular ways and radiography imaging. Evaluation of the history of the patients shows majority of them did not have the history of connection with tuberculosis patients.Reported rate of drug resistance for year88 and earlier was2 cases,for the year 89 this value increased by 24 cases,In 90 it was11subjects,in91and92this value was0and this rate was2 casesfor93.

Conclusion:incidence of drug resistance in89to90shows a significant difference,A reduction of 90to93 years was significant, resulting from reduction of subjects from24 to11in90and finally to 0between91and92and2cases of drug resistance in 93.the rate of incidence between patients during this period did not show a significant difference.Evaluation of diagnostic ways shows smear preparation and radiography significantly are more appropriate ways to identify the patients in this region during this time

Keywords:pulmonary Tuberculosis;sistan;drug-resistant

**P952 - 919: THE DETECTION OF UNIQUE STRAIN OF TUBERCULOSIS DISCOVERED IN
QOM PROVINCE AND ADJACENT PROVINCES**

Sina Nimrooz¹, Taghi Zahraei Salehi², Nader mosaveri³

1. Department Microbiology, Saveh Branch, Islamic Azad university, Saveh, IRAN
2. Department of Microbiology and Immunology, University of Tehran, Tehran, IRAN
3. TB Department, Razi Vaccine and Serum Research Institute, Karaj, IRAN

Background and Aim: TB is an infectious disease caused by the bacterium MTB. Tuberculosis is one of the most important diseases in the world of recent century that has the ability to involve the organs of the body. Knowledge about epidemiology of bovine tuberculosis for rein and eradication of this disease is very important. The Aim of this study is to identify the strains that present in Qom province with adjacent provinces.

Methods: To achieve the objective used in the following the researchers of the recent 5 years in the provinces of Tehran, Arak, Karaj, Isfahan, Qom the RFLP-PVUII method which has been used in the related have been used published article has been used. For this purpose some keywords have been used for example: tuberculosis, Mycobacterium, RFLP, Iran, Tehran, Arak, Karaj, Isfahan and Qom.

Results: In five mentioned provinces four strains were detected that in all provinces have a Common BCG strain. Also a unique strain was found in Qom province.

Conclusion: This research is a part of "National Control and Eradication plan" for "Bovine Tuberculosis" in IRAN. According to the results which obtained from patterns, the mentioned detection strains in Iran will help to control and eradicate TB in the national cattle population.

Keywords: RFLP, Iran, Tehran, Arak, Karaj, Isfahan and Qom

**P953 - 963: ANTITUBERCULAR ACTIVITY AND CYTOTOXICITY EVALUATION OF
NOVEL 4-SUBSTITUTED IMIDAZOLYL-2,6-DIMETHYL-N3,N5-BISARYL-1,4-
DIHYDROPYRIDINE-3,5-DICARBOXAMIDES**

Mehdi Zandhaghighi¹, Farzin Hadizadeh², Zahra Meshkat³, Mohammad Derakhshan⁴, Saman
Soleimanpour⁵, Kiarash Ghazvini⁶

1. Antimicrobial Resistance Research Center & Department of Medical Bacteriology and Virology, Bu-Ali Research Institute & Ghaem University Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
2. Biotechnology Research Center, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran
3. Antimicrobial Resistance Research Center & Department of Medical Bacteriology and Virology, Bu-Ali Research Institute & Ghaem University Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
4. Antimicrobial Resistance Research Center & Department of Medical Bacteriology and Virology, Bu-Ali Research Institute & Ghaem University Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
5. Antimicrobial Resistance Research Center & Department of Medical Bacteriology and Virology, Bu-Ali Research Institute & Ghaem University Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
6. Antimicrobial Resistance Research Center & Department of Medical Bacteriology and Virology, Bu-Ali Research Institute & Ghaem University Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Background and Aim: Drug discovery studies in the field of antitubercular agents have been shown that various substitutions in the 1,4-dihydropyridine molecule can reduce calcium channel blocking activity but provide them some antitubercular properties, so these compounds can act as an effective substances in class of antimycobacterial agents.

Methods: Two newly synthesized dihydropyridine derivatives (F-27 and Cl-33) initially were screened for their in-vitro cytotoxicity (Inhibitory Concentration 50 -IC₅₀) against both normal (mouse spleen lymphocytes) and malignant cell lines (KG-1a, HeLa, RAJI) by the MTT (3-(4, 5-Dimethylthiazol-2-yl)-2, 5-diphenyltetrazolium bromide) assay (tetrazolium salts). MIC₉₀s and MBCs of the compounds were then measured against Mycobacterium tuberculosis (standard strain H37Rv) by a modified broth macro-dilution assay

Results: IC₅₀ of compounds was in the range of 91-186 mg/L (132.5±63.9, $p < 0.05$) and 75-180 mg/L (112.3±74.5, $p < 0.05$) for F-27 and Cl-33, respectively. Compound Cl-33 had MIC₉₀= 16 mg/L and selectivity index <10. Compound F-27 had an excellent feature which had MIC₉₀= 2 mg/L and selectivity index >45, and completely inhibited the growth of Mycobacterium tuberculosis H37Rv at concentration 8 mg/L (MBC= 8 mg/L).

Conclusion: Our compounds showed significantly less toxicity against the cell lines in comparison to the most similar substances. Compounds which have properties such as MIC₉₀ <6.25 mg/L and selectivity index ≥ 10 are interesting compounds as antitubercular agents; hence, we concluded that F-27 is a promising candidate for the development of new antitubercular agent. This research could implicate to introduce new, effective, and well-tolerated treatment for tuberculosis.



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Keywords: Antitubercular activity-cytotoxicity-dihydropyridine

**P954 - 1113: INVESTIGATION AND COMPARING OF EXTRAPULMONARY
MYCOBACTERIUM TUBERCULOSIS CASES (TB) BY TYPE OF SAMPLE IN 2012 AND 2013**

Masoomeh Taziki¹, Ali Akbar Rajablou², Ezat Allah Ghaemi³, Hamid Reza Kamali-Nia⁴, Maryam Shafipour⁵

1. MSc, tuberculosis reference laboratory of Golestan, Gorgan, Golestan, Iran.
2. MSc, head of the laboratory of Golestan Province, Gorgan, Golestan, Iran
3. PhD, Department of Microbiology, Faculty of Golestan University of Medical Sciences, Gorgan, Golestan, Iran.
4. MD, Head of the disease in Golestan Province, Gorgan, Golestan, Iran.
5. MSc, Department of Microbiology, Golestan University of Medical Sciences, Gorgan, Golestan, Iran.

Background and Aim:Recent studies show that about 35 to 40 percent of TB cases, are include extrapulmonary tuberculosis and tuberculosis of the lymph nodes, which is the most common form of extrapulmonary tuberculosis.Extrapulmonary tuberculosis can involve lymph nodes, kidney,intestine and ..., but most patients(90% to 95%) infected secretly.

Methods:From the total of 876 and 922suspected cases of extrapulmonary tuberculosis,who referred to health centers in Golestan province in 2013 and 2012 respectively,samples were isolated according their types and positive or negative smear,and growth or Lack of growth in Levin Stein Johnson medium.

Results:The present study showed that most of the extrapulmonary samples from the total of 876 cases in 2013 were BAL(463 cases, 85/52%),in which 398 cases had negative smear and culture, 41 cases had positive smear and culture,13 cases had positive smear and negative culture and 11 cases had negative smear and positive culture. After BAL,the most samples were urine(156 cases) and the lowest was belonged to stool(1 case).In 2012, from the total of 922 cases,most of the samples of extrapulmonary were BAL(509 cases, 2/55%) in which 441 cases had negative smear and culture,38 cases had positive smear and culture, 19 cases had positive smear and negative culture and 11 cases had negative smear and positive culture. After BAL,most of the samples were urine(164 cases) and the lowest were belonged to Menstruation and synovial fluid(3 cases for each).

Conclusion:With respect to relatively large number of extrapulmonary tuberculosis in two alternative years,more attention and extrapulmonary cases have utmost importance.

Keywords:Mycobacterium tuberculosis, extrapulmonary, BAL, Urine.

P955 - 1114: EVALUATION OF MULTIPLE DRUG-RESISTANT OF MYCOBACTERIUM TUBERCULOSIS (MDR) IN THE GOLESTAN, MAZANDARAN AND SEMNAN PROVINCE

Masoomeh Taziki¹, Ali Akbar Rajablou², Abdolmotallab Mazidi³, Ezat Allah Ghaemi⁴, Hamid Reza Kamali-Nia⁵

1. MSc, tuberculosis reference laboratory area of Golestan, Gorgan, Golestan, Iran.
2. MSc, Head of the Laboratory of Golestan Province, Gorgan, Golestan, Iran
3. MD, Head of city health center in Gorgan, Golestan, Iran.
4. Ph.D., Department of Microbiology, Faculty of Golestan University of Medical Sciences, Gorgan, Golestan, Iran.
5. MD, Head of the disease in Golestan Province, Gorgan, Golestan, Iran.

Background and Aim: Tuberculosis is an infectious disease caused by *M. tuberculosis*, and its fatality rate has declined, but due to increasing of incidence and prevalence of MDR-TB, it remains as a serious warning. MDR is defined as the least resistance to isoniazid and rifampin, which is the most effective drug recommended by the World Health Organization, and is used as a first-line anti TB treatment. Therefore, the main problem in the treatment of TB patients is their resistance to these drugs.

Methods: From the total patients who referred to diagnostic centers in Golestan (Gorgan and Gonbad), Mazandaran (Sari and Babol) and Semnan province (Shahrood and Semnan), 628 positive culture was observed. From these numbers, in order to study drug resistance through Antibigram, 179 samples were chosen, that 116 cases were belonged to Golestan province (Gorgan and Gonbad, 78 and 38 respectively), and 63 cases were belonged to outside of the province (Sari, Babol < Semnan and Shahrood, 45, 11, 4 and 3 respectively).

Results: From the total of 179 Antibigram cases, 7 samples were observed to be drug-resistance (3.91%). Most cases were in Golestan (5 cases, 79/2%), and there were only one case in Semnan and Mazandaran (55/0%). From these 7 cases, 2 samples were part of NTMs that were resistant to three drugs, isoniazid, rifampin and ethambutol. 3 cases were resistant to isoniazid (85/42%), 1 case was resistant to rifampin (28/14%), and 1 case was resistant to isoniazid, ethambutol and rifampin (28/14%).

Conclusion: According to conducted survey, the most cases which were drug-resistant to TB, were observed in Golestan province. Therefore, further investigation on Golestan province samples, and detection or treatment of MDR strains is recommended.

Keywords: Mycobacterium tuberculosis, MDR, Golestan, Semnan, Mazandaran.

P956 - 1182: EVALUATION OF THE RFLP TB/STR ASSAY FOR RAPID DETECTION OF STREPTOMYCIN RESISTANCE IN MYCOBACTERIUM TUBERCULOSIS

Sedique Karimi¹, Bahram Nasr Esfahani², Hossein Mirhendi³, Fateme Riahi⁴, Mahshid Salehi⁵

1. Msc student, Department of Microbiology, Isfahan University of Medical Sciences, Isfahan, Iran
2. Assistant, Department of Microbiology, Isfahan University of Medical Sciences, Isfahan, Iran
3. Assistant, Department of Mycology, Isfahan University of Medical Sciences, Isfahan, Iran
4. PHD student, Department of Microbiology, Isfahan University of Medical Sciences, Isfahan, Iran
5. Staff of Tuberculosis Center of Isfahan Region, Iran

Background and Aim: A total of 400 clinical specimens were collected from individuals with suspected TB by the Tuberculosis Center of Isfahan from which 55 Mycobacterium tuberculosis were isolated by conventional phenotypic methods.

Methods: The MIC of streptomycin for the isolates were determined using the proportion method. We investigated the effect of genetic alterations in the rpsL gene for these resistant isolates by Restriction fragment length polymorphism (RFLP) method.

Results: RFLP analysis showed mutations at codon 43 in 3 strains with point mutations in the same codon.

Conclusion: Our results suggest that RFLP analysis of the rpsL gene is useful for the rapid prediction of streptomycin resistant strains of M. tuberculosis.

Keywords: M. tuberculosis- Streptomycin resistance- RFLP

**P957 - 1184: SCREENING FOR GENETIC PATTERNS OF THE RPSL AND RRS GENES IN
CLINICAL ISOLATES OF MYCOBACTERIUM TUBERCULOSIS IN ISFAHAN, IRAN**

Sedique Karimi¹, Bahram Nasr Esfahani², Hossein Mirhendi³, Fateme Riahi⁴, Mahshid Salehi⁵

1. Msc student, Department of Microbiology, Isfahan University of Medical Sciences, Isfahan, Iran
2. Assistant, Department of Microbiology, Isfahan University of Medical Sciences, Isfahan, Iran
3. Assistant, Department of Mycology, Isfahan University of Medical Sciences, Isfahan, Iran
4. PHD student, Department of Microbiology, Isfahan University of Medical Sciences, Isfahan, Iran
5. Staff of Tuberculosis Center of Isfahan Region, Iran

Background and Aim: Drug-resistant tuberculosis is a major universal problem. Based on the knowledge of certain mutations occurring in the Mycobacterium tuberculosis genome, drug resistance can be detected early. The goal of this study was to determine the prevalence of the most common mutations associated with resistance to Streptomycin (STR) in Mycobacterium tuberculosis isolates in the Isfahan province, Iran, and to find a proper method for the rapid detection of drug-resistant Mycobacterium tuberculosis isolates

Methods: 400 clinical specimens were collected from individuals with suspected TB by the Tuberculosis Center of Isfahan. The MIC of STR for the specimens were determined using the proportion method with Loewenstein-Jensen (L.J) medium. The rpsL and rrs genes (the 530 loop) were analyzed by PCR sequencing for all STR-resistant isolates and for 5 STR-susceptible isolates randomly

Results: Mutations in the rpsL or rrs genes were detected in 60% of the STR-resistant M.tuberculosis isolates. Mutations in rpsL were observed in 4 isolates (40%) in codons 43 (K/R, n=3) and 88 (K/R, n=1). Mutations in rrs were observed in 2 isolates (20%), at nucleotides 514 (A C) and 517 (C T). Also, in the STR-susceptible isolates were founded no mutation in either genes.

Conclusion: The study highlights the usefulness of rpsL and rrs mutations as molecular markers for STR resistance in M.tuberculosis strains. However, the diversity and presence or absence of mutation suggest the possible circulation of a variety of strains and the role of additional mechanisms contributing to STR resistance in various geographical regions

Keywords: M.tuberculosis- Streptomycin resistance- PCR-sequencing

**P958 - 1192: MOLECULAR IDENTIFICATION OF MYCOBACTERIUM TUBERCULOSIS
COMPLEX BY RD-TYPING TECHNIQUE**

Seyedeh Zeinab Mirzaki¹, Nader Mosavari², Raziye Nazari³

1. Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran
2. Razi Vaccine and Serum Research Institute, Agricultural, Education and Extension Organization, Tehran, Iran
3. Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran

Background and Aim: Tuberculosis is one of the most common zoonotic infectious disease in the world. Identification of Mycobacterial isolates is essential for proper treatment of tuberculosis, so the aim of this research was identification of mycobacterial isolates of TB patients from Alborz Province by RD-Typing technique.

Methods: Fifty positive samples from tuberculosis patients of Alborz Province cultured at pyruvate and glycerinated Lowenstein-Jensen Medium. Then DNAs were extracted by van Solingen Method and PCR-16S rRNA, PCR-IS6110 and RD Typing (RD1, RD4, RD9, RD12) PCRs were done respectively.

Results: Except one isolate which hadn't any band at the IS6110-PCR, the other isolates prepared 543 bp, 245 bp, 146 bp, 172 bp, 235 bp and 369 bp bands in 16S-rRNA, IS6110-PCR, RD-1, RD-4, RD-9 and RD-12 PCRs respectively. So based on obtained results, just one of the isolates identified as *Nocardia* by sequencing of 16S-rRNA and alignment and the others were *Mycobacterium tuberculosis*.

Conclusion: Proper treatment of the tuberculosis needs to identification of Mycobacterial isolates of the patient so this research showed that RD-Typing technique is useful for this purpose.

Keywords: *Mycobacterium tuberculosis* complex, RD-Typing, Tuberculosis, IS6110, 16S-rRNA

**P959 - 1217: ISOLATION AND MOLECULAR IDENTIFICATION OF MYCOBACTERIUM
TUBERCULOSIS COMPLEX FROM MICE INFECTED WITH MYCOBACTERIUM
REGIONAL LIVESTOCK BUIN ZAHRA**

Khatereh Alizadeh¹, dr nader mosavari², dr.raziye nazari³

1. Departement of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran
2. Razi Vaccin and Serum Research Institute, Agricultural, Education and Extension Organization, Tehran, Iran
3. Departement of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran

Background and Aim: Tuberculosis is the most common zoonotic infectious diseases transmissible from animals to humans in the world, and even from one animal species to another. The aim of this study was isolation and identification of Mycobacterium tuberculosis complex molecular RD Typing Method of mice infected with Mycobacterium collected from the livestock area Buin Zahra To investigate the relationship as a reservoir of bovine tuberculosis with mice is possible.

Methods: In this study, 100 samples mice were collected from farms positive reactor. DNA was extracted from the bacterial isolates by the method of Van Solengen and identified to genus level by PCR-16SrRNA. To confirm the mycobacterium tuberculosis complex, PCR-IS6110 and identification species by PCR-RD typing (RD1, RD4, RD9, RD12) was used.

Results: 100 samples were cultured from mice, 6 samples were positive that all isolates, were Mycobacterium bovis.

Conclusion: The results showed that Mycobacterium bovis strains isolated from livestock animals under study, the causative agent Mycobacterium bovis infected cattle and mice are carriers of tuberculosis and evidence of zoonotic tuberculosis and its transmission from one animal species to another species is and this was alarming for the spread of animal strains in the community.

Keywords: Buin Zahra, Mycobacterium tuberculosis complex, Mycobacterium bovis, PCR-RD typing.

**P960 - 1230: ISOLATION, MOLECULAR IDENTIFICATION AND DNA FINGERPRINTING
OF MYCOBACTERIUM FROM FISH CULTURE FARMSE OFFER IN KARAJ CITY**

Atefeh Mobasher amini¹, Nader mosavari², Mahdi ghiyami rad³, keyvan tadayon⁴

1. department of microbiology .faculty of science . islamic azad university ahar branch . ahra iran
2. razi vaccim and serum research institute,agricultural,education and extension organization,tehran,iran
3. department of microbiology .faculty of science . islamic azad university ahar branch . ahra iran
4. razi vaccim and serum research institute,agricultural,education and extension organization,tehran,iran

Background and Aim: TB Mycobacteriosis fish Culture zoonotic diseases transmitted to humans in the world and is caused by mycobacteria. Factors that may predispose the fish to mycobacterial infections, including environmental pollution, diet, stress associated with overcrowding, and poor water quality is suboptimal nutrition.

Methods: Of 100 samples of fish Culture (50 samples of cold-water and 50 samples fishes warm water fish) head, tail and offal separately Shdvps the oscillator sampling and decontamination of Mycobacterium specific environments and cultures were incubated.

Results:. Colony cream and orange were that 15 isolates of fast acid (5 strains of farmed fish and 10 samples of farmed fish of warm water), respectively. Tests to determine the molecular identity of PCR-16S rRNA band was performed 543pb shows. All isolates were mycobacterium TB complex .

Conclusion: There Karaj mycobacterium in farmed fish and the possibility of transmission to humans and cause disease is imminent. In this study, none of the separation does not belong to mycobacterium NTM

Keywords:. mycobacteriosis, mycobacterium, fish Cultur

**P961 - 1257: A SEARCH FOR TRACES OF MOST FREQUENT CLONAL COMPLEXES OF
MYCOBACTERIUM BOVIS IN IRAN**

SARA KEZEMNIA¹, KEYVAN TADAYON², FAHIME NEMAT³, NADER MOSAVARI⁴,
ROHOLAH KESHAVERZ⁵, RAINAK GHADERI⁶, MOHAMMAD SEKHAVATI⁷

1. Islamic Azad University of Pharmaceutical Sciences, Tehran
2. RAZI VACCINE AND SERUM RESEARCH INSTITUTE, KARAJ
3. Islamic Azad University of Pharmaceutical Sciences, Tehran
4. RAZI VACCINE AND SERUM RESEARCH INSTITUTE, KARAJ
5. RAZI VACCINE AND SERUM RESEARCH INSTITUTE, KARAJ
6. RAZI VACCINE AND SERUM RESEARCH INSTITUTE, KARAJ
7. RAZI VACCINE AND SERUM RESEARCH INSTITUTE, KARAJ

Background and Aim: In the world population of *Mycobacterium bovis*, the cause of bovine tuberculosis (BTb), a number of clonal complexes have been characterized with their global distribution predominant in specific parts of the world. The African 1 and African 2 in Africa and the European1 and European2 clones in Europe are known as principle recognizable colonies of *M. bovis* both in farm and wildlife animal hosts. Furthermore, there are convincing evidences to support that BTb has been long active in bovids of Iran. The Old Persian Empire is believed to have accommodated two of the most remarkable birthplaces for cattle and sheep domestication, therefore the chances are that local clone(s) of *M. bovis* have been evolved in Persia.

Methods: In order to better understand clonal structure of *M. bovis* population in Iran, we have initiated a systematic PCR/sequencing backed search plan. Specific genomic loci and/or deletions defined previously were used to track any of the above mentioned clones.

Results: Our observations showed none of the examined 17 local *M. bovis* isolates from across Iran in this study belonged to these clones.

Conclusion: Iran holds a very homogenous population of *M. bovis*. Absence of African 1, African 2, European1 and European2 in the Iranian environment is epidemiologically intriguing. We assume there should be locally-evolved clone(s) of *M. bovis* in this country that have not been characterized so far.

Keywords: *Mycobacterium bovis*, bovine tuberculosis, clonal complex

Vaccine

P962 - 207: MICROBIAL VACCINES

Milad Esmatparast¹, Mazrouei Sebdani Roya ²

1. Department of biology, faculty of science, Islamic Azad University, Urumieh, Iran.
2. Department of biology, faculty of science, Islamic Azad University, Urumieh, Iran.

Background and Aim: It has been estimated that vaccination was responsible for over 10 years of the total increase in the average human lifespan worldwide. There are over 10 million deaths annually worldwide as well as considerable morbidity, mostly among young children, that are attributable to infectious diseases. A very large number of these deaths could be prevented by increased use of existing vaccines, while the great majority of these deaths would be preventable by the future wide-scale use of effective new vaccines now being developed. Approaches: Vaccines are one of the most highly cost-effective modalities in healthcare. In this study we reviewed and collected summaries of important subjects about vaccines generally and bacterial vaccines.

Methods: The development of new vaccine technologies as well as the emergence of new mechanisms for the funding of vaccine development, purchase and distribution worldwide offer hope that the fruits of these technologies will reach an ever-increasing number of people.

Results: This article provides an overview of developments in approaches to identify novel bacterial components for use in recombinant subunit vaccines. In particular it describes the processes involved in “reverse vaccinology”, and some associated complementary technologies that can be used in the identification of new and potentially useful vaccine antigens.

Conclusion: Many vaccines only elicit humoral antibodies while the use of whole virus vaccines has been rejected because of other potential problems. Today, many anti-viral vaccines are available and more are being developed. These vaccines have made a considerable impact on public health.

Keywords: vaccinology, vaccine, microbe.

**P963 - 217: IMMUNOLOGICAL EVALUATION OF SALMONELLA PARATYPHI C
OLIGOPOLYSACCHARIDE DIPHTHERIA TOXOID CONJUGATE IN MICE.**

Neda Behmagham¹, Reza Shapori Ph.D², Mehdi Rahnema Ph.D³

1. Department of Microbiology , Zanjan Brach , Islamic Azad University , Zanjan , Iran.
2. Department of Microbiology , Zanjan Brach , Islamic Azad University , Zanjan , Iran.
3. Department of Microbiology , Zanjan Brach , Islamic Azad University , Zanjan , Iran.

Background and Aim:Salmonella paratyphi C is a agent of paratyphoid disease in human and effective vaccine for the disease has not yet been produced . This study aimed to assess the immunogenicity of Salmonella paratyphi C OPS- diphtheria toxoid conjugate (OPS-DT) in mice.

Methods:After culture of bacteria,the OPS was extracted by hot phenol and acetic acid then ADH as a spacer and EDAC as a linker were used to conjugation of OPS to diphtheria toxoid. Prepared conjugate inoculate intraperitonealy to 15 moture BALB/c mice in three dose with 2 week interval. Then indirect ELISA used to determination of induce antibodies (Abs) titers.

Results:According to the results of ELISA,prepared conjugate was strong immunogenic in mice. Two week after first dose there was no significance difirence between groups that were immunizie by OPS and OPS-DT. But after second and third doses, conjugate showed significance increasing in all types of Abs titers inversus OPS. The results of anti-OPS induction for IgG, IgM, IgA, IgG1, IgG2a, IgG2b and IgG3 were observed OPS-DT> OPS > DT.

Conclusion:These results showed that prepared conjugate was affective and can be sugested as a candidate vaccine.

Keywords:Salmonella paratyphi C, diphtheria toxoid , Conjugation , ELISA , oligopolysaccharides

**P964 - 309: EXPRESSION, PURIFICATION AND PRODUCTION OF A RECOMBINANT
PROTEIN VACCINE AGAINST S. AUREUS BIOFILM-RELATED INFECTIONS**

Masoud Haghkhah¹, Maryam Shahbazi², Younes Ghasemi³

1. Department of Pathobiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
2. Department of Pathobiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
3. Pharmaceutical Sciences Research Center, Faculty of Pharmacy, Shiraz University of Medical Sciences, Shiraz, Iran

Background and Aim: In our previous study a subunit hexavalent protein, vaccine candidate, against *Staphylococcus aureus* and *Candida Albicans* biofilm-related infections, was designed considering the polymicrobial nature of the infections.

Methods: The designed vaccine consisted of the selected fragments of five biofilm-associated proteins of *S. aureus* including ClfA, SdrE, FmtB, Spa, Bap and one important adhesion protein of *C. albicans*, Als. The chosen sequences were fused with appropriate linkers and the cut sites of NdeI and XhoI restriction endonuclease were inserted at the N-terminal and C-terminal of the sequence, respectively. After codon optimization the newly synthesized construct was cloned and expressed successfully in *E. coli* strain BL21 (DE3) using pET23d plasmid vector.

Results: The recombinant protein was purified by Ni-NTA spin column and its 591 amino acid was determined by SDS-PAGE and western blot techniques.

Conclusion: The 80 kDa recombinant protein can be considered as a potential target for immunotherapy against *S. aureus* biofilm related infections.

Keywords: *Staphylococcus aureus*, *Candida albicans*, Vaccine

**P965 - 323: EXTRACTION AND BIOLOGICAL EVALUATION OF MYCOBACTERIUM
AVIUM COMPLEX SUBSP. AVIUM MEMBRANE VESICLES**

Mohammad Kamran sarkandi¹, Seyed Davar Siadat², Farzam Vaziri³, Zahra Hoseini Tavassol⁴

1. Department of Microbiology, Science and Research branch, Islamic Azad University, Tehran, Iran.
2. Department of Mycobacteriology, Pasteur Institute of Iran, Tehran, Iran.
3. Department of Mycobacteriology, Pasteur Institute of Iran, Tehran, Iran.
4. Department of Microbiology, Science and Research branch, Islamic Azad University, Tehran, Iran.

Background and Aim: Mycobacteria have been conventionally classified into several broad taxonomic group on the basis criteria such as pathogenicity for humans and animals, rate of growth at optimum temperature and effect of visible light on pigment production. The Mycobacterium avium Complex (MAC) is such bacteria as acid-fast, slow growth, nonphotochromogenic and opportunistic pathogens with various pigments which is considered as nontuberculous mycobacteria (NTM). One of the best studied aspects of MAC is the structure and function of MAC cell wall and membrane that is able release Membrane Vesicles (MV) into different media.

Methods: Using Claassen I, et al. modified methods (Siadat S . D, et al)

Results: The subjective of this study is to extract aforementioned MV from MAC using Claassen I, et al. modified methods in order to stimulate the immune system and to find a candidate for Adjuvant or being Vaccine. Concluded result illustrate that the MV extracted from MAC has the ability to induct IL-10 and IFN-gamma.

Conclusion: These are convenient candid for treatment, new generation vaccines and reducing the rate of Tuberculosis causing from MAC in AIDS patients.

Keywords: Mycobacterium avium Complex (MAC), Membrane Vesicles (MV), IL-10, IFN-gamma, Adjuvant

P966 - 335: THE STUDY OF PROTECTIVE EFFECT OF HEPATITIS B VACCINE IN 12 TO 24 MONTHS OLD VACCINATED CHILDREN REFERED TO TABRIZ CHILDREN HOSPITAL

Asemeh Teymouri Bilesuar¹, Changiz Ahmadizadeh*², Shahram Abdoli Oskouie³

1. M.Sc in Microbiology ,Islamic Azad University of Ahar ,Ahar, Iran
2. Assistant Professor, PhD Microbiology, Islamic Azad University of Ahar ,Ahar, Iran
3. Associate Professor, Professor of Pediatric Infectious Diseases, Infectious Diseases and Tropical Medicine Research Center Medical Sciences University of Tabriz

Background and Aim: Vaccination is One of the most effective methods of prevention of hepatitis B throughout the world. The aim of this study was to check the level of HBsAb after vaccination in vaccinated 12 to 24 months children referred to Children's hospital in Tabriz.

Methods: This descriptive, cross-sectional study was carried out on 200 children 12 to 24 months randomly. The questionnaires were filled out through interviews with children, For data collection: and child's characteristics nutrition, were recorded. 5ml blood sample were taken, Then antiHBs experiment was done quantitatively with the ELISA method, manufactured And values above 10IU/ml were considered as the optimal safety level. Data were analyzed using statistical software spss-17 and t-test and Pearson correlation coefficient.

Results: 93.5% of studied children over 10 Iu/ml Anti-HBs and showed respond to vaccination. The safety level was not associated with sex of children and weight. Considering antibody titer There was not statistically significant difference among breast-fed babies and formula-fed babies ($p > 0.05$). Anti-HBsAb titers were related to the age of children ($p = 0.001$). The immunity level decreased with increasing age. 6.5% of children were not safe.

Conclusion: This study showed that safety caused by total injection of hepatitis B vaccine is desirable according to National vaccination program.

Keywords: Hepatitis B virus- vaccination -12 to 24 months children- HBsAb

**P967 - 342: MAPPING OF IMMUNOGENIC DISCONTINUOUS EPITOPES ON HUMAN IGG
FC REGION BY COMPUTATIONAL IMMUNOLOGY**

Fatemeh Hajighasemi¹, Soheila Rohani², Fatemeh Sefid³

1. Department of Immunology, Faculty of Medicine, Shahed University, Tehran, Iran
2. Department of Immunology, Faculty of Medicine, Shahed University, Tehran, Iran
3. Department of Immunology, Faculty of Basic Science, Shahed University, Tehran, Iran

Background and Aim: Computational immunology is a division of immunology support clinical and basic research for development of improved and more accurate diagnostic tests. Human immunoglobulin G (IgG) is the greatest abundant antibody in serum and extracellular fluids. Several effector roles are triggered via Fc fragment of IgG. The quantity of serum IgG is correlated to severity of various infections like *Helicobacter pylori*, *Chlamydia pneumonia*, and *Toxoplasma gondii*. Thus IgG has a great diagnostic importance. The aim of this study is mapping of immunogenic discontinuous epitopes of human IgG Fc region by computational immunology methods.

Methods: The sequence of amino acid and third structure of reference human IgG was found in PDB database. The second structure of IgG was determined by Phyre 2 software. The discontinuous epitopes of human IgG were defined by Ellipro and CEP softwares.

Results: Two immunogenic discontinuous epitopes located to human IgG Fc region was determined by Ellipro software and 21 immunogenic discontinuous epitopes located to human IgG Fc region was defined by CEP software. Most of these epitopes were located to CH2 domain of human IgG Fc region.

Conclusion: In this study a lot of discontinuous epitopes located on human IgG Fc region were determined by two softwares and findings of previous experimental studies confirm these results. These epitopes are valuable tools for producing specific monoclonal anti IgG antibodies which improve accuracy of current IgG diagnostic tests in various diseases including infections. Also these epitopes are helpful for epitope mapping of human IgG and phylogenetic studies.

Keywords: Human IgG, computational immunology, discontinuous epitope

P968 - 344: EVALUATION OF PERTUSSIS TOXIN PRODUCTION IN B2 AND THijs MEDIA

Hamid Moradtalab¹, Habib Zeighami², Mojtaba Noofeli³, Fakhri Haghi⁴

1. Department of Microbiology, Zanjan University of Medical Sciences, Zanjan, Iran
2. Department of Microbiology, Zanjan University of Medical Sciences, Zanjan, Iran
3. Department of human bacterial vaccines, Razi Vaccine & Serum Research Institute, Karaj, Iran
4. Department of Microbiology, Zanjan University of Medical Sciences, Zanjan, Iran

Background and Aim:Whole-cell pertussis vaccine (wP) has been highly effective in preventing childhood deaths due to pertussis. Pertussis toxin is one of the major virulence factors of *Bordetella pertussis* and the primary component of all available pertussis vaccines. wP production in according to fermenter culture of *B. pertussis* strains (134 and 509) in B2 medium. The aim of this study was to evaluate *B. pertussis* strain 509 PT production in B2 & THijs media by CHO cell and ELISA methods.

Methods:In this study *B. pertussis* strain 509 was cultured in B2 and THijs media (triplicate). 6 samples were taken during the log growth phase in 2-3 hours intervals. The growth rate by opacity and quantification of cell-associated and free PT by ELISA and CHO cell assays was calculated.

Results:THijs medium was significantly showed increase of the bacterial growth rate. Duration the first 29 hours, bacterial concentration in B2 and THijs culture media were 19 and 29 IOU, respectively. In THijs medium, greater amount of produced toxin was cell-associated. in B2 medium, maximum cell-associated toxin by ELISA and CHO cell were in the optical densities of 1.1 and 0.9 and for THijs medium in the optical densities of 1.6 and 1.1, respectively.

Conclusion:*B. pertussis* (509 strain) in THijs medium produced higher cell mass and cell-associated toxin than B2 medium. It can be used for production of whole-cell vaccine with lower biomass per dose, led to reducing vaccine toxicity and so, it is economically affordable.

Keywords:*B. pertussis*, Whole cell pertussis vaccine, ELISA, CHO cell, Pertussis toxin

**P969 - 345: IN SILICO MODELING AND CHARACTERIZATION OF CHIMERIC VACCINE
USING COMPUTATIONAL TOOLS AND SERVERS**

Hadi Arabi Asciabari¹, Reza Mohammadzadeh², Amin Zarei³

1. Cell and Molecular Biology Department, Maragheh University, IR
2. Cell and Molecular Biology Department, Maragheh University, IR
3. Cell and Molecular Biology Department, Maragheh University, IR

Background and Aim: According to studies Cholera Toxin B (CT-B) is unique in that it not only elicits a strong immune response to itself, but more importantly, when given with other antigens acts as a potent adjuvant. In this study, a novel chimeric protein as a candidate vaccine against HCV, containing CT-B and core antigen of Hepatitis C Virus was theoretically designed.

Methods: Computational packages and online servers are the current tools used in the DNA and protein sequence analysis and characterization. The chimeric gene designed based on the nucleotide sequences and the protein structural prediction, alignments and physicochemical traits of fusion protein structures with different linkers was analyzed by online servers.

Results: After find a suitable peptide linker for the new chimeric protein a manner that none of the peptides intervene the other's function and optimization of construction energy condition, evaluation the stability of the chimeric polypeptide and 3D structural alignments we proposed a novel efficient chimeric vaccine against HCV.

Conclusion: Thus, the chimeric protein linked with (EAAAK4) or (GP GP) linkers might show synergistic and stronger immune response than the separate peptide moieties because they could exert their elicits a strong immune response freely which is not influenced by the other part.

Keywords: Cholera toxin B, Chimeric vaccine, Hepatitis C Core Antigen, bioinformatics

P970 - 385: THE EPSTEIN-BARR VIRUS (EBV) AS A TRIGGER FACTOR FOR SYSTEMIC LUPUS ERYTHEMATOSUS

Shokoufeh Zadeh nasir¹

1. Department of Genetics, Faculty of Biological Sciences, Shahid Beheshti University

Background and Aim: Systemic lupus erythematosus (SLE) is an autoimmune disease that is caused by a combination of genetic and environmental factors including infections. Epstein-Barr virus (EBV) is a ubiquitous infectious agent. EBV infects epithelial cells and B cells and it affects the immune system of the host directly by infection of lymphocytes with subsequent immortalization and indirectly by expression of immunomodulating viral antigens. These immunomodulating functions make EBV a good candidate for initiation of autoimmune diseases and exacerbation of disease progression.

Methods: Using Google Scholar search engines and databases such as Science Direct and Wiley and Springer, EBV and Systemic lupus erythematosus and Immunodeficiencies keywords was searched and selected articles were studied.

Results: In B cell lymphocytes, EBV-encoded proteins have been shown to directly promote immortalization and proliferation through stimulation of the NF- κ B pathway and increased expression of anti-apoptotic genes. In the context of mature T/NK lymphocytes, the virus likely plays a nuanced role. SLE patients have dysfunctional control of EBV infection resulting in frequent reactivations and disease progression. These comprise impaired functions of EBV-specific T-cells with an inverse correlation to disease activity and elevated serum levels of antibodies against lytic cycle EBV antigens. The presence of EBV proteins in renal tissue from SLE patients with nephritis suggests direct involvement of EBV in SLE development.

Conclusion: In our opinion, the evidence for a causative role of EBV in SLE is so compelling that future research should be focused on the additional role(s) of other (herpes)viruses and possible new therapies based on immunomodulation and/or antiviral drugs.

Keywords: Epstein-Barr virus , immunodeficiencies , infections , systemic lupus erythematosus , autoimmune disease

P971 - 389: IDENTIFICATION OF PROTECTIVE B-CELL EPITOPE REGIONS IN PILUS T-SURFACE ANTIGEN SPT-1059 OF STREPTOCOCCUS PNEUMONIAE SEROTYPE 19F

Shirin Tarahomjoo¹

1. Division of Genomics and Genetic Engineering, Department of Biotechnology and Central Lab, Razi Vaccine and Serum Research Institute, Agriculture Research, Education and Extension Organization AREEO, Karaj, Iran

Background and Aim: Streptococcus pneumoniae (pneumococcus) is an important pathogen that causes significant annual mortality in children less than 5 years worldwide. S. pneumoniae serotype 19F is a major cause of pneumococcal disease in children globally. Pneumococcal capsule is the antigen used in the construction of pneumococcal vaccines. However, due to its weak immunogenicity in children, it is coupled chemically to an immunogenic carrier protein. The high manufacturing cost of these vaccines encouraged the development of proteinaceous vaccines against pneumococci. Cell surface proteins are key factors in the infection process of pathogenic bacteria and are attractive as antigens for the vaccine development. Our previous study showed that pilus T-surface antigen SPT-1059 of serotype 19F pneumococcus, is an immunoprotective cell surface protein and is not able to induce autoimmunity. Regarding the importance of inducing the antibody response for protection against pneumococci, in this study, we aim to determine the presence of immunogenic B-cell epitope regions in the T-surface antigen that can be used for the protein based vaccine development against serotype 19F pneumococcus.

Methods: Linear B-cell epitopes of the protein were analyzed using Bepipred and BCPreds. Conformational B-cell epitopes were identified using CBTOPE. VaxiJen was used to determine the epitope region immunoprotective ability.

Results: our analysis revealed the presence of five overlapped immunoprotective B-cell epitope regions in the protein. The epitope region beginning at the amino acid 46 (DDNSAITKANGENNAVVKIN) was the most protective B-cell epitope region.

Conclusion: The identified epitope region can be used in the design of proteinaceous vaccines against serotype 19F pneumococcus.

Keywords: Streptococcus pneumoniae, proteinaceous vaccine, B-cell epitope

**P972 - 411: STABILITY STUDY OF IBIBA FULL DOSE BRUCELLOSIS VACCINE AFTER
RECONSTITUTE**

Sajad Dostdari¹, Ebrahim Hasannia², Abolfazl Khafri³, Anahita Emadi⁴, Ramin Baghernejad⁵

1. Department of Bacterial vaccines Quality Control Department, Razi vaccine and Serum Research Institute, Karaj, Iran
2. Department of Bacterial vaccines Quality Control Department, Razi vaccine and Serum Research Institute, Karaj, Iran
3. Department of Bacterial vaccines Quality Control Department, Razi vaccine and Serum Research Institute, Karaj, Iran
4. Department of Bacterial vaccines Quality Control Department, Razi vaccine and Serum Research Institute, Karaj, Iran
5. Department of Brucella Vaccine Production, Razi vaccine and Serum Research Institute, Karaj, Iran

Background and Aim: Stability studies play a critical role in assuring product quality at all points in the vaccine life cycle and have a major impact on the success of immunization programs worldwide. on the other hand, in attention to that brucellosis Iriba full dose vaccine produced in pack of 20 doses and scattering sheep and goats in the field, stability study of the Iriba full dose vaccine after reconstitute is necessary. The purpose of this study is determination of the vaccine quality under the influence of environmental temperature factors and a determination shelf - life Iriba full dose Brucellosis vaccine after reconstitution of lyophilized vials vaccine of with study viable count test after reconstitute lyophilized vials Iriba full dose Brucellosis vaccine.

Methods: For this study after reconstitute 3 vials of Iriba full dose Brucellosis vaccine, In different temperature conditions 4°C, 25°C and 37°C were put, and at time zero, one hour, four hours and twelve hours, accordance with OIE 2012 live bacteria in vaccine (viable count test) was examined.

Results: The results of this study showed suspension Iriba is tested in different three temperatures, 4°C, 25°C and 37°C even up to 12 hours is stable and has passed OIE specification 2012(10-34× 10⁹ cfu/dose) standard.

Conclusion: According to the results, Iriba full dose Brucellosis vaccine can be stabled at least 12 hours after reconstitution at 37°C.

Keywords: Stability study, Iriba, vaccine

**P973 - 418: CLEANING VALIDATION OF MMR VACCINE PRODUCTION DESK TO ASSESS
THE EFFICIENCY OF DECONTAMINATION OF MEASLES, MUMPS AND RUBELLA
VIRUSES DURING CAMPAIGN**

Maryam Talebshoostari¹, Zohre-Azita Sadigh², Ashraf Mohammadi³, Ladan Mokhberralsafa⁴

1. Razi Vaccine and Serum Institute
2. Razi Vaccine and Serum Institute
3. Razi Vaccine and Serum Institute
4. Razi Vaccine and Serum Institute

Background and Aim: Validation is an element of GMP which assures that the equipments and methods are under defined conditions. Therefore, high quality product continuously is being produced. Cleaning validation studies provides high-grade documentary evidence that indicated the cleaning procedure is sustainable. The aim of this study was cleaning validation to assess the efficiency of decontamination of the measles, Rubella and mumps viruses by ethanol 70 percent.

Methods: The effectiveness of the cleaning method was evaluated by inoculation of samples into five different cells (CEF, HeLa, MRC-5, RK13 and Vero). Then, Cell cultures were observed daily by inverted microscope for any CPE. Moreover, Cell cultures were also examined by haemadsorption and haemagglutination assay for detection of Mumps and Rubella viruses respectively. Samples were isolated from five high-risk points before and after treatment (campaign). Totally 2160 samples were collected and inoculated into cells.

Results: During 14 days, although no CPE observed in post-treatment samples, CPE observed in 3 points of before-treatment samples. The efficiency of method was calculated by Wilcoxon signed-rank and McNemar's tests. Before-treatment swab specimens compared with after-campaign swab specimens show significant differences (P values of 0.001, Chi-square = 268).

Conclusion: According to this study and statistical results, cleaning process by ethanol 70 percent during campaign, is valid.

Keywords: Measles, Mumps, Rubella vaccine, Validation, Cleaning process

**P974 - 421: ANALYSIS OF IMMUNOGENIC B-CELL EPITOPE REGIONS IN PLASMID
STABILIZATION PROEIN OF STREPTOCOCCUS PNEUMONIAE SEROVAR 19F**

Shirin Tarahomjoo¹

1. Division of Genomics and Genetic Engineering, Department of Biotechnology and Central Laboratory, Razi Vaccine and Serum Research Institute, Agriculture Research, Education and Extension Organization (AREEO), Karaj, Iran

Background and Aim: Streptococcus pneumoniae (pneumococcus) is an important pathogen that causes significant annual mortality in children less than 5 years worldwide. S. pneumoniae serotype 19F is a major cause of pneumococcal disease in children globally. Pneumococcal capsule is the antigen used in the construction of pneumococcal vaccines. However, due to its weak immunogenicity in children, it is coupled chemically to an immunogenic carrier protein. The high manufacturing cost of these vaccines encouraged the development of proteinaceous vaccines against pneumococci. Cell surface proteins are key factors in the infection process of pathogenic bacteria and are attractive as antigens for the vaccine development. Our previous study showed that plasmid stabilization protein (PSP) of serotype 19F pneumococcus, is an antigenic cell surface protein and is not able to induce autoimmunity. Regarding the importance of inducing the antibody response for protection against pneumococci, in this study, we aim to determine the presence of immunoprotective B-cell epitope regions in PSP that can be used for the protein based vaccine development against serotype 19F pneumococcus.

Methods: Linear B-cell epitopes of the protein were analyzed using Bepipred and BCPreds. Conformational B-cell epitopes were identified using CBTOPE. VaxiJen was used to determine the epitope region immunoprotective ability.

Results: Our analysis revealed the presence of eight overlapped immunoprotective B-cell epitope regions in the protein. The epitope region beginning at the amino acid 570 (KIVTNNLSDKNEKEKNKEEKQSNSNVIDSNQKNGEFNSSKDNRMNDKIDNKQDNKTEEVNY KIVGDGRETNHIN) was the most protective B-cell epitope region.

Conclusion: The identified epitope region can be used in the design of proteinaceous vaccines against serotype 19F pneumococcus.

Keywords: Streptococcus pneumoniae, proteinaceous vaccine, B-cell epitope

P975 - 431: IDENTIFYING CONFORMATIONAL B-CELL EPITOPES OF DIPHTHERIA TOXIN AT DIFFERENT PHs AND TEMPERATURES USING MOLECULAR DYNAMICS SIMULATIONS

Soheila Ghaderi¹, Mohamadreza Bozorgmehr², Shirin Tarahomjoo³

1. Department of Central Laboratory, Razi Vaccine and Serum Research Institute, Agriculture Research, Education and Extension Organization AREEO, Karaj, IRAN
2. Department of Chemistry, Faculty of Science, Mashhad Branch, Islamic Azad University, Mashhad, IRAN
3. Division of Genomics and Genetic Engineering, Department of Biotechnology and Central Laboratory, Razi Vaccine and Serum Research Institute, Agriculture Research, Education and Extension Organization (AREEO), Karaj, Iran

Background and Aim: Variations in temperature and pH condition results in the conformational changes of the diphtheria toxin structure. Conformational B-cell epitopes affects significantly the toxin immunogenic activity. In this study therefore we aim to investigate effects of pH and temperature on the toxin conformational B-cell epitopes.

Methods: We used different temperatures (300K, 320K) and pHs (pH4, pH5, pH6.5, pH8 and pH10) for evaluation of conformational B-cell epitopes of diphtheria toxin using molecular dynamics simulations and bioinformatics tools.

Results: The conformational B-cell epitopes contain amino acids C186-N203, D48, D49, H391 and D392 exclusively at pH 4.0. Moreover, the conformational B-cell epitopes contains the amino acids G171-R173 and G147 exclusively at pH 5.0. However, increasing the pH to more than 6.5 did not affect the epitopes significantly. At 320 K, the epitopes included the amino acids G52, A71, A294, N296 and V443, whereas these residues were not parts of the conformational epitopes at 300 K.

Conclusion: Our results indicated the importance of selecting appropriate pH and temperature conditions to keep the toxin conformational B-cell epitopes at a suitable state for enhancing the protein immunological activity.

Keywords: Conformational B-cell epitope, Diphtheria toxin, Immunological activity, Molecular dynamics simulations, pH, Temperature

**P976 - 437: RECOMBINANT HMW1 CORE BINDING DOMAIN AS A VACCINE CANDIDATE
FOR NONTYPEABLE HAEMPHILUS INFLUENZAE**

Sepideh Meidaninikjeh¹, Seyed Davar Siyadat², Farzam vaziri³, Ghasem Abbaszadeh-Goudarzi ⁴, Kazem Abbaszadeh-Goudarzi⁵

1. Department of Microbiology, Faculty of Advanced Sciences & Technology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran - Iran (IAUPS)
2. Research Center of Microbiology, Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran.
3. Research Center of Microbiology, Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran.
4. Department of Medical Biotechnology, School of Advanced Technologies in Medicine, Tehran University of medical Sciences, Tehran, Iran
5. Department of Medical Biotechnology, School of Advanced Technologies in Medicine, Tehran University of medical Sciences, Tehran, Iran

Background and Aim: Colonization of Nontypeable Haemophilus influenzae in nasopharynx causes respiratory tract diseases. HMW proteins are the major adhesions and induce protective antibodies in the hosts. Moreover, HMW1 and HMW2 core binding domains are necessary for full level adhesion. Therefore, they can be used as vaccine candidates. In this study, we performed cloning, expression, purification and bactericidal activity of HMW1 core binding domain.

Methods: hmw1 core binding domain gene of NTHi PTCC 1766 strain (350 bp) was amplified by PCR. Next, the resulted amplicon was cloned into TA vector and confirmative tests such as colony-PCR, double digest and sequencing was performed. After sub-cloning, the recombinant bacteria were grown in broth medium containing IPTG for overexpression and the determined by SDS-PAGE and western blot. Afterward, the protein purified by using affinity chromatography and for immunization of BALB/c mice, purified HMW1 core binding domain protein with Ferund's adjuvant subcutaneously injected the animals. Eventually, anti HMW1 core binding domain IgG was assessed by Elisa and SBA methods.

Results: Purified HMW1 core binding domain protein could induce mice immune system and it was obvious from increasing antibody responses in immunized mice in comparison with control group. Interestingly, antibodies produced by purified HMW1 core binding domain protein also showed bactericidal activity against NTHi.

Conclusion: In this study collected sera from immunized mice illustrate remarkably increase in antibody responses and bactericidal activity in comparison with control group. Therefore, HMW1 core binding domain protein can be considered as one of NTHi vaccine components candidate for designing subunit vaccines.

Keywords: Nontypeable Haemophilus influenzae; Colony-PCR; Double digest; pET28-a; Ni-NTA agarose; Western blot.

**P977 - 441: EVALUATION THE MAST CELLS RECRUITMENT IN LONGITUDINAL
ISCHIATIC NERVE POST INJECTION OF FORMAL SALINE 5% IN RAT'S PLANTAR
DERMIS**

rasoul shahrooz¹, mahdi bakht², Zahra Bakhtiary³

1. Department of Basic science, Faculty of Veterinary Medicine, Urmia University, Urmia, Iran
2. Department of Basic science, Faculty of Veterinary Medicine, Urmia University, Urmia, Iran
3. Department of Basic science, Faculty of Veterinary Medicine, Urmia University, Urmia, Iran

Background and Aim: Mast cells play a major role in immunological and inflammatory reactions. Therefore, in this study the recruitment of mast cells in the ischiatic nerve trunk after plantar dermis inflammatory reaction in different times was evaluated.

Methods: 18 Wistar rats were randomly and equally divided in 6 groups. Control group was injected normal saline (50µl) in the dermis of right plantar region and after 2 hours ischiatic nerve samples were taken. In the next groups, formal saline 5% (50µl) was injected in dermis of right plantar skin and after 1, 2, 6, 24, 96 hours ischiatic nerve samples obtained respectively. Samples were fixed in formal saline 10%, passaged and prepared paraffin sections. Then, hematoxylin-eosin and toluidine staining methods for histological study and mast cells recruitment were performed.

Results: In histological study myelinated nerve fibers and endo, peri and epineuriums in the ischiatic nerve trunk were evaluated. Whereas, histomorphometrical study of ischiatic nerve in the first hours after injection of formal saline 5% showed the high number of mast cells in comparison to control group. The average number of granulated mast cells in 1 hour after injection and degranulated mast cells in 2 hours after formalin injection were increased in comparison to control group. But, the mean number of mast cells were increased significantly after 24 hours ($P < 0.05$). These cells were extremely decreased after 96 hours.

Conclusion: The observations of this study showed a notably recruitment of mast cells around the ischiatic nerve trunk in the first hours of plantar inflammatory reaction induced by formalin injection.

Keywords: Mast cell, Ischiatic nerve, Plantar dermis

P978 - 455: EFFECT OF TEMPERATURE AND CONCENTRATION OF BETA-PROPIOLACTONE ON INACTIVATION OF CELL DERIVED RABIES VIRUS

Zohre Eftekhari¹, Narges Miandehi², Sey-yed Hesam Tafreshi³, Arsalan Afrasiabi⁴, Ali Khodaeipour⁵,
Zohreh Parhizkar⁶

1. Department of Research and Development, Research and Production Complex, Pasteur Institute of Iran, Tehran, Iran
2. Viral Vaccine Production Department ,Pasteur Institute of Iran
3. Department of Research and Development, Research and Production Complex, Pasteur Institute of Iran, Tehran, Iran
4. Master of Science Microbiology ,Tehran Shomal University
5. Master of Science Microbiology ,Tehran Shomal University
6. Viral Vaccine Production Department ,Pasteur Institute of Iran

Background and Aim: Rabies virus is a single stranded negative sense RNA virus that belongs to the genus lyssavirus of the rhabdoviridae family. In the production process of vaccines, inactivation plays a crucial role in the vaccine efficacy. β -Propiolactone (BPL) is compounds that frequently used for the inactivation of viruses and the production of vaccines, such as rabies vaccines. In this study the effect of temperature on the infectivity of the rabies virus has been investigated.

Methods: BHK21C13 cell grown fixed rabies virus PV strain was treated with 1:3000, 1:4000 and 1:5000 final concentrations of BPL at 4 °C, 21°C and 37°C and evaluated after 24h, 48h, 72h and 5 days. Each aliquot was titrated after various intervals for viral infectivity using titration in BSR cell. The BSR cell was infected by triple serial dilution of the Rabies Virus PV strain, and then detects the fluorescent focus by FITC labeling anti- nucleocapsid of rabies virus monoclonal antibody. All the samples were assayed by Fluorescence Focus Units (FFU).

Results: Complete loss of infectivity of the virus treated with 1:3000 and 1:4000 of BPL was evident at the end of the 24h and 48 hour in 4 °C. Absolute loss of infectivity of the virus treated with 1:3000, 1:4000 and 1:5000 final concentrations of BPL was evident at the end of the 72 days in 21°C and 37°C.

Conclusion: These findings suggest that the temperature has the most important role on PBL inactivation effect which used as an inactivating agent for the fixed rabies virus grown in the cell culture.

Keywords: Temperature, Concentration, Beta-Propiolactone , Rabies Virus

**P979 - 458: EVALUATION OF OMP2A, OMP2B COMBINATION AS A NEW VACCINE
CANDIDATE AGAINST BRUCELLOSIS**

Maryam Meskini¹, Amir Hossein Abadi², Sepideh Hassanirad³, Davoud Esmaeili⁴

1. Department of Microbiology, Baqiyatallah University Medical of Sciences, Tehran, Iran
2. Department of Microbiology, Baqiyatallah University Medical of Sciences, Tehran, Iran
3. Department of Pharmaceutical Chemistry, Faculty of Pharmaceutical Chemistry, Pharmaceutical Science Branch, Tehran, Iran (IAUPS)
4. Department of Microbiology, Baqiyatallah University Medical of Sciences, Tehran, Iran

Background and Aim: Brucellosis is one of the commonest zoonotic disease that is spread throughout world. Brucella outer membrane proteins (OMPs) have been extensively studied because of their potential role as virulence factors, antigenic factors, and molecular typing tools. Studies have shown that these purines omp2a and omp2b the pore structure of the permeability of the membrane as a way to provide optimal growth conditions and protection against harmful compounds and periplasmic immunogenic protein. The recent studies indicate, omps of Brucella can induce Th1 response and IgG2 α antibody to Stimulation IFN- γ of cellular immune response against Brucella. Since, omp2a, Omp2b of Brucella spp. as potential immunogenic and protective antigens and a candidate's subunit vaccine for human and animals.

Methods: This paper is a review article through library research and internet search sites, PubMed, Sid and Google Scholar keyword (omp2a, omp2b, Brucella, immunization, vaccine) is collected in the 2015.

Results: This study indicate omp2a and omp2b are main structure compounds and periplasmic immunogenic protein. In past studies indicate production of IFN- γ , IgG and IgM with omp2a, Omp2b was higher than those with rSodC in immunized mice.

Conclusion: There is no immunization strategy for human thus development of an effective subunit vaccine against brucellosis is necessary. Brucellosis is immune cellular immunity and immune response towards Th1 and IFN- γ can be effective in building safety department. Sin, omp2b can be appropriate vaccine candidate against Brucellosis.

Keywords: Key words: omp2a, omp2b, Brucellosis, vaccine

**P980 - 468: OMP34KDA AS A VACCINE CANDIDATE AGAINST ACINETOBACTER
BAUMANNII**

Aleme Naghipoureramy¹, Iraj rasooli²

1. biology department of shahed university
2. biology department of shahed university

Background and Aim: *Acinetobacter baumannii* is an extracellular opportunistic multidrug resistant pathogen causing nosocomial infections such as pneumonia, bacteremia, urinary tract infections, meningitis, and skin and soft tissue infections with a human mortality rate of >70%. A specific Outer membrane protein of 34 kDa is a cell surface porin in the pathogen associated with its carbapenem resistance and is involved in interaction the bacteria to host cell via binding to fibronectin. Mutation of Omp34 decreases virulence and fitness of *A. baumannii*. High prevalence of an immunogen is one of criteria in vaccine candidate selection. In this study, prevalence of Omp34kDa is analyzed via an in silico approach among *A. baumannii* strains.

Methods: All strains of *A. baumannii* were selected from taxonomy of NCBI at <http://www.ncbi.nlm.nih.gov/taxonomy/>. A protein sequence of Omp34 kDa served as a query for protein BLAST at <http://blast.ncbi.nlm.nih.gov/Blast.cgi> against non-redundant protein sequence database limited to *A. baumannii*. Strains of the pathogen were searched in the BLAST result.

Results: 1057 strains of *A. baumannii* were recorded in NCBI taxonomy. One hundred twenty six hits were found for Omp34kDa as the BLAST result. Omp34kDa was found in 815 of 1057 recorded strains. So >75% of *A. baumannii* strains bear the protein.

Conclusion: In addition to the role of Omp34kDa in virulence and fitness of *A. baumannii*, its high prevalence in *A. baumannii* strains, it could be considered as a suitable vaccine candidate against *A. baumannii*.

Keywords: *Acinetobacter baumannii*; Vaccine; Omp

**P981 - 472: RECOGNITION OF ANTIGENIC REGION IN FHAB AND FHAC PROTEINS ON
ACINETOBACTER BAUMANNII**

Farnoush Ezati mehrabani¹, Iraj rasooli²

1. biology department of shahed university
2. biology department of shahed university

Background and Aim: *Acinetobacter baumannii* is a multi drug resistant bacterium emerged as one of the most troublesome pathogens worldwide. The secretion of virulence factors through general secretory pathways in Gram-negative pathogens is a ubiquitous phenomenon. Filamentous hemagglutinin adhesins (FHA) as the two partner secretion system (TPS) is the key factors for bacterial attachment and subsequent cell accumulation on substrates. Arrangement of the genes encoding TPS are *fhaB1* and *fhaC1* in one ORF and *fhaB2* and *fhaC2* in the other. In this study we focus on antigenic conserved region on *A. baumannii* ATCC19606 with its other substrains and subsequently choose the best sequence for high stimulating immune response.

Methods: *A. baumannii* ATCC19606T was searched for autotransporter domains (*fhaB*, *fhaC*) using the NCBI data base. Three parameters of high immunogenicity, availability on outer membrane and conservity were chosen. Immunogenicity was checked by 5 online bioinformatic tools; bcepred, IEDB, Imed, SVM Trip, ABCprediction. Each online software has its own algorithm for introducing antigenic region. Topology was seen on <http://octopus.cbr.su.se/>, <https://www.predictprotein.org> and <http://www.bioinformatics.biol.uoa.gr/PRED-TMBB>. Conservity was searched at <https://blast.ncbi.nlm.nih.gov/Blast.cgi> and CLC

Results: *FhaB1* and *fhaB2* were aligned to select common conserved regions. This sequence has specific antigenicity with high score

Conclusion: *fhaB1* and *fhaB2*, *fhaC1* and *fhaC2* can stimulate immune response by a single conserved antigenic region. This region is present in >95% of *Acinetobacter baumannii* strains

Keywords: *Acinetobacter baumannii*; TPS; *FhaB*, *FhaC*, Antigen

**P982 - 474: PROTEIN LIPL32 IS A CANDIDATE SUBUNIT VACCINE AGAINST
LEPTOSPIROSIS**

Gholamreza Hashemi Tabar¹, Nikoueeayan, Helia², Hafiez, Maryam³

1. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.
2. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.
3. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.

Background and Aim:: In recent years there have been major advances in the understanding of leptospiral biology and the molecular basis of pathogenesis, yet the protein LipL32 remains an enigma of leptospiral biology. LipL32 (also known as Hap1) is an outer membrane, surface exposed lipoprotein and is the most abundant protein in the cell. LipL32 is found exclusively in pathogenic leptospires, is highly conserved, expressed in vivo and is highly immunogenic.

Methods: In an attempt to enhance the immune response, LipL32 coupled to or co-administered with the B subunit of the Escherichia coli heat-labile enterotoxin (LTB) in a hamster model of leptospirosis. After homologous challenge with 5× the 50% lethal dose (LD (50)) of *Leptospira interrogans*, animals vaccinated with LipL32 co-administered with LTB and LTB. Another study provides evidence that LipL32 is involved in the protective response against *L. interrogans* serovar Canicola in hamsters and is the first reported link to LipL32-induced protection against kidney invasion.

Results: It has been shown that LipL32 had significantly higher survival rates ($P < 0.05$) than animals from the control group. This is the first report of a protective immune response afforded by a subunit vaccine using LipL32 and represents an important contribution toward the development of improved leptospirosis vaccines. Also it is the first reported link to LipL32-induced protection against kidney invasion.

Conclusion: It has been shown that vaccination with LipL32 protein alone could provide a protective response against challenge with *L. interrogans* serovar Canicola to hamsters.

Keywords: Leptospirosis, Protein LipL32, Subunit vaccine,

**P983 - 501: DEVELOPMENT OF ANTI-BOVINE IGGIMMUNOGLOBULIN Y (IGYS) IN
QUAIL**

Yoones Attari roodi¹, kave veisi², khalil alo³, gholamreza nikbakht boroujeni⁴

1. main author

Background and Aim: IgY is the functional equivalent of mammalian IgG, but it is structurally different, and has been found to exhibit several important differences, including its physico-chemical properties and immunological capabilities. Recently, considerable research has focused on the use of IgY as an alternative to mammalian antibodies for several applications, including for various immunodiagnostic and immunotherapeutic applications. The use of IgY offers several advantages, including providing a much more hygienic, cost efficient, convenient, humane and plentiful source of antigen-specific antibodies.

Methods: Six weeks old quail were obtained from a local breeding unit. These quails received 0.2 ml bovine IgG. The bovine IgG were injected in the breast muscle of quails and booster doses were given 2 and 6 weeks after first injection. Eggs were collected weekly after first immunization for 12 weeks. Yolk IgY was isolated using precipitation method of water dilution combined with chloroform. ELISA were used for determining the quantifying the titer of IgY in egg yolks.

Results: Reactive egg yolk samples were used for ELISA checkerboard titration. According to the checkerboard titration, the best concentrations were found and we used those concentrations. ELISA showed acceptable amount of anti-bovine IgG in most weeks after immunization and the peak value was in the 5th week.

Conclusion: Egg yolk antibodies have been used as powerful and specific tools in many diagnostic and biomarker discovery applications. Our previous results suggest that anti-bovine IgG IgY produced in quails could be recruited as a specific probe for detection of bovine IgG-specific proteins.

Keywords: IgY- quail- bovine IgG

**P984 - 502: TESTING OMPS+RCAGA COMBINATION AS A NEW IMMUNIZATION
CANDIDATE FOR SPLENIC, GASTRIC CLEARANCE OF BRUCELLA ABORTUS 544 AND
HELICOBACTER PYLORI SS1 STRAIN INFECTIONS IN BALB/C MICE**

Amir Hossein Abadi¹, Davoud Esmaeili², Abbas Bahador³, Mehdi Mahdavi⁴

1. Microbiology Research Center and Department of Microbiology, Baqiyatallah University of Medical Science, Tehran, Iran.
2. Applied Microbiology Research Center and Department of Microbiology, Baqiyatallah University of Medical Science, Tehran, Iran.
3. 1 Department of Medical Microbiology, Faculty of Medicine, Tehran University of Medical Sciences, Tehran, Iran.
4. Department of Immunology, Pasteur Institute of Iran, Tehran, Iran.

Background and Aim: Brucellosis is the most common zoonotic disease in the world. *Helicobacter pylori* the causative agent of peptic ulcer disease (PUD), chronic gastritis, and MALT lymphoma in human. The *Brucella* spp. outer membrane proteins (OMPs) have been extensively characterized as potential immunogenic and protective antigens and CagA (Cytotoxin-associated gene A) of *Helicobacter pylori* is an immunodominant antigen from CagA island. Aim of this study, evaluation of OMPs and recombinant CagA to induce cellular, humoral immune response and clearance of *Brucella abortus* 544 and *Helicobacter pylori* SS1 strain infection in gaster, serum and spleen of BALB/c.

Methods: We immunization in four mice group OMPs+rCagA with Freund's incomplete in different formulation. After three times subcutaneous at 14-day, three week after latest immunization challenged by 3×10⁸ 544 and SS1 strain. Serum, gasters and spleens were cultured. Antibody response evaluated using ELISA test and cytokine response evaluated by RT-PCR.

Results: We observed OMPs and rCagA are an appropriate formulation to induce humoral (IgG2a/IgG1>1) and cytokines cellular immune response, witch adequate for clearance 544 strain infection in blood and spleen and aren't an appropriate candidate against *H.pylori*.

Conclusion: The recent studies indicate, that effective immune against *Brucella* and *Helicobacter pylori* is cellular immune response. Therefore, mix of formulation OMP+rCagA are appropriate to clearance of *Brucella*.

Keywords: *Brucella*, *Helicobacter pylori*, OMPs, rCagA, immunization, vaccine, clearance

**P985 - 513: CLONING EXPRESSION AND CHARACTERIZATION OF A RECOMBINANT
TRUNCATED CAPSID PROTEIN OF HEV IN ROSETTA EXPRESSION STRAIN**

Marzieh Divbandi¹, mohammad reza aghasadeghi², asghar abdoli³

1. pharmaceutical sciences university
2. pasteur institute
3. pasteur institute

Background and Aim: Hepatitis E virus (HEV) is one of the major causes of hepatic failure world wide and has high mortality among pregnant women. Hepatitis e virus transmission is mostly through fecal-oral especially with contaminated food and water. Recently chronic HEV infections were reported. Therefore, it is necessary to develop an effective vaccine against this virus. The aim of this study is to clone and express the truncated open reading frame 2 (ORF2) proteins- a hepatitis E virus capsid protein- in E. coli(Rosetta), which might be a potential HEV vaccine candidate in future.

Methods: The truncated orf2 gene which encodes 368-606 aminoacid of the protein ORF2 (this part of the protein is named HEV239), synthesized in pUC18 and sub cloned into PET26b expression vector. The construct was confirmed by PCR and digestion. After transforming into E.coli the protein of interest was produced after induction by IPTG. The production of HEV239 protein was confirmed by SDS-PAGE and Western blotting.

Results: The highest amount of protein production in Rosetta was obtained by adding IPTG at a final concentration of 1mM at 37 °C for 2;30 hours. expression and purification of HEV239 protein was confirmed by SDS-PAGE and western blotting. The size of the protein was 26/7 kDa.

Conclusion: In this study, HEV239, was expressed in E. coli and purified successfully for future purposes such as designing vaccine against HEV infection.

Keywords: Hepatitis E virus; capsid protein; rosetta

P986 - 534: PRODUCTION OF AUTOLYSIN PROTEIN OF METHICILIN-RESISTANT STAPHYLOCOCCUS AUREUS AND EVALUATION OF PROTECTIVE ACTIVITY IN BALB/C MICE BY PASSIVE VACCINATION

Yasamin Kalali¹, Setareh Highighat ², Mehdi Mahdavi ³

1. Department of Biotechnology, Faculty of Advanced and Technology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran - Iran (IAUPS)
2. Department of Microbiology, Faculty of Advanced Sciences and Technology, Pharmaceutical Sciences branch, Islamic Azad University, IAUPS, Tehran, Iran
3. Department of Immunology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Staphylococcus aureus is a major human and animal pathogen. In recent years, there has been a marked increase in the incidence of invasive community-acquired (CA) methicillin-resistant S. aureus (MRSA) among patients worldwide. Autolysin is one of the virulence factor that express during infection, regulate the growth, cell lysis, daughter-cell separation and biofilm formation. Our study focuses on passive immunization with rabbit IgG antibody against MRSA infection.

Methods: Atl gene which had been cloned into a suitable plasmid was kindly gifted and transformed into competent E. coli BL21. Expression of the recombinant autolysin (r-autolysin) was evaluated by SDS-PAGE and Western blot analysis. Rabbit was vaccinated subcutaneously (S.C.) vaccine consists purified r-autolysin in presence of complete Freund's adjuvant (CFA) for the first administration. Rabbit was boosted 2 times at 2 weeks intervals with the same vaccine dose formulated in incomplete Freund's adjuvant (IFA). Then, Immunization of mice models with MRSA by Antibody against autolysin was performed. Finally IgG levels in mice models were analyzed by ELISA.

Results: We successfully expressed r-autolysin with SDS-PAGE and western blot analysis. The passive immunization with rabbit polyclonal anti- IgG significantly improved survival rates when BALB/c mice challenged by S. aureus compared with the controls.

Conclusion: Our results suggest that the passive immunization may lead to good strategies to control infections caused by MRSA.

Keywords: methicillin resistance staphylococcus aureus, autolysin, passive immunization

P987 - 545: PRODUCTION AND PURIFICATION OF PENICILLIN BINDING PROTEIN2A (PBP2A) OF METHICILIN-RESISTANT STAPHYLOCOCCUS AUREUS: IMMUNOGENICITY STUDY

Seyedehshadi Mortazavi¹, Setareh Haghighat², Mehdi Mahdavi³

1. Department of Microbiology, Faculty of Advanced Sciences and Technology, Pharmaceutical Sciences branch, Islamic Azad University, IAUPS, Tehran, Iran
2. Department of Microbiology, Faculty of Advanced Sciences and Technology, Pharmaceutical Sciences branch, Islamic Azad University, IAUPS, Tehran, Iran
3. Department of Immunology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Staphylococcus aureus is an important cause of both hospital and community-associated MRSA infections worldwide. High level β -lactam resistance of S. aureus has been attributed to the penicillin binding protein 2a (PBP2a). Here, we aimed to evaluate the immunogenicity of PBP2a and its potential as a vaccine candidate.

Methods: Mec A-pET24a plasmid transformed into BL-21 E. coli cells and expression induced with adding 1 mM IPTG in the culture condition. PBP2a protein was expressed as evaluated by SDS-PAGE and Western blot. Recombinant protein was purified via NiNTA column and after dialysis versus PBS the protein was characterized and used for further studies. Afterward, three groups of female BALB/c mice, each one consisting of 20 mice were immunized using 20 μ g of purified PBP2a formulated in Montanide ISA 266 or alum adjuvants injected subcutaneously three times with two weeks intervals. As control group, mice were injected with PBS. Two weeks after last immunization, sera were collected and specific total IgG was evaluated by ELISA. Then, the level of cytokines such as IFN- γ , IL-4 and IL-17 were identified with commercial ELISA kits.

Results: SDS-PAGE and western blot analysis showed that recombinant protein with molecular weight of 13 kDa is over expressed. Interestingly, Vaccine formulations induced specific IgG and also raised IFN- γ and IL-17 cytokines secretion.

Conclusion: The results of the present studies provide evidences for immunogenicity of PBP2a protein as a vaccine candidate. However challenge study is running today.

Keywords: MRSA, PBP2a, Immunogenicity, Montanide ISA 266, Alum.

**P988 - 550: SIGNIFICANTLY HIGHER THAN THE OTHER MICE GROUPS. THE AAAAA
AAAAAAA AAAAA AAAAA**

Mohammad Reza Asadi Karam¹

1. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Urinary tract infections (UTIs) are among the most common infections in human. Innate immunity recognizes pathogen-associated molecular patterns (PAMPs) by Toll-like receptors (TLRs) to activate responses against pathogens. Recently, we demonstrated the fusion MrpH.FimH consisted of MrpH from *P. mirabilis* and FimH from Uropathogenic *E. coli* (UPEC) showed higher efficacy compared with FimH and MrpH only.

Methods: In this study, we evaluated the innate immunity and adjuvant properties induced by FimH in fusion MrpH.FimH through in vitro and in vivo methods. FimH and MrpH.FimH induced significantly higher IL-8 and IL-6 responses than untreated or MrpH alone in cell lines tested. The neutrophil count in fusion group was significantly higher than the other mice groups. The IL-8 and IL-6 production reached a peak after 6 h, and with significant decline at 24 h post-instillation in both bladder and kidney.

Results: Mice instilled with fusion and challenged with UPEC or *P. mirabilis* showed significant decrease in number of bacteria in bladder and kidney compared to control mice. We demonstrated the dual role of FimH as an immunogen and adjuvant that could be an approach for development of vaccines against UTIs. Furthermore, MrpH.FimH was presented as a promising vaccine candidate against UTIs caused by UPEC and *P. mirabilis*.

Conclusion: We demonstrated the dual role of FimH as an immunogen and adjuvant that could be an approach for development of vaccines against UTIs. Furthermore, MrpH.FimH was presented as a promising vaccine candidate against UTIs caused by UPEC and *P. mirabilis*. We demonstrated the dual role of

Keywords: qqqq, wwwwww, sssss

**P989 - 557: INVESTIGATING EFFECTS OF CARBON AND NITROGEN SOURCES ON THE
CAPSULE PRODUCTION BY STREPTOCOCCUS PNEUMONIAE SEROTYPE 19F**

Shirin Tarahomjoo¹, Mohsen Jalali²

1. Division of Genomics and Genetic Engineering, Department of Biotechnology and Central Laboratory, Razi Vaccine and Serum Research Institute, Agriculture Research, Education and Extension Organization (AREEO), Karaj, Iran
2. Department of Chemical Engineering, North Branch, Azad University of Tehran, Tehran 19585-936, Iran

Background and Aim: *S. pneumoniae* serotype 19F is a major cause of pneumococcal disease in children globally. Pneumococcal capsule is the antigen used in the construction of pneumococcal vaccines. However, due to its weak immunogenicity in children, it is chemically coupled to an immunogenic carrier protein. High manufacturing costs of these vaccines limit their implementation in developing countries. Optimizing cultivation conditions of microbial products has been used to improve the product yield and hence to reduce the manufacturing cost. In this study therefore we aim to evaluate effects of using different carbon and nitrogen sources in the culture medium on the serotype 19F pneumococcal capsule production.

Methods: *S. pneumoniae* ATCC 49619 was cultivated in Hoeprich's modified medium (HMM) at 37 °C for 18 h under static conditions. The pH of the medium was adjusted to 7.5. The capsule measurement was done using the stains all solution and reading the sample absorbance at 640 nm.

Results: HMM contains glucose and soytone as carbon and nitrogen sources respectively. The capsule production in HMM was 0.34 mg/ml. Replacing soytone with casamino acid as the nitrogen source increased the capsule production 1.3 fold. Using sucrose as the carbon source instead of glucose enhanced the capsule production 3.4 fold. Moreover the capsule production in the presence of lactose as the carbon source was comparable with that in the presence of sucrose. However lactose is cheaper than sucrose.

Conclusion: Lactose and casamino acid were appropriate carbon and nitrogen sources respectively for serotype 19F pneumococcal capsule production.

Keywords: Pneumococcal conjugate vaccine, capsular polysaccharide

مشکلات عفونی در نوزادان نارس بیمارستان تک تخصصی زنان حضرت ام البنین(س) مشهد: 565 - P990

Sakine Seddighi¹, Marzieh Ghazi², Akram Jafarzade Noghani (MSC)³, Fatemeh MoghaddShaer am⁴,
zahra asefi⁵, maliheh fareghi⁶, Batoul Khairkhah⁷

1. SeddighiS1@mums.ac.ir
2. GhaziM3@mums.ac.ir
3. JafarzadeNA1@mums.ac.ir
4. ShaerMF1@mums.ac.ir
5. AsefiBZ1@mums.ac.ir
6. FareghiM1@mums.ac.ir
7. KhairkhahB1@mums.ac.ir

Background and Aim: بیمارستانی مراقبتهای ویژه نوزادان، یکی از بخش های حساس بیمارستان از نظر عفونت های بخش: بیمارستانی در نوزادان را عفونتهای خون و سپتیمی تشکیل می است که کنترل آن اغلب با مشکل روبرو می شود. شایعترین عفونتهای

Methods: شد. ابراز جمع اوری اطلاعات، شامل پژوهش، توصیفی مقطعی بوده که از ابتدای سال ۱۳۹۴ تا پایان سال انجام این پرسشنامه بررسی رعایت بهداشت دست توسط پرسنل با استفاده از روش مشاهده پرسشنامه مشخصات دموگرافیک و عوامل درمان و و کمتر از ۳۰ با علل مراجعه نارس، هایپوگلیسمی و ابراز چک لیست بود. معیارهای ورود به مطالعه شامل کلیه نوزادان ۳۰ روزه ای راداشتند، بودند برای نیازمند مداخله که پس از ۴۸ ساعت بستری در بخش علایم بالینی عفونت و نیز نوزادان (RDS) و نشانگانز جرتنفس و تنظیم جداول توزیع فراوانی استفاده شد spss استفاده از نرم افزار تجزیه و تحلیل داده ها از روش های آمار توصیفی با

Results: که ۴۲/۸۵٪ مذکور در گروه تشخیص داده شده است این مطالعه ۱۲ مورد عفونت بیمارستانی در نوزادان بستری در نظر سن بارداری اکثریت ۷۸/۵۷٪ پره ترم بودند. بررسی مطالعه بر حسب سنی ۱۰-۱ روز بوده و زیر ۱/۵ کیلوگرم وزن داشتند. از بیماری مزمن ریوی ۱۴/۲۸٪ بوده درمانی نشان داد که علت اولیه بستری در مطالعه حاضر ۷۸/۵۷٪ موارد نارس و عوامل دارو ها اکثریت آنتروباکتری ۴۱/۶۶٪، کلبسیلا و استافیلوکوک ۲۵٪ بوده است. از بین است. ارگانیزم های جدا شده از کشتهای بترتیب باشند به ایمپنم حساس و به وانکو مایسین مقاوم و به سفنازودایم بینابین می

Conclusion: پرسنل در زمان کار به پژوهش لزوم دقت بیشتر در علل پیدایش پیشگیری از نارس و همچنین توجه بیشتر یافته های ها. توصیه میشود ویژه رعایت بهداشت فردی از همه مهمتر شستشوی مرتب دست

Keywords: عفونت، بخش مراقبت ویژه نوزادان، نوزادان

P991 - 582: MIR-20A AND MIR-17 AND THEIR POTENTIAL TARGETS IN JURKAT CELLS

Maryam Mapar¹, Seyed mehdi Sadat ², Najmeh Ranji ³, Mehrdad Hashemi⁴

1. Department of new science, Islamic Azad University, Tehran Medical Branch, Tehran,Iran
2. Department of Hepatitis and AIDS, Pasteur Institute of Iran, Tehran, Iran
3. Department of Genetics, College of Science, Rasht Branch, Islamic Azad University, Rasht, Iran.
4. Department of new science, Islamic Azad University, Tehran Medical Branch, Tehran,Iran

Background and Aim: Activation of the T cell-mediated immune response has been related with changes in the expression of specific microRNAs. Interleukin-2 plays a major role in activation of ways that lead to the proliferation, survival and production of cytokine of effector T cells. MicroRNAs play critical roles in Post-transcriptional gene expression. Recent studies have been done on the effect of IL-2 to cell proliferation but the role of miRNAs on these cells is not clear .The purpose of this study was evaluation of the effects of miRNAs cell signaling pathways under induction with IL-2 in Jurkat cells.

Methods: Transfection of miR-20a ,miR-17 and miR-neg genes was performed to Jurkat cells using Lipofectamine 2000 reagent. Putative targets of up/ down regulated miRNAs were predicted using Targetscan and miRWalk softwares. Cell viability was measured using XTT assay and expression of several putative targets JAK, AKT1 and AKT3 genes was evaluated by quantitative RT-PCR.

Results: Apoptosis induction by miR-20a and miR-17 in Jurkat cells was confirmed by XTT assay. Also, the expression of their potential target genes such as JAK, AKT1 and AKT3 were significantly down-regulated two-fold or more compared with the control cells.

Conclusion: miR-20a and miR-17 are two members of the miR-17-92 cluster, showed tumor suppression activity in Jurkat cells and during the process they could be able to down-regulated some of the genes involved in cell proliferation pathways such as JAK / STAT and PI3K / AKT and thereby inhibit their proliferation.

Keywords: Il-2, Jurkat cell, miR-20a, miR-17, XTT assay

P992 - 587: THE PREVALENCE OF SEXUAL RISK BEHAVIOR AND PROGNOSIS OF HIV INFECTION IN ADOLESCENTS AND YOUNG ADULTS IN LARESTAN CITY

Eghbal Sekhavati¹, Mojtaba rahimian boogar ², zahra raeisi³, sara bostani⁴, Nasrin sarafraz ⁵

1. Larestan school of medical sciences, Larestan, Iran
2. Larestan school of medical sciences, Larestan, Iran
3. Larestan school of medical sciences, Larestan, Iran
4. Larestan school of medical sciences, Larestan, Iran
5. school of nursing and midwifery , Islamic azad University , Larestan branch, Iran.

Background and Aim: HIV/AIDS, is one of the world's most serious health and development challenges. This research aimed to investigate the prevalence of sexual risk behavior and the prognosis of HIV infection in adolescents and young of Larestan city

Methods: This cross-sectional descriptive study was conducted with a survey, 960 samples was determined and selected by cluster sampling between the schools and universities of Larestan city. Data were collected by using researcher questionnaire which contains demographic information and attitude-care factors. And finally the statistics of frequency, percentage and average were used for the analysis of assumptions.

Results: The age range of participants in the study was 13 to 25 years old with an average of ($M = 19.84$; $SD = 2.17$). Results showed the high prevalence of sexual risk behavior among the study sample. Also, participants in the knowledge level variables, self-efficacy and self-care received low marks that express their poor performance in carrying out preventive measures of HIV infection. The findings suggest that transmission of the virus from mother who suffering from HIV, sex with high-risk with heterosexual and physical contact with infected patients infected with the virus are the most important factor in transmission of the virus.

Conclusion: Due to the poor performance of adolescents and young in self-care and the high prevalence of risk behavior in these groups, it is essential that measures is done to promote knowledge and skills of adolescents and young self-care

Keywords: risk behavior, HIV, knowledge, self-efficacy, self-care

P993 - 588: PREVALENCE OF PEDICULOSIS IN STUDENTS OF LARESTAN CITY IN 2015

Eghbal Sekhavati¹, Mojtaba Neydavodi², Mojtaba Rahimian boogar³, Kobra Abedi⁴, Zahra Mohammadi⁵,
Zahra raeisi⁶

1. Larestan school of medical sciences, Larestan, Iran
2. Larestan school of medical sciences, Larestan, Iran
3. Larestan school of medical sciences, Larestan, Iran
4. Larestan school of medical sciences, Larestan, Iran
5. Larestan school of medical sciences, Larestan, Iran
6. Larestan school of medical sciences, Larestan, Iran

Background and Aim: pediculosis is one of the most common infectious diseases in the community and according to the WHO Reports. Therefore, this study aimed to determine the prevalence of pediculosis in students of larestan city in 2015.

Methods: In this retrospective- descriptive study, all contaminated students with pediculosis statically was selected and studied that they were identified in health department screening program of Larestan and list of their information was registered in the system of this center. The instrument included a researcher-made checklist including demographic information. Finally the data was analyzed by using statistical-descriptive method and percentage and nonparametric inferential statistics and chi-square.

Results: The findings of this study reported that the overall prevalence of the contamination of pediculosis in students of Larestan was 2.4% (774 people) that according to these number, the prevalence by gender was estimated 4.6% for girls (719 patients) and 03/0 % for boys (n = 55) which this difference is approved by using chi-square significance index and in the significance level of 95% ($P < 0.05$). Also, pediculosis contamination in terms of location and level of education was a significant difference between the samples ($P < 0.05$).

Conclusion: Although based on findings is expected that the prevalence of this disease is lower in Larestan in compare with the global and country prevalence but it must be said that this amount is very significant at the regional level and it needs serious planning for controlling and eradicating of the contamination.

Keywords: contamination prevalence, pediculosis, Student

**P994 - 615: COMPARATIVE EVALUATION OF IMMUNE RESPONSES TO
LIPOPOLYSACCHARIDE AND DETOXIFIED LIPOPOLYSACCHARIDE OF LEGIONELLA
PNEUMOPHILA ALONE AND IN COMBINATION WITH BOVINE SERUM ALBUMIN IN
BALB/C MICE.**

Shaghayegh Papian¹, Ashraf Mohabati Mobarez², Armin Adelinik³

1. Tarbiat Modares University, Faculty of Medical Sciences, Department of Bacteriology, Tehran, Iran.
2. Tarbiat Modares University, Faculty of Medical Sciences, Department of Bacteriology, Tehran, Iran.
3. Islamic Azad University, Hamedan Branch, Faculty of Basic Sciences, Department of Molecular Biology

Background and Aim: Legionella pneumophila is capable of causing respiratory infections in patients who are sometimes caused death. Investigation the strategies that led to the induction of protective immunity against intracellular infections are of great importance in the prevention and treatment of patients at risk. Legionella lipopolysaccharide is one of the main factors in the pathogenesis of bacteria and clarifying the type and level of host immune responses to this structure will be effective the design of vaccines or treatments for these bacteria.

Methods: LPS of Legionella were extracted through hot phenol procedure and detoxified by alkaline treatment without chain fatty acids in the lipid A is obtained. Female BALB/c mice, aged between 6-8 weeks were immunized with LPS and d-LPS combination of BSA. Evaluation of antibodies and cytokines were measured by ELISA method and data analysis was performed using One-way ANOVA statistical method.

Results: The results show that the lipopolysaccharide and lipopolysaccharide detoxified Legionella pneumophila with fractions 5 bovine serum albumin (BSA) has been increased IgG antibody response and the cytokines IL-4, IL-12 and INF γ compared with Inserts alone lipopolysaccharide received. It seems lipopolysaccharide endotoxin property can by itself is stimulating cytokines. dLPS induced antibody response and cytokine stimulation.

Conclusion: We suggest that the present combined antigen may serve as a potent candidate in vaccine researches against Legionellae pathogens

Keywords: Legionella pneumophila, LPS, dLPS, BSA

**P995 - 634: IMMUNOGENICITY OF VACJ, AN OUTER MEMBRANE LIPOPROTEIN OF
ACINETOBACTER BAUMANNII**

Saideh Masoumkhani¹, Iraj Rasooli², Abolfazl Jahangiri³, Shakiba Darvish Alipour Astaneh⁴

1. M.Sc. Student, Department of Biology, Faculty of Basic Sciences, Shahed University, Tehran, Iran
2. Professor, Department of Biology, Faculty of Basic Sciences, Shahed University, Tehran, Iran
3. Ph.D. Candidate, Applied Microbiology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran
4. Assistant professor, Faculty of Biotechnology, Semnan University, Semnan, Iran

Background and Aim: *Acinetobacter baumannii* is a gram negative, strictly aerobic nonmotile bacterium with a DNA G-C content of 39% to 47%. *A. baumannii* is an important opportunistic pathogen that causes pneumonia, bacteremia, urinary tract infections, meningitis, skin and soft tissue infections. The major concern about *A. baumannii* is emergence of resistant strains which necessitates development of new prevention, control and treatment methods. Bacterial lipoproteins recently are used for inducing protective immunity against some of infectious diseases. VacJ is a highly conserved outer membrane lipoprotein that exists in many *A. baumannii* strains.

Methods: In this study, the genes encoding mature VacJ of *A. baumannii* strain ATCC19606 was cloned and over-expressed in *Escherichia coli* as a fusion protein. The recombinant VacJ (rVacJ) was purified. The purified rVacJ was used for immunizing mice with adjuvants (FCA).

Results: The rVacJ was successfully produced. The purified protein of ~31kDa was used to immunize mice. Antibody titre was read on an ELISA reader. The mice groups were challenge with live *A. baumannii* to find if the immunization was protective.

Conclusion: The rVacJ can be used as a candidate antigen for vaccine development against *A. baumannii*.

Keywords: *Acinetobacter baumannii* ; Immunogenicity; Outer membrane protein; Recombinant lipoprotein; VacJ.

**P996 - 676: COMPARATIVE CHEMO-PHYSICAL OUTER MEMBRANE VESICLES (OMVS)
ANALYSIS OF PSEUDOMONAS AERUGINOSA SENSITIVE , RESISTANT AND STANDARD
STRAINS**

Fereshteh Satarian¹, Seyed Davar Siadat², Farzam Vaziri³, Ava Behrouzi⁴

1. Islamic Azad University Science and Research Branch
2. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, IR Iran
3. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, IR Iran
4. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, IR Iran

Background and Aim: *Pseudomonas aeruginosa* is an opportunistic mucosal human pathogen causing acute and chronic infections in multiple organ systems and like the other gram negative bacteria secretes outer membrane vesicles (OMVs) in a variety of environments which play critical roles in pathogenicity in hosts. The OMV production and its composition have been found to be strain and environmental stress dependent .

Methods: *P. aeruginosa* sensitive , resistant and standard (ATCC 17933) strains were obtained from the standard Bacterial Collection of Pasteur Institute of Iran. OMVs were purified using differential centrifugation with deoxycholate and EDTA. The protein content of OMV were measured by Nano-drop and SDS-PAGE, eventually electron microscopy was performed to verify stability and totality.

Results: The results of electron microscopy and SDS-PAGE showed that *P. aeruginosa* standard and sensitive strains OMV were similar in size and density but different in protein composition and more bands in the standard strain . Resistant *P. aeruginosa* strain had dense OMV with different sizes and approximately sharper bands.

Conclusion: Previous findings indicate that naturally produced *P. aeruginosa* OMV modulate immune responses but the signaling pathway is not clearly understood so these data would be use for developing vaccines against Pseudomonal infections as a common nosocomial infections.

Keywords: OMV; chemo-physical analysis; *Pseudomonas aeruginosa*

**P997 - 686: EVALUATING THE PROTECTIVE EFFECTS OF POLYVALENT ANTIGEN OF
PSEUDOMONAS AERUGINOSA IN ANIMAL MODEL AS A POTENTIAL VACCINE**

Sanam Rezaei benem¹, Asghar Tanomand²

1. Department of Microbiology, Islamic Azad University, Ahar branch, Ahar, Iran
2. Department of Microbiology, Maragheh University of Medical sciences, Maragheh, Iran

Background and Aim: *Pseudomonas aeruginosa* (*P. aeruginosa*) is one of the opportunist pathogens that takes the advantage of patient's immunodeficiency and is one of the major causes of nosocomial infections. Multivalent vaccines such as using the collection of secretory antigens and inactivated or killed whole-cell can be effective in preventing the infections. Results of ELISA and pure microbial injection to probe the rate of prevention for mice showed that the sonicated antigens can have a more effective role in immunization and the prevention of mice death against *pseudomonas* infections.

Methods: In this study, sonicated multivalent antigen was provided and active immunization of mice between 6-8 weeks (4 groups each with 7 mice) was carried out by subcutaneous, intraperitoneal and intramuscular injections on days 0, 14 and 28. The fourth group was selected as the control group of the study. One week after each injection, on days 7, 21 and 35 blood samples were taken from mice and after isolating the serum, indirect ELISA was carried out to evaluate the produced IgG antibody against sonicated multivalent antigen of *P. aeruginosa*.

Results: According to the results, due to the complexity of *P. aeruginosa* pathogenicity, using multivalent vaccines such as the collection of somatic and secretory antigens, can be effective in the prevention of infections. The Elisa results showed significantly antibody production in subcutaneous, intraperitoneal and intramuscular injections groups comparing control group

Conclusion: Comparing the immunization of antigen based on the route of injection showed that there was not any significant difference in induced immunization by different groups (subcutaneous, intraperitoneal and intramuscular injections).

Keywords: *Pseudomonas aeruginosa*, multivalent antigen, immunization, vaccine candidate

**P998 - 700: ANTIMICROBIAL SUSCEPTIBILITY OF CLOSTRIDIUM ISOLATES FROM
OSTRICHES**

Majid Ezzatkah¹, Majid Ezatkah², Mojtaba Alimolaei³

1. Department of Anaerobic Bacterial Vaccine Research and Production, Kerman branch, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran
2. Department of Molecular Microbiology, Kerman branch, Razi Vaccine and Serum Research Institute, Kerman branch, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran

Background and Aim: Clostridium species are gram-positive, spore forming, and anaerobic bacteria. The purpose of this study was to evaluate of antimicrobial susceptibility clostridial isolates from ostriches.

Methods: A total of 40 Clostridium isolates (30 *C. perfringens* isolates, 3 *C. sphenoides* isolates, 2 *C. innocuum* isolates, and one isolate from every of *C. baratii*, *C. septicum*, *C. butyricum*, *C. putrificum*, and *C. histolyticum* isolates) that previously were confirmed by biochemical tests as described in Bergey's manual. These isolates were screened for antibiotic resistance profiles with 14 antimicrobial discs by Kirby-Bauer disc diffusion method as described by the National Committee for Clinical Laboratory Standards (NCCLS).

Results: Results were shown the relative susceptibility to the most of tested antibiotics. The highest prevalent resistance rates were recorded against penicillin and streptomycin (70% and 65%, respectively).

Conclusion: High resistance rates of clostridial isolates to penicillin and streptomycin antibiotics may be related to the high usage of Pen/Strep compound in veterinary medicine, potentially reflecting the high usage of these antibiotics in ostrich farms.

Keywords: Clostridium, Ostriches, Antimicrobial susceptibility, Antibiotics

**P999 - 701: POSSIBLE RELATIONSHIP BETWEEN CYTOMEGALOVIRUS INFECTION AND
NEUROMYELITIS OPTICA AND MULTIPLE SCLEROSIS**

Mahboobe Jazini¹, Roghanian Rasoul ², Mirmosayyeb Omid³, Zarkesh Esfahani Sayyed Hamid ⁴,
Shaygannejad Vahid ⁵

1. Microbiology M.Sc. student, Department of Biology, Faculty of Sciences, University of Isfahan
2. Associate professor, Department of Biology, Faculty of Sciences, University of Isfahan
3. Medical student, Department of Neurology, Isfahan Neuroscience Research Center (INRC), Isfahan University of Medical Sciences, Isfahan, Iran
4. Associate Professor, Department of Biology, Faculty of Sciences, University of Isfahan
5. Professor, Department of Neurology, Kashani Hospital, Isfahan Neuroscience Research Center (INRC), Isfahan University of Medical Sciences, Isfahan, Iran

Background and Aim: Neuromyelitis optica (NMO) is a demyelinating disease of the central nervous system that autoantibodies react against aquaporin-4(AQP4) expressed on astrocytes. NMO has clinical manifestations resembling those of Multiple Sclerosis (MS). The presence of AQP4 antibody in NMO patients is a hallmark factor that differentiate the NMO from MS. Viruses can cause inflammation in white and grey matter of the brain. Inflammatory alterations facilitate transfer of autoantibody from blood-brain barrier. The aim of this study was to evaluate the possible association between Cytomegalovirus (CMV) infection and NMO and MS.

Methods: In order to assess the presence of CMV, Real Time PCR was performed on serum samples from 25 NMO patients, 30 MS patients and 30 healthy individuals as control.

Results: Despite validity of Real Time PCR assay which was confirmed using internal controls and housekeeping genes, none of the sample was positive for CMV in any of the patients or the controls.

Conclusion: Despite high incidence of CMV infection and high sensitivity of Real Time PCR for detection of CMV virus, we could not detect any CMV contamination in any of the samples.

Keywords: Neuromyelitis optica -Cytomegalovirus -Aquaporin-4

P1000 - 703: PRODUCTION OF IGY ANTI MOUSE IGG ANTIBODY IN QUAIL.

Kaveh Veisi¹, Yoones Attari², Khalil Ghoriani³, Khalil Alalo ⁴, Gholamreza Nikbakht⁵

1. Department of Microbiology and immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
2. Department of Microbiology and immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
3. Department of Microbiology and immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
4. Department of Microbiology and immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
5. Department of Microbiology and immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran

Background and Aim: Egg yolk antibodies (IgY) have increasing role as an alternative Polyclonal antibodies in mammals. This antibodies are using in the prevention, diagnosis and treatment of diseases. The aim of this study Production production of IgY anti mouse IgG antibody in quail.

Methods: Six weeks old quail were obtained from a local breeding unit. These quails were immunized with mouse IgG and booster doses were given 2 and 6 weeks after first injection. Eggs were collected weekly after first immunization for 12 weeks. Yolk IgY was isolated using precipitation method of water dilution combined with chloroform. ELISA were used for determining the quantifying the titer of IgY in egg yolks.

Results: Reactive egg yolk samples were used for ELISA checkerboard titration. According to the checkerboard titration, the best concentrations were found. ELISA showed acceptable amount of anti-mouse IgG in most weeks after immunization and the peak value was in the 6th week.

Conclusion: According to ELISA results, anti mouse IgG could be produced. our results suggest that qualis could be used instead of hens for efficient production of specific IgY antibodies.

Keywords: IgY, anti mouse IgG antibody, quail, ELISA

P1001 - 709: COMPARATIVE SENSITIVITY ANALYSIS BETWEEN TWO METHODS FOR SPECIES DIFFERENTIATION AND INTERSPECIES CROSS CONTAMINATION IN ANIMAL CELL CULTURE

ASHRAF MOHAMMADI¹, Abolhasan Foroughi², Raihaneh Ghorbani³, Fatemeh Esnaashari⁴, zohreh Azita Sedigh⁵, Behnam Alirezaii⁶

1. SCIENTIFIC MEMBER of RAZI VACCINE AND SERUM RESEARCH INSTITUTE
2. SCIENTIFIC MEMBER of RAZI VACCINE AND SERUM RESEARCH INSTITUTE
3. SCIENTIFIC MEMBER of RAZI VACCINE AND SERUM RESEARCH INSTITUTE
4. SCIENTIFIC MEMBER of RAZI VACCINE AND SERUM RESEARCH INSTITUTE
5. SCIENTIFIC MEMBER of RAZI VACCINE AND SERUM RESEARCH INSTITUTE
6. SCIENTIFIC MEMBER of RAZI VACCINE AND SERUM RESEARCH INSTITUTE

Background and Aim: The present article focuses on design and development of a highly sensitive and convenient approach for rapid detection of animal species and cross contamination quickly during cell cultures as most important document for manufacturing working cell bank system.

Methods: A PCR _RFLP assay was optimized based on the use of a pair of primers that anneal to a portion the cytochrome b gene in all the species. The amplification product was digested with a panel of six restriction enzyme and the pattern derived was resolved on 3% high resolution agarose gel for 2 species, human & primate. As a control test we used from conventional method iso enzyme assay.

Results: This protocol produced a unique restriction pattern and the origin of this animal cells resulted to be confirmed by this analysis. Its sensitivity in detecting interspecies cross contamination was at least 100 pg DNA/reaction, which was sufficient for detection of each species of DNA.

Conclusion: Using the method (PCR-RFLP) developed during this research not only significant differences between human and non human also cross- contamination between different cell lines can simply distinguish.

Keywords: cell authentication cross contamination-PCR-RFLP assay-restriction enzyme

**P1002 - 710: OPTIMIZATION OF VERO / MICROCARRIER CELL CULTURE FOR
PRODUCTION OF HIGH TITER VIRUS VACCINE SEED**

Ashraf Mohammadi¹, Abolhasan Foroughi², Raihaneh Ghorbani³, Fatemeh Esnaashari⁴, zohreh Azita Sedigh⁵, Behnam Alirezaii⁶

1. SCIENTIFIC MEMBER of RAZI VACCINE AND SERUM RESEARCH INSTITUTE
2. SCIENTIFIC MEMBER of RAZI VACCINE AND SERUM RESEARCH INSTITUTE
3. SCIENTIFIC MEMBER of RAZI VACCINE AND SERUM RESEARCH INSTITUTE
4. SCIENTIFIC MEMBER of RAZI VACCINE AND SERUM RESEARCH INSTITUTE
5. SCIENTIFIC MEMBER of RAZI VACCINE AND SERUM RESEARCH INSTITUTE
6. SCIENTIFIC MEMBER of RAZI VACCINE AND SERUM RESEARCH INSTITUTE

Background and Aim: The cell line Vero is a continuous, adherent cell line, which has been recommended by the World Health Organization for the production of human vaccines. For the large-scale production of vaccines, microcarriers which are microspheres that serve as support for the cells are being increasingly used. The use of micro carriers in stirred bioreactors allows high cell densities and, consequently, high virus titers to be achieved

Methods: With the aim of Selecting appropriate culture conditions for the cultivation of Vero cells at high cell densities, in this work the Influence of several variables (agitation rate, ratio of inoculated cells to microcarrier mass and fetal bovine serum concentration) PH of media and the amount of microcarrier on cell growth on Cytodex 1 microcarriers was studied.

Results: We can adjusted the condition of Cytodex 1 microcarriers /Vero considering the PH of media ,agitation rate of stirrer , the amount of bead , time and amount of changing media , Kinetics of cell growth and polio T1 virus production were investigated in spinner flask and in compare of Roux bottle 175 cm²..

Conclusion: Under the best conditions determined, a comparison with Vero cell cultivation on mono layer in roux flask and microcarrier was carried out. we can get >1.5 log TCID₅₀ in viral vaccine titre considering to Vero/cytodex Culture.

Keywords: Vero cells, microcarriers, Cytodex 1, spinner flask, high-cell-density cultivation

**P1003 - 732: THE RECOMBINANT ANTIGENS USED AS EXPERIMENTAL VACCINES
AGAINST OLD WORLD CUTANEOUS LEISHMANIASIS : A SYSTEMATIC REVIEW**

Pooya Ghasemi Nejad Almani¹, Iraj Sharifi², Samira Salari³

1. Department of Medical Parasitology and Mycology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran
2. Leishmaniasis Research Center, Kerman University of Medical Sciences, Kerman, Iran
3. Department of Medical Parasitology and Mycology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran

Background and Aim:Leishmaniasis is a major health challenge worldwide. First-line drugs are no longer effective as before, therefore; development of an innovative vaccine is highly essential. The objective of this review was to explore the recombinant or DNA vaccines against Old World cutaneous leishmaniasis (CL) through a systematic review of the literature.

Methods:Literature databases including MEDLINE, EMBASE, and the Cochrane library from 2006 up to 2016 and keywords including Cutaneous, Leishmania, recombinant, vaccine, protein, and antigen were searched. Totally, 58 articles were found. Finally, 31 articles were included in the research topic.

Results:The recombinant antigens used as vaccines are as follows: heat shock protein 70 (HSP70), Leishmania homologue of receptors for activated C kinase (LACK), nucleosomal histones (H2A, H2B, H3 and H4), cysteine proteinase type I (cpa), II (cpb) and III (cpc), stress-inducible protein 1 (LmSTI1), recombinant nucleoside hydrolase, trypanothione peroxidase (TRYP), thiol-specific antigen (TSA), Leish-111f (TSA, LmSTI1 and LeIF), Leish-110f, MAP kinase 10 (LmjMAPK10), lipophosphoglycan 3 (LPG3), amastin, gamma glutamyl cysteine synthetase (GCS), kineto-plastid membrane protein 11 (KMP11), sterol 24-c-methyltransferase (SMT), A2, KSAC, recombinant major surface glycoprotein of Leishmania (rgp63), recombinant ribosomal proteins L3 or L5, peroxidoxin-1 (LdPxn-1), poly (A) binding proteins (LiPABPs) and sand fly salivary antigen : PpSP15 and LJM11

Conclusion:Based on the current evidence, most antigens used as vaccines have respectively been as follows : LmSTI1, cysteine proteinase, LACK and nucleosomal histones. Development of protective vaccines against Leishmania depends on antigens and adjuvants that induce appropriate immune responses.

Keywords:cutaneous, Leishmania, recombinant, vaccine, protein, antigen

**P1004 - 733: COMPARISON INTERACTIONS BETWEEN IMMUNOGENIC EPITOPES OF
TOXOPLASMA GONDII AND MHC CLEFT IN HUMAN AND SHEEP USING MOLECULAR
DYNAMICS SIMULATIONS**

Soudabeh Soltani¹, Karim Mahnam², Behnaz Saffar³, Mostafa Shakhsi Niaii⁴, Mohammad Reza
Mahzunieh⁵

1. Master of Microbial Biotechnology, University of Shahrekord, Shahrekord, Iran
2. Department of Biochemistry, College of Sciences, University of Shahrekord, Sharekord, Iran
3. Department of Genetic, College of Sciences, University of Shahrekord, Sharekord, Iran
4. Department of Genetic, College of Sciences, University of Shahrekord, Sharekord, Iran
5. Department of Immunology, College of Veterinary Medicine, University of Shahrekord, Sharekord, Iran

Background and Aim: Toxoplasmosis is an important zoonosis and cause of congenital disease and abortion in sheep and human. The immune system is engaged in a constant antigenic control by the Major Histocompatibility Complex (MHC) class I antigen presentation pathway therefore this is an effective mechanism for detection of intracellular infections.

Methods: In this work some of immunogenic epitopes of toxoplasma gondii were selected with on-line prediction softwares and then 3D structure of them were built by Hyperchem 8 and used for molecular dynamic simulation by Gromacs 5 for 100 ns in NPT ensemble in presence of water molecules and ions, then 3D structure of MHC class I in human and sheep were built by modeler 9.16 and the best models were user for 10 ns MD simulation at NPT ensemble. Finally, the obtained structures of epitopes were docked to MHC class I cleft in human and sheep by HADDOCK web server.

Results: According to docking results, the selected immunogenic epitopes can bind to both MHC cleft in human and sheep and have negative binding energy.

Conclusion: The approach used in this work allows the selection of epitopes with potential to induce immune responses and the development of more comprehensive vaccines for both sheep and human.

Keywords: Epitopes of toxoplasma gondii, MHC cleft, Molecular dynamics simulations, Vaccine

**P1005 - 735: MOLECULAR DYNAMICS SIMULATIONS IMMUNOGENIC EPITOPS OF
SURFACE ANTIGEN 1 (SAG1) FROM TOXOPLASMA GONDII AND HUMAN LEUKOCYTE
ANTIGEN (HLA) FOR THE DESIGN OF EFFECTIVE VACCINE**

Soudabeh Soltani¹, Behnaz Saffar², Karim Mahnam³, Mostafa Shakhshi Niaii⁴, Mohammad Reza
Mahzunieh⁵

1. Master of Microbial Biotechnology, University of Shahrekord, Shahrekord, Iran
2. Department of Genetic, College of Sciences, University of Shahrekord, Sharekord, Iran
3. Department of Biochemistry, College of Sciences, University of Shahrekord, Sharekord, Iran
4. Department of Genetic, College of Sciences, University of Shahrekord, Sharekord, Iran
5. Department of Immunology, College of Veterinary Medicine, University of Shahrekord, Sharekord, Iran

Background and Aim:Infection with *Toxoplasma gondii* occurs in worldwide that cause infection of humans. *Toxoplasma gondii* is an important parasite that transmit from animals to humans by meat, mainly from pigs and lambs, and oocysts throw by cats into the environment. SAG1, the major surface antigen of *Toxoplasma gondii*, is a highly immunogenic protein which cause invasion of host cells.

Methods:In this study, 65-72, 101-109, 199-206 and 270-278 residue fragment of SAG1 sequence were selected and after making 3D structure of them by Hyperchem 8 were used for 100 ns MD simulation. The nearest crystal structure to HLA-A obtained from the Protein Data Bank (PDB code: 2XPG). Then the final structure obtained from MD simulation of SAG1 epitopes fragments were docked to HLA-A structure for investigated binding of discontinuous and linear epitopes with HLA-A using Haddock web server.

Results:Our docking results confirmed that selected epitopes could bind to HLA-A cleft.

Conclusion:These results can use to design of efficient vaccine for toxoplasmosis in human.

Keywords:Molecular dynamics simulations, SAG1, HLA-A

P1006 - 783: CLONING, EXPRESSION, PURIFICATION AND IMMUNIZATION OF HMW1, HMW2 AND HIA ADHESIN PROTEINS AS A VACCINE CANDIDATES OF NONTYPEABLE HAEMOPHILUS INFLUENZAE(NTHI)

Kazem Abbaszadeh Goudarzi¹, Kazem Abbaszadeh-Goudarzi², Ladan Teimoori-Toolabi³, Seyed Davar Siadat⁴, Mohammad Reza Khorramizadeh⁵, Saeid Bouzari⁶, Sassan Rezaie⁷, Ghasem Abbaszadeh-Goudarzi⁸, Mahdi Davari⁹

1. Department of Medical Biotechnology, School of Advanced Technologies in Medicine, Tehran University of medical Sciences, Tehran, Iran
2. Department of Molecular Medicine, Biotechnology Research Center, Pasteur Institute of Iran, Tehran, Iran
3. Department of Tuberculosis and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran
4. Department of Medical Biotechnology, School of Advanced Technologies in Medicine, Tehran University of medical Sciences, Tehran, Iran
5. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
6. Department of Medical Mycology & Parasitology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
7. Department of Medical Biotechnology, School of Advanced Technologies in Medicine, Tehran University of medical Sciences, Tehran, Iran
8. Department of Tuberculosis and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Nontypeable *H. influenzae* (NTHi) is ordinarily commensal of human upper respiratory tract and pathogenesis begins with bacterial colonization of nasopharynx resulting in human respiratory tract diseases such as otitis media, sinusitis and pneumonia. Although effective vaccines against Hib-strains have been widely used, there is no vaccine against NTHi-induced diseases. HMW1, HMW2 and Hia are the major virulence factor of NTHi, they have important roles in attachment to epithelial cells and could be a good vaccine candidates to provide protection against NTHi infections.

Methods: Binding domain of HMW1, HMW2 and Hia genes were amplified by PCR and then genes cloned and subcloned into PTG19-T and pET-28a as a cloning and expression vectors respectively and confirmative tests such as colony-PCR, enzymatic digestion and gene sequencing were performed. Expression vectors transformed into competent BL21(DE3). Recombinant proteins were overexpressed with IPTG. SDS-PAGE and western blotting performed to evaluate protein determination and verification after purified by Ni-NTA. BALB/c mice immunized subcutaneously with HMW1, HMW2 and Hia proteins mixed with Freund's adjuvant. Eventually, antibody responses and functionality were determined by ELISA and SBA respectively.

Results: The antibodies responses significantly increased in immunized group with purified HMW1, HMW2 and Hia proteins mixed with Freund's adjuvant in comparison with control. Antisera produced against HMW1, HMW2 and Hia proteins showed significantly bactericidal activity against NTHi-strain in comparison with control.

Conclusion: Antisera from immunized animals with HMW1, HMW2 and Hia showed significantly increase in antibodies responses and shown bactericidal activity against NTHi-strain. These results suggest that HMW1, HMW2 and Hia adhesin proteins are potential vaccine candidate for prevention of NTHi infections.



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Keywords: NTHi, HMW1, vaccine candidate, pET-28a

**P1007 - 807: EVALUATION OF AN INCREASE IN PROTEIN SYNTHESIS IN THE PARASITE
PLASMODIUM VIVAX DUFFY BINDING FORM AS A MARKER PROTEIN HEMATOMA
STAGE MALARIA VACCINE ARASBARAN, IRAN.**

Saeed Tarzi¹, Farzin Habashi²

1. MSc student of Microbiology, Azad University of Ahar, Iran
2. MSc student of Microbiology, Azad University of Ahar, Iran

Background and Aim: Malaria is a parasitic disease and is one of the most important health issues, a number of countries, especially in tropical countries around the world. Palodism names such as malaria, fever and chills, ague and fever frequently called

Methods: since the molecular diagnosis of Plasmodium vivax malaria in blood samples obtained from endemic areas in the city of Tabriz in 100 samples using primers complementary Arasbaran sequence contains the amino acid II the protein was 15. And nucleic acid sequences and amino acid sequences for the desired SAL-I isolated Plasmodium vivax isolates were compared with other established and common forms were identified

Results: so in this research finding adequate amounts of antigen pv-DBP-II to satisfy the goals of the later research which is to study antigenicity and discovering the natural form of protein, by means of antibodies produced against a recombinant form which is detected in serum of the inhabitants of the endemic spot of malariya, was made possible

Conclusion: 95% of cases of Plasmodium vivax malaria in endemic areas of south-eastern Iran. Given the importance of this issue in Iran and the Ministry of Health plans to remove it from endemic areas by 2020, achieve effective vaccine in the methods of control, necessary and needed. Duffy protein (DBP) in a major role in the evolution of the parasite Plasmodium vivax blood-stage infection during non-sexual. Mrvzvyythay the parasite to invade human erythrocytes requires the Duffy blood group antigen (DARC) as a receiver surface and should DBP-DARC interaction for the invasion of the host cell used

Keywords: Plasmodium vivax, Duffy binding protein, synthesis system Pqe30, E.coli

**P1008 - 819: COMPARISON INTERACTIONS BETWEEN IMMUNOGENIC EPITOPES OF
TOXOPLASMA GONDII AND MHC CLEFT IN HUMAN AND SHEEP BY MOLECULAR
DYNAMICS SIMULATIONS**

Soudabeh Soltani¹, Karim Mahnam², Behnaz Saffar³, Mostafa Shakhsi Niaii⁴, Mohammad Reza
Mahzunieh⁵

1. Master of Microbial Biotechnology, University of Shahrekord, Shahrekord, Iran
2. Department of Biochemistry, College of Sciences, University of Shahrekord, Sharekord, Iran
3. Department of Genetic, College of Sciences, University of Shahrekord, Sharekord, Iran
4. Department of Genetic, College of Sciences, University of Shahrekord, Sharekord, Iran
5. Department of Immunology, College of Veterinary Medicine, University of Shahrekord, Sharekord, Iran

Background and Aim:Toxoplasmosis is an important zoonosis and cause of congenital disease and abortion in sheep and human. The immune system is engaged in a constant antigenic control by the Major Histocompatibility Complex (MHC) class I antigen presentation pathway therefore this is an effective mechanism for detection of intracellular infections.

Methods:In this work some of immunogenic epitopes of *Toxoplasma gondii* were selected with on-line prediction softwares and then 3D structure of them were built by Hyperchem 8 and used for molecular dynamic simulation by Gromacs 5 for 100 ns in NPT ensemble in presence of water molecules and ions, then 3D structure of MHC class I in human and sheep were built by modeler 9.16 and the best models were used for 10 ns MD simulation at NPT ensemble.

Results:Finally, the obtained structures of epitopes were docked to MHC class I cleft in human and sheep by HADDOCK web server. According to docking results, the selected immunogenic epitopes can bind to both MHC cleft in human and sheep.

Conclusion:The approach used in this work allows the selection of epitopes with potential to induce immune responses and the development of more comprehensive vaccines for both sheep and human.

Keywords:Epitopes of *Toxoplasma gondii*, MHC cleft, Molecular dynamics simulations, Vaccine

**P1009 - 826: INVESTIGATION OF L1 GENE EXPRESSION FROM TYPE33 OF HUMAN
PAPILLOMA VIRUS IN ESCHERICHIA COLI**

Parinaz Mohtasebi¹, Hossein Rassi²

1. Department of Biology , Karaj Islamic Azad University
2. Department of Biology , Karaj Islamic Azad University

Background and Aim: Human papillomavirus (HPV) infection is the most common sexually transmitted disease in the world and is related to the etiology of cervical cancer.

Methods: This study was carried out for the 40 fresh samples from patients in gynecology department that was investigated in Kamali hospital. After, DNA extraction from archival samples HPV types detected by multiplex PCR with HPV-16, HPV-18, HPV-33, HPV-35 primers. Then, full L1 gene of HPV33 cloned and expressed in E.coli.

Results: Results show that HPV type 33 accounts for about 5% of all HPV infections. Amplification of L1 gene by PCR reaction with L1 primers contain EcoRI and XhoI restriction site was done, then the gene were cloned into the pTG-19 vector. Recombinant vector were transferred in the E.coli (DH5 α) and recombinant bacteria in the LB culture were screened using X-Gal and IPTG. L1 were cloned into the pET32a for expression. The recombinant vector were transformed in the E.coli BL21DE3 and correction of transformation tested by using colony PCR.

Conclusion: The results confirmed by the extraction of proteins in SDS-PAGE electrophoresis and estimated at 57 kD. In general, the procedure for L1 gene expression in bacteria is inexpensive and it can be a candidate for cervical cancer as a nano-particles viral vaccine.

Keywords: L1 gene expression , HPV type33 , Escherichia coli

**P1010 - 840: PPD MODIFIED IMMUNE RESPONSES VERSUS KILLED LEISHMANIA
VACCINE**

FARZANEH BALKANIAN¹, Mohsen Zagar ², Fariborz Bahrami ³, Mehdi Mahdavi ⁴

1. Department of Microbiology, Qom branch, Islamic Azad University, Qom, Iran
2. Department of Microbiology, Qom branch, Islamic Azad University, Qom, Iran
3. Department of Immunology, Pasteur Institute of Iran, Tehran, Iran
4. Department of Immunology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim:Leishmaniasis are parasitic diseases caused by protozoan flagellates of the genus Leishmania. There is no effective vaccine against Leishmania infection. The success of adjuvants in enhancing the immune response to antigens has led many researchers to re-focus their vaccine development programs. Here, PPD is used as an adjuvant to improve immune response versus killed leishmania vaccine model.

Methods:Leishmania Major were propagated in culture and killed via exposure to thiomersal. Balb/c mice were immunized s.c with killed Leishmania with 1, 10 and 50 µg of PPD and PBS group was considered as negative control. Mice immunized three times with two weeks interval and two weeks after last immunization total IgG, IgG1 and IgG2a isotypes, IL-4 and IFN-γ cytokines assessed with ELISA. Lymphocyte proliferation assessed with BrdU method

Results:Results of the present study show that formulation of killed Leishmania vaccine with PPD enhances IFN-γ cytokine response and shifted immune response toward strong Th1 pattern.

Conclusion:PPD as an immunomodulator can be used as an adjuvant to improve Th1 cytokine pattern.

Keywords:Adjuvant, PPD, Killed Leishmania, Th1

**P1011 - 844: IMMUNIZATION WITH HPV16E7D VACCINE MODIFIED CYTOKINES
PATTERN IN TUMOR MICROENVIRONMENT**

Pariya Mahin samadi¹, Mohammad Hossein Yazdi ², Setareh Haghighat ³, Mehdi Mahdavi ⁴

1. 1Department of Microbiology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, Iran
2. Department of Research and Development, Pasteur Institute of Iran, Karaj, Iran
3. 1Department of Microbiology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, Iran
4. Department of Immunology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Immune response pattern in tumor environment determines the outcome of tumor and disease prognosis. Therefore, induction of cellular immune response in this condition and decrease of suppressor immune responses may result in controlling and suppression of tumor progression. In the present study, after immunization with HPV17E7d vaccine in tumor bearing mice, the balance of inflammatory and anti-inflammatory cytokines was evaluated in the tumor microenvironment

Methods: Tumor from TC1 cell line was developed in C57BL/6 mice with transplantation. Experimental C57BL/6 tumor bearing mice were vaccinated three times with two weeks intervals with 20 µg of E7d protein formulated in alum and Montanide ISA 206 adjuvants with proper control groups. Two weeks after final immunization, tumor homogenate was prepared and the concentration of it was determined via Bradford method. Then the quantity of TGF-β, IL-17, TNF-α and IL-2 cytokines were evaluated with commercial ELISA kits.

Results: Results show that immunization with vaccine candidate decreased TGF-β as suppressive cytokine in tumor microenvironment versus PBS control group. In addition, it can increase IL-2 and IL-17 as stimulant cytokines in this condition.

Conclusion: Overall, results of the present study show that immunization with E7d vaccine candidate can modify tumor microenvironment and thereby could change outcome on tumor prognosis.

Keywords: HPV16E7d, Tumor, Cytokines, Tumor environment

**P1012 - 847: COMPARISON OF THREE NEW VARIETIES OF NEOSPORA CANINUM TO
INDUCE IMMUNE RESPONSE IN MOUSE**

Maryam Sabouri shirazi¹, Mehdi Namavari²

1. Department of Microbiology, Islamic Azad University, Shiraz, Iran
2. Razi Vaccine and Serum Research Institute, Shiraz, Iran

Background and Aim: Neospora caninum is a protozoan parasite that infects a large spectrum of domestic and wild mammals. There is no efficient vaccine or drug to prevent abortion or transplacental infection in cattle. Currently is the best choice to achieve effective vaccine is a live vaccine. On base these facts the aim of this study evaluation of 3 new varieties of N. caninum as experimental live vaccine to introduce for further researches.

Methods: Thirty and two female BALB/c mice with average age of 6-8 weeks were randomly divided in to 4 groups. The groups 1-3 immunized by varieties 1-3 of N. caninum respectively. The 4th group as control was received cell culture media. All groups were inoculated subcutaneously two times with 14 days interval. Blood samples were collected from the mice 3 weeks after the second injection and the humoral immunity were assessed by ELISA.

Results: The results of present study showed there were no dead or pathological signs of neosporosis in all groups therefore the 3 new varieties of N. caninum were non virulent. Results of ELISA assay showed significant difference between groups 1-3 and control group this finding means all 3 varieties could induce immune responses against of N. caninum.

Conclusion: Among these varieties, The variety No. 3 created higher humoral immune response than others. Hence the variety No. 3 could be used as candidate for further research to develop live vaccines against N. caninum.

Keywords: Neospora caninum, 3 new varieties, ELISA

P1013 - 855: MOLECULAR CHARACTERIZATION OF RAZI PM 0002/1982, AN AVIAN VACCINE STRAIN OF PASTEURELLA MULTOCIDA, BY MULTI LOCUS SEQUENCE TYPING (MLST)

MAHIA IRANSHAHI¹, KEYVAN TADAYON², LISA SPRAGUE³, PATRICK BLACKALL⁴,
HEINRICH NEUBAUER⁵, RAINAK GHADERI⁶, MOHAMMAD SEKHAVATI⁷, REZA
BANIHASHEMI⁸, SABA ZATI BORHANI⁹, SAHAR ABBASI¹⁰

1. Islamic Azad University of Rasht, Science & Research Branch of Guilan, Rasht, Iran
2. Razi Vaccine Serum Research Institute
3. Friedrich-Loeffler-Institut Bundesforschungsinstitut für Tiergesundheit Federal Research Institute for Animal Health Naumburger, Jena, Germani
4. Poultry CRC Head Office, University of New England, Armidale, Australia
5. Friedrich-Loeffler-Institut Bundesforschungsinstitut für Tiergesundheit Federal Research Institute for Animal Health Naumburger, Jena, Germani
6. Razi Vaccine Serum Research Institute
7. Razi Vaccine Serum Research Institute
8. Razi Vaccine Serum Research Institute
9. Islamic Azad University of Rasht, Science & Research Branch of Guilan, Rasht, Iran
10. Islamic Azad University of Rasht, Science & Research Branch of Guilan, Rasht, Iran

Background and Aim: In Asia, *Pasteurella multocida*, the causative agent of fowl cholera is still a serious threat to poultry farming with considerable economic losses. In 1982 a surge of fowl cholera was reported in the Northern Iranian provinces of Mazandaran and Gilan that continued for three consecutive years. The strain of *Pasteurella multocida* (later named as Razi Pm 0002/1982) associated with this outbreak was selected for vaccine preparation. The strain has been continuously used for fowl cholera vaccine production since then.

Methods: To genetically characterize this strain, the Australian version of a Multi Locus Strain Typing (MLST) genotyping system was used. In this system, specific partial segments of 7 housekeeping genes (*etd*, *adk*, *est*, *gdh*, *mdh*, *pgi*, *pmi* and *zwf*) are analyzed for Single Nucleotide Polymorphisms (SNPs).

Results: The individual allelic profile of the examined strain for *adk*, *est*, *gdh*, *mdh*, *pgi*, *pmi* and *zwf* genes proved to be 21, 33, 26, 2, 17, 20 and 20, respectively.

Conclusion: According to the Australian RIRDC (the Rural Industries Research and Development Corporation)-MLST database, this combination represents ST 129 sequence type. This well-known clone encompasses 52 strains with only three not being associated with poultry (one from cow/buffalo, one from a pig and one from anemu) across the world. It is likely that further strains of ST 129 are circulating in poultry in Iran. Further study is required.

Keywords: *Pasteurella multocida*, MLST, vaccine, Fowl Cholera

**P1014 - 917: COMPARATIVE ASSESSMENT OF WHOLE CELL PERTUSSIS VACCINE
POTENCY WITH SEROLOGICAL AND INTRACEREBRAL MOUSE PROTECTION
METHODS**

Davoud Mohammadbagher¹, Mojtaba Noofeli², Gharib Karimi³

1. Department of human bacterial vaccines, Razi Vaccine and Serum Research Institute, Karaj, Iran
2. Department of human bacterial vaccines, Razi Vaccine and Serum Research Institute, Karaj, Iran
3. Blood Transfusion Research Center, High Institute for Research and Education in Transfusion Medicine, Tehran, Iran

Background and Aim:: Based on WHO requirements, one of the most important QC tests of whole cell pertussis vaccine(WCPV) is potency test. Current and mandatory method(Mouse Protection Test, MPT) is associated with large variability in results and severe animal distress. The aim of this study is to assess a serological alternative method(Pertussis Serological Potency Test, PSPT), for the Intracerebral challenge method(MPT) in mice to determine the potency of WCPV.

Methods:Potency of three batches of WCPV and one NIBSC standard vaccine were assessed by MPT and PSPT methods. In MPT, mice immunized with three doses of tests and standard vaccines, two weeks later mice challenged with *Bordetella pertussis* (strain of 18323) via intracerebral route. Two weeks after challenge, numbers of dead and alive mice were counted and potency of vaccines calculated with parallel line analysis. In PSPT, mice were immunized as like as MPT and bled after four weeks, then sera titrated in WCP-ELISA and potency was estimated based on vaccine dose dependent antibody response with parallel line analysis. Correlation of MPT and PSPT results was assigned with pearson statistical method.

Results:Potency of three batches of WCPV with respect in MPT(11.14, 5.02 and 4.24 Iu/ml) and in PSPT(10.32, 4.11 and 3.06 Iu/ml) was assigned. Correlation of MPT and PSPT results was appointed(0.807).

Conclusion:The results of this study confirmed suitable correlation between MPT and PSPT results in assessment of WCPV potency. PSPT showed more advantages to compare with MPT including ethical approaches and less variability in results.

Keywords:Whole cell pertussis vaccine, MPT, PSPT, Potency, ELISA.

**P1015 - 973: RESOLUTION POWER OF TWO TANDEM REPEAT LOCI IN
DIFFERENTIATION BETWEEN THE RAZI BP0134 & RAZI 0509 VACCINE STRAINS OF
BORDETELLA PERTUSSIS**

MASOMEH FATAH MOGHADAM¹, KEYVAN TADAYON², MOJTABA NOUFELI³, RAINAK
GHADERI⁴, PEJVAK KHAKI⁵, MOHAMMAD SEKHAVATI⁶, FARNAZ BOROUMAND⁷,
EBRAHIM ABBASI⁸

1. ISLAMIC AZAD UNIVERSITY of DAMGHAN, DAMGHAN, IRAN
2. RAZI VACCINE AND SERUM RESEARCH INSTITUTE
3. RAZI VACCINE AND SERUM RESEARCH INSTITUTE
4. RAZI VACCINE AND SERUM RESEARCH INSTITUTE
5. RAZI VACCINE AND SERUM RESEARCH INSTITUTE
6. RAZI VACCINE AND SERUM RESEARCH INSTITUTE
7. Razi Vaccine AND Serum Research Institute
8. RAZI VACCINE AND SERUM RESEARCH INSTITUTE

Background and Aim: The Iranian government commits to fund its national children immunization scheme against pertussis, a plan that has been running since 1950's with vaccination a cornerstone in this program. Two imported strains of Bordetella pertussis, namely Razi Bp 0134 and Razi BP0509 are currently used at Razi institute for manufacturing the whole-cell pertussis vaccine.

Methods: In search for a reliable and straightforward method capable to differentiate between these two strains, 8 VNTR loci including VNTR1, VNTR2, VNTR3, VNTR5, VNTR7, VNTR8, VNTR9 and VNTR10 were assessed.

Results: Although simultaneous assessment of all these loci was possible through application of appropriate adjustments in PCRs but in the end it were only VNTR3 and VNTR9 that differentiate the two strains. As at VNTR3 with a 5 bp unit repeat there were 7.2 and 5.2 copies in the genome of the Bp 0134 and Bp 0507 strains, respectively. At VNTR9 on the other hand, there were 5 and 4 copies of a 6 bp unit repeat in the genome of the Bp 0134 and Bp 0507 strains, respectively.

Conclusion: In the vaccine manufacture's view, where little differences between individual production strains are important, the observed dissimilarities between these two strains detected by VNTR3 and VNTR9 can be very helpful in vaccine production, regulatory and legal aspects.

Keywords: Pertussis, Tandem Repeat, Strain, Vaccine

**P1016 - 1014: DESIGNING AND IN SILICO STUDIES OF FUSION PROTEIN FLIC.MRP_H
AGAINST URINARY TRACT INFECTIONS CAUSED BY PROTEUS MIRABILIS**

Ali mohamad Shirzad dreshir¹, Mohammad Reza Asadi Karam², Saeid Bouzari³, Mehri Habibi⁴

1. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
2. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
3. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
4. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran; m_habibi1362@yahoo.com

Background and Aim: *Proteus mirabilis* are frequently associated with urinary tract infections, particularly in patients with urinary catheterization. Flagellin (FliC) is the major structural component of flagella in *P. mirabilis*. Studies have shown that flagellin is able to activate innate immune responses via activation of Toll-like receptor 5 (TLR-5). In this study, we predicted the best structure of fusion protein FliC.Mrp_H as a novel vaccine candidate against UTI caused by *P. mirabilis*.

Methods: In this study, we planned to design a novel fusion protein against UTIs by incorporating the FliC and Mrp_H from *P. mirabilis*. In this light, we modeled two fusion protein forms consisting of FliC and Mrp_H computationally using the I-TASSER server and evaluated the interaction of the fusion forms with TLR-5 by Hex docking. According to various parameters in the Hex docking server, the best fusion form was selected and subjected for cloning and expression.

Results: FliC and Mrp_H form two different models FliC.Mrp_H and Mrp_H.FliC but just one of them had the best interaction to TLR-5. According to the bioinformatics analyses, it was predicted that FliC.Mrp_H would have the best interaction to TLR-5 and selected for further studies.

Conclusion: Development of effective strategies to prevent UTIs has become an important goal in public health. Nowadays, bioinformatics tools have opened new doors for vaccine design and accelerate the design of fusion proteins as vaccine candidates. Our data indicate that fusion FliC.Mrp_H can be considered as a vaccine candidate against UTIs caused *P. mirabilis*. Evaluation of the fusion protein against UTIs is in progress.

Keywords: Urinary tract infection, *P. mirabilis*, Vaccine candidate, Fusion protein, Flagellin, TLR-5

**P1017 - 1037: CLONING AND EXPRESSION NOVEL TRUNCATED RECOMBINANT FUSION
PROTEIN AGAINST URINARY TRACT INFECTIONS CAUSED BY ESCHERICHIA COLI
(UPEC) AND PROTEUS MIRABILIS**

Zakaria Bameri¹, saed bouzari², mohammadreza asadikaram³, mana oloomi⁴, mehri habibi⁵, parastoo
ehsani⁶

1. pasture institute of Iran. molecular biology department
2. pasture institute of Iran. molecular biology department
3. pasture institute of Iran. molecular biology department
4. pasture institute of Iran. molecular biology department
5. pasture institute of Iran. molecular biology department
6. pasture institute of Iran. molecular biology department

Background and Aim: FimH and MrpH are the most important antigens of Escherichia coli and Proteus mirabilis, respectively. FliC of Salmonella typhimurium has showed good efficacy that stimulates multiple signaling pathways of innate immunity, resulting in a strong antibody and cellular responses. In this study we designed and cloned novel fusion protein MrpH.FimH.FliC. We are going to test this fusion protein as vaccine candidate in vitro and in vivo

Methods: C-terminal domains of MrpH (first 405 nucleotides) and FimH (first 495 nucleotides) that have antigenic property and whole gene of fliC selected in fusion protein. We amplified fusion gene mrpH.fimH.fliC by overlap PCR. Amplified segment was digested by NcoI and HindIII enzymes and then ligated in Pet28a vector. Ligated vector was transformed in BL21(DE3) competent. After that induction was done by IPTG as inducer. We confirmed expression novel construct by SDS-page and western blot

Results: Among different models MrpH.FimH.FliC was best model. Amplification showed 2300bp segment. Sequencing amplified and cloned segment showed that segment was inserted in appropriate frame. SDS-page and western blot showed 90 KD bond and western blot confirmed it

Conclusion: UTI are commonly managed with antibiotic therapy but they are less successful in the case of antibiotic-resistant strains. Existing commercial complex vaccines appear to have limited and short-lived protection. Therefore we need to examine different candidate to access best vaccine against UTI infections. We are going to determine efficacy this new fusion protein in vitro and in vivo

Keywords: E.coli, P.mirabilis. fusion protein

**P1018 - 1041: ORAL ADMINISTRATION OF DISPLAYED ACINETOBACTER BAUMANNII
BIOFILM-ASSOCIATED PROTEIN INDUCES A PROTECTIVE IMMUNE RESPONSE IN
MICE**

Elaheh Zadeh Hosseingholi¹, Iraj Rasooli², Seyed Latif Mousavi Gargari³

1. Department of Cellular and Molecular Biology, Faculty of Sciences, Azarbaijan Shahid Madani University, Tabriz, Iran
2. Department of Biology, , Faculty of Sciences, Shahed University, Tehran-Qom Express Way, Opposite Imam Khomeini's Shrine, Tehran-3319118651, Iran
3. Department of Biology, , Faculty of Sciences, Shahed University, Tehran-Qom Express Way, Opposite Imam Khomeini's Shrine, Tehran-3319118651, Iran

Background and Aim: *Acinetobacter baumannii*, a major threat for hospitalized patients, intensive care units (ICUs) residents, military forces, is a public health problem due to increasing rate of antibiotic resistance. A specific cell surface protein named biofilm associated protein (Bap) was defined in a bloodstream isolate of *A. baumannii*. This protein play an important role in bacterial infectious processes. It was proven that immune responses elicited by antigens expressed on *L. lactis* surface are stronger than those expressed intracellularly. In the present study Biofilm associated protein (Bap) were displayed on *Lactococcus lactis* and the efficacies of these recombinant bacteria as oral vaccines were evaluated in murine model

Methods: A chimeric gene was designed and subcloned into a lactococcal vector in order to expression of Bap under the control of nisin A inducible promoter. Mice vaccine group received four cycles of orogastric immunizations at 2-week intervals. Each cycle consisted of gavaging 2×10^9 CFU for 3 consecutive days of induced recombinant *L. lactis* suspended in 100 μ L sterile PBS. Control group received *L. lactis*:vector in the same manner. The resulted serum IgG immune responses were analyzed and the mice were challenged with lethal doses of *A. baumannii*

Results: Mice Immunized with recombinant *L. lactis*, showed 100% protection against 108, 109 and 1010 bacterial challenge. 80% protection was achieved at 1011 bacterial challenge level. All the control groups died within 24 hours of challenge.

Conclusion: the results support the possibility of developing this recombinant strain as a vaccine for controlling *A. baumannii* infection

Keywords: *Acinetobacter baumannii*; Biofilm associated protein; *Lactococcus lactis*; Immunity; Display

P1019 - 1142: MDRA GENE AS A CANDIDATE FOR DEVELOPING VACCINE AGAINST UTI

Hamideh Tokhmechi¹, Nour Amirmozafari², Mohaddeseh Mohsenpour³

1. Department of Microbiology, Faculty of Basic Sciences, Lahijan Branch, Islamic Azad University, Lahijan, Iran
2. Iran University of Medical Sciences, Faculty of Medical Sciences, Department of Microbiology, Tehran, Iran
3. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran

Background and Aim: Urinary tract infections (UTIs) are the most common infections. we performed a study to find new targets for developing vaccine against UTI.

Methods: the complete genome sequence of UPEC strain 536 (Accession number :CP000247) and non pathogenic E. coli K-12 were derived from NCBI site .Then complete genome of UPEC strain 536 and human were compared by Nucleotide Blast software .Blast results were analyzed and sequences with scores below 100 were selected as different sequences which were compared with entire genome of E. coli K-12. Detection of *mdrA* gene was performed by amplifying the gene by PCR. E. coli ATCC 35218 was used as a template.

Results: Expected size of amplicon (445 bp) was ascertained by electrophoresis in a 1% agarose gel with appropriate molecular size markers (100 bp DNA ladder , Fermentas) Amplified products were sequenced to ensure fidelity of the PCR .

Conclusion: As C-terminal domain of *mdrA* gene is a conserved sequence among UPEC

Keywords: Uropathogenic Escherichia coli, *mdrA* gene, vaccine

**P1020 - 1144: HUMAN IMMUNE RESPONSES AND VACCINE CANDIDATES AGAINST
BRUCELLOSIS**

Mohsen Heidary¹, Reza Mirnejad², Mohammad Javad Nasiri³, Fazlollah Shokri⁴, Mehdi Goudarzi⁵

1. Department of Medical Microbiology, Iran University of Medical Sciences, Tehran, Iran
2. Molecular Biology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran
3. Department of Medical Microbiology, Shahid Beheshti University of Medical Sciences, Tehran, Iran
4. Department of Medical Genetics, Shahid Beheshti University of Medical Sciences, Tehran, Iran
5. Department of Medical Microbiology, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim:Brucellosis remains one of the most common zoonotic diseases worldwide with more than 500,000 human cases reported annually. The aim of this review is to discuss the importance of developing the Brucella vaccines.

Methods:A database was built for current challenges and future approaches of Brucella vaccine for human using PubMed, Scopus and Science direct.

Results:Although several studies has been done to develop safer Brucella vaccines to prevent the infection in animals, but there is currently no licensed vaccine for brucellosis in humans. Therefore, there is a desire to develop an ef?cacious vaccine for the protection of general populations living in endemic areas, at-risk workers, and for military personnel for protection against Brucella used in biowarfare.

Conclusion:Subunit vaccines are able to induce protection against Brucella. Some antigens are able to protect BALB/c mice as effectively as a live control vaccine challenge. These include the 22.9-kDa protein, SOD, L7/L121-Omp16 or Omp31.

Keywords:Brucella, vaccine, Brucellosis, human, immunity.

**P1021 - 1202: DESIGNING A CHIMERIC CONSTRUCT AS A SUITABLE IMMUNOGEN
CANDIDATE AGAINST VIBRIO CHOLERAЕ**

Atina Vakili¹, seyed Latif Mosavi², Shahram Nazarian³, Jafar Amani⁴

1. Msc student, Department of Cell Biology, Shahed university
2. Prof. of Cell Biology, Shahed University
3. assistant Prof. Imam Hossein University
4. associate Prof. Baghiyyatollah University of medical sciences

Background and Aim: Vaccination is one of the most efficient options for eradicating infectious diseases in humans and animals. Attenuated or inactivated pathogens are traditionally used as vaccines. But nowadays, scientists are searching for novel recombinant vaccines. Chimeric constructs, offering more possibility for presenting antigens, could be assigned as one of the best recombinant vaccine candidates.

Methods: In this work, we selected two most common pathogenic genes, ompW and ctxB from V.cholera, and a construct consisting these two genes was designed with appropriate linker in between to provide the best proper 3D structure. The primers were designed with suitable restriction sites according to the selected vector. All parameters were checked by recognized soft wares. The vector and PCR product of the ompW were digested and ligated together. The second gene (ctxB) was ligated tandemly to the first construct to obtain the final construct.

Results: The positive clones had been selected and used for protein expression.

Conclusion: The recombinant protein could assume as an effective immunogen candidate to act against Vibrio cholerae infection.

Keywords: Vibrio cholerae, Recombinant vaccine, chimera.

**P1022 - 1220: IN SILICO DESIGN OF A MULTI-EPITOPE DNA VACCINE AGAINST
BRUCELLA SPP**

Sogol Sattari¹, Jafar Amani², seyed Latif Mosavi³, Shahram Nazarian⁴

1. Departement of Biology, shahed university
2. associate Prof. Baghiyyatollah University of medical sciences
3. Prof. of Cell Biology, Shahed University
4. assistant Prof. Imam Hossein University

Background and Aim:Brucellosis is one of the most common worldwide zoonotic diseases. At present, there is no effective and safe Brucella vaccine for humans and existing animal vaccines have limitations such as causing abortions in pregnant animals. Recent trend in vaccine design has shifted to epitope-based vaccines which are safe and efficacious both in humans and animals. TF, OMP31, BLS, SOD, BP26, L9 proteins of Brucella abortus, melitensis and ovis have shown protective antigens for brucellosis.

Methods:In this study, we designed a chimeric protein containing fragments of TF, OMP31, BLS, SOD, BP26, L9 proteins which have a high density of B- and T-cell epitopes. These genes were fused together by repeats of hydrophobic amino acids as linkers. The secondary and tertiary structures of the chimeric protein and other properties such as stability were analyzed.

Results:The epitopes in the chimeric protein are likely to induce both the B-cell and T-cell mediated immune responses. Predicted mRNA structures indicated good stability of the mRNA to increase the efficiency of translation in the target host.

Conclusion:The chimeric protein may be used as a suitable multi-epitope candidate to develop vaccine against Brucella.

Keywords:DNA Vaccine, brucellosis, chimeric protein

P1023 - 1235: INACTIVATION OF ECOLI O157:H7 BY FORMALIN AND HEAT

Nasim Arshadi¹, Shahram Nazarian², seyed latif mousavi³, jafar amani⁴

1. Master of Science
2. Assistant Professor
3. professor
4. associate professor

Background and Aim: Enterohemorrhagic *Escherichia coli* (EHEC) O157:H7 is a food-borne pathogen, causing diarrhea, hemorrhagic colitis, thrombotic thrombocytopenic purpura and a life-threatening sequela called hemolytic uremic syndrome in humans. Healthy cattle are a reservoir of *E. coli* O157:H7 and bovine food products and fresh produce (products) contaminated with bovine waste are the most common sources for disease outbreaks in the developing countries.

Methods: In the present study, we optimized the formulation of an inactivated *E. coli* O157:H7 on the basis of three main components: kind of killing (way of inactivation), antigenic dose, concentration of inactivating agent. Three groups of mice (five in each) were used, the first group was orally gavaged on days 0, 7, 14, 28 with 1×10^9 C.F.U of heat killed *E. coli* O157:H7. The second group was immunized in a similar way with formalin killed *E. coli* O157:H7 and the third group was gavaged with phosphate buffer saline (PBS) and considered as a control group. Blood samples were collected 12, 20, 30 days after the first immunization and sera were assayed for antibody response by ELISA test. Six weeks after vaccination, the immunized and control mice groups were challenged with *E. coli* O157:H7.

Results: We found significant increase in specific systemic antibodies (IgG) and IgA levels elicited by formalin killed *E. coli* O157:H7.

Conclusion: In conclusion immunogenicity of *E. coli* O157:H7 is greatly affected by the inactivation conditions employed for vaccine production and the Formalin treatment shows better response compared to heat killed one.

Keywords: *E. coli* O157:H7, heat killed, formalin killed, oral immunization

**P1024 - 1244: EFFECT OF DIFFERENT CONCENTRATION OF FECL₃ ON SOME
PATHOGENIC BACTERIA FOR PREPARATION OF IRON-INACTIVATED AGENTS**

Maryam Homayoon¹, Yahya Tahamtan ², Mohammad Kargar³

1. Microbiology Department, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. Microbiology Department, Razi Vaccine and Serum Research Institute, Shiraz, Iran
3. Microbiology Department, Jahrom Branch, Islamic Azad University, Jahrom, Iran

Background and Aim:Metals play a vital role in the metabolic processes of the microorganism and some of heavy metals are required by the organisms as micro nutrients. However, in high concentrations, heavy metal ions react to form toxic compounds in bacterial cells. Effect of different concentration of ferric chloride (FeCl₃) on Pasteurella, Salmonella, E. coli, Listeria and Clostridium was investigated in the present study.

Methods:All bacteria were inoculated in BHI broth supplemented with 10 mM, 50mM and 100mM ferric chloride, and the incubation were done at 37 °C for 24 h. Total bacterial counts and viable bacterial counts were done by Brown opacity tubes and spread plate method, respectively. The data obtained was used for deciding the inactivating concentration of FeCl₃.

Results:Total bacterial counts of all bacteria at 10mM, 50mM and 100mM FeCl₃ did not increase significantly after 24 h inoculation. Viability of Salmonella and E. coli at 10mM FeCl₃ in BHI broth was less than 5×10⁸ CFU/ml and was completely lost at 50mM and 100mM FeCl₃ in BHI broth, when measured at 24 h. Viability of Pasteurella, Listeria and Clostridium at 10mM FeCl₃ was completely lost even when measured after incubation for 4h.

Conclusion:This work suggests that use of iron as inactivated agent can improve novel inactivated vaccines for their use in developing countries. The inactivating effect of FeCl₃ is achieved by its ability to precipitate proteins in the cell walls and to degrade/damage nucleic acids and lipids through free radical reactions.

Keywords:FeCl₃, Iron-inactivated, Vaccine, Bacteria

Veterinary Microbiology

P1025 - 179: EVALUATION OF ANTIMICROBIAL PROPERTIES OF HEMISCORPIOUS LEPTURUS SCORPION VENOM AGAINST E.COLI

Ehsan Zayerzadeh¹

1. Department of Biology, Faculty of Food Industry and Agriculture, Standard Research Institute, Karaj, Iran.

Background and Aim: Scorpions are venomous arthropod animals belonging to the class Arachnida. Venoms from scorpions are complex mixtures of compounds and majority of them are some polypeptides with neurotoxicity. These neurotoxins affect a variety of ion-channels of cells. Up to now, some scorpion venoms were reported with antibacterial activities. Hemiscorpius lepturus is one of the major scorpions in Iran and has highly cytotoxic venom, which can cause serious wounds and inflammations. On the other hand, drug resistance poses an increasing threat to global public health, and new antibiotic-resistant pathogens have continued to emerge. The aim of this work is evaluation of potential antibacterial activity of Hemiscorpius lepturus scorpion venom against Escherichia coli.

Methods: In the present work here, we investigated antimicrobial activity of Hemiscorpius lepturus scorpion venom against Escherichia coli bacterial strain. Escherichia coli were exposed with various concentrations of crude venom and antibacterial activity of Hemiscorpius lepturus scorpion venom was analyzed by disc-diffusion test.

Results: The results of these study showed that some concentrations of Hemiscorpius lepturus crude venom have significant antibacterial activity against Escherichia coli.

Conclusion: In conclusion, Hemiscorpius lepturus crude venom has potential antibacterial effects against Escherichia coli and may be use as alternative antibiotic for disease induced by E.coli.

Keywords: antimicrobial activity, Hemiscorpius lepturus scorpion venom, Escherichia coli, disc-diffusion.

**P1026 - 235: INVESTIGATION OF THE IMMUNOGENICITY OF TRIVALENT
INACTIVATED VACCINE AGAINST COLIBACILLOSIS IN POULTRY**

Hojatolah Noori¹, Dr Pejvak Khaki², Dr Behzad Hematti³

1. Islamic Azad University Karaj Branch
2. Department Of Microbiology Razi vaccine And Serum Research Institute Karaj,IRAN
3. Islamic Azad University Karaj Branch

Background and Aim: Escherichia coli septicaemia or colibacillosis is a serious disease which generally occurs in poultry and which is responsible for considerable losses. In Iran the most common serotypes of E.coli associated with colibacillosis in poultry are O1, O2 and O6. Little is known of the virulence factors which play a role in the pathogenesis of the colibacillosis in poultry. Up till now, there exist no vaccines, offering both a good and broad protection against the wide range of pathogenic avian E.coli. Therefore the multivalent vaccine may provide good protection against colibacillosis in poultry.

Methods: The vaccine including serotypes O1, O2 and O6 were provided. All quality control tests including sterility, safety and potency were performed. Chickens were vaccinated once subcutaneously at 12 days of age with dose of approximately 2×10^9 cells in 0.3 ml. The chickens were analyzed for colibacillosis for 45 days. The efficacy of the vaccine was evaluated by mortality, challenge and determination of antibody titer by agglutination test.

Results: The challenge of vaccinated chickens indicated that there was no any mortality and morbidity in them. The antibody titer in vaccinated chickens were 1/244. Antibody titer was not observed in unvaccinated chickens.

Conclusion: The results revealed that this vaccine provided good protection against colibacillosis in poultry. The results suggesting that the trivalent inactivated vaccine may be useful for protection against colibacillosis in poultry.

Keywords: Ecoli, vaccine, colibacillosis, poultry

**P1027 - 293: LPS-PCR TYPING OF OVINE PASTEURELLA MULTOCIDA ISOLATES FROM
IRAN BASED ON(L1 TO L8)OUTER CORE BIOSYNTHESIS LOCI**

Sedeh fahimeh Merhaghgoe jalali¹, Seyedh fahimeh Merhaghgoe jalali², Ahmad Reza Jabbari³, Majid
Esmaelizad⁴

1. MSC Student Razi Vaccine and Serum Research Institute, Karaj, Iran
2. National Pasteurella Research Laboratory Razi Vaccine and Serum Research Institute, Karaj, Iran
3. Central Lab Dept Razi Vaccine & Serum Research Institute

Background and Aim:pasteurella multocida is a gram negative bacterial pathogen that is causative agent a wide range of diseases in many animal species and human.What is clear that LPS is an important virulence factor that even very minor change to the LPS structure can have dramatic effect on the ability of P.multocida to cause disease in its host and can be used for the identification and classification of strains with somatic typing systems.

Methods:in this study, was detected the LPS genotype to ovine P.multocida isolates with using of eight specific primers for LPS outer core biosynthesis loci by PCR. The amplified LPS genes by PCR, then were sequenced and compared to the sequences deposited in the GenBank database from the world.

Results:in First, type capsular isolates were determined that all of them contained capsule type A, then LPS genotypes 32 ovine isolates were determined which 9 isolates included L3 genotype(%28.12), 21 isolates included L6 genotype(%65.62), 1 isolate contains both L3,L6 genotype(%3.12), 1isolate remained untypeable(%3.12). In this method all ovine P.multocida isolates belonging to the L3, L6 genotypes that was most frequency related to the L6 genotype.

Conclusion:LPS-PCR is an accurate LPS genotyping method that accurate differentiate P.multocida strains into one of the eight distinct LPS genotypes that ovine isolates were only contain L3, L6 genotypes.

Keywords:P. multocida, ovine, LPS outer core, PCR-typing

**P1028 - 382: PREVALENCE OF ESCHERICHIA COLI AND ANTIBIOTIC SUSCEPTIBILITY
PATTERN OF ISOLATES IN BOVINE CLINICAL MASTITIS IN TABRIZ**

Samira Vahabian¹, Mahdi Ghiamirad²

1. M.S.C of Microbiology, Higher Education Institute of Rabe-Rashid, Tabriz, Iran.
2. Department of Microbiology, Faculty of Sciences, Islamic Azad University, Ahar branch, Ahar, Iran.

Background and Aim: Inflammation of the mammary glands regardless of its reasons is called mastitis. This illness can cause economical damages. The aim of this study was evaluating the frequency and identifying the pattern of the antibiotic susceptibility of the E. coli isolated from the clinical mastitis cases in cows in Tabriz to common antibiotics.

Methods: 240 milk samples which were sampled in a standard way from the cows with clinical mastitis, were taken to the laboratory. After cultivation, purification and differential Microbial testing, E.coli positive samples were chosen. The susceptibility pattern of the isolates to common antibiotics were examined by combined disk test method.

Results: 50 samples of 240 samples were E.coli. These isolates show resistance to Cefotaxime (88.9%) and Ceftazidime (94.5%). There is no resistance for Co-trimoxazole (100%) and Gentamicin (88.8%).

Conclusion: According to the observed resistance to β -lactams and the possibility of their spread to the human population, the necessity of correct use of antibiotics and not using of raw milks of infected livestock and also observance of contradiction in this period, are vital.

Keywords: Antibiotic Susceptibility, Bovine Clinical Mastitis, E. coli, Tabriz

**P1029 - 409: STUDY OF THE PRESENCE OF BORDETELLA AVIUM AND
ORNITHOBACTERIUM RHINOTRACHEALE IN NATIVE FLOCKS OF TURKEYS AND
DETERMINATION DRUG SENSITIVITY IN ISOLATED SAMPLE**

Elnaz Mohammadi aghbash¹, Babak khabaz², Avesta sadrzade zadeh³

1. Graduated from DVM course , Faculty of Veterinary Medicine, Islamic Azad University , Babol Branch, Babol, Iran
2. clinician and Graduated from DVM course , pars veterinary clinic, mazandaran, chalos ,Iran
3. Department of Clinical Sciences, Faculty of Veterinary Medicine, Islamic Azad University , Garmsar Branch, Garmsar, Iran

Background and Aim: *Bordetella avium* and *Ornithobacterium rhinotracheale* have strategic and economical importance in Turkey industry.

Methods: In this study we referred to native turkey flocks with clinical signs of Respiratory infection (similar to *Bordetellosis* and *Ornithobacteriosis*) or with the background of Respiratory problem and weak growth with the age of 4-8 weeks, in two provinces of Iran (Mazandaran and Guilan) we collected 100 blood samples of turkey were sent to Kousar Veterinary Laboratory in Tehran. Samples were cultured in Mac Conkey agar and Blood agar containing 10 microgram Gentamicin per mL for determination of the presence of *Bordetella avium* and *Ornithobacterium rhinotracheale* respectively. After 48 hours incubation, negative lactose colonies on Mac conkey agar in differential media have been studied. By confirmation of the presence of *Bordetella avium*, antibiotic resistance paradiagram determined through diffusion disk method in Muller-Hinton media and by confirmation of the presence of *ORT*, it was determined through disk diffusion Method in Blood agar. In the next step, ELISA and PCR method were applied to identify any bacteria.

Results: In this study, the presence of *Ornithobacterium rhinotracheale* and *Bordetella avium* in native flocks was determined and confirmed.

Conclusion: In this study, primary antibiotics for *Bordetella avium* treatment are Fosfomycin, gentamicin, Enrofloxacin, Oxytetracycline, Tetracycline, Neomycin, Doxycycline, Colistin, Flumequine and Florfenicol and primary selected antibiotics for *Ornithobacterium rhinotracheale* treatment in turkeys are respectively Florfenicol, Fosfomycin, ampicillin and amoxycilin which response to treatment

Keywords: *Bordetella avium*, *Ornithobacterium rhinotracheale*, Blood agar, ELISA

P1030 - 430: EPIDEMIOLOGICAL STUDY OF ABORTION CAUSED BY CAMPYLOBACTER FETUS IN BALUCHI SHEEP IN THE NORTHERN OF SISTAN AND BALUCHESTAN PROVINCE USING MOLECULAR METHOD (PCR).

Ebrahim Hossein abadi¹, Daryush Saadati², Mohsen Najimi³

1. Student of Veterinary medicine, Faculty of veterinary Medicine, University of Zabol, Iran
2. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, University of Zabol
3. Department of Pathobiology, Faculty of Veterinary Medicine, University of Zabol

Background and Aim: Abortion cause excessive loss in in sheep flock. Campylobacter species are a major cause of gastroenteritis in human and animals. Campylobacteriosis is also characterized by still births, birth of weak lambs and Abortion, which is usually seen in the last 6 weeks of gestation in ewes due to bacteraemia and placentitis. Campylobacteriosis is one of the most important cause of abortion after Brucellosis in Iran. Although we haven't enough information about campylobacteriosis in iran, in many areas there's the possibility of Contamination.

Methods: a total 156 samples were obtained from stomach content and spleen of aborted lamb in autumn 2015. DNA was extracted from samples using a commercial Kit (Sinnagen DNPTM KIT) according to the manufacturer's instructions and stored in -20°C. Primers were designed using past studies and molecular detection was done by PCR.

Results: From all 156 samples, 6 positive cases were found, in which 2 cases were from spleen and 4 cases from stomach content of specific aborted lambs.

Conclusion: Protection can be achieved by the use of an inactivated vaccine consisting of a single strain of ovine C. fetus fetus which has been available since 1980. Inasmuch as campylobacteriosis is a zoonotic disease so it is important for public health and there for a proper understanding of the epidemiology of Campylobacter infections in human and animals is necessary for the planning of effective prevention and control measures.

Keywords: Campylobacter, Abortion, Baluchi sheep, molecular method (PCR)

**P1031 - 433: EPIDEMIOLOGICAL STUDY OF ABORTION CAUSED BY CHLAMYDOPHILA
ABORTUS IN BALUCHI SHEEP IN THE NORTHERN OF SISTAN AND BALUCHESTAN
PROVINCE USING MOLECULAR METHOD (PCR).**

Ebrahim Hossein abadi¹, Mohsen Najimi², Daryush Saadati³

1. Student of Veterinary medicine, Faculty of veterinary Medicine, University of Zabol, Iran
2. Department of Pathobiology, Faculty of Veterinary Medicine, University of Zabol
3. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, University of Zabol

Background and Aim: Chlamydiae are obligate intracellular bacteria, which depend on the host cell for energy and share a unique two-stages developmental cycle, elementary and reticulate bodies. Chlamydia abortus is one of Chlamydiae spp. that cause enzootic abortion in sheep and also cause make problems such as abortion in Human which makes it a zoonotic agent. The environment would be contaminated by infected placenta, feces and uterine discharges, thereby, disease can spread to susceptible animal and humans through exposure of these infected materials. In non-pregnant animals, C. abortus causes a subclinical infection due to existence in lymphoid tissue where it remains until the beginning of pregnancy

Methods: a total 156 samples were obtained from stomach content and spleen of aborted lamb in autumn 2015. DNA was extracted from samples using a commercial Kit (Sinnagen DNPTM KIT) according to the manufacturer's instructions and stored in -20°C. Primers were designed using past studies and molecular detection was done by PCR.

Results: of the 156 samples from 78 aborted lambs and were examined with PCR method, no positive cases were found

Conclusion: although PCR is a proper detection method, because Chlamydiae organisms are intracellular agents, it suggested that for accurate detection of this agents used Nested PCR method, due to high sensitivity and specificity. Particular care must be taken when introducing a new animal into a Chlamydiae-free farm. Chlamydial abortion in ewes can be controlled by means of attenuated or inactivated vaccination for C. abortus.

Keywords: chlamydiae, Abortion, Baluchi sheep, molecular method (PCR).

P1032 - 444: MOLECULAR EPIDEMIOLOGY OF BOVINE CORONAVIRUS IN SAMPLES OF DIARRHEIC CALVES COLLECTED FROM 14 PROVINCES OF IRAN

Ahmad Nazaktabar¹, Omid Madadgar², Taghi Zahraei Salehi³

1. Department of Pathobiology, faculty of veterinary, Amol university of special modern technology, Mazandaran, Iran
2. Department of Microbiology, Faculty of Veterinary of Medicine, University of Tehran, Tehran, Iran
3. Department of Microbiology, Faculty of Veterinary of Medicine, University of Tehran, Tehran, Iran

Background and Aim: Bovine coronavirus (BCV) is one of important pathogens causing neonatal calf diarrhea. As our knowledge no broad study has been done determining the rule of this virus in calf diarrhea in Iran. We investigate the frequency of coronavirus infection in diarrheic calves among 14 provinces of Iran, using RT-PCR.

Methods: 587 stool samples were collected from diarrheic calves under 1 month old rearing in industrial or rural dairy farms in 14 provinces as Tehran, Alborz, Qazvin, Qom, Markazi, Isfahan, Fars, Zanjan, East Azarbaijan, Sistan and Baluchistan, Razavi Khorasan and South Khorasan. All samples investigated with a very sensitive RT-PCR to detect coronavirus infection.

Results: Infection of coronavirus was detected in 33 of 587 samples and detection rate was determined as 5.6% but the rate of detection was not same in all provinces.

Conclusion: Results of this study showed quite high rate of coronavirus infection among calves of dairy farms. Although, this rate is not same in all provinces. For example, in some provinces like Fars and Zanjan the frequency of detection was as high as almost 22 and 24% respectively. Improving of management skills and vaccination is recommended to reduce and control of coronavirus infection in newborn calves

Keywords: coronavirus, calf diarrhea, molecular epidemiology, Iran

**P1033 - 475: PHYLOGENETIC ANALYSIS OF COXIELLA BURNETII ISOLATES FROM
DAIRY FARMS IN TEHRAN**

Changiz Ahmadizadeh¹, Farhad Musakhani², Rozita Tamjidifar³, Fatemeh Shahnazian⁴

1. Assistant Professor, Department of Microbiology, Islamic Azad University of Ahar
2. Assistant Professor, Department of Microbiology, Islamic Azad University of Karaj
3. Master of Science Microbiology
4. Master of Science Microbiology

Background and Aim: Q fever is a zoonotic disease with worldwide distribution Caused by a Rickettsia called coxiella burnetii through the mass of aborted fetuses, urine, and feces excreted in the milk of infected animals. Thus, consumption of unpasteurized milk contamination can be a source of infection for humans

Methods: In this study, a total of 50 dairy farms around Tehran in 150 milk samples were received from the reservoir tank and all the samples using primers specific genes, transposons IS1111a coxiella burnetii, the PCR test were Of the total samples, 18 samples positive coxiella burnetii frequently randomly selected 12 samples were sent for sequencing to Korea Macrogen company

Results: The results showed that cow's milk is one of the potential reservoirs coxiella burnetii in Iran. The aim of this study phylogenetic analysis Coxiella burnetii was isolated from dairy farms in Tehran After obtaining the desired gene sequence of the bacterium Coxiella burnetii, the sequences obtained were compared with sequences in the gene bank.

Conclusion: The result of this comparison showed that the transposons IS1111A Coxiella burnetii gene isolated from milk farms around Tehran with more than 99% sequence similarity to the gene bank

Keywords: coxiella burnetii, phylogenetic analysis, PCR

**P1034 - 496: A SERO-EPIDEMIOLOGICAL STUDY OF BOVINE LEPTOSPIROSIS IN EAST
REGION OF GUILAN PROVINCE**

Seyedeh Tooba Shafighi¹, Meysam koochaki alikolayeh², Tooba Shafighi³, Gholamreza Abdollahpour⁴

1. Master of Science (M.Sc) In Microbiology, Department. of Microbiology, Faculty of Basic science, Islamic Azad University, Rasht Branch, Iran
2. Assistant Professor, Department. of Microbiology, Faculty of Basic science, Islamic Azad University, Rasht Branch, Iran
3. Associate professor, Department of Internal medicine, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran

Background and Aim: Leptospirosis is a zoonotic disease caused by *Leptospira* species. A serological study was conducted in order to investigate the present status of leptospirosis in cattle in east region of Guilan province.

Methods: Between May and August 2015, 100 random blood samples were collected from non vaccinated cattles. All serum samples were serologically tested by microscopic agglutination test (MAT) using live antigens representing *Leptospira interrogans* serovars: Hardjo, Icterohaemorrhagiae, Canicola, Pomona and Gripotyphosa.

Results: Serologic evaluation of cattles revealed MAT titre $\geq 1:100$ in 33(33%) samples against one or more serovars. The most prevalent *Leptospira* serovars was Pomona 19(19%) samples, Hardjo 9(9%) samples, Gripotyphosa 4(4%) samples and Canicola 2(2%) samples, respectively. The most prevalent serological titre was 1:100(29 samples) and the highest serological titre was measured to be 1:200 (5 samples). The highest rate of positive MAT was found in three years old cattles.

Conclusion: It was concluded that leptospiral infection is magnified in cattle in east region of Guilan province and cattle have a major role in maintaining Pomona serovar. Therefore, vaccination of the cattles with endemic serovars to reduce the prevalence of leptospirosis in cattle population is suggested.

Keywords: leptospirosis, epidemiologic study, Bovine

**P1035 - 498: PREVALENCE OF STAPHYLOCOCCUS AUREUS AND COAGULASE-
NEGATIVE STAPHYLOCOCCI IN BOVINE MASTITIS IN TABRIZ**

Naeimeh Rezaei ansaroudi¹, mehdi ghiyamirad²

1. department of microbiology, faculty of science ,Islamic azad university ahar branch ,Ahar,Iran
2. department of microbiology, faculty of science ,Islamic azad university ahar branch ,Ahar,Iran

Background and Aim: Mastitis, or inflammation of the mammary gland parenchyma, is one of the most important diseases of dairy cows in the cattle industry. The disease is caused by bacteria, fungi and yeasts. This disease occurs in 3 forms including clinical, subclinical and chronic mastitis. *Staphylococcus aureus* and coagulase-negative *Staphylococci* bacteria are amongst causing bovine clinical mastitis. This form of mastitis is the most common form of bovine mastitis in the world. The aim of this study was to isolate and identify coagulase-negative staphylococci (CONS) and *Staphylococcus aureus* in bovine mastitis in dairy cattle around Tabriz.

Methods: This cross-sectional study has been done on 182 samples of milk collected from cows with clinical mastitis in Tabriz city from 2014 to 2015. Milk samples were transferred to the laboratory and cultured in selective media, then confirmatory tests including gram staining, catalase, oxidase, coagulase, Aesculin hydrolysis, hemolysis on blood agar, and mannitol were performed.

Results: From 182 samples, in 40 cases (21.9%), *Staphylococcus aureus* and 15 cases (8.2%) coagulase-negative staphylococci were found. Coagulase-negative staphylococci included: 12 cases (6.6%) *S. epidermidis*, 3 cases (1.7%) *S. saprophyticus*.

Conclusion: The prevalence of (30.1%) *Staphylococcus aureus* and coagulase-negative staphylococci in bovine mastitis cases at this study was found, so the correct diagnosis and treatment of staphylococcal infections in mastitis is necessary.

Keywords: clinical bovine mastitis, *Staphylococcus aureus*, coagulase negative staphylococci, Tabriz

**P1036 - 526: DETERMINATION OF ANTIBIOTICAL RESISTANCE PATTERN IN
SALMONELLA ENTERITIDIS STRAINS ISOLATED FROM POULTRY SAMPLES AND
THEIR DETECTION OF VIRULENCE GENES**

Elaheh Salami khanehan¹, Mehdi Parviz², Gholamali Moradli³

1. MSc. in Microbiology, Department of Microbiology, Saveh Branch, Islamic Azad University, Saveh, IR Iran.
2. Instructor, Department of Microbiology, Saveh Branch, Islamic Azad University, Saveh, IR Iran.
3. Assistant Professor, Department of Microbiology, Saveh Branch, Islamic Azad University, Saveh, IR Iran.

Background and Aim:Salmonella, as one of the most important bacterial diseases, In a global issue in poultry industry. Thus, industrial aviculture is an important source of salmonella which may cause food born disease in human. The aim of this study is detection of virulence genes *invA*, *int*, *flost*, *spvc* in salamonella enteritidis strain isolated from poultry sample in Tehran and their antibiotic susceptibility pattern.

Methods:salmonella Enteridis used in this cross-sectional study were isolated frim stool samples of the suspicious poultry casecasses in Tehran poultry farms. Serelological and biochemical tests were used to indentification of serotype. PCR method was used to study virulence genes and antibiotal resistance was performed by disk diffusion method.

Results:Overall, 160 stool samples were collected from poultry, From which 27 salmonella enteritidis strains were isolated. From 27 isolated salmonella enteritidis 44.4% were positive for *spvc* genes which 7.4% of them had multiple drug resistance to antibiotic, And 22.3% show resistance, at least, to one of twelve antibiotics. The most antibiotic resistance was seen to ampicillin.

Conclusion:In the current study, All isolatet were sensitive to imipenem, gentamicin, amikacin, florfenicol, enrofloxacin and ceftriaxone and given the studies in iran resistance to the anbiotic imipenem was not observed.resistance to gentamicin and amikacin was very low.these antibiotics can be used to treat in fections caused by these bacteria. Virulance plasmid genes among Salmonella Enteritidis strains isolated in this study can cause serious health problems for poultry and community health.

Keywords:poultry ‘salmonella ‘spv

**P1037 - 531: PREVALENCE OF METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS
AND COAGULASE-NEGATIVE STAPHYLOCOCCI IN BOVINE CLINICAL MASTITIS IN
TABRIZ**

Naeimeh Rezaei ansaroudi¹, mehdi ghiyamirad²

1. department of microbiology, faculty of science ,Islamic azad university ahar branch ,Ahar,Iran
2. department of microbiology, faculty of science ,Islamic azad university ahar branch ,Ahar,Iran

Background and Aim: Mastitis, is one of the most important diseases of dairy cows. The disease occurs by bacteria, fungi and yeasts. Staphylococcus species is the most bacterial agent that can cause mastitis in bovine. The aim of this study was to determine prevalence of methicillin resistance in Staphylococcus species, isolated from bovine mastitis in Tabriz.

Methods: In this study 182 milk samples obtained from cows with clinical mastitis, transferred to laboratory and staphylococcus species were identified with standard methods. Antibiotic susceptibility pattern was characterized with disk diffusion method using common antibiotic disk. Susceptibility to methicillin was measured with oxacillin agar screening method.

Results: In 15 cases, coagulase negative Staphylococci (CONS) and in 40 cases Staphylococcus aureus were identified respectively. 4 isolates (10%) of S. aureus and 3 coagulase-negative staphylococci (20%) were resistant to methicillin. Antibiotic resistance pattern in S. aureus was as follows: Penicillin 100%, Trimethoprim 11%, Ceftriaxone 11%, Tetracycline 16.5%, Cefixime 89%, Gentamicin 16.5%, Tylosin 72% and Enrofloxacin 11%. And about CONS: Penicillin 93.3%, Trimethoprim 20%, Tylosin 60%, Tetracycline 6.6%, Cefixime 73%. There was no resistance to Enrofloxacin, Gentamicin, Ceftriaxone. The resistance was not found.

Conclusion: According to observation of methicillin-resistant Staphylococcus species at the cattle, resistance can transfer to humans, and according to the occurrence of resistance in staphylococci isolates to commonly used antibiotics for mastitis treatment, doing a proper antibiotic susceptibility test before starting treatment with antibiotics and use of the effective antibiotics is necessary.

Keywords: Clinical bovine mastitis, Staphylococcus, methicillin-resistant, Tabriz

**P1038 - 591: MOLECULAR CHARACTERIZATION OF COMPLETE CODING SEQUENCE OF
PHOSPHOPROTEIN GENE NEW IRANIAN VIRULENT NDV DISEASE**

Samira Roustaei¹, Majid Esmaelizad², A.S. Tabatabaeipناه³

1. Islamic Azad University of Erth Tehran, Tehran, IRAN
2. Central Laboratory Department, Razi Vaccine and Serum Research Institute, Karaj, Alborz, IRAN
3. Islamic Azad University of Erth Tehran, Tehran, IRAN

Background and Aim: Newcastle disease (ND) is one of the most devastating diseases to the poultry industry. (NDV) is single-stranded RNA virus and encodes six genes (in the order 3'-NP-P-M-F-HN-L-5') and in general there are two class (class I, class II) and three pathotype(Velogenic, mezogenic, lentogenic). The phosphoprotein of NDV plays an important role in virus replication and is also a virulence factor. In this study we attempt to identify the nucleotide pattern of two new velogenic NDV isolates from north of Iran.

Methods: Two NDV viruses (Beh and Maz) were isolated from chicken in Mazandaran province of Iran. Viral RNA was extracted from infective allantoic fluid using the High Pure Viral RNA kit. Two degenerated primers were designed in flanking of phosphoprotein gene by Oligo5 software. Complete coding sequence of Phosphoprotein gene amplified by RT-PCR technique. PCR products were sequenced by Sanger method. Nucleotide and amino acid sequences of Iranian isolates were compared to all GenBank sequences by MegAlign software.

Results: In this study, the complete coding sequences of phosphoprotein in two new velogenic Iranian isolates were amplified by degenerated primers successfully using RT-PCR. Phylogeny tree showed that Beh and Maz isolates closely related to genotype VII and subgenotype VIId. Beh and Maz isolates showed 100% similarity in nucleotide level. 20% divergence was found between Class I and Class II.

Conclusion: Our data demonstrated that Beh and Maz isolates belong to class II and closely related to genotype VIId. According to this study we conclude that the Newcastle disease viruses could be classified based on phosphoprotein gene.

Keywords: Newcastle disease viruses. Velogenic. phosphoprotein

**P1039 - 608: STUDY OF CLINICAL OBSERVATIONS OF EXPERIMENTAL INFECTION
WITH AEROMONAS HYDROPHILA IN YELLOWFIN SEABREAM ACANTHOPAGRUS
LATUS**

Fatemeh Azadbakht¹, Solmaz Shirali², Mohammad Taghi Ronagh³, Eshagh Zamani⁴

1. Khorramshahr University of Marine Science and Technology
2. Khorramshahr University of Marine Science and Technology
3. Khorramshahr University of Marine Science and Technology
4. Khorramshahr University of Marine Science and Technology

Background and Aim: The *Aeromonas hydrophila* is an opportunistic pathogen bacteria in aquatic environment both fresh water and brackish waters. Yellowfin Seabream *Acanthopagrus latus* is an important commercial species in the Persian Gulf. The present study was conducted to evaluate the alterations of skin in *Acanthopagrus latus* after exposure to the *Aeromonas hydrophila*.

Methods: In this study, to evaluate the clinical signs of *Acanthopagrus latus* after exposure to *Aeromonas hydrophila*, the fish were collected from naseri pond were carried out in biology lab of Khorramshahr University of Marine Science and Technology. Then, 70 fish were divided in to 3 groups. One group did not affect by bacteria and therefore was considered as control group. Other two groups were exposed to 103 and 106 concentration of bacteria in immersion way. Fish were kept under experimental condition for 21 days and clinical signs were recorded during this period.

Results: According to results of clinical observations in both groups exposed to bacteria, decay tail rot and pectoral fins, paleness (due to the reduced thickness of the chromatophore layer in histological study), skin blemishes (caused by loss of scales), hemorrhage on the skin surface and hemorrhage on the ventral surface and anus were recorded.

Conclusion: According to results of present study, high doses of *Aeromonas hydrophila* can cause clinical signs in fish and on the other hand, these clinical signs can help to conduct us to distinguish of *Aeromonas hydrophila* infection in fish.

Keywords: *Aeromonas hydrophila*, *Acanthopagrus latus*, paleness, skin blemishes

**P1040 - 661: STUDY ON THE CONTAMINATION OF RAW MILK WITH E.COLI O157: H7 IN
KHOUZESTAN PROVINCE**

Iman Zarnegar¹, Ali Fazlara ², Milad Chadorbaf³

1. Graduate of the faculty of veterinary Medicine, Shahid Chamran University of Ahvaz, Iran
2. professor, department of food hygiene, faculty of veterinary Medicine, Shahid Chamran University of Ahvaz, Iran
3. Graduate of the faculty of veterinary Medicine, Shahid Chamran University of Ahvaz, Iran

Background and Aim: coliform bacteria are important group of bacteria associated with foods. among the bacteria of this group, E.coli is studied because of its pathogenesis and prevalence in many kinds of foods. Recently one serotype of this microorganism (O157:H7) is considered as a foodborne pathogen by the most food safety researchers and organization. this serotype is associated with hemorrhagic colitis and hemolytic uremic syndrome (HUS) in human.

Methods: this study was conducted to determine the contamination of raw milk with E.coli O157:H7 in Khuzestan province. two hundred samples of raw milk were collected from different parts of the province; bacteriological examination were done by using Escherichia Broth (ed, novobiocin) as an enrichment media and then MC concky Sorbitol as a selective plating media. Suspected colonies were checked by IMViC tests and serological examinations were done to confirm the E.coli O157:H7.

Results: In bacteriological examinations, 83 suspected colonies were isolated. Serological tests with O and H antisera showed that 9(4.5%) of the isolates were O157 and none of them was O157:H7. Indeed 22 serotypes of E.coli other than O157 were isolated from the samples.

Conclusion: The results of this study showed that the samples collected from the west of the province were shown the most (7.14%) and the north were shown the least (3.61%) contamination with E.coli.

Keywords: Raw milk, E.coli O157:H7, Khuzestan province

P1041 - 679: EPIDEMIOLOGICAL STUDY OF ABORTION CAUSED BY MYCOPLASMA AGALACTIAE IN BALUCHI SHEEP IN THE NORTHERN OF SISTAN AND BALUCHESTAN PROVINCE USING MOLECULAR METHOD (PCR).

Ebrahim Hossein abadi¹, Daryush Saadati², Mohsen Najimi³

1. Student of Veterinary medicine, Faculty of veterinary Medicine, University of Zabol, Iran
2. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, University of Zabol
3. Department of Pathobiology, Faculty of Veterinary Medicine, University of Zabol

Background and Aim: Mycoplasmae are the smallest bacterial cells yet discovered, several species are pathogenic in humans which are known as zoonotic agents. Mycoplasmae species have membrane associated protein antigen that allows them to adhere to epithelial cells. Mycoplasma agalactiae is one of the organisms which cause a highly infectious disease in small ruminants that called contagious agalactiae. Disease probably introduce by carrier animals, which are very important in epidemiology of the disease. This infection in ewes manifested by mastitis, arthritis, keratoconjunctivitis, respiratory problems and occasionally abortion.

Methods: a total 156 samples were obtained from stomach content and spleen of aborted lamb in autumn 2015. DNA was extracted from samples using a commercial Kit (Sinnagen DNPTM KIT) according to the manufacturer's instructions and stored in -20°C. Primers were designed using past studies and molecular detection was done by PCR.

Results: from all 156 sampled were examined, overall 24(30.7%) cases were positive in which 13 positive cases were from spleen samples, 8 positive cases were from stomach content samples and 3 positive cases were simultaneity from both spleen and stomach content samples.

Conclusion: The high rate of abortion in this region indicate the high pollution in farms. Contagious Agalactiae can persist in a herd for several months unless adequate measures such as vaccination in sensitive livestock are taken in time. The vector animals carrying infection without clinical signs in the herd, which can transmit the organism for 1 to 8 years considered to be a great risk for other sensitive livestock a major treat to livestock.

Keywords: Mycoplasma, abortion, Baluchi sheep, molecular method (PCR).

**P1042 - 696: THE FIRST SURVEY OF ANTIBODY TO BLUETONGUE VIRUS (BTV) IN
SMALL RUMINANTS FLOCKS IN SISTAN & BALUCHESTAN PROVINCE, IRAN**

Mojtaba Alimolaei¹, Majid Ezatkhah², Maryam Amini³

1. Department of Molecular Microbiology, Kerman branch, Razi Vaccine and Serum Research Institute, Kerman branch, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran
2. Department of Anaerobic Bacterial Vaccine Research and Production, Kerman branch, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran
3. Kerman branch, Razi Vaccine and Serum Research Institute, Kerman branch, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran

Background and Aim: Bluetongue (BT) is an arthropod-borne viral disease of domestic and wild ruminants. It is considered to be one of the most important diseases of domestic livestock. We report the results of the first survey of antibody to bluetongue virus in Sistan & Baluchestan province, Iran.

Methods: A total of 325 sera were collected from clinically healthy sheep and goats in this province, and screened by competitive-Enzyme Linked Immunosorbent Assay (c-ELISA). The test was carried out as described in the protocol supplied by the manufacturer.

Results: Seropositive results were found in 26.67 % and 35.79 % of the male and female sheep and in 60.60 % and 89.01 % of the male and female goats, respectively.

Conclusion: Seropositive rates for sheep were variable, due to a small sample size and a small sheep population. Further investigations about prevalence of this virus are needed to increase the knowledge on its epidemiology.

Keywords: Bluetongue, c-ELISA, Seroprevalence, Sistan & Baluchestan, Iran

**P1043 - 698: HIGH SEROPREVALENCE OF BLUETONGUE VIRUS ANTIBODIES IN GOAT
FLOCKS IN NORTH KERMAN, IRAN**

Majid Ezzatkhah¹, Majid Ezatkhah², Mojtaba Alimolaei³, Mehrdad Shamsaddini-Bafti⁴

1. Department of Anaerobic Bacterial Vaccine Research and Production, Kerman branch, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran
2. Department of Molecular Microbiology, Kerman branch, Razi Vaccine and Serum Research Institute, Kerman branch, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran
3. Department of Anaerobic Bacterial Vaccine Research and Production, Kerman branch, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran

Background and Aim: Bluetongue is an insect-borne viral disease of domestic and wild ruminants. Bluetongue listed in “List A” of Office of International Epizootics (OIE). This disease has a considerable impact on the health of livestock. The aim of this study was to describe the seroprevalence rate of BTV in goat flocks in north Kerman of Iran.

Methods: Simple random sampling was performed from ten flocks in north Kerman of Iran. A total of 273 goat blood samples were randomly collected in the winter of 2012. Samples were screened by bluetongue Virus Vp7 Antibody competitive-Elisa (c-Elisa) kit, as described in the protocol supplied by the manufacturer.

Results: The overall prevalence of BTV antibodies was found to be 98.9 % (270 from 273 goats). The seroprevalence rates were 99.02 % and 98.53 % in female and male goats respectively.

Conclusion: Goats are not the main host of bluetongue disease and show clinical signs, rarely. Thus, goats can be act as a reservoir for the virus that causes spreading of bluetongue disease. High titer of BTV serum antibodies in goats is a warning for bluetongue outbreaks that requires more attention in epidemiological monitoring.

Keywords: Bluetongue Virus, Goat, Competitive-Elisa, Kerman

P1044 - 814: PASTEURELLA MULTOCIDA ST 325, A NEWLY REPORTED MULTI LOCUS SEQUENCE TYPE (MLST) CLASSIFIED WITHIN THE ST122 CLONAL COMPLEX

SABA ZATI BORHANI¹, KEYVAN TADAYON², LISA SPRAGUE³, PATRICK BLACKALL⁴,
HEINRICH NEUBAUER⁵, RAINAK GHADERI⁶, MOHAMMAD SEKHAVATI⁷, REZA
BANIHASHEMI⁸, AHMADREZA JABBARI⁹, GHOLAMREZA SHOKRI¹⁰

1. Islamic Azad University of Rasht, Science & Research Branch of Guilan, Rasht, Iran
2. Razi Vaccine Serum Research Institute, Karaj , Iran
3. Friedrich-Loeffler-Institut, Bundesforschungsinstitut für Tiergesundheit Federal Research Institute for Animal Health Naumburger, Jena, Germany
4. Poultry CRC Head Office, University of New England, Armidale, Australia
5. Friedrich-Loeffler-Institut, Bundesforschungsinstitut für Tiergesundheit Federal Research Institute for Animal Health Naumburger, Jena, Germany
6. Razi Vaccine Serum Research Institute, Karaj , Iran
7. Razi Vaccine Serum Research Institute, Karaj , Iran
8. Razi Vaccine Serum Research Institute, Karaj , Iran
9. Razi Vaccine Serum Research Institute, Karaj , Iran
10. Razi Vaccine Serum Research Institute, Karaj , Iran

Background and Aim: *Pasteurella multocida* remains a major pathogen of bovine and ovine populations farmed in large parts of Iran. Back in 1938, a very virulent local strain of *P. multocida* isolated from diseased cattle/buffalos was used in preparation of the hemorrhagic septicaemia (HS) vaccine at the Razi institute, Iran and is still used in production. In order to characterize this commercially valuable strain, the Australian web-based genotyping scheme known as the RIRDC (the Rural Industries Research and Development Corporation) MLST was employed.

Methods: In order to characterize this commercially valuable strain, the Australian web-based genotyping scheme known as the RIRDC (the Rural Industries Research and Development Corporation) MLST was employed.

Results: Consulting the RIRDC MLST database, the alleles of this strain in connection with the individual genes of *adk*, *est*, *gdh*, *mdh*, *pgi*, *pmi* and *zwf* were found to be 52, 37, 21, 17, 4, 2 and 17, respectively

Conclusion: Interestingly, the *adk* allele of the strain (52) was found new. This allele has not been previously recognized. The Iranian strain was typed as sequence type (ST) 325, a new ST currently represented only by this single strain from Iran. The ST 325 lies within clonal complex ST122 which is essentially the HS clonal complex and which occurs across the world. Whether other *Pasteurella multocida* STs are currently circulating in the bovine and ovine populations of Iran and the geographical range, requires further study.

Keywords: *Pasteurella multocida*, MLST, Iran, Sequence Type

**P1045 - 843: INTERACTION OF HETEROPHILS WITH DIFFERENT PHYLOTYPES OF
ESCHERICHIA COLI ISOLATED FROM CHICKEN COLIBACILLOSIS**

Somayeh Ahmadi¹, Habib Dastmalchi Saei², Seyyed Meysam Abtahi Froushani³

1. MS student in Bacteriology, Department of Microbiology, Veterinary faculty, Urmia University, Urmia, Iran.
2. Assistant professor of microbiology, Department of Microbiology, Veterinary faculty, Urmia University, Urmia, Iran.
3. Assistant professor of Immunology, Department of Microbiology, Veterinary faculty, Urmia University, Urmia, Iran.

Background and Aim: Colibacillosis is one of the principal causes of economic losses in poultry industry. As heterophils, the avian equivalent of neutrophils, are an innate responder and typically the first cell type to fight infection, the objective of this study was to investigate whether or not there is any difference in the in vitro interaction between heterophils and four phlotypes of E. coli: A, B1, B2 and D.

Methods: E. coli isolates from chicken colibacillosis were phylogenetic grouped based on the Clermont phlotyping using chuA and yjaA genes and DNA fragment of TSPE4.C2. Then, in vitro effects of E. coli isolates (five for each phlotype) on the phagocytosis, respiratory burst and germicidal effects of heterophils were investigated.

Results: Results showed that opsonized E. coli isolates belonging to phlotype B1 significantly enhanced the levels of phagocytosis and respiratory burst in heterophils compared to other

Conclusion: Phlotype B1 may cause more severe pathologic conditions because of induction higher levels of potentially harmful reactive oxygen substances and resistance to killing by heterophils.

Keywords: Colibacillosis, Phlotypes, E. coli, Heterophils.

**P1046 - 868: IDENTIFICATION AND ANTIBIOTIC RESISTANCE OF COAGULASE-
NEGATIVE STAPHYLOCOCCI ISOLATED FROM NASAL CAVITY OF HEALTHY
ANIMALS IN IRAN**

Habib Dastmalchi saei¹, Somayyeh Hosseinzadeh²

1. Department of Microbiology, Faculty of Veterinary Medicine, Urmia University, P.O. Box 1177, Urmia, Iran
2. Department of Microbiology, Faculty of Veterinary Medicine, Urmia University, P.O. Box 1177, Urmia, Iran

Background and Aim: Coagulase-negative staphylococci (CoNS) are recognised as a major cause of respiratory infections, therefore, the aim of this study was an analysis of the CoNS of the nasal cavity of apparently healthy cows (n=69), sheep (n=51) and goats (n=18) from 3 different areas of Iran, and determine the genes involved in resistance to penicillin (blaZ) and methicillin (mecA).

Methods: From the total of 138 nasal swabs, 26 CoNS were isolated. All isolates possessed the gap gene.

Results: On the basis of PCR-RFLP analysis of gap gene, 19.11% CoNS were identified: *S. piscifermentans* (n=8; 30.76%), *S. simulans* (n=6; 23.07%), *S. xylosus* (n=5; 19.23%), *S. succinus* (n=4; 15.38%), *S. chromogenes* (n=2; 7.69%), and *S. capitis* (n=1; 3.84%). To our knowledge, this was the first isolation of *S. piscifermentans* from nasal cavity of animals. Antimicrobial resistance genes were determined by PCR. Methicillin-resistant coagulase negative staphylococci harbouring *mecA* were not detected in any species, while the *blaZ* gene were detected in 11.53% (n= 3) different species of all CoNS.

Conclusion: In conclusion various CoNS can be colonized in the nasal cavity of healthy ruminants which may be capable of causing disease if they pass across the normal defences of host. This study also showed these isolates might be a reservoir of β -lactamase resistance.

Keywords: Coagulase-negative staphylococci, Nasal carriage, ruminants, gap, blaZ, mecA

**P1047 - 869: PRESENCE OF PENICILLIN G RESISTANCE OF STAPHYLOCOCCUS AUREUS
ISOLATED FROM MASTITIS IN CATTLE AND SHEEP**

Habib Dastmalchi saei¹, Sina Zakeri², Somayyeh Hosseinzadeh³

1. Department of Microbiology, Faculty of Veterinary Medicine, Urmia University, P.O. Box 1177, Urmia, Iran
2. Graduated from Faculty of Veterinary Medicine, Urmia University, P.O. Box 1177, Urmia, Iran.
3. Department of Microbiology, Faculty of Veterinary Medicine, Urmia University, P.O. Box 1177, Urmia, Iran

Background and Aim: Staphylococci are part of the normal microflora of humans and animals and some are potential pathogens that have become resistant to almost all known antibiotics. Resistance of *Staphylococcus aureus* to penicillin G is common among isolates from bovine mastitis.

Methods: This study was aimed at investigating the molecular basis of resistance to penicillin G in cows and sheep staphylococcal isolates.

Results: In the present study, 74 isolates of *Staphylococcus aureus* identified in cows (29 isolates) and sheep (45 isolates) using *nuc* gene, respectively. A 518bp fragment of the structural *blaZ* gene which codes for β -lactamase production in staphylococci was amplified by polymerase chain reaction (PCR). β -lactam resistance was found in 38 isolates which 15 (51.72%) isolates from cows and 23 (51.11%) isolates from sheep.

Conclusion: Due to the presence of *blaZ* in more than half of the samples, these findings can be utilized in mastitis treatment programmes and antimicrobials strategies in organized herds.

Keywords: Mastitis, *Staphylococcus aureus*, penicillin G, *blaZ* gene

**P1048 - 870: SEROLOGICAL DETECTION OF ANTI NEWCASTELL DISEASE VIRUS
ANTIBODIES IN FREE RANGE CHICKEN OF FARS PROVINCE OF IRAN**

Yasamin Dehghani¹, Mohammad Hossein Hosseini², Mehdi Namavari³, Elhame karimi nezhad⁴

1. Islamic Azad University Damghan-Branch, Iran
2. Razi Vaccine and Serum Research Institute, Shiraz, Iran
3. Razi Vaccine and Serum Research Institute, Shiraz, Iran
4. Razi Vaccine and Serum Research Institute, Shiraz, Iran

Background and Aim: Newcastle disease (ND) is one of the most important viral diseases of poultry world wide as well as Iran. It is also the most important infectious disease affecting free range chickens. As infection in free range chicken could act as sores of infection to other specially industrial poultry therefore this study was performed to understand the infection situation in this type of chicken

Methods: In this survey, 197 serum samples of free range chickens were collected from rural area of two regions (Neyriz and Zarghan) of Fars province of Iran. Sera were tested for anti Newcastle disease virus antibodies by haemagglutination inhibition test (HI) following OIE protocol

Results: Of 197 serum samples being tested 153 (77.66%) were positive for NDV antibodies in HI test with mean antibody titer being 5.17. No significant differences observed among the two sampled region ($P > 0.05$).

Conclusion: In this study 44 serum samples (22.33%) were negative for NDV antibodies either not showing any titer or may show HI titer of 2-3, and 77.66% of samples showed titer greater than 4 up to 10. High percentage of positive HI titer among free range chicken indicates that NDV is presented in rural area chicken. Such high prevalence of infection among rural area chicken may emphasize their role as a source of NDV infection

Keywords: Newcastle, free range chicken, haemagglutination inhibition test

P1049 - 881: DETERMINATION AND COMPARISON OF ANTIMICROBIAL SENSITIVITY OF ESCHERICHIA COLI ISOLATED FROM HEALTHY OSTRICHES IN COMPARISON WITH ISOLATES FROM INFECTED POULTRY WITH COLIBACILLOSIS

Afsane Hosseini¹, Saeed Salari², Mojtaba Kiani³

1. Department of Pathobiology, Faculty of Veterinary Medicine, University of Zabol, Zabol, Iran
2. Department of Pathobiology, Faculty of Veterinary Medicine, University of Zabol, Zabol, Iran
3. Veterinarian, Birjand, Iran

Background and Aim: Ostrich carcasses during processing can become infected by their stool and thereupon stool can be considered as a potential source of contamination of environment with resistant bacteria. The objective of this study was to determine the antimicrobial sensitivity of *Escherichia coli* isolated from healthy ostriches and compare with *Escherichia coli* isolated from infected poultry with colibacillosis.

Methods: As a case-control survey, *Escherichia coli* from 43 and 39 feces samples were collected from healthy ostriches and infected poultry with colibacillosis, respectively, and its antibiotic sensitivity for 8 antibacterial agents were determined by disc diffusion method. Statistical analysis were interpreted via K-square and Fisher's exact tests and P value were considered < 0.05 .

Results: the Ostrich-origin *E. coli* had maximum resistance to Ampicillin, Gentamycin and Amoxicillin (100%) antibiotics while resistance to lincospectin and Sultrim (2.3%) was minimum. The *E. coli* isolates obtained from poultry with colibacillosis showed 100% and 35.9% resistances to Ampicillin and Lincospectin antibiotics, as maximum and minimum, respectively. X2 test showed that the sensitivity to three antibiotics including Lincospectin, Sultrim, Oxytetracyclin and Chloramphenicol was significantly different based on origin of *E. coli* ($P < 0.05$).

Conclusion: Regarding to the important role of ostrich in public health, studies considered the antibiotic resistance and application of antibiogram before the treatment of diseased ostrich would be essential. Our results demonstrated that the effects of antibiotic are different between poultry and ostriches. So, for the treatment of identical infectious diseases in ostriches and poultry, a uniform antibiotic medication wouldn't be applicable.

Keywords: Antimicrobial sensitivity, *Escherichia coli*, Healthy ostrich, Poultry with colibacillosis

**P1050 - 1007: ANTIBIOTIC PROPHYLAXIS IN RABBIT OVARIOHYSTERECTOMY
SURGERY**

Leila Mohammadiar¹, Behzad Riaie², Azin Tavakoli³

1. Islamic Azad University, Garmsar Branch
2. Islamic Azad University, Garmsar Branch
3. Islamic Azad University, Garmsar Branch

Background and Aim: One of the most common surgical operations in veterinary is ovariohysterectomy. Nowadays, post-surgical infection is reduced due to performing sterilization during operation procedures. However, dosage and protocols of administration of antibiotics are still unclear in veterinary practice.

Methods: In the present study, 21 rabbits were divided in three groups randomly and undergone ovariohysterectomy surgery in common sterility condition. In the first group, 20 mg/kg IV cefazolin was administered just one hour before surgery. In the second group, rabbits were taken the same dosage one hour before and every 24 hours after surgery for 3 days. In the third group, Cefazolin with the same dosage was used just after surgery every 24 hours for 3 days. Blood samples were collected on the 1st, 2nd, 3rd, and 7th post operation to compare the blood factors (eg. PCV, TP, WBC). The cases were observed for presence of any ulcer infections, inflammations, abscess formations, or wound secretion.

Results: There was no significant difference in the post-surgical wound healing duration or factors between the groups.

Conclusion: The study showed that one dose of antibiotic prophylaxis will be enough in the common rabbit veterinary surgical conditions and probably in other animals.

Keywords: prophylaxis, antibiotic, rabbit, surgery

P1051 - 1042: FIRST DETECTION OF BOVINE TOROVIRUS CAUSING DIARRHEA IN NEW BORN CALVES, IN IRAN

Ahmad Nazaktabar¹, Omid Madadgar², Taghi Zahraei Salehi³

1. Department of Pathobiology, faculty of veterinary, Amol university of special modern technology, Mazandaran, Iran
2. Department of Microbiology, Faculty of Veterinary of Medicine, University of Tehran, Tehran, Iran
3. Department of Microbiology, Faculty of Veterinary of Medicine, University of Tehran, Tehran, Iran

Background and Aim: Bovine torovirus (BToV), a member of the family Coronaviridae, is known as an enteric pathogen of calves, but its epidemiology and etiological role in causing diarrhea in newborn calves of Iran has been unclear. In this study we investigate its frequency in 587 samples collected from diarrheic calves among 14 provinces of Iran, using RT-PCR. As our Knowledge it is the first report of detection of bovine toroviruses in Iran.

Methods: 587 stool samples were collected from diarrheic calves under 1 month old rearing in industrial or rural dairy farms in 14 provinces as Tehran, Alborz, Qazvin, Qom, Markazi, Isfahan, Fars, Zanjan, East Azarbaijan, Sistan and Baluchistan, Razavi Khorasan and South Khorasan. All samples investigated with a very sensitive RT-PCR to detect torovirus infection.

Results: Torovirus was detected in only 6 samples which were collected from provinces Fars and Isfahan (3 samples from each one). Positive samples were collected from industrial farms in which administration of colostrum were done.

Conclusion: The results of this study proved the presence of torovirus infection in Iran. Although, the infection rate is rare but it should be considered as a potential risk as a new emerging infection particularly under the pressure of rotavirus A immunity.

Keywords: Bovine torovirus, calf diarrhea, molecular epidemiology, Iran

**P1052 - 1043: FIRST DETECTION OF BOVINE ROTAVIRUS GROUP C CIRCULATING IN
CALF POPULATION OF DAIRY FARMS OF IRAN**

Ahmad Nazaktabar¹, Omid Madadgar², Taghi Zahraei Salehi³

1. Department of Pathobiology, faculty of veterinary, Amol university of special modern technology, Mazandaran, Iran
2. Department of Microbiology, Faculty of Veterinary of Medicine, University of Tehran, Tehran, Iran
3. Department of Microbiology, Faculty of Veterinary of Medicine, University of Tehran, Tehran, Iran

Background and Aim: Rotaviruses are important agents of gastroenteritis in humans and animals Which are divided in 8 groups based on antigenic features of protein of their intermediate capsid, VP6. Group C rotaviruses (RVC) were first isolated in piglets in 1980 and in humans and bovine in 1982 and 1991, respectively. The zoonotic potential and interspecies transmission of RVC has been demonstrated which increasing the importance and interesting questions about their unclear aspects of their biology. In present study epidemiology of this virus has been investigated among calf population in the broad area of our country and as our knowledge this the first attempt to detect and reveal the epidemiology of RVC in Iran.

Methods: 587 stool samples were collected from diarrheic calves under 1 month old rearing in industrial or rural dairy farms of 14 provinces as Tehran, Alborz, Qazvin, Qom, Markazi, Isfahan, Fars, Zanjan, East Azarbaijan, Sistan and Baluchistan, Razavi Khorasan and South Khorasan. All samples investigated with a very sensitive RT-PCR to detect rotavirus group C infection.

Results: Four samples of all examined samples where positive. The infected calves were reared in provinces Tehran (1 sample), Sistan and Baluchestan (1 sample), Fars (1 sample) and Zanjan (2 samples). The positive samples were collected from both industrial and rural farms.

Conclusion: The results of this study demonstrated the presence of bovine rotavirus C infection in Iran. Considering the zoonotic potential, presence of the virus in both industrial and rural farms and potential of interspecies transmission to human population living nearby the farms is important.

Keywords: Rotavirus C, calf diarrhea, molecular epidemiology

**P1053 - 1097: TURKEY ENTERITIS PREVENTION USING GARLIC AND SHALLOT
POWDER**

Abdolreza Nabinejad¹

1. Isfahan Res center of Agriculture

Background and Aim: Turkey meat with some specific characters could be a suitable and cheap alternative for human usage, Now the social taste are going to increase for turkey meat therefore its health is important. Turkey breeding duration is more than 140 days and its body weight would be more than 15 kg , these birds could be infected with some infectious agent ,turkeys gastroenteritis is one of the most popular infection which execute by Enterobacteriaceae and complicate with some viruses and parasites followed by clinical sign such as emaciation, weakness,diarrhea and finally death can occur. The morbidity rate of turkey gastroenteritis is about 10% and using antibiotics is first indication for treatment, in other hands the antibiotics have some known and unknown side effects so herbal medication could be recommended for prophylaxis and treatments

Methods:Garlic(*Allium sativum*) and Shallot (*Allium hirtifolium*) with some antimicrobial contents such as allicine and a suitable taste for human are good candidate for turkeys farm.

Results:In current work prevention of gastroenteritis in 2 turkey farms with a population of 4000 birds were studied , so garlic and shallot powder in a equal ratio and totally as 0.02 % of growing and finishing diet were used

Conclusion:Regarding to the results the rate of gastroenteritis were decreased in the studied farms comparing ti the others, Geougenum mucosal layer microscopy of treated birds showed increasing of papilla diameter and length

Keywords:Turkey, gastroenteritis, prevention, Garlic, shallot

**P1054 - 1152: A REVIEW OF THE EPIDEMIOLOGY OF MALARIA AND
IMMUNOINFORMATIC STUDY OF SG1, SG2 AND SG3 PROTEINS OF SALIVARY GLAND
IN ANOPHELES GAMBIAE**

Seyed Sajjad Hasheminasab¹, sara khalili²

1. 2Department of Parasitology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
2. 2Department of Parasitology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran

Background and Aim: Malaria is the most important parasitic disease in the world and remains of highest public health significance. About 280 million people in eight countries in the Eastern Mediterranean were at some risk of malaria, with 104 million at high risk. Six countries have areas of high malaria transmission (Afghanistan, Djibouti, Pakistan, Somalia, the Sudan and Yemen), transmission is focal in Iran and Saudi Arabia.

Methods: Studies were identified by using electronic databases in various research areas related to such as PubMed, Elsevier Search by keyword as Epidemiology of malaria, Anopheles mosquitoes and bio control etc. The amino acid sequence of salivary gland of anopheles proteins retrieved from UniprotKB databases. Then physico-chemical properties of sequence were evaluated. Using immunoinformatics servers we predicted B-cell epitopes and antigenicity testing by Kolaskar & Tongaonkar method.

Results: Results revealed 19, 4 and 6 antigenic epitopes for SG1, SG2 and SG3, respectively. Based on SVM method, all predicted epitopes were allergenic. The minimum score for SG1, SG2 and SG3 was 0.890, 0.880 and 0.906, respectively, and also the maximum score was 1.230, 1.318 and 1.210 respectively. The 19 antigenic epitopes in SG1 were between 4 to 396bp, The 4 antigenic epitopes in SG2 were between 4 to 101bp and finally the 6 antigenic epitopes were between 4 to 130bp.

Conclusion: Malaria is commonly associated with poverty and has a major negative effect on economic development. Bioinformatics analysis results showed that this protein has several peptides that are responsible for its antigenicity.

Keywords: malaria, epidemiology, proteins of salivary gland, Anopheles

**P1055 - 1177: EVALUATION THE PATTERN OF ANTIBIOTIC SENSITIVITY AND
RESISTANCE OF ESCHERICHIA COLI AND SALMONELLA ISOLATED FROM
AVICULTURE IN THE TABRIZ CITIES**

Yasin Bageri¹, Adel Feizi², Benyamin aqchehli³, Sina Moshtagh⁴

1. Young Researchers And Elite club, Tabriz Branch Islamic Azad university, Tabriz, Iran
2. Department of Avian Diseases, Faculty of Veterinary Medicine, Islamic Azad University Tabriz, Tabriz, Iran
3. student of medical Sciences Islamic Azad University Gorgan Branch, Medical laboratory Department, Gorgan, Iran
4. DVM student, College of Veterinary Medicine, Islamic Azad University, Tabriz Branch, Tabriz, Iran

Background and Aim: Drug-resistance prevalence in Salmonella and colibacillosis, is one of the concerns of broiler farms and human societies. The indiscriminate use of antibiotics in broiler farms has been resulted to increases the amount of resistance in this type of diseases. The aim of this study is evaluation the pattern of antibiotic sensitivity and resistance of Escherichia coli and Salmonella isolated from broiler farms in the cities around Tabriz.

Methods: Resistance level of four Salmonella isolates from 50 stool samples was conducted against antimicrobial compounds based on standard disk diffusion method. Also 75 stool samples for E. coli were collected and antibiotic sensitivity was performed by disk diffusion method (Kirby-Bauer).

Results: All isolated Salmonella were sensitive to cefixime, ceftriaxone, gentamicin, fosbac and felorfenicle. Also all Salmonella isolates were resistant to gentamicin, doxycycline and flumequine. As well as, multi-resistant was prevalent between four Salmonella isolates. The most resistance of E. coli was related to flumequine and doxycycline and the least one expressed for gentamicin.

Conclusion: It is recommended to select the best antibiotic before treating poultry flock, must be used antibiotic sensitivity test.

Keywords: Escherichia coli, Salmonella, poultry, antibiotic sensitivity and resistance

P1056 - 1251: PARATUBERCULOSIS IN IRAN, HAS THE TIME ARRIVED FOR A NATIONAL CONTROL PLAN?

LIDA ABDOLMOHAMMADI KHIIV¹, MASOUD HAGHKHAH², KEYVAN TADAYON³, NADER MOSAVARI⁴, MOHAMMAD TABATABAI⁵, ABDOLLAH DERAKHSHANDE⁶

1. Shiraz College of Veterinary Medicine, Shiraz, Iran
2. Shiraz College of Veterinary Medicine, Shiraz, Iran
3. RAZI VACCINE AND SERUM RESEARCH INSTITUTE
4. RAZI VACCINE AND SERUM RESEARCH INSTITUTE
5. Shiraz College of Veterinary Medicine, Shiraz, Iran
6. Shiraz College of Veterinary Medicine, Shiraz, Iran

Background and Aim: There are a number of convincing evidences to implicate importation of live animal stocks in introduction of paratuberculosis (PTb) to Persia. Regardless of the original source, PTb is now extensively scattered across the country.

Methods: In order to improve the current epidemiological understand of PTb, clinical specimens (feces and blood) from 142 cattle, sheep and goats representing Alborz, Fars, Isfahan, Kerman, North Khorasan, Tehran and Qazvin provinces were subjected to diagnostic molecular (IS900-PCR, F57-PCR), and traditional (ELISA, bacterial culture on specific media) tests

Results: In ELISA 90 and in bacterial culture 30 out of 142 examined animals were tested positive with IS900-PCR and F57-PCR also positive in all culture-positive specimens.

Conclusion: Given that reports on high frequency of PTb in Iranian farm animals are on rise, we assume the time has arrived to re-think about implementation of a State-funded plan to bring PTb under control.

Keywords: Paratuberculosis, Persia, F57

Viruses

P1057 - 21: DO COMMON MITOCHONDRIAL DNA POLYMORPHISM ASSOCIATION WITH HUMAN T-CELL LEUKEMIA VIRUS TYPE I

Toktam Zolfaghari¹, Massoud Houshmand², Ehsan Ghayoor Karimiani³

1. Department of Medical Biotechnology Research Center, Ashkezar Branch, Islamic Azad University, Ashkezar, Yazd, Iran.
2. Department of Medical Genetics, National Institute of Genetic Engineering and Biotechnology (NIGEB), Tehran, Iran.
3. Department of molecular Genetics, Razavi Hospital, Mashhad, Iran and Department of Medical Genetics, Mashhad University of Medical Sciences, Mashhad, Iran.

Background and Aim: Human T-cell leukemia virus type I infection is endemic in Razavi Khorasan, Northeast of Iran. Accumulation of single nucleotide polymorphisms (SNPs) in the displacement loop (D-loop) of mitochondrial DNA (mtDNA) may be associated with an increased HTLV1 risk. In the present study we investigated the association between D-loop SNPs in a case-control study and the outcome of HTLV-I infection in Iranian patients.

Methods: We sequenced the D-loop region in 36 samples of Patient's with HTLV1, as well as matched 116 normal group.

Results: The frequencies of the major mitochondrial CR polymorphisms were significantly higher in patients with HTLV1 compared to the controls. The control region SNP A73G, commonly found were more frequent in the patient's with HTLV1 than in healthy control, whereas the minor allele of nucleotides C16519T associated with the decreased risk of HTLV1 disease.

Conclusion: Our results suggest that mtDNA variations could be involved in HTLV1 etiology and pathogenesis, although the functional consequence of CR polymorphisms remains to be elucidated.

Keywords: Human T-cell leukemia virus type I, D-loop mutation, haplogroups, Mashhad

P1058 - 110: INVESTIGATION OF PAPILLOMA VIRUS GENOTYPES IN PATIENT'S ORAL LESIONS WITH HEAD AND NECK CANCER IN THE YEAR 1393 IN IRAN

Elham Pouide¹

1. Dr.Ehsan Arefaniyan

Background and Aim: Introduction: Squamous cell carcinoma comprises approximately 94% of all oral cavity. Malignancies that involve jaw, mouth, tongue, tonsils and salivary glands. One of the most important reasons for this cancer, is Human Papilloma Virus (HPV). It has different genotypes but. Just some of them can make this cancer. Finding the most common genotypes will be hope full to control and prevent of spreading this virus.

Methods: In this study 70 paraffin blocks were collected from cancer department of Imam Khomeini hospital in Tehran. All of these samples included histopathological report of dysplastic lesions. They were considered about 6 months. First the samples were deparaffinated. Then some primers were designed for polymerase chain reaction technique (PCR). All the samples were transferred to electrophoresis tank. At last, positive samples were sequenced by Mega 4.

Results: • Finding the relation between papilloma virus and mouth cancer. • Finding the common genotypes of HPV in mouth cancer • Finding if there is a relation between sex and age with papilloma virus in mouth cancer. • Consideration of HPV spreading

Conclusion: 8 HPV+ samples include of 3 HPV+6 and HPV+16. HPV6 is the cause of genital warts that can spread by skin contact or oral-sexual behavior. 3 positive samples were found in women and the others were in men. (2% more in men). People between 30 to 45 is more sensitive for HPV than the other group. People up to 60 years old are sensitive too. All the samples were collected from different cities of Iran but most of the positive samples were found in Tehran and Islam Shahr.

Keywords: Carcinoma. Human papilloma virus, Squamous cell, Polymerase Chain Reaction (PCR).

**P1059 - 119: MOLECULAR DIAGNOSIS OF HUMAN PAPILLOMAVIRUS (HPV)
GENOTYPES IN TEHRAN CITY**

Bahareh Soltanahmadi¹, Ali_Reza Ahmadi, ², Naeimeh Najafi ³, Ali Islamifar⁴

1. Department of Biology, Faculty of Science, Payam Noor Tehranshargh University
2. Department of Biomedical Sciences, Alzahra University, Tehran, Ira
3. Department of Biomedical Sciences, Alzahra University, Tehran, Ira
4. Department of Clinical Research, Pasteur Institute, Tehran, Iran

Background and Aim:The human papilloma virus is known as one of the cause's anogenital cancers, including cervical cancer there is a strong link between presences of different types of human papilloma viruses to the development of genital lesions. HPV16 and HPV18 were defined as most important etiologic agents for cervical dysplasia and carcinoma. The aim of present research was to find genital HPV genome in patients with cervical cancer and control group and to investigate incidence of HPV16, HPV18, HPV31, HPV33, HPV45 and HPV51 types among patients admitted to medical centers.

Methods:For this purpose, DNA was extracted and purified using a DNA Extraction Kit (Cinnagen, Tehran, Iran) from 50 patients with cervical cancer attending the Imam Khomani Hospital (Tehran, Iran) and amplified by PCR. The nucleotide sequences were analyzed using the BLAST program (<http://www.ncbi.nlm.gov/BLAST>).

Results:The molecular and pathological investigation of samples showed that %71 of cases were HPV-positive. Out of them, %41 of samples was determined HPV 16 , %28 HPV18, %10 HPV31, %5 HPV33, %7 HPV45 and %9 HPV51 .

Conclusion:As a matter of fact, the virus is not related to significantly detectable symptoms, and also the extreme prevalence of HPV in Iran, early detection of HPV can prohibit preventing cancer development from pre-cancer lesions. Therefore, using molecular techniques like PCR may contribute effectively to identifying HPV cases to diagnose in a proper time.

Keywords:Human Papilloma Virus, Cervical Cancer, Molecular Diagnosis, Genotypes

**P1060 - 155: EXPRESSION AND SOLUBILITY DETERMINATION OF HEPATITIS B CORE
ANTIGEN IN E.COLI**

Malihe sadat Hashemi khah¹, Hafez Heydari-Zarnagh²

1. Department of microbiology, Damghan branch, Islamic Azad university, Damghan, Iran
2. Assistant Professor of Dept of Clinical Biochemistry School of Medicine Sabzevar University of Medical Sciences

Background and Aim: Hepatitis is a major cause of mortality in the world. HBC is one of the hepatitis B proteins, having a strong immunogenic protein and one of the serological markers of acute infection with HBV is the virus. Protein expression in E.coli expression system often leads to the formation of insoluble structures is Anklvzhn-Bady. Processes related to proper folding and protein solution are usually complex and time-consuming this is. The aim of this study the expression of HBc in E.coli expression system is the solution.

Methods: In order to genotype D, HBc coding sequences derived from the database Uniprot according to codon usage in E. coli was optimized and the position vector pET32a was subcloned BamHI and ECORI. Recombinant vector in BL21 cells that were transformed into chemical was to prepare. HBC protein expression was induced by adding IPTG. The bacteria were collected by centrifugation and then frozen and Rfryz, using the enzyme lysozyme and sonication the solid and liquid phases were separated both on SDS-PAGE gel

Results: SDS PAGE showed that HBS successfully expressed in E. coli cells. The results of the SDS PAGE indicate that protein using the above methods as well as the solution phase.

Conclusion: HBc protein in the cells of E-coli expression by adding IPTG was good and determine the solubility, using methods such as freeze-Rfryz, using the enzyme lysozyme and sonication was determined by purifying the protein can also be used to measure HBV infection can be used.

Keywords: protein expression, hepatitis B, core antigen, E. coli

**P1061 - 156: CONSTRUCTING, MOLECULAR MODELLING AND EVALUATING A NOVEL
CHIMERIC ANTIGEN CONTAINING GP46 AND P19 LINEAR EPITOPES FOR HTLV-I
INFECTION SCREENING**

Malihe sadat Hashemi khah¹, Hafez Heydari-Zarnagh²

1. Department of microbiology, Damghan branch, Islamic Azad university, Damghan, Iran
2. Assistant Professor of Dept of Clinical Biochemistry School of Medicine Sabzevar University of Medical Sciences

Background and Aim: The aim of the present study was to design a single chimeric peptide (SCP) to detect HTLV-I 29 antibodies. A chimeric peptide for C-terminal epitopes of p19 (100–130) and gp46 (175–213) 30 was designed and was initially studied using computational tools

Methods: Peptide was synthesized and 31 used as antigen. Ninety serum samples obtained from the blood center of Mashhad, previously 32 analyzed by ELISA and Western blotting, were evaluated by the chimeric peptide designed 33 here.

Results: The results indicated that SCP was able to detect HTLV-I infected sera with high 34 sensitivity and specificity.

Conclusion: With further validation, SCP described in the present study could be 35 introduced as a novel candidate for high specific screening of HTLV-I infection in endemic 36 regions.

Keywords: HTLV-I, synthetic peptides, p19, gp46, antigenicity

**P1062 - 173: A SURVEY OF THE FREQUENCY OF CYTOMEGALOVIRUS-ASSOCIATED
DIARRHEA IN HIV/AIDS PATIENTS USING NON-INVASIVE METHOD**

Mahmoud agholi¹, Jamal Sarvari², Gholam Reza Hatam³

1. Department of Microbiology, Fasa University of Medical Sciences, Fasa, Iran
2. Department of Bacteriology and Virology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran
3. Department of Parasitology and Mycology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran

Background and Aim: Cytomegalovirus infection is the most common infectious complication in immunocompromised patients. The development and performance of a robust and sensitive PCR assay are described and evaluated for detection of CMV DNA in human fecal specimens. Our aim was to detect CMV DNA in stool samples of HIV/AIDS with chronic persistence diarrhea in Iran

Methods: A total of 356 subjects diagnosed as with HIV/AIDS suffering from chronic diarrhea were consecutively included in this study. CMV DNA was extracted from stool samples using phenol chloroform method. CMV DNA was identified by polymerase chain reaction using sequence specific primers on genomic DNA

Results: Of the 356 patients with an age range of 10–69 years, 273 (76.68%) were males and 83 (23.31%) females. The mean age of the male and female patients was 38.68 and 35.69 years, respectively. From 356 subjects 6 subjects were positive for CMV DNA

Conclusion: The results of this study were shown that the cause of chronic diarrhea in some HIV/AIDS patients is CMV infection which might be detected by non-invasive method. Accordingly, we recommended non-invasive method, stool sample, as a first line of diagnosis of colitis when the physician suspected to the CMV colitis in this group of patients.

Keywords: Cytomegalovirus; stool samples; HIV/AIDS; chronic diarrhea

**P1063 - 208: CLONING AND EXPRESSION OF VP1 GENE OF FOOT AND MOUTH DISEASE
VIRUSE AND FLIC GENE OF SALMONELLA IN E.COLI**

Mehrnoosh Qadir¹, mahmoud azimi²

1. Department of Microbiology, Faculty of Sciences, Karaj Branch, Islamic Azad University, Karaj, Iran
2. Assistant professor of Razi Vaccine & Serum Research Inst. FMD Dept

Background and Aim:Foot& mouth disease (FMD) is a viral vesicular disease which severe damage has been caused livestock. Now FMD is controlled by traditional inactivated vaccine. Due to short duration of immunity, using molecular adjuvant is recommended to increase efficiency of vaccine. Purpose of this study is synthesis fusion protein from VP1 protein of FMDV (Opanasia2) and flagelline of the salmonella (FliC) in E. coli.

Methods:1D gene that is responsible for producing vp1 protein was produced by PCR(800bp)and cloned in PTZ57 vector.After cutting cloned fragment from the recombinant plasmid by HindIII & XhoI, inserted to expression vector (pET41b) that contain FliC of the salmonella. The construct was transfected to competent E. coli (BL21DE3) cell. The expression was induced by IPTG (0.5mM) and purified by Ni-NTA Resin. Production of recombinant protein was resolved by SDS-PAGE in 12% acrylamide gel and western blotting.

Results:Recombinant fusion protein was evaluated by PCR and enzyme digestion. By molecular analysis, PCR product by length 700 and 1500 bp was observed.Ni-NTA Resin and gradient pH was used for purification that the most amount of protein recovering was observed in PH 4.5. Recombinant protein by molecular weight of 76 KDa determined in SDS-PAGE (12% acrylamide gel) and was confirmed by western blot by AntiHis.

Conclusion:In this study, the fused gene of FMDV vp1 and flagellin of salmonella (FliC /2200 bp) was cloned successfully in E.coli and recombinant protein (76 KDa) was expressed and purified.

Keywords:VP1-FMDV-FLAGELLIN SALMONELLA

P1064 - 277: POTENTIAL ANTIGENICITY OF THE G1- EPITOPE BEFV ISOLATED IN IRAN

Fereshteh YAZDANI¹, Mehran bakhshesh², Majid Esmaeilizad³, Zohreh Azita sadigh⁴

1. Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
2. Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
3. Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
4. Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran

Background and Aim: Bovine ephemeral fever is an acute and arthropod-borne viral disease of cattle and water buffalo. The surface glycoprotein G of BEFV is composed of 4 antigenic sites (G1-G4) and plays the main role for eliciting neutralizing antibodies and protective immunity. In order to detect anti-BEFV antibodies, establishment of an ELISA test using G1-epitope as a specific coating antigen has been investigated in a couple of research.

Methods: Using PCR and specific primers, a length of 88 amino acid of the G glycoprotein of BEFV including G1- epitope was amplified and cloned into the expression vector pGEX-4T-1, with the GST moiety. The recombinant plasmid (pGEX-4T-1-G1) was then transformed into E.coli BL21 and expression of fusion protein was induced by 0.1 mM IPTG at different times.

Results: The fusion protein G1 plus GST was successfully expressed in the prokaryotic system and the maximum expression of was obtained at 16h post induction as verified by SDS-PAGE electrophoresis. It was also confirmed that this protein bearing G1- epitope is biologically active to bind to anti-BEFV serum in Western blot experiment.

Conclusion: These data could be constructive for development of a specific and inexpensive ELISA test based on the recombinant G1- epitope as a coating antigen.

Keywords: BEFV, G1- Epitope, Ecoli, ELISA

**P1065 - 315: EVALUATION SEROPREVALENCE HEPATITIS B AND C VIRUS IN SAHNEH
CITY OF KERMANSHAH PROVINCE OF IRAN DURING MARCH 2010-MARCH 2016**

Mehrdad Pooyanmehr¹, Qobadi Esmaeil², Amini Zohreh³

1. 1Department of Pathobiology, microbiology section, Faculty of Veterinary Medicine, Razi University, Iran
2. 2Veterinary Student, Faculty of Veterinary Medicine, Razi University, Iran
3. 2Veterinary Student, Faculty of Veterinary Medicine, Razi University, Iran

Background and Aim: Hepatitis B is considered as a cause for serum hepatitis which may lead to liver cells cancer. Hepatitis C is major cause of chronic hepatitis in developed countries. It can cause both acute and chronic infections. this study was conducted to evaluate the prevalence of Hepatitis B and C in Sahneh City in Kermansha Province of Iran during a period of five years (March2010 – March2016).

Methods: This study performed include 5000 patients with age 20 -60 years on serum samples were tested for determining of HBsAg and total anti-HBcAb by Enzyme-linked immunosorbent Assay (Elisa) quantitatively in during five years (March2010 – March2016). Titers of higher than 10 mIU/ml were considered protective. Serum samples were collected from the patients who sent to the central lab (HEALTH CENTER) in Sahneh City during a period of five years. Only samples positive for HBsAg and total anti-HBcAb were used for the study.

Results: The findings showed that Blood samples were taken from 49 patients 35 male (71.43%) and 14 female (28.57%). total samples had positive result for HBsAb and total anti-HBcAb during period (2010 - 2016), 2010 (0.24 %), 2011 (0.18%), 2012 (0.22%), 2013 (0.18%), 2014 (0.08%) and 2015 until March 2016 (0.08%) years respectively.

Conclusion: According to our findings health education and evaluation of immune responses against hepatitis is necessary. Although the prevalence of hepatitis B and C infection in Sahneh City are similar to the general population of Iran And during last five years has not significant increase.

Keywords: Seroprevalence, hepatitis B and C, Elisa

**P1066 - 515: PODOVIRIDAE BACTERIOPHAGES ISOLATION AND MICROSCOPIC
CHARACTERIZATION FROM URMIA LAKE, IRAN**

Arash Mohammadpoor Arjmand¹, Ehsan Arefian², Mohammad Ali Amoozegar³

1. Department of Microbiology, School of Biology, College of Science, University of Tehran, Tehran, Iran
2. Department of Microbiology, School of Biology, College of Science, University of Tehran, Tehran, Iran
3. Extremophile laboratory, Department of microbiology, faculty of biology, college of science, university of Tehran, Tehran, iran

Background and Aim: Urmia Lake is one of the most important hypersaline marine area in Iran with specific situation due to drought and loss of many biological species. Because of the important role of phages in the ecosystem of the lake, to create a balance between bacteria in the Lake, it is important to isolate and characterize lake environmental bacteriophages. The aim of the current study is isolation and characterization bacteriophages from Urmia Lake by plaque assay and TEM microscope.

Methods: Saline water samples were collected from the lake. The bacterial strains were isolated from the water samples on Sea Water Nutrient (SWN 3% salt). After molecular characterization and identification of the environmental lake bacteria strains, the method of top agar was used to isolate bacteriophages. In this way plaques, areas on the medium that the host bacteria are destroyed by the phages, were produced on bacteria cultured media. Plaques were purified by three times sub-culturing. Final samples were collected from purified plaques and stained on the grids then Phages were detected and surveyed by Transmission Electron Microscopy (TEM).

Results: The results showed that a tailed bacteriophage belong to podoviridae is illustrating lytic cycle in its host, gram-negative cocci, that both of them were isolated from Urmia lake.

Conclusion: Finally, we ought to survey Urmia Lake Podovirus and compare sizes of these phages with marine Podovirus phages. Furthermore, molecular characterization of these phages should be investigated in the future.

Keywords: Bacteriophages, Urmia Lake, saline areas, TEM

**P1067 - 544: DETECTION OF SOME VIRULENCE FACTORS OF ESCHERICHIA COLI
ISOLATED FROM URINARY TRACT INFECTION BY MULTIPLEX PCR IN MASHHAD,
NORTH EAST OF IRAN**

Tahereh Gholamhosiani moghadam¹, Mahdis Ghavidel², Kiarash Ghazvini³

1. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.
2. Antimicrobial Resistance Research center, School of Medicine Mashhad University Of Medical Sciences, Mashhad, Iran.
3. Antimicrobial Resistance Research center, School of Medicine Mashhad University Of Medical Sciences, Mashhad, Iran.

Background and Aim: Urinary tract infections (UTIs) are one of the most common infectious diseases. Although different bacteria can be responsible for UTIs. E.coli is the most frequently isolated pathogen in UTIs. The pathogenic potential of E. coli strains dependent on the presence of virulence factors. The aim of this study was to determine the presence of main virulence genes by multiplex PCR among clinical isolates in northeast of Iran.

Methods: Seventy Escherichia coli isolates obtained from patients with urinary tract infection (UTI) referred to the Ghaem Hospital Microbiology Laboratory, Mashhad, Iran. A Multiplex polymerase chain reaction (PCR) was used for the amplification of genes encoding pyelonephritis associated pili (pap genes), S-family adhesions (sfa gene), type1 fimbriae (fimH gene), aerobactin (aer gene).

Results: Frequencies of fimH, aer, pap and sfa in total of 70 E. coli isolates were 82.86% (58), 78.57% (55), 32.86% (23) and 0% respectively. Based on presence of different virulence factors observed 7 patterns included: only aer+, only fimH+, and only pap+ were 11.43%, 15.71% and 1.43% respectively. Another pattern were: 40% aer+ and fimH+, 16% aer+, fimH+ and pap+, 4.28% aer+ and pap+, 4.28% pap+ and fimH+.

Conclusion: Based on our finding, fimH is the most frequent virulence factor among these isolates surprisingly this result is in contrast to other previous studies. According to many previous reports, pap has more significant role in UTI. In addition, our findings show that Multiplex PCR is an efficient, rapid and economical tool for identification of virulence profile of E. coli isolated from UTI.

Keywords: UTI, E.coli, virulence factors, Multiplex PCR

**P1068 - 554: EXPRESSION AND PURIFICATION OF IMMUNO-DOMINANT PEPTIDE
DERIVED FROM GP46-II FOR DETECTION OF HTLV-II SPECIFIC ANTIBODIES**

Maryam Miyanabadi¹, hafez heydari zarnagh², malihe sadat hashemi khah³

1. 1Department of Microbiology, Neyshabur Branch, Islamic Azad University, Neyshabur, Khorasan Razavi, IR Iran
2. Asistent or professor of Department of Clinical Biochemistry School or Medicin Sabzevar Univrsity of Medical Sciences
3. department of microbiology,Damghan branch,Islamic Azad university,damghan.semnan.

Background and Aim:: K55 is a fusion protein that includes His-GST and a44 amino acid peptide derived from a conserved region of gp46-II of human T-cell leukemia virus (HTLV)-II. This protein is used in the detection of HTLV-II infection.

Methods:: Synthetic DNA encoding K55 was sub-cloned into pGEX-4t-1 expression vector and then transformed into chemically competent *E. coli* cells. The expression of K55 was induced using 1 mM IPTG. The expression and solubility of K55 was evaluated by SDS-PAGE. The recombinant protein was purified using affinity chromatography. The immune reactivity of purified protein with antibodies present in infected serum was evaluated using ELISA.

Results:The SDS-PAGE results indicated that K55 is expressed as a soluble form in *E. coli* cells. In addition, ELISA results indicated that this protein interacts with anti-HTLV-II-specific antibodies in a concentration-dependent manner.

Conclusion:The K55 prepared in *E. coli* cells specifically reacts with anti-HTLV-II antibodies and could be used in the preparation of diagnostic reagents.

Keywords:HTLV-II, Screening, gp46-II, Protein Purification

**P1069 - 612: A FATAL CRIMEAN-CONGO HEMORRHAGIC FEVER FOLLOWING
INFECTION WITH AN AP92 LIKE STRAIN OF CRIMEAN-CONGO HEMORRHAGIC
FEVER VIRUS**

Yasaman Jamshidi¹, Mostafa Salehi-Vaziri², Mehdi Fazlalipour³

1. Department of Arboviruses and Viral Hemorrhagic Fevers (National Ref Lab), Pasteur Institute of Iran, Tehran, Iran
2. Department of Arboviruses and Viral Hemorrhagic Fevers (National Ref Lab), Pasteur Institute of Iran, Tehran, Iran
3. Department of Arboviruses and Viral Hemorrhagic Fevers (National Ref Lab), Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Crimean-Congo Hemorrhagic Fever (CCHF) is serious tick-borne viral, zoonose with a mortality rate up to 50% in humans¹. CCHF virus can be transmitted to people via infected tick bites or through exposure to blood or tissues of patients or viremic animal. The disease is endemic in Africa, Southeast Europe, Asia and the Middle east ^{2,3}. It has been proposed that the AP92 strain of CCHF virus poses no virulence, and has been suggested as a vaccine candidate. However, in recent years some study reported a mild clinical disease following infection with this strain. Here, we report a fatal case of CCHF following AP92 like strain of Crimean-Congo Hemorrhagic Fever virus in Iran.

Methods: In October 2015, a serum sample from an old man probable to CCHF was sent to the department of Arboviruses and Viral Hemorrhagic Fevers (National Ref Lab), Pasteur institute of Iran. He had Pyrexia, myalgia, sever hemorrhage and low platelet count on admission. CCHF virus infection was confirmed by the use of reverse transcriptase polymerase chain reaction (RT-PCR).

Results: Sequence analysis of RT-PCR product revealed high similarity this isolate to the AP92 strain. The isolate was nominated as Iran-4675 and the sequence was submitted in GenBank with the accession number KT899991.

Conclusion: This report describe a case of fatal CCHF following infection with a CCHF virus AP92 like strain which is genetically varied from other strains reported from Iran. In addition, this is the first report of AP92 like strain in Iran.

Keywords: Crimean-Congo hemorrhagic fever virus, Phylogenetic analysis, Iran

**P1070 - 651: EVALUATION OF RISK FACTORS AND CLINICAL COURSE IN PATIENTS
WITH HIV INFECTIONS AT TABRIZ CITY DURATION 2013-15**

Yasin Bageri¹, Mojtaba Varshochi², Sina Moshtagh³, Benyamin aqchehli⁴

1. Young Researchers And Elite club, Tabriz Branch Islamic Azad university, Tabriz, Iran
2. Associate Professor of Infectious Diseases, Dept. of Infectious Diseases, Tabriz University of Medical Sciences, Tabriz, Iran
3. DVM student, College of Veterinary Medicine, Islamic Azad University, Tabriz Branch, Tabriz, Iran
4. student of medical Sciences Islamic Azad University, Medical laboratory Department, Gorgan, Iran

Background and Aim: In this study we intended to evaluate the patients with HIV in this province during current 3 years so that obtained information may be used to prevent and treat this illness in these patients.

Methods: Check lists were completed for all subjects who were enrolled in this study. Check lists were included demographic information such as possible ways of infection, patient's status at diagnosis, disease progress, onset and duration of treatment, co morbidities, consumption of anti-viral drugs, cause of death and interval from diagnosis to death, malignancy, family status in terms of disease and sexual risks.

Results: information of 20 patients with HIV was evaluated that 65% were men and the mean age was 40.20 years. Thirty percent of patients were married. In evaluation of potential transmission ways of HIV, 55% were with intravenous injection, 40% sexual contact, and 5% were with blood products. In evaluation the history of risk factors in patients, 70% were with intravenous addiction, 15% with tattoos, 10% with prison history and 5% were with bloodletting history. The mean CD4 count in patients was 252 cells per ml. Fever with 70%; aphthous with 45% and diarrhea with 30% were the most common symptom among patients and also multi-symptom was observed in some patients.

Conclusion: This study showed that injective addiction were the most common risk factor and intravenous injection was the most common way to transmission the HIV virus. Hepatitis C was the most common co morbid and opportunistic disease in this study. Also use of HAART treatment increased survival of patients.

Keywords: infection, HIV, Tabriz province

**P1071 - 668: FREQUENT UL27 MUTATIONS IN HIV INFECTED CLINICAL SAMPLES MAY
SUGGEST ITS ROLE IN VIRUS INFECTION**

Azam Mirarab¹, Alireza Mohebbi², Alijan Tabarraei^{2,3}, Abdolvahab Moradi⁴, Naeme Javid⁵, Mohammad
A. Vakili⁶

1. 1Student Research Committee, Golestan University of Medical Science, Gorgan, Iran
2. 1Student Research Committee, Golestan University of Medical Science, Gorgan, Iran
3. Infectious diseases research centre, Golestan University of Medical Science, Gorgan, Iran
4. Infectious diseases research centre, Golestan University of Medical Science, Gorgan, Iran
5. Infectious diseases research centre, Golestan University of Medical Science, Gorgan, Iran
6. Infectious diseases research centre, Golestan University of Medical Science, Gorgan, Iran

Background and Aim:: Drug resistance isolates of Human Cytomegalovirus (HCMV) is matters of developing new anti-CMV drugs. Maribavir (MBV) is a novel inhibitor of viral kinase. Clinical and laboratory isolate resistance to MBV are maps to UL27 mutations, a viral nuclear protein

Methods: DNA extracted from 20 CMV positive HIV (9/20) and congenitally infected (11/20) patients used for Polymerase Chain Reaction (PCR) amplification for UL27.

Results: Sequencing of products and Multiple Sequence Alignment (MSA) have shown significant mutation rate in HIV infected samples ($P=0.038$).

Conclusion: Our results shows, there may be a pressure incorporated by HIV counterparts to CMV UL27 gene products, which need more investigations

Keywords: HCMV, Congenital infection, HIV, Mutation, UL27

**P1072 - 677: ASSOCIATION OF EPSTEIN-BARR VIRUS WITH TUMOR SIZE OF PATIENTS
WITH ESOPHAGEAL SQUAMOUS CELL CARCINOMA**

Ali Moradi¹, Amir Avan², Soodabeh ShahidSales³, Faezeh Ghasemi⁴, Kazem Anvari⁵, Saeideh Ahmadi
Simab⁶, Seyed Mahdi Hassanian⁷, Safieh Ebrahimi⁸, Mohammad Taher Boroushaki⁹

1. Molecular Medicine Group, Department of Modern Sciences and Technologies, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
2. Molecular Medicine Group, Department of Modern Sciences and Technologies, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
3. Cancer Research Center, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
4. Molecular Medicine Group, Department of Modern Sciences and Technologies, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
5. Cancer Research Center, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
6. Cancer Research Center, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
7. Department of Medical Biochemistry, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
8. Department of Medical Biochemistry, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
9. Department of Pharmacology and Pharmacological Research Center of Medicinal Plants, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, I. R. Iran

Background and Aim: Esophageal squamous cell carcinoma (ESCC) is among the leading cause of cancer related death within gastrointestinal tumors. There is growing body of evidence showing the association of Epstein Barr Virus (EBV) infection with the development of malignancies including B-cell non-Hodgkin lymphoma, Hodgkin disease and Burkett lymphoma, although its potential association with ESCC is still controversial. Therefore in the present study we explored the association of EBV with pathological information and clinical outcome of ESCC patients.

Methods: One hundred and eight patients were recruited. The ESCC tissue was stained with H&E, followed by DNA extraction. The presence of EBV was evaluated using an Epstein-Barr virus PCR detection Kit. Univariate/multivariate analyses were employed to investigate the association of EBV with overall survival and progression free survival.

Results: Among the patients, 48% of patients were female, and 52% were male with mean age of 59.2±11.1yr. 5.6%, 21.3%, and 71.3% patients were T1, T2, T3, respectively, while 32.4% of patients had lymph node metastases. Of note we observed the presence of EBV in 6.5% patients, and 100% of EBV infected patients were at T2 and T3, while 42.8% of these patients had lymph node positive.

Conclusion: Our findings demonstrate the presence of EBV in 6.5% of Iranian patients and its potential link with tumor size, supporting further studies in multi center setting to determine its association with development and progression of ESCC.

Keywords: Esophageal squamous cell carcinoma; Epstein Barr Virus, PCR

**P1073 - 683: MECHANISM OF INFECTIOUS BRONCHITIS VIRUS
IMMUNOPATHOGENESIS**

Shahin Masoudi¹, Shahla Shahsavandi², Mohamad Majid Ebrahimi³

1. Razi vaccine and serume research institute
2. Razi vaccine and serume research institute
3. Razi vaccine and serume research institute

Background and Aim: Infectious Bronchitis Virus (IBV) is one of the most important pathogens in poultry and is a member of group 3 coronavirus. While infectious bronchitis is a disease of the respiratory tract, tissue tropism and pathogenicity of virus strains are different

Methods: Regardless of tissue tropism of virus strain (respiratory, kidney and reproductive organs) the main site of IBV replication is the upper respiratory tract, followed by viremia and dissemination of virus in other tissues. IBV is epitheliotropic, and replicates in many types of epithelial cells, including epithelial cells of the respiratory, kidneys and the reproductive organs and produces lesions. Some strains of the virus replicate in the alimentary tract, often with mild pathobiological changes. One of the most important viral strains can cause bilateral pectoral myopathy. All strains of the virus cause lesions in the respiratory tract with different severity.

Results: Therefore, IBV often causes increased susceptibility to secondary respiratory infections or damage caused by primary respiratory pathogens. Immunogenic components of the virus, the S proteins and the N nucleoprotein, stimulate the humoral, local and cellular immune responses against the virus.

Conclusion: Apparently the changes in the S1 protein may be associated to the differences in tissues tropisms of the virus strains. It is likely that in the future, the emergence of new strains of viruses will involve organs or systems that are not normally affected.

Keywords: Coronavirus, infectious bronchitis, pathogenesis, immunity

P1074 - 728: PREVALENCE OF HERPES VIRAL ENCEPHALITIS IN CHILDREN WITH ASEPTIC MENINGOENCEPHALITIS IN IMAM REZA HOSPITAL IN THE FALL OF 1394, NORTH KHORASAN, BOJNURD

Saghar Safamanesh¹, Sara Nojoomi², Seyed Ahmad Hashemi³, Majid Ghafouri⁴, Mahsa Khosrojerdi⁵, Amir Azimian⁶

1. Department of Pathobiology and Laboratory Sciences, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran
2. Medical Diagnostic Laboratory, Emam Reza Hospital, North Khorasan University of Medical Sciences, Bojnurd, Iran
3. Department of Internal Medicine, Emam Reza Hospital, North Khorasan University of Medical Sciences, Bojnurd, Iran
4. Department of Internal Medicine, Emam Reza Hospital, North Khorasan University of Medical Sciences, Bojnurd, Iran
5. Department of Pediatrics, School of Medicine, Semnan University of Medical Sciences, Semnan, Iran
6. Department of Pathobiology and Laboratory Sciences, School of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran

Background and Aim: Herpes viruses are relatively common viral causes of nervous system diseases. HSV-1 has been the most common cause of acute sporadic encephalitis in the world. The initial CSF examination may be normal in patients with encephalitis with HSV-1. Today, PCR on the CSF, the main method diagnosis of herpes encephalitis-causing agents, with high sensitivity and specificity.

Methods: In this cross-sectional study all CSF samples from children admitted to Imam Reza Hospital in the fall of 94, who were with the aseptic meningoencephalitis symptoms, were evaluated with PCR method for the presence of HSV1, 2. Aseptic Meningitis diagnostic criteria were: fever, a symptom of nausea, vomiting, headache, seizures, drowsiness and symptoms of central nervous system involvement. Exclusion criteria were including positive bacterial cultures, changes in CSF in favor of bacterial meningitis and the presence of other diseases such as cerebral hemorrhage, tumor or metabolic diseases, etc.

Results: Of 52 samples suspected to aseptic Meningoencephalitis 8 cases (15.38%) were positive for herpes viruses.

Conclusion: One of the problems that were found in this study was to rule out other viral cause's children meningoencephalitis. Most patients with symptoms of meningitis at the age of 5 years, but due to the low number of positive samples, we cannot definitively conclude. PCR is a sensitive and specific method for diagnosis of Herpes simplex virus in CSF. It is suggested due to the absence of accredited laboratory tests for the diagnosis of herpes viruses such as serological tests, PCR method for the detection of the virus to be fast and accurate.

Keywords: Herpes Simplex Virus, PCR, Meningoencephalitis

**P1075 - 741: SCREENING OF MAJOR BLOOD-BORNE VIRUSES IN HEMODIALYSIS
PATIENTS IN ZANJAN, IRAN**

Elham Samadi¹, Hessam Mirshabi², Nima Motamed³, Paniz Shirmast⁴

1. MSc student, Department of Microbiology and Virology, Faculty of medicine, Zanzan University of medical sciences, Zanzan, Iran
2. PhD, Department of Microbiology and Virology, Faculty of medicine, Zanzan University of medical sciences, Zanzan, Iran
3. Department of Community Medicine, Faculty of Medicine, Zanzan University of Medical Sciences, Zanzan, Iran
4. MSc student, Department of Microbiology and Virology, Faculty of medicine, Zanzan University of medical sciences, Zanzan, Iran

Background and Aim: The prevalence of hepatitis viruses have been reported in hemodialysis patients much more than in the general population. Hepatitis viruses (HBV, HCV) and human immunodeficiency virus (HIV) are the major causes of mortality among hemodialysis patients. The prevalence of these infections is known widely in different regions of the world. It has been proven that 400 million, approximately 175 million and 35 million people worldwide are infected with hepatitis B, C and HIV virus, respectively. These infections become chronic and lead to liver failure, cirrhosis and liver cancer. The aim of this study was to detect the serum prevalence of HBV, HCV and HIV in hemodialysis patients in Zanzan city

Methods: In this cross sectional study, 136 serum samples of hemodialysis patients were collected from Valiasr hospital of Zanzan. These samples were used for detection of markers for hepatitis B surface antigen (HBsAg), hepatitis B surface antibody (HBsAb), antibody to HCV (anti-HCV), HIV antibody by ELISA.

Results: This group was comprised of 77(56.6%) males and 59 (43.3%) females. The mean age of the patients was 58±16.05 year. Positive HBsAg was found in .7%, HBsAb 66.2% and HCVAbs .7% of cases. HIVAb cases were negative in these patients.

Conclusion: Hemodialysis patients are at risk of HBV, HCV and HIV transmission through blood transfusion devices. Prevalence of HBV and HCV in hemodialysis patients was low in Zanzan city. Protection principles can reduce transmission rate of blood borne viruses like HBV, HCV and HIV.

Keywords: Hepatitis B Virus, Hepatitis C Virus, HIV, haemodialysis

**P1076 - 763: PREVALENCE OF OCCULT HBV INFECTION IN HAEMODIALYSIS PATIENTS
WITH CHRONIC HCV IN THE PROVINCE OF TEHRAN (IRAN)**

Mohammad Mehdi Attarpour Yazdi¹

1. Department of Microbiology, Faculty of Medicine, Shahed University, Tehran, Iran

Background and Aim:Background: Occult hepatitis B is defined by the presence of HBV DNA in serum or liver in the absence of HBsAg. Low serum HBV DNA titers, in the range of 100 to 1000 copies/ml, are typical in occult HBV infection. HBV infection can lead to chronic disease, cirrhosis and liver cancer. For this reason the aim of this research was to find out the prevalence and clinical effects of occult HBV infection in haemodialysis patients with chronic HCV in Tehran (Iran).

Methods:Methods: 45 chronic hemodialysis patients with negative HBsAg, and positive anti-HCV were included in the study. These patients were divided into two groups: HCV-RNA positive and HCV-RNA negative, based on the results of HCV-RNA PCR. HBV-DNA was studied using the PCR method in both groups.

Results:Results: None of the 19 HCV-RNA positive patients and 26 HCV-RNA negative patients revealed HBV-DNA in serum by PCR method. The average age was 56.0 ± 12.0 in the HCV-RNA positive group and 30 ± 15.0 in the HCV-RNA negative group.

Conclusion:Conclusion: The prevalence of occult HBV infection is not high in haemodialysis patients with chronic HCV in Tehran (Iran). This result of our study has to be evaluated in consideration of the interaction between HBsAg positivity (7%-11%) and frequency of HBV mutants in Tehran (Iran).

Keywords:Keywords: Occult HBV infection, Chronic HCV, Haemodialysis, Tehran

**P1077 - 859: RESISTANCE TO ADEFOVIR DIPIVOXIL IN LAMIVUDINE RESISTANT
CHRONIC HEPATITIS B PATIENTS IN GOLESTAN PROVINCE-IRAN**

Masoomeh Rezanezhadi¹, Alijan Tabarraei², Sareh Zhand³, Abdolvahab Moradi⁴

1. Islamic Azad University of Damghan, Department of Microbiology, Damghan, Iran
2. Infectious diseases research centre, Golestan University of Medical Sciences, Gorgan, Iran
3. Infectious diseases research centre, Golestan University of Medical Sciences, Gorgan, Iran
4. Infectious diseases research centre, Golestan University of Medical Sciences, Gorgan, Iran

Background and Aim: Adefovir dipivoxil (ADV)-resistant mutations have been identified in treating hepatitis B virus (HBV) infection. Most ADV-resistant strains display amino acid substitutions of rtN236T (substitution of asparagine by threonine) and rtA181V/T (substitution of alanine by valine or threonine) in the D and B domains of HBV polymerase. In this study, we intended to determine the pre-existing adefovir-resistance mutations in patients infected with LAM resistant mutants prior to starting adefovir therapy.

Methods: this cross sectional study, 55 patients with proved chronic HBV infection with lamivudine resistance mutations were recruited.

Results: After HBV-DNA extractions, direct sequencing and alignment of P gene with reference sequence from Gene Bank database, the rtN236T mutation was observed in one (1.81 %) patients, while forty four others had neither rtN236T, nor rtA181V/T mutation. All 55 patients were infected with genotype D of hepatitis B virus.

Conclusion: The early mutation analysis of LAM-resistance mutations could be effective for drug selection and treatment of CHB.

Keywords: HBV, adefovir dipivoxil, Lamivudine, resistance mutation.

**P1078 - 891: MOLECULAR BIOLOGY, DIAGNOSIS, TREATMENT AND PREVENTION OF
HUMAN T CELL LEUKEMIA VIRUS(HTLV-1,2)**

Abdol Reza Salamat Zadeh¹, Arezou Kafshdar Jalali²

1. Department of Microbiology, Faculty of Sciences, Lahijan Branch, Islamic Azad University, Lahijan, Iran.
2. Department of Microbiology, Faculty of Sciences, Lahijan Branch, Islamic Azad University, Lahijan, Iran.

Background and Aim: human T cell leukemia virus (HTLV) is family of Retroviridae. HTLV1, HTLV2 are two important viruses in this group. HTLV1 is a viral oncogene that causes ATLL or Adult T-cell Leukemia / Lymphoma and TSP or Tropical Spastic Paraparesis and HTLV2 causes hairy cell leukemia. In this study, we decide that the complete information presented about this group of viruses to the broaden measures of its prevalence choose in country.

Methods: In this article, references to more than 50 books and articles published during the last decade, molecular biology, life cycle, diagnosis, treatment and prevention of viruses HTLV1, 2 for a detailed discussion has been addressed.

Results: HTLV type 1 and 2 with 5 Brigade, which is more common. Genome HTLV1, 2 in connection with other retrovirus similar to HIV-1 genome. ATLL infection incubation period is about 20 to 30 years and aged between 30 and 50 years, usually within one year after symptoms occur, death can occur. Blood screening to prevent infected mothers from breastfeeding helps prevent HTLV infection. Test for the detection of ELISA, cell preparation and PCR is used, there is no cure or vaccine for HTLV.

Conclusion: Based the Iran is one of endemic countries on HTLV infection and one of the main routes transmission is blood transfusion, to prevent blood screening is recommended.

Keywords: HTLV-1, 2, blood screening, diagnosis, treatment, prevention

**P1079 - 899: HIGH-LEVEL EXPRESSION AND ONE- STEP PURIFICATION OF
RECOMBINANT ANTIGEN CONTAINING HTLV-I/-II LINEAR EPITOPES**

Roxana Faramarzi¹, Dr.Samane Dolatabadi², Dr. Hafez Hidary Zarnagh³

1. Department of biologyt, Neyshabur Branch, Islamic Azad university, Neshabur, Iran
2. Department of biologyt, Neyshabur Branch, Islamic Azad university, Neshabur, Iran
3. Department of clinical biochemistry faculty of medicine Sabzevar university of medical science Sabzevar Iran

Background and Aim:gp46-I, gp46-II, gp21 and p19 are regarded as the major diagnostic proteins of HTLV-I/-II infection. Our aim in this study was to high-level expression and purification of chimeric antigen (CA) containing HTLV-I/-II immunodominant epitopes. Large-scale preparation of the this antigen may have diagnostic value.

Methods:The synthetic DNA encoding chimeric antigen was subcloned into BamHI/EcoRI restriction stite of pGS21a expression vector. The pGS21a-CA was transformed into chemically compotent Escherichia coli BL21 (DE3) cells. expresssion, solubility of CA were determined using 12% SDS-PAGE. The protein was purified by utilizing Ni-NTA agarose beads. The purified protein was concentrated by ultrafiltration. Antigenicity of protein was evaluated by antigen sandiwich ELISA.

Results:The results of SDS-PAGE has been showed CA overexpressed as soluble in E.coli BL21 (DE3) cells. The soluble protein was purified by utilizing Ni-NTA under native conditions. The final yield was approximately 25 mg of immunoreactive protein per liter of culture medium. SDS-PAGE revealed that the purified protein was more than 90% pure. ELISA results showed that this protein could specifically bind to anti-HTLV-I/-II antibodies.

Conclusion:CA could be a candidate for HTLV detection

Keywords:HTLV, chimeric antigen, protein expression, purification

**P1080 - 947: INVESTIGATION OF ASSOCIATION OF A SINGLE NUCLEOTIDE
POLYMORPHISM (RS1179251) IN INTERLEUKIN 22 GENE WITH CHRONIC HEPATITIS B**

PANIZA Asadi¹, Seyed Masoud Hosseini², Seyed Reza Mohebbi³, Maryam Karkhane⁴, Mahsa Saeidi Niasar⁵, Yasin Hatami⁶, Afsaneh Sharifian⁷, Mohammad Reza Zali⁸

1. Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
2. Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, Tehran, Iran
3. 1-Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
4. Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
5. 1-Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
6. 1-Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
7. Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
8. Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: Hepatitis B virus is one of the main causes of chronic liver disease that can lead to serious complications including liver cirrhosis and hepatocellular carcinoma. Interleukin 22 (IL22) is a member of IL10 family which has recently discovered and is mainly produced and secreted by T cells. The main biological function of this cytokine is cell growth and proliferation and it is an important mediator of pro-inflammatory responses in HBV infection. The aim of this study is to investigate the association between a single nucleotide polymorphism (rs1179251) in Interleukin 22 gene and chronic hepatitis B.

Methods: In this case-control study, blood samples were collected from 60 chronic HBV infected patients and 60 healthy controls. Genomic DNA was extracted using salting out method and genotype of IL22 SNP rs1179251 was determined by PCR-RFLP method.

Results: Based on the results, genotype frequencies of CC and GC were found to be 47.7%, 53.3% respectively in chronic patients and 55%, 45% in the control group. Homozygote GG was not observed in any of studied groups. Results showed a slight lower CC genotype among patients in comparison with control group, but no statistically significant difference was found ($P=0.361$). Allele frequency was not statistically different among two groups ($P=0.454$).

Conclusion: Our results suggest that there is no correlation between IL22 SNP rs1179251 polymorphism with HBV chronic infection and that it could not be regarded as a host genetic factor associated with the outcome of HBV infection.

Keywords: Interleukin 22, Hepatitis B virus, chronic infection, single Nucleotide polymorphism

P1081 - 1040: THE ROLE OF HUMAN PAPILLOMAVIRUS IN CANCER

Behzad Jamali¹, sajjad jamali²

1. Young Researchers and Elite club, Tabriz Branch, Islamic Azad University, Tabriz, Iran
2. Young Researchers and Elite club, Tabriz Branch, Islamic Azad University, Tabriz, Iran

Background and Aim: Human papilloma virus, cutaneous and mucosal epithelial tissue genitals, hands or legs infect and cause various diseases such as skin warts, genital warts, warts and laryngeal epithelial neoplasia of the genital area is usually also moves towards malignancy. In this article, in addition to the viral replication cycle and the mechanisms of cancer development, to the ways of transmission and pathogenesis of papillomavirus pay.

Methods: A systemic search was performed to identify studies published in pubmed and the cochrane database up to july2015 and recently published abstracts were also reviewed .to review research articles on The role of human papillomavirus in cancer had been discussed.

Results: So far, more than 100 types of human papillomavirus have been identified; about of them, infect epithelial cells of the genital area. Human papilloma virus, cutaneous and mucosal epithelial tissue genitals, hands or legs infect and cause various diseases such as skin warts, genital warts, warts and laryngeal epithelial neoplasia of the genital area is usually also moves towards malignancy.

Conclusion: Papilloma virus, causing benign and malignant tumors of the skin and mucous membranes of humans. Including diseases and cancers associated with human HPV, can be noted cervical cancer, skin, throat, head and neck, breast, genital warts, eyes conjunctival diseases and mucosa. Thus, knowledge of HPV, cause cancer and its spread, could help vaccine design, to use the appropriate vaccine, to cover higher safety in society.

Keywords: papilloma viridae, neoplasms, role, cancer

P1082 - 1062: RNA DETECTION OF RABIES VIRUS IN THE BRAINS OF SUSPECTED RABID ANIMALS USING RT-LAMP METHOD COMPARE TO REAL TIME RT-PCR TEST AS A QUANTITATIVE MOLECULAR TECHNIQUE AND DFA AS A SEROLOGIC METHOD

Elahe Naji¹, Jamileh Nowroozi², Alireza Gholami³, Behzad Pourhossein⁴, Maryam Fazeli⁵

1. Department of Biology, College of basic science, Tehran Science and Research branch, Islamic Azad University, Tehran, Iran
2. Department of Microbiology, Islamic Azad University, Tehran North Branch, Tehran, Iran
3. WHO-Collaborating Center for Reference and Research on Rabies, Pasteur Institute, Tehran, Iran
4. Department of Virology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
5. WHO-Collaborating Center for Reference and Research on Rabies, Pasteur Institute, Tehran, Iran

Background and Aim: Rabies is endemic in most Middle Eastern countries. It is the most important zoonotic disease and major public health problems in Iran. Rabies is preventable by proper vaccination, even after exposure. Therefore, it seems a fast, sensitive and reliable rabies diagnostic method is required, which might pose a financial burden as well as physiological stress on patients because of the extremely high fatality rate of the disease.

Methods: In this study, we developed reverse transcription loop-mediated isothermal amplification (RT-LAMP) method as a fast, sensitive, specific and cheap method for rapid detection of rabies virus in two ways (colorimetric and electrophoresis). The sensitivity and specificity of RT-LAMP were determined compared to Real Time reverse transcriptase polymerase chain reaction (Real Time RT-PCR) test as a quantitative molecular technique and direct fluorescent antibody (DFA) as a serologic gold standard method of the World Health Organization (WHO).

Results: The sensitivity of rabies specific LAMP method, reached about 500 copies/tube that lower than Real Time RT-PCR with 100 copies/tube while both tests had the same specificity (99.9%). The agarose gel electrophoresis containing safe stain and also, sybr green dye directly detected rabies virus LAMP products in reactions. Also, rabies RT-LAMP assay was more simple and less time-consuming compared to Real-Time RT-PCR.

Conclusion: Although, further studies are required to establish more universal primers for both methods, RT-LAMP and Real Time RT-PCR, set up of these methods as sensitive, specific and reliable tests is an effective step in diagnosis of rabies and play an important role for the comprehensive rabies elimination programme.

Keywords: reverse transcription loop-mediated isothermal amplification (RT-LAMP), Real Time reverse transcriptase polymerase chain reaction (Real Time RT-PCR), sensitivity, specificity

P1083 - 1081: EVALUATION OF SERUM LEVELS OF IL-12 IN PATIENTS IN VARIOUS CLINICAL PHASES OF HEPATITIS B VIRUS INFECTION

Parvaneh Mohammadi¹, Seyed Reza Mohebbi², Parvin Khodarahmi³, Mahsa Asadi Niasar⁴, Paniza Asadi⁵, Afsaneh Sharifian⁶, Mohammad Reza Zali⁷

1. 1-Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran 2-Basic and Molecular Epidemiology of Gastrointestinal Disorders Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
2. Basic and Molecular Epidemiology of Gastrointestinal Disorders Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. - Department of biology, Faculty of biological sciences, Parand branch, Islamic Azad University, Tehran, Iran
4. 1-Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
5. 1-Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
6. 1-Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
7. 1-Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: Hepatitis B virus (HBV) infection is one of the most important public health problems in the world. IL-12 is a heterodimer cytokine that is mainly produced by activated macrophages and dendritic cells. IL-12 can activate and differentiate T cells into TH1 cells and can increase cytotoxic activity of natural killer cells (NK). It can also promote and increase interferon gamma production and secretion from NK cells. The aim of this study was to evaluate serum level of IL-12 in patients in various clinical phases of hepatitis B virus infection.

Methods: A Total of 80 individuals including patients with active chronic infection, liver cirrhosis, inactive carriers and healthy controls were sampled. Confirmatory serological tests including HBs Ag, Anti-HBc Ab, HBe Ag and anti-HBe Ab were performed on these samples using ELISA method. Hepatitis B virus DNA level was determined by a quantitative Taq Man Real time PCR method. Finally, serum Interleukin 12 level was determined in patients in various clinical phases and healthy controls using a quantitative ELISA method.

Results: The mean serum level of IL-12 in all studied samples was 34.96 ± 25.73 pg/ml and in different groups were 49.28 ± 7.97 (cirrhotic patients), 64.94 ± 11.21 (active chronic patients), 14.48 ± 4.99 (inactive carriers) and 11.13 ± 4.3 (control group) respectively and showed a statistically difference among studied groups ($p < 0.001$).

Conclusion: Analysis of serum levels of IL-12 in individuals in different clinical groups showed that IL-12 levels increased with disease progression and severity of liver injuries. Thus, this factor can be used for a more precise determination of patients' clinical status.

Keywords: Hepatitis B virus, Interleukin 12, chronic infection, Clinical phases, liver cirrhosis

**P1084 - 1083: ASSOCIATION OF INTERLEUKIN-21 GENE POLYMORPHISM (RS2055979)
WITH SUSCEPTIBILITY TO CHRONIC HEPATITIS B VIRUS INFECTION**

PANIZA Asadi¹, Yasin Hatami^{1,2}, Seyed Reza Mohebbi³, Hossein Maghsoodi⁴, Maryam Karkhane^{1,5},
Mahsa Saeidi Niasar^{1,6}, Paniza Asadi^{1,7}, Afsaneh Sharifian^{1,8}, Mohammad Reza Zali⁹

1. 1-Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Ira3- Department of biology, Basic sciences faculty, Payame Noor University, Tehran, Iran3- Department of biology, Basic sciences faculty, Payame Noor University, Tehran, Iran
2. Basic and Molecular Epidemiology of Gastrointestinal Disorders Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. - Department of biology, Basic sciences faculty, Payame Noor University, Tehran, Iran
4. 1-Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
5. 1-Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
6. 1-Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
7. 1-Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
8. 1-Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim:Infection with hepatitis B virus is a major cause of chronic liver diseases and variations within cytokine genes may affect the host immune response to hepatitis B infection. Interleukin-21 (IL-21), as a multifunctional cytokine, plays an important role in many diseases, such as cancer, inflammatory and autoimmune diseases. The aim of this study was to investigate whether IL-21 rs2055979 G/T single nucleotide polymorphism is involved in the progression of chronic hepatitis B infection.

Methods:A total of 100 chronic hepatitis B patients and 100 healthy subjects were examined for differences in genotype and allele frequencies in this case-control study. PCR-RFLP method was applied for analyzing the polymorphism site.

Results:Genotype frequencies of GG, TG and TT were found to be 35%, 50% and 15% in chronic patients and 16%, 67% and 17% in the control group. Results suggested a higher GG genotype among chronic patients (35% vs. 16%) and a statistically significant difference was observed in the frequency of IL-21 gene polymorphism (rs2055979) between chronically infected patients and healthy controls for genotype frequencies (P-value=0.008).

Conclusion:Our findings indicate that IL-21 rs2055979 G/T might be associated with HBV infection and the SNP can serve as a biomarker predictive of risk for the development of HBV chronic infection in Iranian patients.

Keywords:Hepatitis B virus, Interleukin 21, chronic infection, genetic variation, immune response

**P1085 - 1098: DEVELOPMENT AND EVALUATION A NOVEL REAL TIME PCR TEST
BASED ON SYBR GREEN CHEMISTRY FOR QUANTIFICATION OF HEPATITIS B VIRUS
DNA**

Alaa Kamill¹, Seyed Masoud Hosseini², Seyed Reza Mohebbi³, Shabnam Kazemian⁴, Behta Keshavarz
Pakseresh⁵, Afsaneh Sharifian⁶, Mohammad Reza Zali⁷

1. Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
2. Department of Microbiology, Faculty of Biological Sciences, Shahid Beheshti University, Tehran, Iran
3. Basic and Molecular Epidemiology of Gastrointestinal Disorders Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
4. Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
5. Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
6. Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
7. Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: Hepatitis B virus (HBV) infection is a serious worldwide public health problem. Although various diagnostics methods have been established for detection of HBV infection, molecular tests based on Real time PCR method play an important role in monitoring disease progression and also assessing proper response to antiviral treatments. The aim of this study was to develop and evaluate a real-time polymerase chain reaction (PCR) assay based on SYBR green dye technology for detection and quantification of HBV DNA.

Methods: Proper primers were designed for the HBV surface gene and then quantitative real-time PCR assay was carried out using SYBR-Green chemistry. For establishing a quantification standard a fragment of surface gene was amplified and cloned into TA cloning TOPO vector. The concentrations of the plasmids were measured and ten-fold dilution series of the plasmid was used as quantification standard. The accuracy of the developed test was evaluated using a commercial HBV quantification kit.

Results: The cloned plasmid was analyzed and confirmed by PCR to verify existence of the inserted HBV fragment (98 bp). Quantification of HBV loads of 20 clinical samples from chronic patients using developed assay in comparison with commercial quantification kit showed a 100% detection rate and lower detection limit was determined.

Conclusion: The developed real-time PCR assay based on SYBR green technology provided a suitable approach for routine diagnostic and HBV quantification purposes and also showed a good sensitivity, high specificity, high reproducibility, and good linearity over a broad dynamic range of quantification.

Keywords: Hepatitis B virus, Viral load, Quantification test, Real time PCR

P1086 - 1099: INFECTIVITY OF HUMAN T -CELL VIRUS TYPE 1

Behzad Jamali¹, sajjad jamali²

1. Young Researchers and Elite club, Tabriz Branch, Islamic Azad University, Tabriz, Iran
2. Young Researchers and Elite club, Tabriz Branch, Islamic Azad University, Tabriz, Iran

Background and Aim: hiv infection usually through blood and breast milk and saliva and rarely sexually is transmitted. After transmission of the virus from an infected person to a healthy person. can cause leukemia, lymphoma in adults, tropical spastic paralysis, spastic paresis and some other diseases the nervous system.

Methods: A systemic search was performed to identify studies published in pubmed and the cochrane database up to march 2015, and recently published abstracts were also reviewed. To review research articles on The infectivity of human t -cell virus type1 had been discussed.

Results: The virus is not the only factor for HAM/TSP but in a small percentage of people create various viral diseases such as arthropathy associated (HAAP) HTLV-I, T Skin cell lymphoma, Graves' disease, polymyositis, chronic respiratory diseases, lymphadenopathy, uveitis, arthritis, myositis alveolitis, Sjogren syndrome and dermatitis.

Conclusion: hiv infection usually through blood and breast milk and saliva and rarely sexually is transmitted. After transmission of the virus from an infected person to a healthy person. can cause leukemia, lymphoma in adults, tropical spastic paralysis, spastic paresis and some other diseases the nervous system. according the complications and diseases dangerous caused by pollution to this virus and treatment of approx indecisive these diseases, pollution prevention and spreading the disease to others is important .

Keywords: humans , t-lymphocytes, viruses

**P1087 - 1194: FREQUENCY OF HCV GENOTYPES 1A AND 1B IN HCV POSITIVE PATIENTS
REFERRED TO CLINICAL LABORATORIES IN RASHT**

Mahnaz Hooshmand rad¹, Leila Asadpour², Zeinab Khazaei³

1. Department of Biology, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran
2. Department of Biology, Rasht Branch, Islamic Azad University, Rasht, Iran
3. - Department of Biology, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran

Background and Aim: Hepatitis C virus is a major etiologic agent of chronic liver disease and can lead to progressive liver cirrhosis and hepatocellular carcinoma. . HCV has six major genotypes. It has been investigated that patients with genotype 1 infection are less likely to have a sustained response to antiviral therapy. The present study was aimed to investigate frequency of genotypes 1a and 1b in HCV positive patients referred to clinical laboratories in Rasht City.

Methods: Viral RNA was extracted from 225 HCV antibody positive plasma by Roche viral nucleic acid extraction kit and 5'UTR specific primers were used to amplify a 220bp HCV specific fragment of this region using one-step RT—PCR . The amplified product was sequenced and subsequently analyzed by online Blast Software for genotyping .

Results: Assessment of 225 plasma samples determined that 142 samples (63.2%) were negative for hepatitis C virus in molecular investigation. Out of 83 HCV positive samples, 29 samples belonged to genotype 1a (% 34.94) and five samples were recognized as genotype 1b (6.03%).

Conclusion: The results of the present research showed the high frequency of genotype 1 in HCV positive patients in Gilan province and indicate the importance of genotyping in treatment of HCV infection.

Keywords: hepatitis C, 1a, 1b, genotyping

P1088 - 1219: ZIKA VIRUS AS A PUBLIC HEALTH EMERGENCY OF INTERNATIONAL CONCERN; A REVIEW ARTICLE

Siavash Hamzepour¹, Siavash Hamzeh pour², Salman varmaghani³, Parisa Javanali azar⁴, Mahshad pourjahan⁵

1. Department of Biology, Higher Education Institute of Rabe – Rashid
2. Department of Biology, Higher Education Institute of Rabe – Rashid
3. Department of Biology, Higher Education Institute of Rabe – Rashid
4. Department of Biology, Higher Education Institute of Rabe – Rashid

Background and Aim: The widespread epidemic of Zika virus infection in South and Central America and the Caribbean in 2015 along with increased incidence of microcephaly in fetuses born to mothers infected with Zika virus and a potential for a worldwide spread indicate the need to review the current literature regarding vectors, reservoirs and amplification hosts.

Methods: Multiple information sources were employed to support the review. These included publically available literature in pubmed Between 1990 and 2016, patents, official communications, English and Lusophone lay press. Zika virus software using the genetic map of the snepgene was analyzed. Computational epitope analysis as well as infectious disease outbreak modeling and forecasting were implemented. Field observations were compiled and interviews conducted with public health officials.

Results: During the Yap outbreak, the main clinical manifestation (incidence in parentheses) were maculopapular rash (90%), fever (65%), arthritis/arthralgia (65%), conjunctivitis (55%), myalgia (48%), headache (45%), retro-orbital pain (39%), oedema (19%), and vomiting (10%). There is a possible association between ZIKV and microcephaly in newborn babies with maternal ZIKV infection, and some infected adults with neurologic conditions like Guillain-Barre syndrome (GBS) were also reported.

Conclusion: Zika-related disease has its most devastating effects on the unborn fetus with a delay to diagnosis. The transplacental pathology is not understood. The occurrence of GBS suggests that Zika virus associated disease has an autoimmune component. It is epidemic in a region with a high degree of global connectivity; cases will be widely disseminated. The Zika epidemic is moving very rapidly.

Keywords: Zika virus, Aedes, Arboviruses, Flavivirus, Outbreak

Zoonosis

P1089 - 5: SPATIAL AND TEMPORAL DISTRIBUTIONS AND PREVALENCE OF CUTANEOUS LEISHMANIASIS: EVALUATION OF 499 CASES IN THE BADROOD REGION OF IRAN

Hamid Kassiri¹, Rohollah Dehghani ², Narges Mehrzad ³, Nilofar Ghasemi ⁴

1. School of Health, Ahwaz Jundishapur University of Medical Sciences, Ahwaz, Iran
2. School of Health and Research Center on Social Determinants of Health, Kashan University of Medical Sciences, Kashan, Iran
3. School of Health, Kashan University of Medical Sciences, Kashan, Iran
4. School of Health, Kashan University of Medical Sciences, Kashan, Iran

Background and Aim: This study was conducted to investigate the status of Cutaneous Leishmaniasis (CL) during 2008 through 2012 in Badrood City. This region is considered as one of the major CL foci in Isfahan Province due to the geographical, climatic, and ecological conditions and the high prevalence rate of the disease.

Methods: The statistical population consisted of all patients, who were under treatment and follow up with the diagnosis of CL through laboratory confirmation and clinical symptoms. The impression smears were prepared from the sides of ulcers of all patients by scraping; then, they were fixed in methanol, stained by standard Geimsa method, and observed exactly under the microscope. A questionnaire was completed and the results were analyzed using the SPSS version 17.

Results: Among the number of 499 patients studied, 297 cases (59.5%) were male. Slides prepared from the lesions of these patients had a Leishmania parasite with large vacuole (the features of Leishmania major). The highest cases of disease were related to the year 2012 with 190 patients. In total, 26 patients (5.2%) have had the disease history. The highest incidence of the disease was respectively in the month of September (143 cases). The most ulcers (38.08%) were observed on the hand. Also, in most patients (53.9%) were observed over an ulcer.

Conclusion: The results of this study showed an increase in the prevalence of CL during the years 2008 to 2012. The increased disease process can be controlled through education and appropriate prevention methods.

Keywords: Cutaneous leishmaniasis, Epidemiology, Prevalence, Leishmania major, Iran

**P1090 - 10: EPIDEMIOLOGY OF CUTANEOUS LEISHMANIASIS IN NEYSHABUR
DISTRICT, DURING 2010-2014**

Mohammad Salehi¹, Abdolmajid Ghasemian², Seyyed Khalil Shokuhi Mostafavi³

1. Medical Diagnostic Laboratory of Neyshabour, Center of Medical, Pathological and Genetic Diagnostic Services, Iranian Academic Center for Education, Culture and Research (ACECR), Mashhad Branch, Mashhad, Iran
2. Department of Microbiology, Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran
3. Department of Microbiology, Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran

Background and Aim: Leishmania tropica and L. major are among neglected tropical diseases of Middle East and North Africa and Over 90% of CL cases are present in seven countries; including: Afghanistan (Eastern Iran), Algeria, Peru, Brazil, Iran, Saudi Arabia and Syria. This study was performed to determine the prevalence of CL in Neyshabur, Northeastern Iran during 2010-2014.

Methods: This descriptive-analytical and epidemiological survey was performed to detect CL cases in Neyshabur city, Northeastern Iran during 2010-2014. A total of 543 patients included in the study. The sampling of wound secretions was done and then the samples were streaked on glass slide. After 20-30min, the slides were stained with Giemsa and the microscope slides were scanned with 100 immersion lenses. The amastigotes were observed under light microscopy.

Results: The highest prevalence of CL was among 21-30 (p value=0.007) years and the lowest rate belonged to age range of 51-60 years old (p value=0.156). The overall prevalence of CL in Neyshabur from 2010-2014 was 32.2% (n=175).

Conclusion: The highest prevalence of CL was among 21-30 years old and the lowest rate belonged to age range of 51-60 years old. The overall prevalence of CL in Neyshabur from 2010-2014 was 32.2% (n=175). It was declined from 2010 to 2014, but not significant results were observed.

Keywords: cutaneous leishmaniasis, Neyshabur city, Northeastern Iran

**P1091 - 84: A STUDY OF THE SMALL RUMINANTS' ABORTION DUE TO SALMONELLA
SPP. IN IRAN**

Rabehe Karimi sari¹, Mona Hamed², Hossein Esmaeili³, Rabee Karimi Sari⁴, Mohammed Javad Ragh⁵

1. Department of microbiology, Faculty of veterinary medicine, University of Tehran, Tehran- Iran
2. Department of microbiology, Faculty of veterinary medicine, University of Tehran, Tehran- Iran
3. MSc in biology- genetics, University of Payame noor, Tehran- Iran
4. Livestock research institute, Faculty of veterinary medicine, University of Tehran, Tehran- Iran

Background and Aim:Salmonellosis is one of the most important zoonoses and by inducing complications such as abortion, can also results economic losses in small ruminants industry. Livestock and their products are the major sources of Salmonella for humans. Placental membrane of the aborted ewes and does are severely infected by the agent and lack of hygiene could result infection in farmers. The present study evaluates the role of Salmonella in small ruminants' abortion and emphasizes on the necessity of the bacterium as a hazardous cause of disease in humans, especially farmers.

Methods:The specimens were collected from abomasal contents of 432 aborted fetuses. Samples were enriched in selenite F broth and then a loop of the broth was inoculated in to the Xylose Lysine Deoxycholate (XLD) medium. Positive colonies were confirmed using biochemical tests.

Results:In the XLD agar, red colonies with black centers were isolated in 14 samples. The results of TSI, Urease and IMViC tests were Alk/Acid H₂S +, negative and +-+ respectively.

Conclusion:Salmonella is an opportunistic bacterium which in the presence of predisposing factors such as stress and lack of hygiene, could result abortion in ewes and does. Farmers are usually in near contact with animals and their post parturition or abortion discharges, so they are at high risk of infection with zoonotic agents such as Salmonella. Isolation of Salmonella in the present study, indicatives the importance of the bacterium in causing disease in humans alongside Brucella and Chlamydia.

Keywords:Abortion, zoonose, Salmonella and small ruminants.

P1092 - 85: ISOLATION OF E. COLI O157:H7 FROM FECAL SAMPLES OF OSTRICH USING CULTURE AND MULTIPLEX PCR IN LORESTAN PROVINCE

Nemat Shams¹, Mohamad Nayeb Aghae², Sepideh Asadi³

1. Department of microbiology, Faculty of Veterinary Medicine, Lorestan University, Khorramabad, Iran
2. Department of microbiology, Faculty of Veterinary Medicine, Lorestan University, Khorramabad, Iran
3. 2. MSc in Microbiology, Faculty of Veterinary Medicine, Lorestan University, Khorram-Abad, Iran

Background and Aim: E.coli O157:H7 is recognized globally as pathogen that cause diarrhea, hemorrhagic colitis (HC) and haemolytic uremic syndrome (HUS) in humans. The natural reservoirs of E. coli O157:H7 are domestic and wild animals, which shed the bacteria with their feces into the environment. The aim of the present study was to assess the prevalence of E. coli O157:H7 in fecal samples of ostrich using culture and multiplex PCR from ostrich farms in Lorestan province.

Methods: In this study, at all 100 fecal samples of ostrich were collected from ostrich farms in Lorestan province during March to May 2015. A 10-g of fecal sample was added to 90 ml of Trypticase soya broth containing novobiocin. One loop of each enrichment sample was streaked on selective sorbitol Macconkey agar plates supplemented with Cefixime and tellurite (CT-SMAC) for screening test. Diagnostic E. coli- O157 antisera (Baharafshan; Iran) were used for serological identification of E. coli O157:H7. After biochemical and serological identifications, E. coli O157:H7 isolates were subjected to multiplex PCR.

Results: From 100 fecal samples, nonsorbitol fermenting colonies were isolated from 15 samples after enrichment and selective plating, but 6 isolate was confirmed as E. coli O157 by E. coli- O157 antisera. In m-PCR assay, only 4 isolate was confirmed as E. coli O157:H7.

Conclusion: The present study is the first report on isolation of E. coli O157:H7 from ostrich fecal sample in Iran. This study shows the importance of ostrich fecal as potential sources of human E. coli O157:H7/NM infection.

Keywords: E. coli O157:H7, Ostrich, Feces, Multiplex PCR

P1093 - 98: ETIOLOGIC DIAGNOSIS OF BOVINE INFECTIOUS ABORTION BY PCR

Ali Sharifzadeh¹, Sajjad Goodarzi², Mohammad Hagherian³

1. 1Department of Microbiology, Faculty of Veterinary Medicine, Islamic Azad University, Shahrekord Branch, Shahrekord, Iran
2. 2Faculty of Veterinary Medicine, Islamic Azad University, Shahrekord Branch, Shahrekord, Iran.
3. 2Faculty of Veterinary Medicine, Islamic Azad University, Shahrekord Branch, Shahrekord, Iran.

Background and Aim:Infectious abortion is a significant cause of reproductive failure and economic losses in cattle. The goal of this study was to detect nucleic acids of several infectious agents known to cause abortion including *Brucella abortus*, *Leptospira* sp, *Mycoplasma* Sp. and *Clostridium* Sp

Methods:DNA samples were PCR tested for detection of 2 infectious agents known to cause abortion in cattle, including *Brucella abortus*, *Leptospira* sp, *Mycoplasma* Sp. and *Clostridium* Sp

Results:*Leptospira* sp was detected in 26.6% (25/94) of the samples. *Brucella abortus* was detected in 2% (2/94) and *Mycoplasma* Sp. and *Clostridium* Sp not detected

Conclusion:The PCR protocols employed in this study efficiently amplified sequences from the DNA samples from aborted fetuses.

Keywords:cattle, abortion, *Brucella abortus*, *leptospira*, *mycoplasma*, *clostridium*

**P1094 - 103: SURVEY ON PREVALENCE RATE OF HUMAN INTESTINAL VERMINOUS
INFECTIONS IN URMIA**

Sohrab Rasouli¹, Mohammad Sadaghian², Omid Mohammadpour³, Hadi Nejadrezaei ⁴

1. associate professor of parasitology and member of scientific advisory board in Islamic azad university branch urmia-iran
2. assistant professor of parasitology and member of scientific advisory board in Islamic azad university branch shabestar-iran
3. student of veterinary medicine in Islamic azad university branch urmia-iran
4. graduate doctor of veterinary medicine in Islamic azad university branch urmia-iran

Background and Aim: Intestinal worms are widespread parasites of human communities in all over the world specially developing countries including Iran. Bad sanitary condition can provide the high chance for fecal-oral transmission of this parasites and prevalency of these infections. This study aims to determine the prevalency of intestinal helminths' infection in human community of Urmia.

Methods: In this study 1836 sample of gathered feces from different medical laboratories of urmia were evaluated on these faces were tested via flotation of feces with the method of formaline-ether (telman). this evaluation was done according to the quality of the pollution of parasite and the collected data were analysed via the software of Excell-v.2007 and SPSS-v.16

Results: According to the results, 41 out of 1836 (2.23%) examined persons were infected to intestinal worms including *Ascaris lumbricoides*, *Entrobis vermicularis*, *Trichuris trichura*, *Trichostrongylid* nematode, *Taenia* spp and *Hymenolepis* spp.

Conclusion: Data analysis using Chi-square test showed that there are no significant difference about age groups and sex groups' prevalence rate ($P > 0.05$). However *Entrobis vermicularis* was the most prevalent parasite (0.87%) in studied persons whereas *Trichuris trichura* was the least (0.05%) ($P < 0.05$).

Keywords: Intestinal worms, Human, Urmia.

P1095 - 108: THE PREVALENCE RATE OF HUMAN BRUCELLOSIS IN GHASCHASRAN COUNTY, SOUTH WEST OF IRAN.

Omolbanin Ghasemian karyak¹, Siamak Asri –Rezaei²

- 1- Young Researchers and Elite Club, Behbahan Branch, Islamic Azad University, Behbahan, Iran.
2. Department of Veterinary, Urmia University, Urmia, Iran

Background and Aim:Brucellosis is a bacterial infectious diseases common between humans and animals. Disease widely distributed around the globe,The reason is that, the spread of infection in domestic or wild animals.In this study, published literature on the sero-prevalence of brucellosis in human in 2013- 2014, in Ghachsaran city, Kohgilouyeh and Boyerahmad province was subjected to statistical analysis.

Methods:This research is a descriptive cross-sectional study on 1379 patients per 100,000 people with brucellosis referred to health- medical centers of the Ghachsaran county during the year 2013-2014. Also, 558(40.46%) were male and 821 (59.53%) female. Samples were patients who referred with clinical complaints compatible to brucellosis, and their Standard Agglutination Test (SAT) tests were positive. The results were analyzed using SPSS softwar

Results:During this study, 1379 participants were found positive. According to SAT = titer 1:160, As common cut off level for the diagnosis of brucellosis, the highest rate of infection with Brucellosis was seen in male group (10.57%) more than female(5.1%) which it was due to this fact that the men is primarily composed of milk and dairy products by Occupational exposure.

Conclusion:Based on acquired results in this study, the authors recommended to livestock vaccination in Ghaschasran County emphatically and veterinary network is required to consider livestock health and their resistance to disease following vaccination. Designing and introduce training programs could enhance society and Practitioner awareness in term of Brucellosis.

Keywords:Human Brucellosis, Prevalence Rate, Ghaschasran County.

P1096 - 138: EVALUATION OF BRUCELLA CONTAMINATION IN RAW MILK IN KERMAN DAIRY FARMS BY PCR

Farzaneh Salari ali abadi¹

1. Farzaneh Salari ali abadi

Background and Aim: Human brucellosis is a significant public health problem in many middle east countries including Iran. In endemic developing countries, dairy products produced from untreated milk are a potential threat to public health. The gold standard for the diagnosis of brucellosis is isolation of Brucella bacteria. However, to isolate Brucella bacteria is time- and resource-intensive; it requires level 3 biocontainment facilities and highly skilled technical personnel to handle samples and live bacteria for eventual identification and biotyping. Handling all live Brucella involves risk of laboratory infection and very strict biosafety rules must be observed. In order to avoid these disadvantages, methods based on the polymerase chain reaction (PCR) are becoming very useful and considerable progress has been made recently to improve their sensitivity, specificity, and technical ease and to lower costs. The aim of this study was to detect Brucella Spp in milk from dairy cattle farms in Kerman by PCR (Iran).

Methods: Forty and eight Bulk Tank Milk (BTM) were collected from 48 dairy cattle farm including 4200 cow. All milk samples were examined by PCR to detect Brucella-specific DNA targeting IS 711

Results: Using IS711 primer were detected in 4 samples (8.3%) Brucella spp from 48 BTM samples in this area..

Conclusion: The results indicate that brucellosis by Brucella species is endemic in the Kerman dairy farms. Consumption of dairy products produced from non-pasteurized milk by individual farmers operating under poor hygienic conditions represents an unacceptable risk to public health. The need for implementing control measures and raising public awareness on zoonotic transmission of brucellosis are recommended

Keywords: Milk, Brucellosis, PCR, Kerman

**P1097 - 142: SURVEY OF THE PORK ROLE IN DIFFERENT TISSUES INFECTION AND
DESTRUCTION IN RELEVANCE TO DISCOVERY OF FORBIDDANCE REASONS THESE
DRINKS IN QURAN AND ISLAM**

Sayed alireza Mirsane¹, Shima Shafagh², Nasrin Oraei³, Sayed Mojtaba Mirsane⁴

1. Surgical Technologist, Kashan University of Medical Sciences, Kashan,I.R.IRAN
2. General Surgery Specialist, Medical School, Kashan University of Medical Science,Kashan,I.R.IRAN
3. Khansar education office,Esfahan, ,I.R.IRAN
4. Khansar education office,Esfahan, ,I.R.IRAN

Background and Aim:Praise be to Allah, the Lord of the Worlds; and blessings and peace be upon our Prophet Muhammad and upon all his Family. All Muslims are agreed that eating of pork is impermissible. Cysticercosis is a tissue infection caused by the young form of the pork tapeworm. The purpose of this review was to elucidate role of the Cysticercosis in different tissues infection

Methods:We did a review of 26 studies identified by searching PubMed, Ovide ,Elsevier and ProQuest

Results:Studies showed the larval stage of the pork tapeworm (*Taenia solium*) infects the human nervous system, causing neurocysticercosis also this disease is one of the main causes of epileptic seizures in many countries and is also increasingly seen in more developed countries. Analysis showed Cysticercosis is a common tropical disease that disseminated cysticercosis have involvement of the subcutaneous tissues, skeletal muscles, right orbit and thyroid gland and likewise some studies showed this disease have high morbidity that those due to immense symptomatic in the ocular organs, oral region, tongue, lower lip, cutaneous, mucocutaneous and neurocutaneous.

Conclusion:Due to the reviewed articles , Cysticercosis can be damage to nervous system,subcutaneous tissues, skeletal muscles, right orbit and thyroid gland ,ocular organs, oral region, tongue, lower lip, cutaneous, mucocutaneous and neurocutaneous.. Finally One of the reasons of pork eating forbiddance in islam and Quran was discovered.

Keywords:Cysticercosis,Pork,Quran, Islam

**P1098 - 151: Q FEVER SEROLOGICAL SURVEY IN FEBRILE PATIENTS IN
KHORRAMABAD CITY**

Amin Jaydari¹, Nemat Shams², Hadis Morad Joodaki³, Farnaz Ferdowsi⁴

1. Assistant Professor, Department of Microbiology, Faculty of Veterinary Medicine, Lorestan University, Khorramabad, Iran.
2. Assistant Professor, Department of Microbiology, Faculty of Veterinary Medicine, Lorestan University, Khorramabad, Iran.
3. Master of Science student in bacteriology, Faculty of Veterinary Medicine, Lorestan university, Khorramabad, Iran
4. Master of Science student in bacteriology, Faculty of Veterinary Medicine, Lorestan university, Khorramabad, Iran

Background and Aim: Q fever is an infectious zoonotic disease characterized by sudden fever, headache, and atypical pneumonia, caused by *Coxiella burnetii* an obligatory intracellular parasite. Q fever is a widespread in the world zoonoses. Its main reservoir in the rural environment are farm animals: cows, sheep, goats, and urban pets such as dogs, cats, rabbits. It causes infections in humans that may be subclinical or acute (classical Q fever) or lead to chronic disease (endocarditis, hepatitis). The diagnosis test normally employed are complement fixation (CF), indirect immunofluorescent assay (IFA) and ELISA. ELISA test due to its high specificity and good sensibility, have proved greatly useful both for epidemiologic screening and diagnostic test for human Q fever. Given that there is little information about the Q fever in most parts of Iran, the aim of this study was to serological survey *C. burnetii* in febrile patient with historical contact with animal or animal products referred to clinical laboratories in Khorramabad city.

Methods: *C. burnetii* phase II IgG antibodies were measured by a commercial enzyme -linked immunosorbent assay (ELISA) in sera from 183 febrile patients.

Results: phase II IgG antibodies were detected in 52 subjects (28.41%).

Conclusion: This study demonstrated a high scales of *C. burnetii* exposure in the sampled febrile patients.

Keywords: Q Fever, ELISA, Khorramabad

**P1099 - 152: SEROPREVALENCE OF Q FEVER DISEASE IN SHEEP AND GOAT IN
KHORRAMABAD USING ELISA METHOD**

Amin Jaydari¹, Shahram Maleki², Gelareh majidi³

1. Assistant Professor, Department of microbiology, Faculty of Veterinary Medicine, Lorestan university, Khorramabad, Iran.
2. Assistant Professor, Department of Large animal, Faculty of Veterinary Medicine, Lorestan university, Khorramabad, Iran.
3. Master of Science student in Bacteriology, Department of Microbiology, Faculty of Veterinary Medicine, Lorestan university, Khorramabad, Iran

Background and Aim: Q fever is a zoonotic disease caused by *Coxiella burnetii*. In humans, the disease is seen as acute or chronic. In domestic animals, Q fever is usually subclinical although is along with abortion and stillbirths in sheep and goats. Domestic animals are the reservoir of *Coxiella* and release it through milk, urine, feces and respiratory and reproductive secretions. Inhalation of contaminated aerosols is the main way to contaminate human and animals. The aim of this study is to determine the seroprevalence of Q fever in sheep and goats in Khorramabad that also investigate the role of host factors.

Methods: In this study, blood samples were collected from 104 sheep and goats (male and female) at random in Khorramabad (53 sheep samples and 46 goat samples). Prepared serum were tested for *C. Burnetii* by ELISA.

Results: Seroprevalence of Q fever in this study was 33.64 percent that Seroprevalence of Q fever in sheep was 16.34 and Seroprevalence of Q fever in goat was 17.3.

Conclusion: The results of this study showed that *C. burnetii* contamination is present in different sites of Khorramabad. Also results of this study showed that contamination in sheep and goat population is high that, according to the zoonosis of this disease should be considered to health community.

Keywords: Q Fever, ELISA, khorramabad

**P1100 - 165: THE EFFECT OF ARTEMISININ PLUS SHARK CARTILAGE EXTRACT ON
LEISHMANIA MAJOR IN IN-VITRO CONDITION**

Soheila Molaie¹, Ghaffarifar fatemeh²

1. tarbiat modares university
2. tarbiat modares university

Background and Aim:: Leishmaniasis is one of the neglected tropical diseases. Cutaneous leishmaniasis is the chronic form of the disease and health problem of many countries. In this study we examined anti-leishmanial and apoptotic effects of Artemisinin and shark cartilage extract on Leishmania Major invitro conditions.

Methods:: In this experimental study the effect of Artemisinin was evaluated at different concentration and shark cartilage extract after 72hr by counting and MTT assay and the apoptosis was evaluated with flow cytometry assay.

Results:: IC50 of drugs Artemisinin were determined after 72 hours 50µg/ml. Cytotoxicity for 50µg/ml of Artemisinin and shark cartilage extract was 19% and 11% respectively. Flow cytometry analysis showed that the percent of apoptosis in control, 50 and 100µg/ml concentration of artemisinin were 2.41%, 50% and 49.5% respectively. Apoptosis of shark cartilage on Promastigotes were 39%. Statistical analysis showed significant differences between treated and control groups ($P < 0.05$).

Conclusion: This study supports Artemisinin and shark cartilage showed significant effectiveness on promastigotes and amastigotes, and can be used as alternative drugs in- vivo studies.

Keywords: Artemisinin, shark cartilage, leishmania major, invitro

**P1101 - 178: DETERMINATION OF ESCHERICHIA COLI PHYLOGENETIC GROUPS
ISOLATED FROM BROILERS COLIBACILLOSIS IN SEMNAN BY USING TRIPLEX-PCR
TECHNIQUE.**

Hamid staji¹, Elham Atefitabar², Elham Shahaboddin³

1. Department of Pathobiology, Faculty of Veterinary Medicine, Semnan University, Semnan, Iran.
2. Student in DVM degree, Faculty of Veterinary Medicine, Semnan University, Semnan, Iran.
3. Student in DVM degree, Faculty of Veterinary Medicine, Semnan University, Semnan, Iran.

Background and Aim: The aim of the present study was to determine the phylogenetic groups of E.Coli isolates from poultry colibacillosis in Semnan as potential zoonotic source for human infections.

Methods: In this study 50 strains of E. coli were isolated from internal organs of fifty five broilers suspected to colibacillosis. E. coli isolation and identification was carried out based on standard biochemical procedures, then strains were analyzed for the presence of yjaA, chuA and Tspe4.C2 markers by PCR for phylogenetic typing.

Results: PCR results showed that the strains fall in to 4 main Phylogenetic group as follow: nineteen isolates (38%) in phylogroup B2, eighteen isolates (36%) in group D, ten (20%) isolates in group A and three (6%) isolates belonged to group B1, subsequently. Also the strains belonging to phylogroups B2 & D included the majority (74%) of related strains.

Conclusion: Based on previous studies chicken meat and products, could be a reservoir for human zoonotic pathogens and there are several evidences that members of phylogroups B2 and D are responsible for human infections especially extra intestinal sites invasions, so strains of poultry colibacillosis in Semnan can be a hazardous source of human extraintestinal infections. On the other hand, strains belonging to A and B1 groups are considered as commensal bacteria, but these agents are capable to persist in environment and transmit the virulence genes like antimicrobials resistance genes to other phylogroups via horizontal gene transfer mechanisms and play an important role in presence of virulent and resistant pathogens.

Keywords: Escherichia coli, Phylogenetic groups, poultry colibacillosis, Semnan, Iran.

P1102 - 214: OVIPOSITION INDUCER BACTERIA OF GRAVID PHLEBOTOMUS PAPATASI

Naseh Maleki Ravasan¹, Naseh Maleki-Ravasan², Mohammad Ali Oshaghi³, Amir Ahmad Akhavan⁴,
Zahra Saeidi⁵, Mona Koosha⁶

1. -
2. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran (PII), Tehran, Iran
3. Department of Medical Entomology and Vector Control, School of Public Health, Tehran University of Medical Sciences (TUMS), Tehran, Iran
4. Department of Medical Entomology and Vector Control, School of Public Health, Tehran University of Medical Sciences (TUMS), Tehran, Iran
5. Department of Medical Entomology and Vector Control, School of Public Health, Tehran University of Medical Sciences (TUMS), Tehran, Iran
6. Department of Medical Entomology and Vector Control, School of Public Health, Tehran University of Medical Sciences (TUMS), Tehran, Iran

Background and Aim: It is revealed that oviposition of gravid *Phlebotomus papatasi* is excited by microbial flora of the environment. The most important breeding place of these sandflies is the *Rhombomys opimus* nests. Chemical communication between bacteria and their host's guarantees harmonization of behavior. Behavior was mediated through quorum sensing and hormones in the prokaryotic and eukaryotic cells respectively. We aimed to trace bacteria that are known to be involved in the inter-kingdom communication of eukaryotic sand flies and prokaryotic bacteria.

Methods: Samples from *Rhombomys opimus* nest materials comprising soil and vegetarian food residues plus *P. papatsi* dissected alimentary canal were checked for the presence of accused bacteria using 16S rRNA gene sequence analysis.

Results: In this survey we found twelve isolates and five species including four *Bacillus* species *B. pumilus*, *B. cereus*, *B. firmus*, *B. licheniformis* and one Coagulase-negative *Staphylococcus*, *S. saprophyticus*. Except for *S. saprophyticus*, other four bacteria were present in the sandfly gut. Two species of *B. pumilus* and *S. saprophyticus* were found in the nest materials where sand flies lay eggs.

Conclusion: Presence of some sand fly oviposition inducers such *Bacillus* spp. and *S. saprophyticus* support association between gut flora and oviposition induction. Inter-kingdom signaling mediates symbiotic and pathogenic relationships between bacteria, arthropods, plants and mammalian hosts.

Keywords: Oviposition inducer bacteria, *Phlebotomus papatasi*, symbiosis

P1103 - 216: AEROBIC GUT BACTERIA OF PHLEBOTOMUS PAPATASI FROM DIFFERENT ECOTOPES

Naseh Maleki Ravasan¹, Naseh Maleki-Ravasan², Mohammad Ali Oshaghi³, Amir Ahmad Akhavan⁴,
Mohammad Hossein Arandian⁵

1. -
2. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran (PII), Tehran, Iran
3. Department of Medical Entomology and Vector Control, School of Public Health, Tehran University of Medical Sciences (TUMS), Tehran, Iran
4. Department of Medical Entomology and Vector Control, School of Public Health, Tehran University of Medical Sciences (TUMS), Tehran, Iran
5. Isfahan Health Research Station, National Institute of Health Research (NIHR-IHRS), Esfahan, Iran

Background and Aim: Zoonotic Cutaneous Leishmaniasis (ZCL) is a public health problem with a clear and disturbing increase in the number of cases in 17 out of 31 provinces of Iran. The causative agent, *Leishmania major*, is mainly vectored by the *Phlebotomus papatasi*. There is no efficient control measure or vaccine available for this widespread insect-borne infectious disease until the present time. The aim of the study was determining correlation between sandflies gut bacteria and their breeding places.

Methods: In this study, the presence and distribution of gut microbiota of 390 *P. papatasi*, were investigated from rodent colonies, cattle farm and uninhabited home.

Results: 170 bacterial isolates included 40 distinct species isolated from the guts of *P. papatasi*. We found 24, 18, and 12 bacterial species from guts of captured sandflies from rodent colony, cattle farm and human dwellings, respectively. Members of families Microbacteriaceae, Staphylococcaceae and Xanthomonadaceae were the most prevalent bacteria in the sand flies guts. Comparison of the bacteria isolated from guts of the three locations indicated that species of *Microbacterium*, *Pseudomonas*, and *Staphylococcus* genera were dominant in human dwellings, cattle farms, and rodent colonies, respectively. *Staphylococcus aureus* was the only common bacterium in guts of sand flies of three regions. Also *Microbacterium paraoxydans* was generally found in the greatest abundance.

Conclusion: This study shows there is a wide variety of variation of aerobic gut flora occupying sand fly guts, which possibly reflect the micro-ecological circumstances of the dwelling site where the sandfly breeds.

Keywords: Gut Bacteria, *Phlebotomus papatasi*, ecotopes

**P1104 - 236: A BRUCELLOSIS SURVEY IN GHACHSARAN CITY, KOHGILOUYEH AND
BOYERAHMAD PROVINCE.**

Omolbanin Ghasemian karyak¹, Soheila Nouri ²

1. 1- Veterinary and Animal Sciences Research Center, Behbahan Branch, Islamic Azad University, Behbahan, Iran.
2. Health- Medical Center of Ghachsaran City, Ghachsaran , Kohgilouyeh and Boyerahmad province, Iran.

Background and Aim:Brucellosis is also known as Bang's disease, Malta fever, Mediterranean fever, or undulant fever, and is the most common zoonotic infection worldwide.The purpose of this study was to determine the rate of seropositivity of brucellosis among human in Ghachsaran city, Kohgilouyeh and Boyerahmad province.

Methods:During the year 2015-2016, 894 blood samples were gathered from suspicious patients with brucellosis different ages form Ghachsaran city, and were examined by Standard Agglutination Test (SAT).From 894 suspected patients, 529(59.2%) were male and 365 (40.8%) female. The results were analyzed using SPSS software.

Results:During this study, 894 participants were found positive. According to SAT = titer 1:160, As common cut off level for the diagnosis of brucellosis,64 cases were positive, and the highest rate of infection with Brucellosis was seen in female group (35 cases) more than male(29 cases)

Conclusion:Brucellosis is a preventable disease and its prevention in man is dependent on control of the disease in animals. The screening approach along with public health education enhances the detection rate and reduces the incidence of human brucellosis. Additional efforts are also required between medical and veterinary authorities to control this zoonotic disease in Ghaschasran.

Keywords:Brucellosis, Malta fever, Ghaschasran.

**P1105 - 257: EVALUATION OF THE ANIMAL BRUCELLOSIS CONTROL PROGRAM IN
IRAN FROM 2008 TO 2014**

Mohammad hasan Rabiee¹, Hamideh Hasannejad²

1. PhD Student of epidemiology, faculty of veterinary medicine, university of Tehran
2. Student of Veterinary Medicine, faculty of veterinary medicine, university of Tabriz

Background and Aim:Brucellosis is one of the most common zoonotic diseases. Prevention and control of human brucellosis is based on control of disease in animals, and control program in animals is based on vaccination and test-slaughter strategy. According to the published reports, human brucellosis has seen an increasing trend since 2010. This study investigates animal brucellosis control program In Iran from 2008 to 2014.

Methods:Data related to the control program of animal brucellosis and animal populations in Iran were taken from the Agriculture Ministry. Then the yearly percentage of vaccinated animals and tested animals in regard to brucellosis were calculated.

Results:In 2008, 41 percent of cattle population and 45 percent of sheep and goat population have been covered by vaccination. These percent in 2009 and 2010 decreased suddenly. Since 2011 this trend has started increasing, meanwhile 31 percent of cattle population and 40 percent of sheep and goat population has been covered in 2014. The percent of tested animals show a consistent trend in these years. On average, 10.6 percent of cattle and 0.05 of sheep and goat were tested during 2008 to 2014.

Conclusion:The result suggests that vaccination coverage that was reduced in years 2009 and 2010 has seen an increasing trend in recent years, and this increasing trend needs to be continued, as it is the most important strategy to control the disease in human.

Keywords:brucellosis, animal, control

**P1106 - 266: AN OVERVIEW OF CURRENT STATE AND RECENT OUTBREAKS OF
GLANDERS IN IRAN**

Samed Broumandfar¹

1. Iran Veterinary Organization

Background and Aim: Glanders is oldest and often fatal zoonotic disease that mainly occurs in the solipeds and caused by *Burkholderia mallei*. This article is a briefly review of the current state, epidemiology and outbreaks of glanders in the last decade in Iran.

Methods: A systematic retrospective review and analysis of data related to national glanders control program in IRAN.

Results: Glanders has been eradicated in most countries, but still focal outbreaks and sporadic cases are reported in some countries including IRAN. By attention to the data of Geographical Information System, glanders outbreak prevalence in Iran's equine population due to equines used for goods contraband from west neighboring countries could be understood.

Conclusion: Most important factor for occurrence of sporadic cases in IRAN is transmission of infected animals from neighboring countries to the west provinces of Iran. The key points in the Glanders control program are: Detection and elimination of reactors and affected animals, strict quarantine of premises. Because of the fatal nature of disease, history of use of *B.mallei* as a biological weapon, re-emerging of Glanders in the middle East, increased number of infected solipeds in our country during the recent years and the report of confirmed clinical cases in solipeds and captive carnivores of Tehran zoo, it is necessary to pay special attention to the disease and updating national strategy according to international recommendations and guidelines.

Keywords: *Burkholderia mallei*, Equine, Glanders, Iran

**P1107 - 268: CORRELATION OF BIOFILM PRODUCTION AND VIRULENCE FACTORS IN
EXTRAIESTINAL PATHOGENIC ESCHERICHIA COLI**

NAGHMEH MOORI BAKHTIARI¹, saad Gooraninezhad ², maryam Karami ³

1. 1Department of Pathobiology, Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz, Iran
2. 2Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz, Iran.
3. 3Gratuaded student of Veterinary Faculty, Shahid Chamran University of Ahvaz, Iran

Background and Aim: Escherichia coli are one of the most frequent causes of infections. Biofilm formation allows the strains to persist a long time on the biotic and abiotic surfaces and interfere with bacterial eradication. Different extracellular appendages are implicated in E. coli surface colonization and to ensure productive events leading to mature biofilm formation. In this research, the possible relationship between the presence of fimA (encoding large subunit of type I fimbriae) and csgA (encoding curli fimbriae) genes with biofilm formation, in extra intestinal pathogen E.coli isolates was evaluated

Methods: For this study, thirty isolates of E. coli was collected from different extra intestinal infections in bovine. After isolation and identification of E.coli strains by common biochemical tests, biofilm formation of isolates was examined in LB and BHI containing 1% sucrose by using micro titer plate crystal violet method. Presence of two studied genes in this isolated was evaluated by PCR

Results: Based on results, 100% and 96.7% of isolates have csgA and fimA gene, respectively. By using of BHI medium containing 1% sucrose, 53.3% of strains were average biofilm producer and 16.6% of isolates were strong biofilm producer compared with LB medium which 66.6% of isolates were weak biofilm producer and none of those were strong biofilm producer

Conclusion: In this research BHI medium containing 1% sucrose was better than LB medium in biofilm production and Because of presence of two studied genes in none producer biofilm isolates, correlation of these genes with biofilm production ability is suspect.

Keywords: Escherichia coli, Biofilm, Micro titer plate crystal violet

**P1108 - 270: MOLECULAR ANALYSIS OF VIRULENCE FACTORS IN BACTERIAL
LIPOPOLYSACCHARIDE RAZI INSTITUTE VACCINAL STRAINS OF PASTEURELLA
MULTOCIDA AVIAN FIELD**

Zahra Yazdanpour¹, Ahmad Reza Jabbari², Majid Esmaelizad³

1. MSc student Razi Vaccine and Serum Research Inst, Karaj, Iran
2. National Pasteurella Research Laboratory, Razi Vaccine & Serum Research Institute, Karaj, Iran
3. Central Lab Dept, Razi Vaccine & Serum Research Institute, Karaj, Ira

Background and Aim: Pasteurella multocida is a gram-negative coccobacillus belonging to the Pasteurellaceae family can cause wild range of disease in human and animal. P. multocida Strains can be classified into five capsular serogroups (A, B, D, E, F) using an Indirect hemagglutination test and into 16 somatic or lipopolysaccharide (LPS) serotypes using the Heddlestone gel diffusion precipitin test. The aim of this study was to identify the LPS genotypes L1- L8 among avian

Methods: A collection of 33 bacterial isolates of P. multocida from avian was analysed in this study. All P. multocida Strains were grown at 37°C in Brain Heart infusion broth (BHI). DNA was purified of culture using boiling Method. DNA extracted by this Method allowed amplification and sequencing. The quality DNA Measured by A260–A280 ratio in nonodrap

Results: 60% of isolates contained LPS1, 13.4% LPS2, 16.6% LPS3 and 10% of isolates contained more than one gene and no other genotypes were detected in isolates.

Conclusion: Fowl cholera is endemic in Northern part of Iran, mainly Gilan and Mazandaran provinces. High rainfall, high humidity and heat prepare suitable conditions for the PM for survive and transmission. A local isolate of Pm recovered from FC outbreaks in Gilan Province, Astara, in 1980 is used for making a monovalent vaccine. PCR typing is a suitable typing system for differentiating between Pasteurella multocida genotypes and it is preferable to Heddlestone serotyping

Keywords: p. multocida, avine, LPS-PCR typing

P1109 - 271: SEROPREVALENCE DETERMINATION OF BRUCELLOSIS IN SOME NATIVE DAIRY CATTLE FARMS OF SABZEVAR USING SANDWICH LATERAL FLOW IMMUNOCHROMATOGRAPHIC

Gholamreza Hashemi Tabar¹, Mohammad reza. Raiesnia²

1. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.
2. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.

Background and Aim: Brucellosis is one of the common diseases among humans and animals across the world. The disease mainly involves cattle, sheep, goat, camel and pig and causes many economic losses. The purpose of this study was to investigate the seroprevalence of brucellosis in native cattle using the serological rapid lateral flow immunoassay method.

Methods: Blood samples were taken from 150 unvaccinated native cattle. After centrifugation of the blood samples, 2 ml serum was taken and was stored at -20 ° C. One to two drops of each of serum samples was added to RLFA kits along with buffer recommended by kit and the results was shown in a 1 to 2 minutes period.

Results: The seroprevalence of brucellosis was calculated to be 2% using the RLFA method and, with a 95% confidence level, it is sayable that the prevalence of brucellosis in the study region varies from zero to four percent.

Conclusion: Timely and accurate identification of animals infected with brucellosis plays a key role in preventing large losses of the disease and reducing the incidence of it in humans. Serological rapid lateral flow immunoassay method is one of the new methods for diagnosis of brucellosis which, given the high specificity and sensitivity and also no need of advanced laboratory equipment and experienced personnel, and can be used as an applicable method in the diagnosis of this disease.

Keywords: Brucellosis, cattle, seroprevalence, rapid lateral flow immunoassay.

**P1110 - 284: DIAGNOSIS OF COXIELLA BURNETII IN PATIENTS WITH ACUTE
UNDIFFERENTIATED FEBRILE ILLNESS (AUFI) IN KHORRAMABAD CITY**

Farnaz Ferdosi¹, Amin Jaydari², Nemat Shams³, Hadis Morad Joodaki⁴

1. Master Of Science Student In Bacteriology, Faculty Of Veterinary Medicine Lorestan University
2. Assistant Professor, Department Of Microbiology, Faculty Of Veterinary Medicine, Lorestan University
3. Assistant Professor, Department Of Microbiology, Faculty Of Veterinary Medicine, Lorestan University
4. Master Of Science Student In Bacteriology, Faculty Of Veterinary Medicine Lorestan University

Background and Aim: *Coxiella burnetii* bacteria cause Q fever which is a zoonotic disease and occurs in two forms, acute and chronic. Q fever might cause a various clinical symptoms in patients. The aim of this study is to diagnose and study Q fever among patients with acute undifferentiated febrile illness (AUFI) by molecular method.

Methods: Nested-PCR method was used to diagnose *Coxiella burnetii* genome.

Results: In this study 200 blood samples of patients with suspected Q fever in Khorramabad city were collected where *Coxiella burnetii*'s DNA was identified in 16 samples (8%).

Conclusion: This study reveals that Q fever might be one of the possible reasons in febrile patients that should be considered. In addition, raising awareness of transmission of diseases through contact with animals or consumption of unpasteurized dairy products to patients should be considered.

Keywords: *Coxiella burnetii*, Human, Khorramabad, Nested-PCR, Q fever

**P1111 - 288: INVESTIGATION OF MYCOPLASMA INFECTION IN LUNGS OF CATTLE
SLAUGHTERED IN HAMADAN INDUSTRIAL ABATTOIR**

Saeed Totonchi mashhour¹, Abdolmajid Mohammadzadeh², Alireza Nourian ³, Pezhman Mahmoodi kofi⁴

1. Department of pathobiology, Faculty of Veterinary Science, Bu-Ali Sina University
2. Department of pathobiology, Faculty of Veterinary Science, Bu-Ali Sina University
3. Department of pathobiology, Faculty of Veterinary Science, Bu-Ali Sina University
4. Department of pathobiology, Faculty of Veterinary Science, Bu-Ali Sina University

Background and Aim: Mycoplasmas are very small bacteria which lack a cell wall and therefore, resist the effects of antibiotics that affect the bacterial cell wall. About 20 Mycoplasma species have been detected in cattle. These bacteria exist all around the world and cause respiratory, ocular, mammary, articular, and urogenital infections in their host.

Methods: This study aimed to investigate the prevalence of Mycoplasma infection in lung tissue samples from cattle slaughtered in Hamedan industrial abattoir in cold and warm seasons. A total of 93 lung samples were collected and whole DNA was extracted using commercial kits. After confirming the quality of the extracted DNA by agarose gel electrophoresis, all samples were tested by PCR using primers specific for the genus Mycoplasma.

Results: Results showed that 4 (4/3%) out of 93 lung samples were infected with Mycoplasma.

Conclusion: Based on the results of this study, mycoplasma infection exists in cattle population in the region, and the rate of infection is in agreement with reports from other countries.

Keywords: Mycoplasma, Lungs, PCR

**P1112 - 297: EPIDEMIOLOGICAL FEATURES OF PATIENTS WITH BRUCELLOSIS
REFERRED TO THE BESAT HOSPITAL, SANANDAJ, 2015**

Arezo Omati¹, Khaled Rahmani², Ashkan Zobairi³

1. MSc student of Microbiology, Rasht Sciences and Researches University, Rasht, Iran.
2. PhD student of Epidemiology, Dept. of Epidemiology, School of Public Health, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
3. student of veterinary medicine, Islamic Azad university of Sanandaj, Sanandaj, Iran.

Background and Aim:Brucellosis as one of the most important zoonotic disease is endemic in Kurdistan province of Iran. The aim of present study was to determine the epidemiological features of brucellosis patients in Besat hospital of Kurdistan center, Sanandaj, 2015.

Methods:This was a cross-sectional study that carried out in the year of 2015. All confirmed brucellosis patients admitted in the hospital from January to December of 2015 entered to the study. All analysis including descriptive and analytical conducted in stata version 13.

Results:Ninety sex brucellosis patients with mean (SD) age of 40(17) years admitted in Besat hospital that 55.2% of them were males. From the view of occupational distribution, household (42.7%) and farming/livestock rearing (27.1%) were most prevalent occupations. The main risk factors of patients in this region were consumption of unpasteurized dairy products and exposure to the aborted domestic animal secretions with 80.2% and 71.9%, respectively. Fever (62.5%), lower back pain (55.2%) and muscles pain (50%) were common symptoms of studied patients. About 33% and 21% of patients had high wright's serum agglutination brucellosis antigen ($>1/320$) and 2-Mercaptoethanol ($>1/320$) in time of disease diagnosis, respectively. There was no statistical significant difference between sex and wright's test values ($P=0.3$).

Conclusion:This study indicated that lower back pain is most important clue in diagnosing of brucellosis in Kurdistan region after fever. Our results also reveled that unpasteurized dairy products and exposure to the aborted domestic animal secretions are considered two main risk factors for brucellosis in Kurdistan.

Keywords:Brucellosis, Epidemiologic features, Sanandaj

**P1113 - 313: A REPORT SEROPREVALENCE BRUCELLOSIS IN SAHNEH CITY OF
KERMANSHAH PROVINCE OF IRAN DURING MARCH 2010-MARCH 2016**

Mehrdad Pooyanmehr¹, Qobadi Esmaeil², Amini Zohreh³

1. 1Department of Pathobiology, microbiology section, Faculty of Veterinary Medicine, Razi University, Iran
2. 2Veterinary Student, Faculty of Veterinary Medicine, Razi University, Iran
3. 2Veterinary Student, Faculty of Veterinary Medicine, Razi University, Iran

Background and Aim: Brucellosis is one of the most important zoonotic disease constituting a public health problem worldwide. Brucellosis is usually associated with the consumption of unpasteurized milk and soft cheeses made from infected animals. The aim of this study was to a report prevalence of Brucellosis among people in sahneh City of Kermanshah Province of Iran during five years.

Methods: In this study 5000 person were examined and only patients with a positive result in diagnostic tests Wright - Combs - 2ME in the years of March2010-March2016 were reported. Factors such as age - gender- work with animals the kind of contact with animals , consumption unpasteurized dairy products were studied. Generally, 327 patients (96 female and 224 male) serum specimens that collected in Health center laboratory (five years) were used in Coombs Wright Brucellosis test (In this test, serum titer of $\geq 1:80$ is positive for brucellosis).

Results: Total Patients were 327 person. the age of 20 to 60 were the highest rate of infection (6.54%). 65.95% of men and 34.05% of the patients were women. The people were villager 70.8% and 29.2% were townspeople. 70.8% of the patients had a history of direct contact with their animal and livestock. Consumption of unpasteurized dairy products were found in 93.43% of cases.

Conclusion: The results of this study show that infectious animals must be control for prevention of disease. It is concluded that screening of brucellosis is necessary in our population for basic programming.

Keywords: Seroprevalence, Brucellosis, Kermanshah Province

**P1114 - 314: A REPORT SEROPREVALENCE SALMONELLOSIS IN SAHNEH CITY OF
KERMANSHAH PROVINCE OF IRAN DURING MARCH 2010-MARCH 2016**

Mehrdad Pooyanmehr¹, Qobadi Esmaeil², Amini Zohreh³

1. 1Department of Pathobiology, microbiology section, Faculty of Veterinary Medicine, Razi University, Iran
2. 2Veterinary Student, Faculty of Veterinary Medicine, Razi University, Iran
3. 2Veterinary Student, Faculty of Veterinary Medicine, Razi University, Iran

Background and Aim: Salmonella spp is important zoonotic pathogens. food products of animal origin, particularly meat and eggs are important sources of bacteria of the Salmonella Typhimurium and typhi causes gastroenteritis in humans (Typhoid fever)and other mammals with so modifiable economic losses.

Methods: In this study 5000 person were examined and only patients with a positive result in diagnostic Widal test in the years of March 2010 -March 2016 were reported. Factors such as age - gender- work with animals the kind of contact with animals , consumption meat, eggs and unpasteurized dairy products were studied. Generally, 127 patients (37 female and 90 male) serum specimens that collected in Health center laboratory (five periods) were used by test Widal (In this test, serum titer of $\geq 1:80$ for O Ag and $\geq 1:40$ for H Ag were positive).

Results: Total Patients were 127 person .the age of 18 to 60 were the highest rate of infection (6.54%). 75.95% of men and 24.05% of the patients were women. The people were villager 80.8% and 20.2% were townspeople. 69.5% of the patients had a history of direct contact with their animal and livestock.

Conclusion: The results of this study show that infectious animals and food products of animal origin, particularly meat and eggs must be control for prevention of disease. It is concluded that screening of salmonellosis and educations is necessary in our population for basic programming.

Keywords: Salmonella, zoonotic pathogens, Kermanshah Province

**P1115 - 317: A REPORT PREVALENCE ANTHRAX IN SAHNEH COUNTY OF
KERMANSHAH PROVINCE OF IRAN DURING MARCH 2010-MARCH 2016**

Mehrdad Pooyanmehr¹, Qobadi Esmaeil², Amini Zohreh³

1. 1Department of Pathobiology, microbiology section, Faculty of Veterinary Medicine, Razi University, Iran
2. 2Veterinary Student, Faculty of Veterinary Medicine, Razi University, Iran
3. 2Veterinary Student, Faculty of Veterinary Medicine, Razi University, Iran

Background and Aim: Zoonotic diseases constitute a public health problem throughout the world. Anthrax is a potentially fatal zoonotic disease and is a important zoonotic disease which is primarily a job-related infection caused by *Bacillus anthracis*. The diagnosis of cutaneous anthrax (CA) may be very difficult, particularly in atypical presentations and non-endemic regions. Aim this study, anthrax cases seen between March 2010 – March 2016 (five years) in Sahneh County of Kermanshah Province.

Methods: Two patients with CA were included in this study. The diagnosis of CA was based on clinical findings and/or microbiologic procedures. The data were taken from internal reports of Health Center with Animal Resources in the period five years.

Results: Each 2 patients with a diagnosis of CA were followed up. two patients had a history of animal contact. The clinical presentation of CA was typical in 2 patients in 2011 (1 case) and 2012 (1 case). one patients were initially misdiagnosed with insect bites and one patient with angioedema. Cultures from the lesions were positive for *Bacillus anthracis* in two cases. Gram stain from the lesions revealed Gram-positive rods in two cases. Patients were diagnosed by clinical presentation and a history of contact with sick animals and/or contaminated animal products.

Conclusion: CA is a very contagious and important infectious disease worldwide. Early and accurate diagnosis dramatically affects the prognosis of the disease. The diagnosis of CA may be difficult, especially in atypical presentations and nonendemic areas. Thus, CA should be kept in mind, especially in these situations.

Keywords: *Bacillus anthracis*, Zoonotic diseases, kermanshah

**P1116 - 329: COXIELLA BURNETII IN MILK SAMPLES FROM DAIRYS GOAT FARMS IN
THE BONAB, IRAN IN 2014**

Peyman Khademi¹, Mohammadreza Mahzounieh², Mahmoud Esmaeili³, Ramin Khademi⁴

1. PhD Student of bacteriology School of Veterinary Medicine Department of Pathobiology Urmia University, Urmia, Iran.
2. Professor, Pathobiology Department, Faculty of Veterinary Medicine and Research Institute for Zoonotic Diseases, Shahrekord University, Iran.
3. Master of Science Food Hygiene and Quality Control, Department of Food Hygiene and Quality, Shahrekord University, Iran.
4. Lecturer, Computer Engineering Department, Faculty of Engineering, Khorramabad Branch, Islamic Azad University, Khorramabad, Iran.

Background and Aim: Q fever is a zoonotic agent that is endemic in the very parts of the World. It has animal origin as consider as an emerging zoonoses in many countries, including Iran. Cattle, sheep, and goats are the primary reservoirs although a variety of species may be infectious. Bacteria are found in milk of infected animals. PCR-based methods have been widely used for the detection often because isolation of *C. burnetii* is time-consuming. Recent reports showed that PCR-positive rates of Q fever infection widely vary. We have evaluated the PCR and nested PCR assays currently used in Iran.

Methods: A nested PCR method was developed for the detection of *Coxiella burnetii* in goat milk and samples. Two pairs of oligonucleotide primers were designed to amplify a 438-bp fragment of the *com1* gene encoding a 27-kDa outer membrane protein of *C. burnetii*. To analyze the sequencing data, BLAST comparison was performed with the NCBI/ GeneBank database accession number; KM263614.

Results: that 49 samples from 160 samples of goat milk (30.62%) were positive for *C. burnetii*.

Conclusion: The analysis of the collected data in different seasons and areas revealed that, 69.38 percent of the samples were negative and 30.62 percent were positive in terms of *Coxiella burnetii* presence. It can be concluded Goat milk can be one of the potential sources of *Coxiella burnetii* in Iran.

Keywords: Q fever, *Coxiella burnetii*, Goat, Nested-PCR

**P1117 - 353: COMPARISON OF MACROSCOPIC AND MICROSCOPIC METHODS FOR THE
DIAGNOSIS OF INFECTIONS WITH PATHOGENIC SARCOCYSTIS SPECIES IN
SLAUGHTERED SHEEP IN DEZFUL ABATTOIR**

Seyed mild Mousvi¹, saloomeh shirali², Leila derakhshan³, seyed milad mousavi⁴

1. -
2. biotechnology ,basic sience faculty , Ahvaz Azad university ,Iran
3. parasitology, veterinary faculty ,shoshtar Azad university ,Iran
4. student ,biotechnology ,basic sience faculty , Ahvaz Azad university ,Iran

Background and Aim:Sarcocystosis is a zoonotic protozoan diseases that caused by different Sarcocystis spp. This parasite is found in many animals and in terms of economic and public healths impose losses in human and animal societies. Given the importance of this infection, the infection rate of macroscopic and microscopic sarcocysts in slaughtered sheep was determined in Dezful abattoir.

Methods:In the autumn of 2015, three tissue samples (esophagus, diaphragm, and heart) of 300 sheep were inspected to detect macroscopic sarcocysts. To detect microscopic cysts these muscles were investigated randomly via impression smear and digestion method.

Results:The results showed that the infection rate of macroscopic cysts was 16/16% and the infection rates of impression smear and digestion method were 63/33% and 70%. Data analysis by Chi square method was shown there was no significant relationship between impression smear and digestion method ($p>0.05$) and there was a significant relationship between the infection rates of macroscopic method with impression smear and digestion method.

Conclusion:Although there was no significant relationship between impression smear and digestion method, digestion method was the most sensitive method for the detection of sarcocystis in sheep.

Keywords:Sarcocysts, sheep, impression smear, digestion method

**P1118 - 357: PREVALENCE OF BOVINE CYSTICERCOSIS OF SLAUGHTERED CATTLE IN
AHVAZ ABATTOIR**

Leila derakhshan¹, Saloomesh shirali², Mohammad Aryanpour³

1. parasitology , veterinary faculty , Shoshtar azad university , Iran
2. biotechnology ,basic sience faculty, Ahvaz azad university , Iran
3. student ,biotechnology ,basic sience faculty, Ahvaz azad university , Iran

Background and Aim: Bovine cysticercosis or *T. saginata* cysticercosis is one of the most important zoonosis parasitic diseases caused by larvae of *Taenia saginata* (*T. saginata*) in cattle muscle while the adult worms in human cause taeniasis. Human infection with adult worms and bovine cysticercosis has been reported from different regions of Iran. The aims of this study were the importance of hygiene and evaluate the prevalence of bovine cysticercosis in Ahvaz slaughterhouse.

Methods: For this purpose in autumn of 2015, 3860 skeletal muscle of cattle observed and evaluated for the presence of cysticercosis. In inspection both live and calcified cyst was observed.

Results: The total amount of pollution in cattle was reported 2/9% and the prevalence of the cyst was 43% in heart, 9% in diaphragm, 62% in triceps muscles, 29% in intercostal and 45% in masseter muscles. In these cases, severe damage was found around the cyst.

Conclusion: Bovine cysticercosis is a zoonotic disease and it transmits to humans, so Simple precautions such as avoiding the use of semi-cooked or raw meat; more attention of abattoir inspectors and detection of infected organs will have a significant impact on reducing pollution.

Keywords: cysticercosis, skeletal muscle, prevalence

**P1119 - 359: STUDY ON CONTAMINATION OF PUBLIC PARK BY TOXOCARA PARASITE
EGGS IN QAZVIN**

Maryam Moradnia¹, masoud panahi fard²

1. M.Sc in Environmental. Health Engineering, Health faculty, Qazvin University of Medical Science, Qazvin, Iran
2. M.Sc in Environmental. Health Engineering, Health faculty, Qazvin University of Medical Science, Qazvin, Iran

Background and Aim:Toxocaridae is one of the most common soil-borne parasites and intestinal nematodes that cause ocular and acute visceral toxoplasmosis. Public parks are important places that may be contaminated by toxocara parasite eggs. The objective of the study was review on contamination of Public Park by toxocara parasite eggs in Qazvin in 2014.

Methods:In the experimental study, 100 samples (The approximate weight of 30 grams) were collected from the grass lawns of a public park (Fadak Park) in Qazvin. The samples were examined by sedimentation – flotation. Samples were taken every 10 to 15 Smear. The specimens were observed with a microscope. The collected data were analyzed by statistical software SPSS17.

Results:It was diagnosed only two of toxocara eggs. In the two samples there was only a lack of a fetal egg. Strongyloides larva was observed in 100% of cases. It also was observed in 55% of samples of larvae, parasitic mites and other eggs.

Conclusion:Toxoplasma parasite eggs were contaminated low efficient in Fadak park lawn. This may be due to some important parameters such as the sufficient care of lawns in the park in terms of traffic control and ownership of stray dogs and cats, the lack of available dogs and cats infected with the parasite toxoplasma efficient in this area, and the topography of the park

Keywords:Toxocara parasite eggs, Public park, Qazvin

P1120 - 420: BRUCELLOSIS EPIDEMIC COMPARISON IN DEHDASHT IN TWO YEARS

Seyyed vahid Ganjiani¹

1. Student of veterinary medicine from Shiraz University, Iran

Background and Aim:Brucellosis is a zoonotic infection specially known by Malta fever that caused by the bacterial genus *Brucella*. The bacteria are transmitted from animals to humans by direct contact with infected animals or ingestion through using milk and meat products from these animals. *Brucella* organisms which are small aerobic intracellular coccobacilli localize in the reproductive organs of host animals, causing abortion and sterility. They are shed in large animals' urine, milk, placental fluid and other fluids. To date, eight species have been identified, named primarily for the source animal or features of infection. The following two are most important than others: • *Brucella melitensis* (from sheep) • *Brucella abortus* (from cattle)

Methods:By wright test, all suspicious clients of Apadana laboratory that is most prominent laboratory in Dehdasht have been checked.

Results:In general, 84 of 912 suspicious clients were wright positive (9.21%) from 20/3/2014 to 20/3/2015 and 77 of 451 suspicious clients was wright positive (17.01%) from 20/3/2015 to 20/3/2016.

Conclusion:There are numerous animal husbandries in Dehdasht vicinity and people use rural products.By comparison between these two years and based on the patients' history, doubling of infected people in this city caused by using of rural or non-pasteurized dairy products. Finally using pasteurized dairy products or heated rural ones is best way for reducing morbidity of brucellosis for typical people.

Keywords:Brucellosis, Malta fever, abortus, melitensis, Dehdasht, Wright

**P1121 - 457: MEASUREMENT OF DIPALMITOYLPHOSPHATIDYLCHOLINE (DPPC)
CONCENTRATION IN BRONCHOALVEOLAR LAVAGED FLUIDS BY HPLC IN
EXPERIMENTAL PNEUMONIA**

Zohre Eftekhari¹, Mohammad Reza Mokhber Dezfouli ², Mohammad Mahdi Dehghan³, Raziieh Toghrol⁴,
Mahiar Jaloudari Mamaghani⁵, Ali Khodaeipour⁶, Arsalan afraziabi⁷

1. Department of Research and Development, Research and Production Complex, Pasteur Institute of Iran, Tehran, Iran
2. Department of Internal Medicine, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
3. Department of Surgery and Radiology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
4. Vat Graduated ,University of Tehran, Tehran, Iran
5. Production Manager,University of Tehran, Tehran, Iran
6. Master of Science Microbiology ,Tehran Shomal University
7. Master of Science Microbiology ,Tehran Shomal University

Background and Aim:Surfactant is composed of six phospholipids and four apoproteins. The components of surfactant include phospholipids, neutral lipids, and proteins. *Pasteurella multocida* causes a range of diseases in mammals and birds which can also cause a zoonotic infection in humans. Evaluation of Dipalmitoylphosphatidylcholine (DPPC) in surfactant content may provide a valuable diagnostic tool for detection of calf pneumonia and also state of treatment.

Methods:Ten Holstein-Frisian bull calves aged 4 months were selected for study in two groups. The *Pasteurella multocida* (PMC66 Razi) was used in the present study for inducing pneumonia. The Bronchoalveolar lavage (BAL) process was done in selected calves. BAL fluid was collected and centrifuged and finally the sediment (crude surfactant) was reserved at -20°C. The cytological evaluation and DPPC content was assayed by HPLC Refractive Index Detector.

Results:Significantly increased in segmented neutrophil, neutrophil band and WBC were occurred in pneumonic calves as compared with control calves ($P < 0.05$). The level of total phospholipids content in pneumonic calves measured 76 ± 8.5 mg/ml and in control group recorded 89.23 ± 14.1 mg/ml which there was not a significant difference between the two conditions but, the amount of DPPC in pneumonic group (3.3 mg/ml) decreased significantly in comparison control group (10.5 mg/ml) which enhanced after treatment in pneumonic group (7.5 mg/ml and TPL $81.13 \pm 0.4.8$ mg/ml).

Conclusion:*Pasteurella* inducing pulmonary can changed the major component of lung surfactant which evaluation of these markers can be helpful as an appropriate tool in diagnostic state of pneumonia and healing.

Keywords:Dipalmitoylphosphatidylcholine, Surfactant,Pneumonia

**P1122 - 487: SURVEY OF PREVALENCE AND VIRULANCE FACTORS OF SALMONELLA
ENTERITIDIS AND SALMONELLA TYPHIMURIUM ISOLATES' FROM SHEEP'S
TRADITIONAL CHEESE BY CULTURE AND PCR TESTS**

Pourya Dadabiglou¹, Younes Anzabi²

1. Student of Veterinary Medicine collage, Tabriz Branch, Islamic Azad University, Tabriz, Iran
2. Department of Pathobiology, Tabriz Branch, Islamic Azad University, Tabriz, Iran

Background and Aim:Salmonella enteritidis and Salmonella typhimurium are among the most important pathogenic bacteria transmitted from milk that the main reason for their pathogenicity is related to virulence factors. Current study to evaluate the frequency and present of virulence genes in mentioned bacterial isolates at sheep's traditional cheese produced in Lighvan region of East Azerbaijan province.

Methods:330 samples of sheep's traditional cheese was collected randomly in sterile containers and transferred to the Microbiology laboratory in Tabriz branch, Islamic Azad University. All samples were cultured in standard conditions for isolation and identification of eventual Salmonella in mentioned samples. Then all isolates transferred to the Genomics laboratory of Biotechnology Research Center of Tabriz branch, Islamic Azad University; in order to get the final confirmation of Salmonella road found the presence of Salmonella enteritidis and Salmonella typhimurium strains virulence genes by simple-PCR and multiplex-PCR tests.

Results:Of the total samples cultivated was found that 9 isolates (2.72 percent) belongs to the Salmonella genus but based on the simple-PCR results only 6 isolates (1.81 percent) belongs to it. According to the results of mentioned research the prevalence amount of Salmonella enteritidis and Salmonella typhimurium was revealed 0.6 and 1.21 percent. Also based on Multiplex-PCR method the presence of virulence genes in all isolates was determined.

Conclusion:The results indicate that there is potential for transmission of Salmonella in unpasteurized dairy products and it seems that usage of traditional sheep's cheese increases the risk of Gastroenteritis related to Salmonella in human.

Keywords:virulence factors, Salmonella, traditional sheep's cheese, culture, molecular test

**P1123 - 537: A COMPARATIVE EVALUATION OF SENSITIVITY OF CASONI'S
INTRADERMAL, INDIRECT HAEMAGGLUTINATION, LATEX AGGLUTINATION AND
GEL PRECIPITATION TESTS IN RECOGNITION OF HYDATIDOSIS IN VARIOUS
LOCALITY OF THE BODY IN ANIMAL MODEL**

Zahra Pourahmad¹, Mehdi Assmar², Ali Reza Masiha³, Zohreh Gholizadeh Siahmazgi⁴

1. Islamic Azad University of Lahijan
2. Islamic Azad University of Lahijan
3. Islamic Azad University of Lahijan
4. Zist Faravard Pars Co.

Background and Aim:Hydatidosis is a zoonotic disease. Due to the importance of diagnosis of cysts in various organs of the body, a comparative evaluation of sensitivity of immune assay methods such as casoni (ID), indirect haemagglutination (IHA), latex agglutination (LA) and gel precipitation (GP) tests was performed.

Methods:infected liver to hydatid cyst were collected from a slaughterhouse. Cyst fluid was aspirated and then the supernatant was separated from protoscoleces. Fifty Balb/c mice were inoculated intraperitoneally by 0.2 ml from the supernatant. Protoscoleces were checked in terms of viability and ten rabbits were inoculated intraperitoneally, intravenously and respiratory (4,4 and 2 respectively) with 0.5 ml of diluted protoscoleces with phosphate buffered saline. After one month, the animal's sera were collected and evaluated by using IHA, LA and GP tests. After preparing the antigen, casoni test was performed for sixty animals.

Results:The sensitivity of IHA, LA and GP was 84%, 82% and 76%, respectively. Casoni was negative for all animals. After autopsy, cysts were observed in various organs of 30% of rabbits. According to the presence of cysts in various organs, the sensitivity of IHA, LA and GP was 100%, 100% and 66.6% respectively. GP test in diagnosis of pulmonary cysts was negative.

Conclusion:According to the locality of cysts, comparative evaluation of sensitivity of methods showed the sensitivity of precipitation (GP) test is lower than agglutination (IHA and LA) tests. So precipitation tests as a GP test is not suitable for diagnosis of pulmonary cysts. Casoni (ID) test was negative in the laboratory animals.

Keywords:Hydatidosis, Immune Assay Methods, Sensitivity, Animal Model

**P1124 - 568: AN EPIDEMIOLOGICAL STUDY OF BRUCELLOSIS IN ARDABIL PROVINCE,
IRAN, IN 2015**

Seyyede negar Modarres sadrani¹, Dr. Sadegh Hazrati², Dariush Emdadi³

1. M.Sc in Biochemistry, Ardabil Province Health Center, Ardabil University of Medical Sciences, Ardabil, Iran
2. Occupational Health PhD, Ardabil Province Health Center, Ardabil University of Medical Sciences, Ardabil, Iran
3. M.Sc in entomology, Ardabil Province Health Center, Ardabil University of Medical Sciences, Ardabil, Iran

Background and Aim:Brucellosis is one of the most widespread zoonotic diseases between humans and animals. Brucellosis as an occupational disease can involve those who have direct or indirect contact with infected animals or their products

Methods:In this descriptive study, all collected 506 cases of human brucellosis were reported and analyzed separately for 10 subsidiary cities according to national guideline for brucellosis control.

Results:The incidence rate of the disease in 2015 was 33 per 100,000 people in the province. Urban (27%) and rural (73%) cases were infectious including 52% males and 48% females. Of the total cases, 82% had contact with livestock and 18% had no contact, 85% of patients used dairy products and 15% did not use; and in terms of occupational were as follows, 37% housewives, 21% students, 14% ranchers, 11% farmers, 6% children and 3% shepherds and 8% other professions.

Conclusion:Considering the high prevalence of the disease in rural areas and among pregnant women and students, it is necessary to train and inform people through the health workers and technicians of rural centers in order to introduce transmission routes and prevent the risk of infection.

Keywords:Brucellosis, Epidemiological Study, Incidence Rate, Ardabil, Iran

**P1125 - 692: MOLECULAR CHARACTERIZATION OF ENTEROHEMORRHAGIC
ESCHERICHIA COLI HEMOLYSIN GENE (EHEC-HLYA)-HARBORING ISOLATES FROM
CATTLE REVEALS A DIVERSE ORIGIN AND HYBRID DIARRHEAGENIC STRAINS**

Mahdi Askari Badouei¹, Stefano Morabito ², Arash Najafifar ³, Emad Mazandarani ⁴

1. Department of Pathobiology, Faculty of Veterinary Medicine, Garmsar Branch, Islamic Azad University, Garmsar, Iran
2. European Union Reference Laboratory for Escherichia coli, Istituto Superiore di Sanita, Dipartimento di Sanita Pubblica Veterinaria e Sicurezza Alimentare, Rome, Italy
3. Department of Pathobiology, Faculty of Veterinary Medicine, Garmsar Branch, Islamic Azad University, Garmsar, Iran
4. Department of Pathobiology, Faculty of Veterinary Medicine, Garmsar Branch, Islamic Azad University, Garmsar, Iran

Background and Aim:The Escherichia coli strains carrying stx and EHEC-hlyA (also designated ehxA) are named enterohemorrhagic E. coli (EHEC). EHEC strains are mostly associated with severe infections in humans and with outbreaks. In the present study we investigated the occurrence of Escherichia coli strains harboring the gene encoding enterohemorrhagic E. coli hemolysin in cattle and the association of this gene with various diarrheagenic Escherichia coli (DEC) pathotypes

Methods:First, a total of 452 E. coli isolates were screened for EHEC-hlyA gene by PCR, and then they were characterized for the phylogenetic groups and the presence of the major virulence genes of different DEC pathotypes including stx, eae, estA, elt, cnf, ipaH, aggR, astA and other genes.

Results:In total, 25 virulence gene profiles were observed in 54 EHEC-hlyA+ isolates that reflect a considerable heterogeneity. The EHEC-hlyA+ strains were mostly associated with EHEC (72%), while only 7.4% were enteropathogenic E. coli (EPEC). We also showed the presence of estA gene of enterotoxigenic E. coli (ETEC) in 6 isolates (11.1%). Interestingly, two of the estA+ strains showed hybrid pathotypes with one carrying eae/estA (EPEC/ETEC), and the other one stx2/astA/estA (EHEC/ETEC). All stx-/eae+ strains carried O island 57 (OI-57) that may indicate these to be the progenitors of EHEC or strains losing stx. The most prevalent phylogroup was B1 (61.1%), but the most heterogenous strains including the hybrid strains belonged to A phylogroup.

Conclusion:Overall, our results indicate that cattle EHEC-hlyA encoding E. coli isolates consist of diverse diarrheagenic strains with the possible existence of hybrid pathotypes.

Keywords:EHEC-hly, E. coli, Pathotypes, Phylogroups, Hybrid

**P1126 - 752: BRUCELLOSIS IN HOSPITALIZED PATIENTS BY BACTEC-MYCO/F BLOOD
CULTURE IN TEHRAN 2013-2015**

Bahareh Abniki¹, Bizhan nomanpour², R.Yaghoubi³, M.Yaghoubi³

1. Microbiology Dept. Azad University –Damghan
2. Microbiology Dept. Kermanshah University Medical of Sciences
3. Aramesh clinical Lab. Tehran-Iran

Background and Aim: Brucellosis, as multi-faces illness, is a persistent zoonotic disease .Outbreak of brucellosis is come to scenes in Iran. Misdiagnosis of brucellosis is not only public health problems also is life-threatening. We survey BacTec-Myco/F medium, by blood, ascites, CSF and synovial fluid inoculation from hospitalized patients with unknown origins of fever accepted to the northern Tehran hospitals from April 2013 to April, 2015.

Methods: Blood, CSF, Ascites , synovial fluid and other body fluids specimens had come to the Aramesh Clinical Lab. For detecting of sources of febrile hospitalized patients were cultured on Bactec Myco/F . Inoculated media by syringes were placed in BACTEC9050 system. Vials were considered negative after 6 weeks. Gram staining, oxidase and catalase tests and finally, IS711 PCR were used for genus identification.

Results: Out of 213 specimens; 157 (74.76%) blood, 23 (10.80%) CSF, 19 (7.87%) synovial fluid and 14 (6.57%) other specimens. Gram negative coccobacilli were recovered from 45 (21.13%) vials and 16 cases were confirmed by catalase , oxidase and PCR as *Brucella* sp. Duration of positive Culture were 13 to 30 days .

Conclusion: Using BACTEC-MYCO/F will be beneficial for febrile patients with unknown origins. Brucellosis were 35.56 % (16/45 cases) of causative agents. Using BACTEC-MYCO/F is cheaper and more sensitive than homemade media (more than 20%). In addition, these results indicate the necessity of designing faster and molecular diagnosis methods.

Keywords: Brucellosis, BACTEC, Myco/F medium, hospitalized patient

**P1127 - 806: INVESTIGATES THE EPIDEMIOLOGICAL SITUATION OF PATIENTS WITH
HYDATID CYST IN MAZANDARAN PROVINCE IN 2014**

Kamran Molaei¹, Kamran Molaei ghara², seyed mohammad hoseini³, mehdi vahidi rad⁴

1. -
2. DVM student of Veterinary Medicine, Faculty of Veterinary Medicine, Young Researchers and Elite Club, Babol branch, Islamic Azad University, Babol, Iran
3. Assistant Professor Department of Pathobiology, Faculty of Veterinary Medicine Islamic Azad University of Babol
4. DVM student of Veterinary Medicine, Faculty of Veterinary Medicine, Young Researchers and Elite Club, Babol branch, Islamic Azad University, Babol, Iran

Background and Aim:Hydatidosis is considered as an important parasitic disease, common to humans and animals which caused by the larval stage of *Echinococcus granulosus*. This disease has a worldwide distribution that annual damage in health economics in veterinary and medical industry. Recognizing Epidemiological aspects of the disease is essential to control and prevention this disease. This study was conducted to determine the epidemiological status of patients with hydatid cyst, admitted to the hospitals of Mazandaran province in 2014.

Methods:This study was conducted retrospective cross-sectional. In this study, medical records of patients with hydatid cyst, who were admitted in Mazandaran hospitals in 2014, were studied. Patients were evaluated according to personal characteristics, including gender, age, occupation, place of residence and affected organs.

Results:among 8 patients, 5 patients (62.5%) were female, and 3 patients (37.5%) were male, and the highest prevalence rate (37.5%) is in the age group 40-50 years. Infection in housewives was higher than other occupational groups (50%), and the percentage of patients living in rural and urban were equal each other (50%). The affected Organs, liver with 50% (4 cases) and the lung with 50% (4 cases) were the most.

Conclusion:Because in this study, 62.5% of patients with hydatid cyst were female, and housewives are more than other occupational groups diagnosed with cysts, it is possible, more contacts with vegetables contaminated with parasitic eggs, is the most important cause of pollution.

Keywords:hydatid cyst, Epidemiology, Iran, Mazandaran

**P1128 - 818: MOLECULAR AND HISTOPATHOLOGICAL STUDY OF HELICOBACTER
PYLORI INFECTION IN THE BODY OF STOMACH OF STRAY CATS IN AHVAZ**

Simin Khalaf deris¹, Annahita Rezaie ², Naghmeh Moori Bakhtiari ³, Bahman Mosalla Nejad ⁴

1. Graduated of doctor of veterinary medicine, faculty of veterinary medicine, Shahid Chamran University of Ahvaz, Ahvaz, Iran.
2. Associate professor of pathobiology department, faculty of veterinary medicine, Shahid Chamran University of Ahvaz, Ahvaz, Iran.
3. Assistant professor of pathobiology department, faculty of veterinary medicine, Shahid Chamran University of Ahvaz, Ahvaz, Iran.
4. Associate professor of clinical sciences department, faculty of veterinary medicine, Shahid Chamran University of Ahvaz, Ahvaz, Iran.

Background and Aim: Helicobacter pylori infection is one of the most common bacterial infections in humans around the world. According to the possibility of transmission of infection from cats to humans, the aim of this study was presence determination of helicobacter pylori infection in body of stomach in stray cats in Ahvaz.

Methods: The biopsies were taken from the body of stomach mucosa and submucosa of 30 apparently healthy adult stray cats for molecular analysis and all layers for histopathological evaluation. The presence or absence of Helicobacter pylori were identified by using polymerase chain reaction (PCR). Mucosal lesions were evaluated by examination of sections stained by haematoxylin and eosin and also distribution of bacteria existence were immunohistochemically investigated.

Results: The presence of Helicobacter pylori in the body of stomach of 12 cats (40 percent) were detected by PCR. Histopathological changes in the lamina propria included mild to moderate epithelial injury, fibrosis, mononuclear inflammation accompanied by the presence of neutrophils and eosinophils and severe lymphoid follicular hyperplasia. In immunohistochemically study, 5 samples were degreed sever infection, which bacteria were visible in the cytoplasm of parietal cells of body part of stomach, 4 and 3 samples were respectively showed moderate and mild infection.

Conclusion: According to relatively high percent of helicobacter pylori in stomach of Ahvaz stray cats and presence of lesions in stomach that may be related to helicobacter infection and zoonotic importance of helicobacter pylori, more studies in the field of treatment and prevention are highly recommended more than past.

Keywords: Cat, helicobacter pylori, stomach, Immunohistochemistry, Ahvaz.

**P1129 - 834: THE PREVALENCE OF BRUCELLOSIS IN PATIENTS REFERRED TO THE
GHAEM HOSPITAL DURING 2015-2016, MASHHAD, NORTHEAST IRAN**

Mahdis Ghavidel¹, Davood Mansury², Kiarash Ghazvini³

1. PhD student, Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
2. PhD student, Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
3. Associate Professor, Antimicrobial Resistance Research Center, Buali Research Institute, Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Background and Aim: Brucellosis is a widespread zoonosis mainly transmitted from animals such as cattle, sheep, goats and camels through direct contact with blood, placenta, fetuses or uterine secretions, or through consumption of contaminated raw animal products (especially unpasteurized milk and soft cheese). In endemic areas, human brucellosis has serious public health consequences. Aim of study was determined brucellosis's epidemiologic base on laboratory diagnostic in Mashhad City, Northeast Iran.

Methods: This is a descriptive cross sectional study (from September 2015 up to January 2016), the subjects of which are composed of 720 patients (from Ghaem Hospital, Mashhad). In this study the diagnosis of Brucellosis is based on serology (Wright and 2ME test).

Results: During 15 months we had 65 patients with Brucellosis from 720 patients that the incidence of brucellosis was 8.9%. About 55.4% of patients were female and 44.6% male. Two patients (3.1%) were under ten years, 45 patients (69.2%) were 10 to 50 years old, 18 patients (27.7%) were more than 50 years. The most common season was autumn for brucellosis incidence. The rate of brucellosis incidence in spring, summer, autumn and winter was 18.5%, 16.9%, 38.5%, 26.2% respectively. Nearly 40 % of human cases were living in rural and 60 % in urban areas.

Conclusion: Based on our finding, we suggest an improved healthcare system and preventive measures are necessary to decrease the infection of brucellosis. Likely, A high incidence of brucellosis in urban areas may be due to consumption of unpasteurized dairy products such as fresh cheese or unpasteurized milk.

Keywords: Brucellosis, prevalence, Wright, 2ME, Mashhad

**P1130 - 836: A CLINICAL CASE OF CUTANEOUS ANTHRAX IN NORTHEAST IRAN,
OCTOBER 2015**

Mahdis Ghavidel¹, Mohsen Karbalaee zadeh babaki², Hadi Farsiani³, Kiarash Ghazvini⁴

1. PhD student, Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
2. PhD student, Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
3. Assistant Professor, Antimicrobial Resistance Research Center, Buali Research Institute, Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
4. Associate Professor, Antimicrobial Resistance Research Center, Buali Research Institute, Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Background and Aim: Anthrax is a zoonotic disease caused by a bacterium called *Bacillus anthracis*. In humans, it causes a cutaneous, gastrointestinal and inhalation form of disease. The disease is especially common in areas with livestock such as sheep and cattle.

Methods: In this report, the patient was a 52 year old female, who lives in Mashhad. During meat handling, her right hand had a black ulcer with swelling and high itching, and almost a week had passed ever since the creation of this wound. Moreover, she made mention of a cut on her finger by a skull of slaughtered sheep. The woman was hospitalized for 4 days before entering the microbiology laboratory and was treated with antibiotics such as cephalexin, ciprofloxacin and clindamycin. The wound finger was sampled under the hood using a sterile swab. One swab was used for culture on blood agar media and the other swab was used for smear preparation. The plate containing the sample was transferred to the incubator for growth of microorganism under aerobic condition, and the smear was stained using Gram staining.

Results: Prior to the patients entrance into the laboratory, antibiotic therapy was administered in the hospital and as a result, the spores of *B. anthracis* were observed to be very low under the microscope.

Conclusion: The diagnosis of anthrax is very important. If a person with symptoms, such as painless papules along with severe itching that is sometimes surrounded with vesicles on affected areas of the skin, is referred to the laboratory, the disease should be suspected.

Keywords: *Bacillus anthracis*, Cutaneous anthrax, a clinical case, Iran

**P1131 - 866: HIGH PREVALENCE OF BRUCELLA INFECTION IN FREE RANGING
CHICKENS (GALLUS DOMESTICUS) IN SOUTH OF IRAN**

Yasamin Dehghani¹, Mohammad Hossein Hosseini², Mehdi Namavari³

1. Islamic Azad University Damghan-Branch, Iran
2. Razi Vaccine and Serum Research Institute, Shiraz, Iran
3. Razi Vaccine and Serum Research Institute, Shiraz, Iran

Background and Aim: Brucellosis is an important zoonotic disease caused by Brucella species. Iran is an endemic area for this infection. Although there are reports related to survey of brucella infection from domestic animals in Iran, there is no information about the prevalence of this infection in free ranging chickens. Therefore, this study was carried out to determine the seroprevalence of brucella infection in chickens in Iran.

Methods: One hundred and ninety seven blood samples were collected from local chickens in Fars province in south of Iran. Sera antibodies were tested for Brucella genus using slide agglutination by rose bengal test and tube agglutination test (TAT) by 2-mercaptoethanol, for the presence of antibodies against Brucella genus

Results: From 197 serum samples 18 samples (9.1%) were positive in RBPT, and 17 samples (8.6%) were positive by Wright test. The difference between two testes is considered to be not statistically significant.

Conclusion: Results of this study revealed the high prevalence of Brucella infection in chickens in Fars province especially when compared with the incidence in other countries. Chickens are cosmopolitan animals and serve as a food source for human and other animals. The prevalence of Brucella infection in chickens is a good indicator of the prevalence of Brucella in the soil because chickens feed from the ground. The results obtained assure the significance of infected chicks, their eggs and droppings in disseminating brucellosis for man and animals.

Keywords: Brucellosis, zoonotic, chickens, rose bengal test

**P1132 - 902: DETERMINATION OF PREVALENCE OF SARCOCYSTIS PARASITE IN
HAMBURGER SAMPLES DISTRIBUTED IN RASHT, IRAN USING PCR METHOD**

Hale Akbari¹, leila manafi², mojtaba bahreh³

1. Ms Health and Food Safety, Zanzan University of Medical Sciences, Zanzan
2. Phd Food Quality Control, Urmia University, Urmia
3. Ms Health and Food Safety, Shahid sadughi Yazd University of Medical Sciences, Yazd

Background and Aim: Hamburger is a popular type of fast foods produced and consumed all over the world. It is possible to be infected by zoonotic parasites. Sarcocystosis is one of the common zoonotic diseases caused by the parasites of genus Sarcocystis. The present study describes the prevalence rate of Sarcocystis parasite in hamburgers in Iran, using PCR.

Methods: Method: 30 raw hamburger samples were randomly purchased from supermarkets and street food sellers located in Rasht City, north Iran. DNA was extracted by salting-out method. To identify Sarcocystis and by using specific primers, fragment of genomic DNA (18S rRNA) was amplified and results of electrophoresis showed the polymerase chain reaction (PCR) product with about 953 bp in length indicating presence of the Sarcocystis genus.

Results: Result: PCR analysis showed that 81.2% of all the hamburger samples were infected with Sarcocystis genus.

Conclusion: The people who consume semi-cooked hamburger must be trained about the life cycle, public health importance and pathogenicity of this parasite. More detailed studies are needed to describe the distribution pattern and species identification of Sarcocystis in other meat products. Detailed studies should also be designed, in future, to achieve more effective and applied approaches for inactivation of this parasite in hamburgers.

Keywords: prevalence, Sarcocystis, PCR, hamburger.

**P1133 - 962: INVESTIGATES THE EPIDEMIOLOGIC SITUATION OF PATIENTS WITH
LEPTOSPIROSIS IN MAZANDARAN PROVINCE IN THE YEAR 2014**

Kamran Molaei¹, Kamran Molaei ghara², seyed mohammad hoseini³, mehdi vahidi rad⁴

1. -
2. DVM student of Veterinary Medicine, Faculty of Veterinary Medicine, Young Researchers and Elite Club, Babol branch, Islamic Azad University, Babol, Iran
3. Assistant Professor Department of Pathobiology, Faculty of Veterinary Medicine, Babol branch, Islamic Azad University, Babol, Iran
4. DVM student of Veterinary Medicine, Faculty of Veterinary Medicine, Young Researchers and Elite Club, Babol branch, Islamic Azad University, Babol, Iran

Background and Aim: Leptospirosis is an infectious disease common to humans and animals which is prevalent in nearly all parts of the world, especially in warm, tropical and subtropical regions and also in hot and humid areas. Spread of disease conditions, provided, often in the Northern provinces of Iran, bordering the Caspian in particular, due to having mild and wet weather. The disease in developing countries, like Iran, is considered as an occupational disease, and it occurs more in agriculture, ranchers, and fishermen, in the warm seasons.

Methods: This study was conducted, retrospective cross-sectional. After reviewing medical records, patients with leptospirosis, who were admitted in hospitals of Mazandaran province, in 2014, and 36 samples from collected serums were assessed with two validated diagnostic methods, ELISA and immunofluorescence. I also analyzed the demographic characteristics of the patients.

Results: among 36 patients admitted to hospitals in Mazandaran province, the majority of patients, 12 patients (33.3%) were related to Qaemshahr city, and from total number of patients, 8 patients (22.2%) were female, and 28 (77.8 %) were male, and the highest prevalence rate (41.7%) are in the age group 40-20 years. Infection in paddy (55.5%) was higher than any other occupational group, and 27 patients (75%) of patients living in rural areas, and the largest outbreak was in May (36.1%).

Conclusion: Given that the largest percentage of outbreaks in people who are somehow involved in paddy And the prevalence of the disease when the rice planting season matches conclude that the prevalence of Mazandaran paddy leptospirosis closely related.

Keywords: Leptospirosis, epidemiology, Mazandaran

**P1134 - 978: EVALUATION OF GENUS HELICOBACTER INFECTION IN THE ORAL
CAVITY AND STOMACH OF STRAY CATS IN AHVAZ**

Simin Khalaf deris¹, Annahita Rezaie ², Naghmeh Moori Bakhtiari³, Bahman Mosalla Nejad ⁴

1. Graduated of doctor of veterinary medicine, faculty of veterinary medicine, Shahid Chamran University of Ahvaz, Ahvaz, Iran.
2. Associate professor of pathobiology department, faculty of veterinary medicine, Shahid Chamran University of Ahvaz, Ahvaz, Iran.
3. Assistant professor of pathobiology department, faculty of veterinary medicine, Shahid Chamran University of Ahvaz, Ahvaz, Iran.
4. Associate professor of clinical sciences department, faculty of veterinary medicine, Shahid Chamran University of Ahvaz, Ahvaz, Iran.

Background and Aim: Helicobacter is important due to its role in gastric disorders in human and other animals and also zoonotic capability so this study was designed to determine the presence of genus helicobacter in the oral cavity and stomach of stray cats in Ahvaz.

Methods: Samples were taken from saliva and three different parts of stomach (fundus, body and antrum) of 30 cats for molecular and histopathological evaluation. PCR was carried out for detection of helicobacter in the mentioned samples. Probable lesions in stomach were studied using section stained by haematoxylin and eosin and localization of bacteria evaluated by immunohistochemistry staining. Semi quantitative results of microscopic parameters in three parts of stomach were statistically analyzed.

Results: Genus helicobacter were detected in 53.3%, 76.6%, 73.3% and 53.3% of saliva, fundus, body and antrum respectively, by PCR. In the histopathological analysis, in lamina propria fibrosis and infiltration of lymphocytes and plasma cells in lamina propria of body and antrum of stomach, there were significant differences between Helicobacter positive and negative ($P < 0.05$). Bacteria were seen immunohistochemically in the cytoplasm of parietal cells of body part of stomach and with low rate in fundus and also were colonized in the lumen of pyloric glands in antrum.

Conclusion: The present study showed high prevalence of genus helicobacter in saliva and stomach tissue of stray cats in Ahvaz so its importance in the public health is considered more than ever.

Keywords: Cat, saliva, stomach, PCR, Histopathology, Immunohistochemistry.

**P1135 - 1094: STUDIES ON SALMONELLA INFECTIONS IN LAYING POULTRY FARMS
AROUND QOM CITY**

Amir Paksayeh¹, Hadi Haghbin Nazarpak²

1. Dvm Student of Veterinary Medicine Faculaty, Garmsar Branch, Islamic Azad university, Garmsar, Iran
2. Department of clinical science, Faculaty of Veterinary Medicine, Garmsar branch, Islamic Azad university, Garmsar, Iran

Background and Aim:Salmonella is a zoonotic disease in the world is economically important. Different Salmonella serotypes distribution in a geographic region varies by region. This study describes the prevalence of Salmonella in poultry laying in Qom (pullets and adults) by biochemical tests.

Methods:The aim of this study was to isolate Salmonella serovars and also to determine the prevalence of infection in egg-laying flocks in Qom province for the first time. Fecal samples were obtained from 20 farms and pooled before culture. For this purpose, a total of 50 samples were taken from each farm and each 10 samples pooled and cultured according to the OIE protocols. All suspect isolates were checked by means of conventional biochemical tests.

Results:In 1000 samples tested, 26 isolates from 2 farms were confirmed belonging to Salmonella serovars based on biochemical diagnosis. Therefore the prevalence were determined as 2.6 % in samples and affected only 10 % of farms in Qom province.

Conclusion:This study has showed the presence of Salmonella in poultry chickens in Qom especially in egg-laying pullets. These findings are important for the poultry industry and people's health especially because of the zoonotic nature of salmonellosis.

Keywords:Biochemical tests, Poultry laying, Qom, Salmonella, Zoonotic

**P1136 - 1133: ISOLATION & IDENTIFICATION OF MYCOBACTERIUM TUBERCULOSIS
COMPLEX BACTERIA OF QOM PROVINCE FROM TUBERCULIN POSITIVE CATTLE
AND RODENTS FROM INFECTED CATTLE FARMS**

Ali Reza Ahmadi¹, Keshavarz R.², Barani S. M.³, Hoseini M.⁴, Moghimi A. H.⁵, Mosavari N.⁶, Aref
Pajouhi R.⁷, Bayat A.⁸

1. Qom Branch of Iran Veterinary Organization
2. Agri Culture research and education organization.Razi institute. Karaj. Iran
3. Qom Branch of Iran Veterinary Organization
4. Qom Branch of Iran Veterinary Organization
5. Qom Branch of Iran Veterinary Organization
6. Agri Culture research and education organization.Razi institute. Karaj. Iran
7. Agri Culture research and education organization.Razi institute. Karaj. Iran
8. Qom Branch of Iran Veterinary Organization

Background and Aim:The Mycobacteria grouped in the Mycobacterium tuberculosis complex are characterized by 99.9% similarity at the nucleotide level and identical 16SrRNA sequences but differ widely in terms of their host tropisms, phenotypes, and pathogenicity. Between 2011-2014 this study was conducted to characterize Mycobacterium tuberculosis complex isolates in tuberculin positive cattle of Qom Province. 137 lymph node specimens of collected and cultured by standard methods. In order to Mycobacterium characterization, tuberculin positive samples were examined by PCR. According to results Mycobacterium Tuberculosis was isolated from 22 samples and all of them had IS6110 in their genome thus they were belong to Mycobacterium Tuberculosis complex. Differentiating among Mycobacterium Tuberculosis members is important as it has health implications.

Methods:This study include Lymphatic Node(Mezantric, Medastinal, Retropharengal and other)Of 137 Tuberculin PositiveCow in Tuberculin Test Of Veterinary Organization in Dairy farm of Qom province

Results:According to results Mycobacterium Tuberculosis was isolated from 22 samples and all of them had IS6110 in their genome thus they were belong to Mycobacterium Tuberculosis complex.

Conclusion:Differentiating among Mycobacterium Tuberculosis members is important as it has health implications.

Keywords:Isolation, Qom, tuberculin positive, PCR

P1137 - 1156: EVALUATION OF PREVALENCE AND FERTILITY RATES OF HYDATID CYSTS IN CATTLE AND SHEEP SLAUGHTERED DURING 2013 AT BOJNOURD ABATTOIR

Mitra Salehi¹, Reza Besharati²

1. Vector-borne Diseases Research Center, North Khorasan University of Medical Sciences, Bojnourd, Iran
2. Vector-borne Diseases Research Center, North Khorasan University of Medical Sciences, Bojnourd, Iran

Background and Aim: Hydatidosis is one the most important parasitic zoonotic diseases that is caused by the larval stage of *Echinococcus granulosus*. This study was undertaken to evaluate the prevalence and the fertility of hydatid cyst in slaughtered sheep and cattle in Bojnourd, North Khorasan Province.

Methods: this descriptive cross-sectional study during 2013, 2343 animals (1673 cattle and 670 sheep) were examined in Bojnourd abattoir. Cysts were collected and information about age, gender and organ involvement were recorded, then sent to laboratory. Fertility of cysts was assessed by examining the cyst fluid for the presence of protoscolices. Chi-square test was used to determine the significant differences between the frequency of hydatid cyst and other variables.

Results: Among 1673 cattle and 670 sheep, 6.75 and 5.52 % were infected with hydatid cyst, respectively. The organ distribution of hydatid cyst in cattle was 3.29% in liver and 6.09% in lung. In sheep, hydatid cysts were recovered from 5.52% of the liver and 4.62% of the lung. The highest and lowest rate of fertility was observed in pulmonary cysts of sheep and pulmonary cysts in cattle. The significant differences was observed between the age of cattle and prevalence rate ($p < 0.05$). Hydatidosis was more prevalent in males than females.

Conclusion: In regards to high rate of hydatid cysts in this area, control programs and the importance of sheep in public health should be noted.

Keywords: Hydatid cyst, slaughter animals, prevalence and fertility.

P1138 - 1199: FIRST REPORT OF SALMONELLA NEWPORT FROM DAIRY HERDS IN IRAN

Dr.Masood Rahmani¹, Dr.Mohamadreza Mahzounieh², Mahshad Shahmoradi³, Milad Parchami⁴,
Dr.Rasool Ahmadi⁵, Dr.Taghi Zahraie⁶

1. Doctor of veterinary medicine and manager at Arian Dam , Isfahan ,Iran
2. Department of Immunology and microbiology, Faculty of Veterinary, University of Shahrekord,Iran
3. Researcher at Arian Dam, Isfahan, Iran
4. Student of Faculty of Veterinary Medicine, University of Shahrekord, Iran
5. CEO at Arian Dam, Isfahan, Iran
6. Department of Immunology and microbiology, Faculty of Veterinary, University of Tehran, Iran

Background and Aim:The emergence of multiple antibiotic-resistant strains of Salmonella Spp. should be of great concern to the public. Among more than 2300 Salmonella serotypes, S. Newport was appeared in dairy cattle herds from 1998 in some United States farms and spread to other farms and countries.

Methods:samples were collected from bulk tank milk, feces and milking system filters. Samples were divided into two groups. First group enriched with lactose broth enrichment media and second group directly used in PCR experiment. One ml of each sample were centrifuged and sediment collected for DNA extraction. All DNA's samples were extracted by DNA extraction kit (Gene All Cell SV). PCR reaction was done using invA gene specific primers. PCR products electrophored in 1.5% agarose and stained with greenwiewer and visualized under UV light. Positive cultures were test by biochemical and serological methods. The O and H antigens were determined by specific antibodies.

Results:Nineteen percent of samples of first group were positive but in second group there wasn't any positive sample. The result showed the S. newport as predominant serotype among samples

Conclusion:The presence of S. newport was confirmed in dairy cattle in Isfahan for the first time. . This serotypes substitute to widespread S.dublin and S.typhimurium. Multiple antibiotic-resistant is the common characteristic of these emerging bacteria. This serotype was previously reported in chicken in Iran but this is the first report in dairy herds. Spreading from carrier cattle's raw milk may be has a public health concern.

Keywords:Salmonella Newport, Dairy Cattle, Iran

**P1139 - 1201: CANINE LEISHMANIASIS, A SPREADING ZOONOSIS IN ALBORZ PROVINCE
: A RAPID RELIABLE DIAGNOSTIC TEST IS NEEDED**

Kasra Esmaeilnia¹

1. Razi Vaccine and serum Research Institute

Background and Aim: Canine Leishmaniasis, a spreading zoonosis in Alborz Province : a rapid reliable diagnostic test is needed

Methods: Leishmaniasis is an endemic arthropod-borne zoonotic disease in Middle East. Its most important source are dogs and wild rodents and the vectors are Psychodidae (sand flies) in Iran

Results: Iran always has been very interesting for WHO because of high prevalence of zoonotic cutaneous Leishmaniasis (ZCL) all over the country and also focal prevalence of Kala Azar (visceral Leishmaniasis) in North-West province (Ardebil). About 30 years ago, a wide research started in Razi Institute for producing the best kind of killed vaccine against ZCL and clinical trials on animal models and then man, that took about 2 decades

Conclusion: So, there were many studies in culture, antigen preparing and frequent assays of it that is continuing in some kinds but unfortunately, the veterinary aspects of Leishmaniasis has not focused very well. Microscopic method only is effective in cutaneous forms, but it is very rare in dogs. The visceral infection is common in dogs, but it's not simple to have proper specimen to test. Veterinary services do not focus on this disease and the human health system has not enough authority and budget to look after infected dogs, so the disease has been neglected in epidemiological aspects.

Keywords: Canine Leishmaniasis, Rapid test, Alborz Province

P1140 - 1205: DIAGNOSIS OF GLANDERS BY CF TEST

Maryam Mehraban¹, Nader Mosavari², Ali Purtaghi³

1. Department of Microbiology, Faculty of Sciences, Islamic Azad University, Karaj, Alborz
2. Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO)
3. Department of Microbiology, Faculty of Sciences, Islamic Azad University, Karaj, Alborz

Background and Aim: Glanders is one of the contagious infectious diseases in solipeds and carnivores maybe infected when consumption of infected meat. Humans also maybe infected in closed contact with infected horses. Causative agent of the disease is a Gram-negative bacteria called *Burkholderia mallei*. One of the important points of the control and eradication program is diagnosis of infected horses with high sensitivity and specificity, so aim of this research is based on diagnosis of infected horses by CF Test.

Methods: One hundred serum samples submitted to the Razi Reference laboratory and aliquoted with 1/5 veronal buffer. Then 25 microliters of five serial dilutions prepared at 96 well plates with sample serums. After that 25 microliters of *Burkholderia mallei* antigen were added to all the wells. Then 25 microliters complement added to the wells for 90 minutes at 37 degree. Then haemolytic system added to all wells for 30 minutes at 37 degree and centrifugate at 3000 RPM.

Results: Three positive out of 100 samples obtained with this technique.

Conclusion: CF test is the first technique which recommend by OIE reference laboratory because higher sensitivity and specificity at compare with other tests more than %90.

Keywords: Glanders, *Burkholderia mallei*, CF test

P1141 - 1208: DIAGNOSIS OF GLANDERS BY ELISA

Maryam Javanmardi¹, Nader Mosavari², Ali Pourtaghi³

1. Department of Microbiology, Faculty of Sciences, Islamic Azad University, Karaj, Alborz
2. Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO)
3. Department of Microbiology, Faculty of Sciences, Islamic Azad University, Karaj, Alborz

Background and Aim: Glanders is one of the contagious infectious diseases in solipeds and carnivores maybe infected when consumption of infected meat. Humans also maybe infected in closed contact with infected horses. Causative agent of the disease is a Gram-negative bacteria called *Burkholderia mallei*. One of the important points of the control and eradication program is rapid diagnosis of the disease, so aim of this research is based on diagnosis of infected horses by ELISA Test.

Methods: Two hundred serum samples submitted to the Razi Reference laboratory and aliquoted with 1/100 PBS-T solution. Then 96 well ELISA plates coated overnight by 100 microliters of 10 micrograms per liter solution of *Burkholderia mallei* antigen. All the wells washed three times with PBS and Bovine Albumine used as coating buffer. Then 100 microliters of samples located at two wells and remained for half an hour and washed three times. Then 1/10000 dilution of anti horse were conjugated with horse radish peroxidase added to all the wells for half an hour and washed again. Then TMB added to all the wells for 10 minutes at dark room and after finishing process with 2% of Hydrochloric acid, results obtained with ELISA reader with OD 450 nm.

Results: Three positive out of 200 samples obtained with this technique.

Conclusion: ELISA is the second technique which recommend by OIE reference laboratory because this method have a reasonable sensitivity and specificity.

Keywords: Glanders, *Burkholderia mallei*, ELISA

**P1142 - 1214: GALNDERS KEEPS THREATENING PERSIAN HORSES, DESCRIPTION OF A
FATAL CASE FROM ISFAHAN PROVINCE**

Shojaat Dashtipour¹, Nader Mosavari², Seyyed Kazem Bidouki³, Keyvan Tadayon⁴

1. Payame Noor University, Tehran Shargh Branch, Tehran, Iran
2. Razi Vaccine AND Serum Research Institute
3. Payame Noor University, Tehran Shargh Branch, Tehran, Iran
4. Razi Vaccine AND Serum Research Institute

Background and Aim: Joseph Désiré Tholozan (1820-18970], the French personal physician to Nasreddin Shah, was first to study glanders in Persia (Iran) in the modern-day world. Nevertheless, Glanders remains a serious threat to horses, donkeys and mules populations in the Iranian environment. This paper describes isolation of *Burkholderia mallei* from a glanders miniepidemic in Isfahan province. In summer 2016 a glanderous-suspected mare tracked by Intera-palpebral mallein test was euthanatized and necropsied.

Methods: Nostrils, lungs, lymph nodes and wounds on for/hind legs were swabbed and collected specimens were used to inoculate glycerinated culture media specific for *B. mallei*. Phenotypic (TSI, SIM and motility) and genotypic (BimA-PCR, IS407/flip-PCR) differential tests were performed to identify the culprit bacterium.

Results: Observations made 48 hours post-incubation detected a single bacterial isolate unable to consume sugars and gas production with no motility. In BimA-PCR and IS407/flip-PCR, the isolate produced two fragments of 989 and 250 bp, respectively. These findings confirmed identity of the pathogen as *B. mallei*, as expected.

Conclusion: While isolation of *B. mallei* in Semirom from a reactor horse confirms usefulness of the mallein test in field diagnosis of the disease in the region. Search for tracking source(s) infection and the index case by molecular epidemiology techniques is strongly recommended

Keywords: Glanders, *Burkholderia mallei*, Horse, flip, IS407

P1143 - 1243: REPORT OF STAPHYLOCOCCUS AUREUS FROM DAIRY HERDS IN IRAN

Dr.Mohamadreza Mahzounieh¹, Dr.Rasool Ahmadi², Dr.Masood Rahmani³, Mahshad Shahmoradi⁴,
Milad Parchami⁵

1. Department of Immunology and microbiology, Faculty of Veterinary, University of Shahrekord, Iran
2. CEO at Arian Dam , Isfahan , Iran
3. Doctor of veterinary medicine and manager at Arian Dam , Isfahan , Iran
4. Researcher at Arian Dam , Isfahan , Iran
5. Student of Faculty of Veterinary Medicine, University of Shahrekord, Iran

Background and Aim:Milk is considered a nutritious food because it contains several important nutrients including proteins and vitamins. Conversely, it can harbor several pathogenic bacteria such as *Staphylococcus aureus*. Among the predominant bacteria involved in the food borne diseases, *Staphylococcus aureus* may cause gastroenteritis resulting in the consumption of contaminated milk. This study aimed to determine the presence of *Staphylococcus aureus* in bulk milk tank.

Methods: The samples were collected from different dairy herd around the Isfahan during 1 year(from June 2015 to June 2016). The samples were collected from bulk milk tank. The milk shake for 30 minutes until its temperature came to 4 degree of centigrade. After cooling, samples were took above the tank. We diluted the milk samples and culturing on specific medium and incubated for 48-96 hours. Results were reported according to CFU/mL. The number of *S.aureus* in milk has a wide range. If the number of bacteria was more than 500 CFU/mL, the sample was considered as hazardous. The number of *S.aureus* between 100 to 500 CFU/mL was considered in borderline and less than 100 CFU/mL was considered as

Results: Results of this study showed that about 80% of samples were safe and remain were considered in threshold number. None of samples was contaminated more than threshold.

Conclusion:The presence of *S.aureus* was confirmed in some dairy cattle farms milk in Isfahan. Fortunately if the milk keep in cold chain, and the bacteria won't increased, raw milk may be has a few concern in public health.

Keywords:staphylococcus aureus, dairy cattle, milk, iran

P1144- 1142: New tandem repeat loci suitable for Multi Locus Variable Number Analysis (MLVA) genotyping of *Burkholderia mallei*, an Iranian experiment

1) Faranak Abna Roud-e-helle
Islamic Azad University, Science and Research Branch, Tehran

2) Seyyed Ali Pourbakhsh
Razi Vaccine & Serum Research Institute

3) Nader Mosavari
Razi Vaccine & Serum Research Institute

4) **Keyvan Tadayon**
Razi Vaccine & Serum Research Institute

Asia, Africa, the Middle East and South and Central America are still strongholds of glanders in the world. The very high pathogenicity, lack of commercially available vaccines and also the threats raised from malicious use of *Burkholderia mallei* as a biological weapon, has rendered development of the genotyping methods of *B. mallei* very urgent. Multi Locus Variable Number Analysis (MLVA) has received much attention at the international level as a useful genotyping method. No global consensus has been reached however, over the tandem repeat (TR) loci to be used in this typing system as new polymorphic loci are still reported by different workers.

To assess the genomic diversity of *B. mallei* in Iran, we have examined four local field isolate and one laboratory strain of *B. mallei* against one TR locus namely VNTR13 that was recently found at Razi institute.

PCR optimizations were made to ensure successful amplification of the locus VNTR13. The amplified fragments were subjected to sequencing to determine the size and nucleotide structure.

The VNTR13 comprises a 12 bp TR. Three different alleles were detected among the examined four isolates and one strain. These were 447, 459 and 471 bp in length.

Given that 3 alleles were detected between 5 *B. mallei* isolates/strain studied here, we assume application of this locus in MLVA genotyping protocol is reasonable.

P1145- 1143: An update on *M. bovis* spoligotypes from Iran, knowing where we are standing now

1) Parham Tadayon

Qazvin University of Medical Sciences

2) **Keyvan Tadayon (corresponding author)**

Razi Vaccine & Serum Research Institute

3) Amir Peymani

Qazvin University of Medical Sciences

4) Nader Mosavari

Razi Vaccine & Serum Research Institute

5) Rohollah Keshavarz

Razi Vaccine & Serum Research Institute

6) Rainak Ghaderi

Razi Vaccine & Serum Research Institute

8) Mahya Beigi Hoseinabadi

Qazvin University of Medical Sciences

9) Ali Sarbazi Golezari

Qazvin University of Medical Sciences

Background:

By July 2016, the number of spoligotypes registered with the international Mycobacterium bovis spoligotyping database (<http://www.mbovis.org/spoligodatabase/user-database-output.php>) reached to 2,389. So far 23 *M. bovis* spoligotypes have been characterized in Iran close to 1% of all the deposited types in the database. There is no doubt that SB0120, the spoligotype representing *M. bovis* BCG, the famous vaccine strain of tuberculosis, is the ancestral genotype of *M. bovis* population in Iran.

Scope:

In order to update population genetics of *M. bovis* in Iran in the light of most recent findings, we have re-visited the international *M. bovis* spoligotyping database.

Materials & Methods:

A minimum spanning tree holding all the reported types from across the world was produced using BioNumerics. Frequency and position of Iranian types within the tree was analyzed.

Results & Discussion:

It is a well-documented fact that *M. bovis* in Iran is very homogenic, whether this observation reflects local evolution of clonal complex/complexes in the region, we assume much further work is needed.

Keywords:

Mycobacterium bovis, spoligotyping, database, Iran

P1146- 1144: Detection of *bla*CTX-M Gene in ESBL-producers *Escherichia coli* Strains Isolated from Urine Specimens in Preschool Children, Jahrom, Iran

Dehghani Aliakbar¹, Rezaeian Abbasali*², kargar jahromi Zahra³, Saadat Sareh⁴, Mardaneh Jalal⁵

1.Department of Microbiology, Student in Islamic Azad University, Jahrom, Iran

2.Department of Microbiology, Professor in Islamic Azad University, Jahrom, Iran

3.Zoonosis Research Center, Jahrom University of Medical Sciences, Jahrom, Iran

4.Microbiology Department, Islamic Azad University, Jahrom Branch (the member of young scientific research club of Islamic azad university of jahrom), Jahrom, Iran

5.Department of Microbiology, School of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran.

Background: Multidrug resistance is now emerging worldwide at an alarming rate among gram negatives, causing both community acquired and nosocomial infections. The goal of this study was screening and confirmation ESBL-producers and detection *bla*CTX-M gene in ESBL-positive *Escherichia coli* strains isolated from urine specimens by PCR assay.

Materials and methods: In this cross-sectional study, *Escherichia coli* isolated consecutively from urinary tract infections (UTI) during 9 month (2014-2015) in Jahrom (IRAN) were tested. Cultures were done on microbiological media and plates were kept under incubation at 35-37°C for 16 to 18 hrs. The isolates were identified as *E. coli* based on **manual morphological and biochemical tests**. Antimicrobial susceptibility testing (disc diffusion) and ESBL detection was performed according to CLSI 2014 guidelines. The *bla*_{CTX-M} gene was detected in the isolates by polymerase chain reaction (PCR) assay.

Results: In the current study, a total 310 isolates of *E. coli* were isolated and investigated. Among studied isolates 43.87% were ESBL-positive according to standard combined disk phenotypic test. As observed, nitrofurantoin (39.35%) were the most effective antibiotics against ESBL-positive isolates. The results of PCR on *bla*CTX-M gene indicated that 18 (13.23%) of the isolates possess the gene.

Conclusion: Results showed the resistance of ESBL-producers *Escherichia coli* isolates to the nalidixic acid, nitrofurantoin, and ciprofloxacin is a serious public health concern. Epidemiologic studies for presentation of public programs aimed at preventing emergence and dissemination of resistant bacteria in community are vital.

Keywords: urinary tract infection, *Escherichia coli*, ESBL-producer isolates, *bla*CTX-M gene.

P1147- 1145: *Escherichia coli* Causing Urinary Tract Infections (UTIs): Characterization Minimum Inhibitory Concentration (MIC) for Ceftazidime, and Detection ESBL Genes in Isolates

Rezaeian Abbasali¹, Dehghani Aliakbar*², kargar jahromi Zahra³, Saadat Sareh⁴, Mardaneh Jalal⁵

1.Department of Microbiology, Professor in Islamic Azad University, Jahrom, Iran

2.Department of Microbiology, Student in Islamic Azad University, Jahrom, Iran

3.Zoonosis Research Center, Jahrom University of Medical Sciences, Jahrom, Iran

4.Microbiology Department, Islamic Azad University, Jahrom Branch (the member of young scientific research club of Islamic azad university of jahrom), Jahrom, Iran

5.Department of Microbiology, School of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran.

Background: Urinary tract infections (UTIs) to be a major international problem both in terms of morbidity and economic losses. Antibiotic resistant of *Escheriachia coli* is an increasing public health emergency since infections from resistant bacteria are more difficult and costly to treat. The aims of the present study were to investigate the isolation of *Escheria coli* from urine samples in south of IRAN (Jahrom), characterization minimum inhibitory concentration (MIC) for ceftazidime, antimicrobial susceptibility pattern of isolates, and detection ESBL genes.

Materials and Methods: Urine samples of patients suspected to UTIs, were collected and culture was done on clinical microbiology media. **In order to characterization of *Escheriachia coli*, conventional biochemical tests were used.** Antibiotic susceptibility test (AST), MICs, and ESBL detection was performed according clinical and laboratory standards institute (CLSI, 2014) procedures.

Results: In the current study, a total of 585 children suspected to UTI were investigated. *Escherichia coli* strains were isolated from 310 (52.99%) patients consisting of 143 males (46%) and 167 females (54%). One-hundred seventy eight isolates (57.41%) were resistant to ciprofloxacin. All (100%) ESBL(+) isolates displayed resistance to ceftazidime in MIC method (MIC ≥ 4 $\mu\text{g/ml}$). The ESBL-encoding gene (*blaSHV*) was detected in 6 (4.41%) isolates.

Conclusion: These data indicate that multidrug-resistant (MDR) strains of *Escherichia coli* are rising, and fewer antibiotics may be useful for treating UTIs infections causing by this isolate and treatment failures can occur. Routine investigation and reporting of antibiotics susceptibility patterns in patients presenting with UTIs infections is suggested.

Keywords: Urinary tract infections (UTIs), *Escherichia coli*, antimicrobial resistance patterns, MIC of ceftazidime, ESBL-encoding genes.

P1148- 1146: Survey of polymerase chain reaction efficiency in detection of Mycoplasma, Listeria and Brucella in culture negative samples obtain from women with abortion during 1390-93

Maryam Rezaei¹, Elham Goudarzi², Jalil Vand yousefi¹, Nadia Kazemipour³, Naser Harzandi²

- 1- Faculty of dental, Department of Science Azad university Tehran
- 2- Department of microbiology, Azad university of karaj
- 3- Department of microbiology, Azad university of Kerman

Introduction and objective: Misabortion is a result and of numerous causes such as infection. It is clear that bacterial infection due to genital Mycoplasma, Listeria and Brucella can cause septic abortion. A right time diagnosis of these infections can improve women fertility. This study was conducted in order to survey the efficiency of PCR in detecting the specimens with negative culture results in women suffering from septic abortion. We also do this with considering individual variables.

Methods: In this analytical and descriptive study, appropriate samples were collected from a total of 87 women with septic abortion who referred to Karaj hospitals. Samples were cultured into Mycoplasma, Listeria and Brucella specific media. Then the bacterial genus verified by different biochemical tests. PCR test is performed on negative culture cases and SPSS-18 software is used for statistical analysis of datas.

Results: From the total of 87 blood samples, 37 samples (%42.5) were positive for Mycoplasma and Ureaplasma (25c cases) and Listeria monocytogenes (12 cases) with both culture and PCR method. Our result showed no positive cases for Brucella. From the total of cultured specimens, 12 cases (%13.8) were positive and 75 cases (% 86.2) were negative. We performed PCR test for negative cultured results. With PCR method 25 cases (%33.33) showed positive and 50 cases (%66.67) showed negative results. Result also showed a significant statistical relation between PCR test results w3ith recurrent abortion and level of education ($p < 0.05$)

Conclusion: Results show that PCR a more sensitive, esier and faster method in comparison to culture for detecting of bacterial cause septic abortion. So it recommended that using PCR in detecting of this bacterial could be more effective.

Keywords: Septic Abortion, Culture and PCR

P1149- 1147: Study of *Bacillus cereus*, mold, arsenic and lead contamination of imported rice

Farahnaz Mehrabi¹, Nahid Rahimifard^{2*}, Mohamad hadi Dehghani³, Mohamad rasoul Hadiani², Roya Behroozi²

1 .Graduated of Hygiene and food safety, Health faculty, Tehran university of medical sciences, Tehran, Iran

2 .Microbiology Department , Food and Drug Control Laboratories (FDCLs), Food and Drug Laboratory Research center (FDLRC),, Ministry of Health (MOH) , Tehran, Iran

3. Health Environment engineering Department , Health faculty, Tehran university of medical sciences, Tehran, Iran

Background and Aim: Rice is a staple food in Asia, especially in Iran. One of the most widely consumed items *oryza sativa* L. Rice as a staple food and an essential source of hydrocarbons in the diet of several Asian countries, including Iran. 12-year-old Iranian Chamber of Commerce estimates that annual rice consumption per capita has done is 42.5 kg. It is not, then the storage policy and other measures to regulate the market has always had to import rice and our country is one of the main importers of this product. Bacteria, fungus or mold toxins, chemicals and pharmaceuticals and pesticides can contaminate the food to be corruption. Contamination of soil and water environments with heavy metals is a serious problem and is expanding. Admission toxic metals from human activities cause pollution of the soil. In examining the toxicity of various metals and complex system plant - soil, there are many factors related to soil properties, plant characteristics and other factors are environmental. The entry of heavy metals into the food chain and reach a critical concentration, metabolic and physiological adverse effects on living organisms on the leaves. Harmful effects of heavy metals on human health has been proven in many different ways. Exposure to these pollutants cause acute poisoning and chronic disease death very well. Bacterial contamination in rice may be in the process of growing, harvesting and other agricultural processes, such as processing and preparation of the product takes place. *Manndasprzhylvs* and grains are common *fungus Penicillium* which produces mycotoxins pose a danger. *Bacillus cereus* poisoning Drbrnj is also very important and debatable.

To evaluate the necessity of product widely used in the food safety assessment carried out in the country.

Methods : 20 imported rices were studied 3 times on each sample. First stage of sample preparation for microbiological tests carried out. At this point, according to Iranian National Standard Methods for the Examination No. 11602 Microbiology rice is done. The standard *mold* count tests has permitted range cfu / g 10^4 and counting *Bacillus cereus* has permitted range is cfu / g 10^3 . For the heavy metals in rice atomic absorption method (Atomic Absorption Spectrometry) is used. After sample preparation, the data devices to measure the amount of lead and arsenic samples show. Summary measure of lead and arsenic in rice: rice sample collection of samples -digestion -Madh samples -wash containers of lead and arsenic (each in separate steps) standard curve by AAS -custom calibration - validation procedure for each of element the accuracy of the measurement method is based on standard 12968

Result : Tested samples of microbial contamination and *Bacillus cereus* were within the allowable range . And contamination with heavy metals (lead and arsenic) were in the range of Iranian national standard

Conclusion : The results indicate that in the case of imported rices microbial contamination and pollution by heavy metals lead and arsenic is less than the allowable range and can be used.

KeyWords: *Bacillus cereus*, mold , arsenic , lead, imported rice

P1150- 1148: A comparison of rate of prevalence of Coagulase- Negative Staphylococcus infections in the male and female patients referred to surgery and emergency wards (ICU and CCU) of the Chalous hospital

Ghasem sharifian –E - Tutkaleh¹ Esmaeil ghorbanalinezhad*²

¹ -M.A. student of Microbiology, Faculty of Biosciences, Islamic Azad University of TONEKABON Branch, Iran.

¹ - Faculty member of Microbiology department, Faculty of Biosciences, Islamic Azad University of TONEKABON Branch, Iran.

Background and objective: Coagulase- negative staphylococci reside in all open organs of body. In the past, they have been counted as weak non-pathogenic factors and secondary infectious factors. It has been passing more than two decades since appearance of Coagulase-Negative Staphylococci as the opportunistic pathogens, especially in the individuals with immunodeficiency and patients with implant. Increasing incidence of hospital infections resulted from these bacteria propounds their identification in the limit of species. Objective of performance of this study was to identify strains of Coagulase – Negative Staphylococci isolated from 100 clinical samples through culturing and biochemical methods.

Materials and methods: 100 samples of the Coagulase – Negative Staphylococci, including samples of urine, skin and ulcer from man and woman patients referred to Ayatollah Taleghani hospital of CHALOUS were isolated from various clinical samples. Phenotypic methods, including culture in blood Agar, Manitol salt agar and DNase as well as biochemical tests, including Oxidase and Catalase test and usage of Bacitracin, Furazolidone and Novobiocin discs were studied.

Results: In this research, we could isolate and identify 35 isolates of the Coagulase Staphylococcus from the desired places through phenotypic methods which the highest percentage of infection was observed in the urinary tracts of women and skin of men.

Discussion:

Due to existence of this bacterium in the urinary tracts of women as a natural flora and probability of contamination at the time of occurrence of other diseases, it is, thus, required that the women hospitalized in the hospital to make a special effort for health of this area, and hospitalized factors assist to control this hospitalized infection via teaching to patients as well.

Key words: Prevalence, *Staphylococcus*, Coagulase-Negative, Hospital