Iran's 19th International Congress of Microbiology

نوزدهمین کنگره بین‌المللی

میکروب شناسی ایران

دانشکده پزشکی، دانشگاه علوم پزشکی تهران

۱۳ الی ۱۵ شهریور ماه ۱۳۹۷، تهران، ایران

انجمن علمی میکروب شناسی ایران
Iranian Society of Microbiology

دانشگاه علوم پزشکی ایلام

معاونت بهداشت

یا من اسمهُ دواء و ذکرهُ شفاء

Iran's 19th International Congress of Microbiology

نوزدهمین کنگره بین المللی میکروبشناسی ایران

دانشکده پزشکی،دانشگاه علوم پزشکی تهران

۱۳ الی ۱۵ شهریورماه ۱۳۹۷،تهران،ایران

محور های کنگره:

- عفونت های بالینی و واکسن
- تشخیص و تایپینگ مولکولی میکرو ارگانیسمها
- مقاومتهای میکروبی و مواد ضد میکروبی
- واکسنهای میکروبی
- سرطانها و عفونتهای میکروبی
- متابولیتهای میکروبی و بیماریها
- بیماریهای عفونی نو پدید و بازپدید
- میکروبیوم
- میکروبشناسی غذایی
- میکروبشناسی کاربردی و محیطی
- زئونوزها و میکروبشناسی دامپزشکی
- پروبیوتیک و پربیوتیک ها
- بیوتکنولوژی و نانوتکنولوی میکروبی
- متابولیتهای میکروبی و درمان سرطانها
- میکروبشناسی دهان
- میکروبیولوژی دارویی

با امتیاز باز آموزی

مهلت ارسال مقالات:۱۵ تیر ماه

Tel:+98-21-88632456 Email:congress@ismcongress.ir http://ismcongress.ir

نوزدهمین کنگره بین‌المللی

میکروب شناسی ایران

دانشکده پزشکی، دانشگاه علوم پزشکی تهران

۱۳ الی ۱۵ شهریور ماه ۱۳۹۷، تهران، ایران

Iran's 19th International

Congress of Microbiology

September 2018 4-6 Tehran - Iran

School of Medicine, Tehran University of Medical Sciences

سرشناسه	:	نوزدهمین کنگره بین‌المللی میکروب شناسی ایران (۱۳۹۷ : تهران)
عنوان و نام پدیدآور	:	نوزدهمین کنگره بین‌المللی میکروب شناسی ایران ۱۳ الی ۱۵ شهریور ماه ۱۳۹۷
وضعیت ویراست	:	به کوشش : محمد رضا آشتیانی
مشخصات نشر	:	تهران : رسانه تخصصی، ۱۳۹۷
مشخصات ظاهری	:	۱۲۴ص.
شابک	:	۹۷۸-۶۰۰-۲۹۳-۳۸۵-۰
وضعیت فهرست نویسی	:	فیپای مختصر
یادداشت	:	فهرست نویسی کامل این اثر در نشانی: http://opac.nlai.ir قابل دسترسی است
شناسه افزوده	:	آشتیانی، محمد رضا

نوزدهمین کنگره بین‌المللی میکروب شناسی ایران

به کوشش : محمد رضا آشتیانی

امور اجرایی و بازرگانی : حمید رضا اسکندری

صفحه آرایی و امور هنری : فرزانه وحدت بهروتی

نوبت چاپ : اول/ ۱۳۹۷

شابک : ۹۷۸-۶۰۰-۲۹۳-۳۸۵-۰

تیراژ : ۲۰۰۰

سیصد و نود و ششمین عنوان از مجموعه کتاب‌های جامع رسانه تخصصی

نشانی، خیابان انقلاب، نرسیده به میدان فردوسی، خیابان کندوان، پلاک ۸، طبقه همکف

تلفن : ۶۶۷۳۷۱۳۳- ۶۶۷۳۷۳۳۲- ۶۶۷۳۷۳۰۸- ۶۶۷۳۷۰۷۴- ۰۹۱۲۳۰۴۹۱۰۹

سامانه پیامکی: ۶۶۷۳۷۳۳۲ ۰۲۱ ۳۰۰

پست الکترونیکی : Rasane_takhassosi@yahoo.com وب سایت: Rasanetakhassosi.ir

فهرست مطالب

پیام کنگره

به نام خالق هستی

همکاران گرامی، از اولین کنگره میکروب‌شناسی در دانشگاه علوم پزشکی مازندران در شهر ساری قریب ۲۵ سال می‌گذرد. در این مدت میکروب‌شناسان با همفکری و همکاری یکدیگر بر بسیاری از چالش‌های میکروب‌شناسی غلبه نموده‌اند و تکنیک‌های جدیدی را برای تشخیص، تایپینگ و شناسایی عوامل جدید میکروبی به جامعه پزشکی معرفی کرده‌اند، ولی ما هنوز با چالش‌های متعددی در زمینه میکروب‌شناسی روبرو هستیم که نیاز به همفکری و همکاری همه متخصصین در زمینه علوم پزشکی دارد تا انشاءالله آنها را نیز از میان برداریم.

نوزدهمین کنگره میکروب شناسی که از تاریخ ۱۳ تا ۱۵ شهریور ماه ۱۳۹۷ در شهر تهران برگزار می‌شود فرصت مناسبی است تا نتایج تحقیقات و تجربیات خود را به صورت سخنرانی، ارائه پوستر، شرکت در پانل‌های تخصصی و کارگاه‌های آموزشی در اختیار دیگر همکاران قرار داده در مورد آن‌ها به بحث و تبادل نظر بپردازیم. کنگره امسال بر روی جدیدترین و آخرین دستاوردها در تمام زمینه‌های بیماری‌های عفونی، مقاومت میکروبی، میکروب‌شناسی مواد غذایی، بیماری‌های نوپدید و باز پدید، میکروب‌شناسی بالینی و واکسن‌های میکروبی، بیماری‌های زئونوز و بیوتکنولوژی میکروبی تمرکز دارد. این کنگره همچنین فرصت مناسبی است تا رو در رو و در ملاقات با دیگر محققین به تبادل اطلاعات و بحث در زمینه دستاوردهای جدید علمی میکروب شناسی بپردازیم و زمینه را برای همکاری‌های مشترک آینده فراهم کنیم.

منتظر ملاقات و دیدار شما در این کنگره هستیم.

دکتر محمد مهدی فیض آبادی	**دکتر محمد مهدی اصلانی**	**دکتر عباسعلی ایمانی فولادی**
رییس کنگره	دبیر علمی کنگره	دبیر اجرایی کنگره

ارکان نوزدهمین کنگره بین‌المللی میکروب‌شناسی ایران

۱۳ الی ۱۵ شهریور ماه ۱۳۹۷، تهران، ایران، دانشکده پزشکی، دانشگاه علوم پزشکی تهران

دکتر محمد مهدی فیض آبادی

رییس کنگره

دکتر محمد مهدی اصلانی

دبیر علمی کنگره

دکتر عباسعلی ایمانی فولادی

دبیر اجرایی کنگره

اعضای کمیته علمی بر اساس ترتیب حروف الفبای فارسی

- غلام حسین ابراهیمی پور / دانشگاه علوم پزشکی شهید بهشتی
- حمید رضا ابطحی / دانشگاه علوم پزشکی اراک
- مصطفی اجتهادی فر / دانشگاه علوم پزشکی اراک
- علیرضا احمدی / دانشگاه الزهرا
- محمد تقی اخی/ دانشگاه علوم پزشکی تبریز
- مهرداد آذین / انجمن علوم و فنون میکروبی
- محمد ارجمندزادگان / دانشگاه علوم پزشکی اراک
- محسن ارزنلو / دانشگاه علوم پزشکی اردبیل
- احسان آرین / دانشگاه علوم پزشکی مشهد
- کیهان آزادمنش / انیستیتو پاستور ایران
- محمدرضا اسدی کرم / انستیتو پاستور ایران
- بهزاد اسفندیاری / انستیتو پاستور ایران
- سهیل اسکندری / سازمان غذا و دارو
- داوود اسماعیلی / دانشگاه علوم پزشکی بقیه الله
- سید سعید اشراقی / دانشگاه علوم پزشکی تهران
- محمدرضا آصف / موسسه تحقیقات آفات و بیماریهای گیاهی

- محمد مهدی اصلانی / انستیتو پاستور ایران
- فرشته افتخار / دانشگاه علوم پزشکی شهید بهشتی
- ابوالفضل اکبری / موسسه تحقیقات واکسن و سرم سازی رازی
- علیشا اکیا / دانشگاه علوم پزشکی کرمانشاه
- حسام الدین اکبرین / دانشگاه تهران
- مسعود آل بویه / مرکز تحقیقات و گوارش و کبد بیمارستان طالقانی
- جعفر امانی / دانشگاه علوم پزشکی بقیه الله
- محمد علی آموزگار / دانشگاه علوم پزشکی تهران
- نور امیر مظفری / دانشگاه علوم پزشکی ایران
- محسن امین / دانشگاه علوم پزشکی تهران
- سید محمود امین مرعشی / دانشگاه علوم پزشکی البرز
- محمد آهنجان / دانشگاه علوم پزشکی ساری
- هرمز اورمزدی / دانشگاه علوم پزشکی ایران
- پرویز اولیا / دانشگاه علوم پزشکی شاهد
- غلامرضا ایراجیان / دانشگاه علوم پزشکی ایران
- محمد ایمان عینی / دانشگاه علوم پزشکی تهران
- عباسعلی ایمانی فولادی / دانشگاه علوم پزشکی بقیه الله
- ناصر بادامی / دانشگاه علوم پزشکی تهران
- حمید باغچه سرایی / دانشگاه علوم پزشکی زنجان
- رامین باقری نژاد / موسسه تحقیقات واکسن و سرم سازی رازی
- حمید بدلی / دانشگاه علوم پزشکی مازندران
- پریسا بدیعی / مرکز تحقیقات میکروب شناسی دکتر البرزی
- عباس بهادر / دانشگاه علوم پزشکی تهران
- علی محمد بهروزیخواه / موسسه تحقیقات واکسن و سرم سازی رازی
- محمدرضا بوجاری / دانشگاه علوم پزشکی ایران
- سعید بوذری / انستیتو پاستور ایران
- ایرج پاکزاد / دانشگاه علوم پزشکی ایلام
- امید پژند / دانشگاه علوم پزشکی سمنان
- فاضل پور احمد / دانشگاه ایلام
- بابک پور اکبری / مرکز تحقیقات عفونی اطفال
- فرهاد پور فرضی / دانشگاه علوم پزشکی اردبیل

- هادی پیری دوگاهه / دانشگاه علوم پزشکی اردبیل
- رضا پیله‌چیان لنگرودی / موسسه تحقیقات واکسن و سرم سازی رازی
- مریم تاج آبادی ابراهیمی / دانشگاه آزاد اسلامی
- حسن تاجبخش / دانشگاه علوم پزشکی تهران
- کیوان تدین / موسسه تحقیقات واکسن و سرم سازی رازی
- احمد رضا جباری / موسسه تحقیقات واکسن و سرم سازی رازی
- فرشته جبل عاملی / دانشگاه علوم پزشکی تهران
- علی جزایری مقدس / دانشگاه علو پزشکی سمنان
- سیروس جعفری / دانشگاه علوم پزشکی تهران
- داریوش جهان پیما / سازمان دامپزشکی کشور
- صدیقه جواد پور / دانشگاه علوم پزشکی هرمزگان
- عباس حاج آخوندی / دانشگاه علوم پزشکی تهران
- محبوبه حاج عبدالباقی / دانشگاه علوم پزشکی تهران
- نسرین حاجی سیدجوادی / انستیتو تحقیقات تغذیه ای و صنایع غذایی کشور
- مژده حاکمی والا / دانشگاه علوم پزشکی شهید بهشتی
- جواد حامدی / دانشگاه علوم پزشکی تهران
- اعظم حدادی / دانشگاه آزاد اسلامی
- حزینی / دانشگاه علوم پزشکی تهران
- شیرین حسنی رنجبر / دانشگاه علوم پزشکی تهران
- سید مسعود حسینی / دانشگاه علوم پزشکی شهید بهشتی
- مسعود حسینی / دانشگاه آزاد اسلامی واحد تهران شمال
- نیما حسینی جزنی / دانشگاه علوم پزشکی ارومیه
- مسعود حق خواه / دانشکده دامپزشکی-دانشگاه شیراز
- راحله حلبیان / دانشگاه علوم پزشکی بقیه الله (عج)
- امیر علی حمیدیه / ستاد توسعه علوم و فناوری های سلول های بنیادی
- رضا خاشعی / دانشگاه علوم پزشکی شیراز
- پژواک خاکی / موسسه تحقیقات واکسن و سرم سازی رازی
- محمود خدادوست / دانشگاه علوم پزشکی شهید بهشتی
- سید سجاد خرم روز / دانشگاه علوم پزشکی یاسوج
- سید عبدالمجید خسروانی / دانشگاه علوم پزشکی یاسوج
- آذر دخت خسروی / دانشگاه علوم پزشکی جندی شاپور

- افرا خسروی / دانشگاه علوم پزشکی ایلام
- محمد خلیفه قلی / دانشگاه علوم پزشکی قم
- محمد خلیلی / دانشگاه کرمان
- احمد خورشیدی مال احمدی / دانشگاه علوم پزشکی کاشان
- حسین دبیری / دانشگاه علوم پزشکی شهید بهشتی
- شهریار دبیریان / شرکت صنایع شیر ایران (پگاه)
- داوود دربان ساروخلیل / دانشگاه علوم پزشکی ایران
- علی دل پیشه / دانشگاه علوم پزشکی ایلام
- سمیه دلفانی / دانشگاه علوم پزشکی لرستان
- سید علی دهقان منشادی / دانشگاه علوم پزشکی تهران
- فرحنوش دوست‌دار / دانشگاه علوم پزشکی شهید بهشتی
- صدیقه ذاکری / انستیتو پاستور ایران
- سعید ذاکر بستان آباد / دانشگاه آزاد اسلامی
- رمضان رجب نیا / دانشگاه علوم پزشکی بابل
- امیر رحیمی راد / دانشگاه علوم پزشکی ارومیه
- ناهید رحیمی فرد / آزمایشگاه کنترل غذا و دارو
- مهدی رزاقی ابیانه / انستیتو پاستور ایران
- ایرج رسولی / دانشگاه شاهد
- مهرناز رسولی نژاد / دانشگاه علوم پزشکی تهران
- فرانک رضایی / دانشگاه علوم پزشکی لرستان
- حسین رضایی زاده / دانشگاه علوم پزشکی تهران
- عبدالناصر رفیع / دانشگاه علوم پزشکی تبریز
- رشید رمضان زاده / دانشگاه علوم پزشکی کردستان
- رضا رنجبر / دانشگاه علوم پزشکی بقیه الله
- محمد رهبر / آزمایشگاه مرجع سلامت
- پژمان روحانی / دانشگاه علوم پزشکی شهید بهشتی
- مهدی رئیسی / مجله میکروب شناسی مواد غذائی
- مجید زارع بیدکی / دانشگاه علوم پزشکی بیرجند
- محمد رضا زالی / مرکز تحقیقات و گوارش و کبد بیمارستان طالقانی
- آرمان زرگران / دانشگاه علوم پزشکی تهران
- غلامرضا زرینی / دانشگاه تبریز

- هنگامه زندی / دانشگاه علوم پزشکی یزد
- تقی زهرائی صالحی / دانشگاه تهران
- محمد حسین سالاری / دانشگاه علوم پزشکی تهران
- ماندانا ستاری / دانشگاه علوم پزشکی شهید بهشتی
- ستاره سروش / دانشگاه علوم پزشکی لرستان
- احمدرضا سروش / دانشگاه علوم پزشکی تهران
- جعفر سلیمیان / دانشگاه علوم پزشکی بقیه الله
- سید داور سیادت / انستیتو پاستور ایران
- آرش سیفی / دانشگاه علوم پزشکی تهران
- رضا شاپوری / دانشگاه آزاد اسلامی واحد زنجان
- 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 / دانشکده علوم تبریز
- شهرام شهرکی / دانشگاه علوم پزشکی زاهدان
- محمد حسن شیرازی / دانشگاه علوم پزشکی تهران
- حوریه صادری / دانشگاه علوم پزشکی شاهد
- نور خدا صادقی فرد / دانشگاه علوم پزشکی ایلام
- محمدرضا صالحی / دانشگاه علوم پزشکی تهران
- غلامرضا صالحی جوزانی / انستیتو بیوتکنولوژی کشاورزی
- میترا صالحی سیرجان / دانشگاه آزاد اسلامی واحد تهران شمال
- مصطفی صالحی وزیری / انستیتو پاستور ایران
- محمد رضا صعودی / دانشگاه الزهراء
- سارا صعودی / دانشگاه تربیت مدرس
- محمود صفاری / دانشگاه علوم پزشکی کاشان
- پروانه صفاریان / دانشگاه آزاد اسلامی واحد علوم تحقیقات
- شیلا صفائیان / سازمان غذا و دارو
- حسین صمدی کفیل / دانشگاه علوم پزشکی تبریز

- مروت طاهری کلانی / دانشگاه علوم پزشکی لرستان
- پیام طبرسی / دانشگاه علوم پزشکی شهید بهشتی
- بهمن عابدی کیاسری / موسسه تحقیقات واکسن و سرم سازی رازی
- عباس عبدالهی / دانشگاه علوم پزشکی فسا
- احیا عبدی عالی / دانشگاه الزهرا
- رامین عبیری / دانشگاه علوم پزشکی کرمانشاه
- محمدرضا عربستانی / دانشگاه علوم پزشکی همدان
- حسین عرفانی / وزارت بهداشت، درمان و آموزش پزشکی
- رمضانعلی عطایی / دانشگاه علوم پزشکی بقیه الله
- آتوسا علی احمدی / مرکز تحقیقات گیاهان دارویی دانشگاه شهید بهشتی
- محمد یوسف علیخانی / دانشگاه علوم پزشکی همدان
- ندا علیخانی
- حمید عمادی کوچک / دانشگاه علوم پزشکی تهران
- محمد جواد غروی / دانشگاه علوم پزشکی ایران
- احسان اله غزنوی راد / دانشگاه علوم پزشکی اراک
- سبحان غفوریان / دانشگاه علوم پزشکی ایلام
- حسین فاضلی / دانشگاه علوم پزشکی اصفهان
- بهرام فتح اله زاده / دانشگاه علوم پزشکی تهران
- کامبیز فرقان پرست / دانشگاه علوم پزشکی گیلان
- خسرو فرهی / دانشگاه علوم پزشکی تهران
- 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
- محمد مهدی فیض آبادی / دانشگاه علوم پزشکی تهران
- رایناک قادری / موسسه تحقیقات واکسن و سرم سازی رازی
- مصطفی قانعی / انستیتو پاستور ایران
- کیارش قزوینی / دانشگاه علوم پزشکی مشهد
- ابوالفضل قلی پور / دانشگاه علوم پزشکی شهرکرد
- روحا کسری کرمانشاهی / دانشگاه الزهرا

- روح اله کشاورز / آزمایشگاه تشخیص تحقیق و تهیه توبرکولین، مالئین و یونین
- داود کلانتر نیستانکی / دانشگاه علوم پزشکی کرمان
- محمد کمالی نژاد / دانشگاه علوم پزشکی شهید بهشتی
- هادی کیوان فر / دانشگاه تهران
- غلامرضا گودرزی / دانشگاه علوم پزشکی لرستان
- محمد مهدی گویا / مرکز مدیریت بیماری های واگیر
- پرویز مالک نژاد / دانشگاه علوم پزشکی تهران
- علی مجتهدی / دانشگاه علوم پزشکی گیلان
- اشرف محبتی مبارز/ دانشگاه تربیت مدرس
- سید رضا محبی / دانشگاه علوم پزشکی شهید بهشتی
- محمد رضا محزونیه / دانشکده دامپزشکی- دانشگاه شهرکرد
- مرجان محمدی / انستیتو پاستور ایران
- پریسا محمدی / دانشگاه الزهراء
- فاطمه محمدی پناه / دانشگاه تهران-دانشکده علوم
- حمیده محمود زاده حسینی / دانشگاه علوم پزشکی بقیه الله(عج)
- طلعت مختاری آزاد / دانشگاه علوم پزشکی تهران
- سهیلا مرادی بیدهندی / موسسه تحقیقات واکسن و سرم سازی رازی
- کریم مردانی / دانشگاه علوم پزشکی ارومیه
- ناهید مژگانی / موسسه تحقیقات واکسن و سرم سازی رازی
- سیامک مسعودی / سازمان حفاظت محیط زیست
- زهره مشاک / دانشگاه آزاد اسلامی واحد کرج
- احسان مصطفوی / انستیتو پاستور ایران
- نادر مصوری / موسسه تحقیقات واکسن و سرم سازی رازی
- نسرین معظمی / سازمان پژوهشهای علمی و صنعتی ایران
- مریم مقدم متین / دانشگاه فردوسی مشهد
- 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

- علی میرحسینی / دانشگاه علوم پزشکی بقیه الله
- سید سعید میردامادی / پژوهشکده زیست فناوری سازمان پژوهش های علمی و صنعتی
- مهدی میرزائی / دانشگاه علوم پزشکی شاهرود
- اکبر میرصالحیان / 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 پیرایه / 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
- مجتبی نوفلی / موسسه تحقیقات واکسن و سرم سازی رازی
- محمد نیاکان / دانشگاه علوم پزشکی شاهد
- ایرج نیکوکار / دانشگاه علوم پزشکی گیلان
- مسعود هاشم زاده / موسسه تحقیقات واکسن و سرم سازی رازی
- غلامرضا هاشمی تبار / دانشگاه فردوسی
- مجتبی هدایتی / دانشگاه علوم پزشکی گیلان
- ناصر هرزندی / دانشگاه آزاد اسلامی واحد کرج
- زویا هژبری ماهانی / دانشگاه علوم پزشکی سمنان
- فرزام وزیری / انیستیتو پاستور ایران
- جلیل وند یوسفی / موسسه تحقیقات واکسن و سرم سازی رازی
- امیر هوشنگ الوندی / دانشگاه علوم پزشکی کرمانشاه
- یوسف یحیی پور / دانشگاه علوم پزشکی بابل
- سمیه یسلیانی فرد / دانشگاه علوم پزشکی البرز
- رسول یوسفی مشعوف / دانشگاه علوم پزشکی همدان

اعضای کمیته اجرایی بر اساس ترتیب حروف الفبای فارسی

محمد طه ابراهیمی
فاطمه اتحاد مروستی
آزاده احمدی
زیبا آذرش
سمانه استاد محمدی
سهیلا استاد محمدی
دکتر پرویز افروغ
الناز افشاری
رقیه آقازاده
مینا آقاصفی
آتوسا آقایی
ملیسا اقبال
ایمان اکبرزاده
بهاره اکبری بیرگانی
الهام امجدی
فاطمه امرایی
مریم امیدوارپناه
کیانا امیری
احمد ایادی
سارا بافنده
شیرین باوری
فاطمه بذر افشان
صبا بشری
سمیه بهرامی
الهه تاکی
طاهره تفرشی مطلق
مینا سادات تقوی
سمیه جاسمی
مهناز جعفری
صبا جلالی فر
شیدا جنتی
ساناز حاجی خانی
تینا حسن خانی
سید مصطفی حسینی
سپیده حق نظری
حمید رضا حوری
سارا حیاتی مهر
زهرا خدابنده لو
امیر درب امامیه
امین دهقان
محمدرضا رجب پور
زهرا رحیمی نادی
یاسین رخشانی
رویا رسولی
اکرم رضایی
الهه رضایی
شبنم رویایی
نگار زینعلی
سمانه ساعدی
نیلوفر سبکرو
فاطمه سپه وند
ارمغان سلطانی شیرازی
شقایق شاه کلاهی
محمد شعله
عارفه شهریاری
علی شیوایی

مهنام صدری
فرانک عبدلی
رضا عزیزیان
صبا عظیمی
طاهر عظیمی
غزاله عفیفی
فاطمه غیاض
الیکا فرج تبریزی
مرصع السادات فرناد
عبدالامیر قدکساز
جابر قربانی
جلیل کاردان
حسین کاظمیان
ایسان گلکار
رضوان گلمرادی
فروغ گودرزی
نسترن محسنی
سمانه محمد جواد
نیما محمدزاده
محمد حسین مصلایی زاده

فریبا مفیدی
یگانه ملک محمدی
مرضیه مهدی زاده
رضوان مهراب
سیده تینا میری
احمد ناصر
رضا نجف پور
سعیده نجفی
زهرا نجفی علیا
مریم نجفی
محسن نظری
آتنا نعمتی
امیر حسام نعمتی
امیر حسین نفری
سارا همتی
منصوره هوشیار
ایثار یحیاوی
سجاد یزدان ستاد
فاطمه یزدانی
ندا یوسفی

حامیان کنگره

۱. دانشگاه علوم پزشکی تهران
۲. وزارت بهداشت، درمان و آموزش پزشکی
۳. موسسه تحقیقات واکسن و سرم سازی رازی
۴. انستیتو پاستور ایران
۵. دانشگاه علوم پزشکی ایلام
۶. مرکز مدیریت بیماریهای واگیر
۷. سازمان نظام دامپزشکی جمهوری اسلامی ایران
۸. سازمان غذا و دارو وزارت بهداشت، درمان و آموزش پزشکی
۹. شرکت صنایع شیر ایران (پگاه)

برنامه روزانه

نوزدهمین کنگره بین‌المللی میکروب‌شناسی ایران

برنامه سخنرانی‌ها در سالن ابن سینا

سه شنبه ۱۳۹۷/۶/۱۳

زمان	عنوان سخنرانی	سخنرانان	تخصص
۸:۰۰ -۸:۰۵	افتتاحیه قرائت قرآن و سرود ملی جمهوری اسلامی ایران		
۸:۰۵ -۸:۱۵	پیام علمی و سخنرانی رئیس انجمن میکروب شناسی ایران	دکتر محمد مهدی فیض آبادی	میکروب شناسی پزشکی
۸:۱۵ -۸:۲۰	سخنرانی دبیر علمی	دکتر محمد مهدی اصلانی	میکروب شناسی پزشکی
۸:۲۰-۸:۴۵	Exploiting Bacteriophages: Phage therapy initiative in finland	Prof. Skurnik Mikael	
۸:۴۵ —۹:۱۰	Bioinformatics in the routine laboratory	Dr. Herbert Tomaso	
۹:۱۰—۹:۳۵	DNA microarray technology and its usefulness in genetic researches of bacteria	Dr. Helmut Hotzel	
۹:۳۵ - ۱۰:۰۰	Infection disease investigation: from field to the lab	Dr. Akbar Dastjerdi	
۱۰:۰۰-۱۰:۳۰	**پذیرایی و بازدید از پوسترها**		
۱۰:۳۰ -۱۰:۵۵	Clostridium difficile as a possible zoonotic agent, strains from animal hosts and their genomic diversity	Dr. Christian Seyboldt	
۱۰:۵۵-۱۱:۲۰	Brucella abortus vaccine strain RB51 efficacy in water buffalo; status of art of an animal experimentation	Dr. Massimo Schacchia	

پانل میکروبیوتا			**۱۱:۲۰ - ۱۲ :۴۰**
رئیس پانل: دکتر سید داور سیادت **اعضای پانل:** Prof Mohammad Reza Zali (Gastroenterology and Liver, Shahid Beheshti, University of Medical Sciences), Prof Mostafa Ghanei(Baqiyatallah University of Medical Sciences), Dr. Pejman Rohani (Department of Pediatric (Mofid), Shahid Beheshti University of medical Sciences), Dr. Shabnam Shahrokh (Gastroenterology and Liver Shahid Beheshti, University of Medical Sciences), Dr. Haleh Massoudi (Department of Pediatric Ramsar Campus, Mazandaran University of Medical Sciences), Dr. Sara Ahmadi Badi (Microbiology Research Center, Pasteur Institute of Iran), Prof. Ashraf Mohebati Mobarez (Faculty of Medine Tarbiat Modares University) , Prof. Saeid Bouzari (Microbiology Research Center, Pasteur Institute of IRAN), Prof. Seyed Davar Siadat (Microbiology Research Center, Pasteur Institute of IRAN).			
The Gut –Liver Axis	Prof Mohammad Reza Zali		
The Gut –Lung Axis	Prof Mostafa Ghanei		
Microbiota and IBD (pediatric)	Dr. Pejman Rohani		
Microbiota and IBD (Adult)	Dr. Shabnam Shahrokh		
The Role of Microbiota in Infantile Colic	Dr. Haleh Massoudi		
The Impact of Microbiota on Epigenetic Modification	Dr. Sara Ahmadi Badi		
Therapeutic Effect of Probiotic in	Prof. Ashraf Mohebati Mobarez		
The Gut-kidney Axis	Prof. Saeid Bouzari		
Blood Microbiota	Prof. Seyed Davar Siadat		
پرسش و پاسخ			
نماز، نهار و استراحت			۱۲:۴۰-۱۴:۰۰
هیئت رئیسه: دکتر رشید رمضان زاده، دکتر محسن ارزنلو، دکتر محسن امین، دکتر مهدی میرزایی ، دکتر شهره فرشاد، دکتر پروانه صفاریان			
	Prof. Dr. Shahana Urooj Kazmi	Early detection of diagnostic markers of measles for better management and control of infection	۱۴:۰۰-۱۴:۲۰

۱۴:۳۰-۱۴:۲۰	MULTILOCUS SEQUENCE TYPING OF PENICILLIN NON-SUSCEPTIBLE S. PNEUMONIAE ISOLATES FROM INVASIVE INFECTIONS	Mohammad Azarsa	
۱۴:۴۰-۱۴:۳۰	MOLECULAR EPIDEMIOLOGY OF PVL HARBORING HOSPITAL-ASSOCIATED METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS IN SEPTICEMIC CHILDREN, NORTHEASTERN IRAN, BOJNURD	Amir Azimian	
۱۴:۵۰-۱۴:۴۰	DETECTION OF LEGIONELLA PNEUMOPHILA IN THE SPUTUM SPECIMENS OF PATIENT WITH RESPIRATORY SYMPTOMS BY CULTURE, PCR AND LOOP-MEDIATED ISOTHERMAL AMPLIFICATION METHODS	Fatemeh shahi	
۱۶:۳۰-۱۴:۵۰	**پانل تشخیص، تایپینگ و اپیدمیولوژی بیماری های عفونی**		
رئیس پانل: دکتر سهیلا مرادی بیدهندی (موسسه رازی) **اعضاء پانل:** دکتر رامین عبیری(دانشگاه علوم پزشکی کرمانشاه)، دکتر داود دربان (دانشگاه علوم پزشکی ایران)، دکتر حسین دبیری (دانشگاه علوم پزشکی شهید بهشتی)، دکتر محمد ایمان عینی (دانشگاه علوم پزشکی تهران)، دکتر مینا ابراهیمی راد (انستیتو پاستو ر ایران)			
	Identification of anaerobic bacteria.	دکتر پرویز اولیا	
	Loop-Mediated Isothermal Amplification as a Reliable Technique for Diagnosis of Microbial Infections	دکتر رامین عبیری	
	Different molecular methods for typing of Staphylococcus aureus; A special focus on spa-typing	دکتر داود دربان	
	Update on Helicobacter pylori epidemiology, diagnosis and treatment in Iran	دکتر حسین دبیری	
	Staphylococci: identification methods	دکتر محمد ایمان عینی	
	Mycobacterium tuberculosis Typing: A Molecular Epidemiologic Strategy to Control and Manage Tuberculosis	دکتر مینا ابراهیمی راد	
۱۶:۳۰ - ۱۶:۱۰	**پذیرایی و بازدید از پوسترها**		

۱۷:۱۰-۱۶:۳۰	**هیئت رئیسه: دکتر هادی پیری دوگاهه، دکتر عباس بهادر، دکتر محمد یوسف علیخانی، دکتر حلیمی، دکتر اسدی کرم، دکتر علیشا اکیا، دکتر نور امیر مظفری**		
۱۶:۴۰-۱۶:۳۰	FFECTS OF A FOOD ENRICHED WITH PROBIOTICS ON STREPTOCOCCUS MUTANS AND LACTOBACILLUS SPP. SALIVARY COUNTS IN PRESCHOOL CHILDREN: A CLUSTER RANDOMIZED TRIAL.	Seyed ehsan Asadi	
۱۶:۵۰-۱۶:۴۰	MOLECULAR DETERMINANTS OF ACQUIRED COLISTIN RESISTANCE AMONG CLINICAL ISOLATES OF KLEBSIELLA PNEUMONIAE	Mehri Haeili	
۱۷:۰۰-۱۶:۵۰	CONSTRUCTION OF PTX-DEFICIENT BORDETELLA PERTUSSIS VACCINE STRAIN 134 BY ALLELIC EXCHANGE	Vajihe Sadat Nikbin	
۱۷:۱۰-۱۷:۰۰	DIAGNOSTIC ACCURACY OF MONOCYTE CHEMOTACTIC PROTEIN (MCP)-2 AS BIOMARKER FOR THE DISCRIMINATION BETWEEN ACTIVE AND LATENT TUBERCULOSIS	Shima Mahmoud	
۱۸:۳۰- ۱۷:۱۰	**پانل چالش های حوزه کنترل کیفیت در بخش های میکروب شناسی آزمایشگاه های پزشکی**		
رئیس پانل: دکتر بابک ولی زاده (دکتری علوم آزمایشگاهی) **اعضاء پانل:** دکتر مرجان فرزامی (متخصص پاتولوژی)، دکتر محمد علی برومند (متخصص پاتولوژی)، دکتر سینا مباشری زاده (دکتری میکروب شناسی)، دکتر محمد رهبر(دکتری میکروب شناسی)			
	گزارشی از وضعیت آزمایشگاه های میکروب شناسی بیمارستانی با تاکید بر حوزه کنترل کیفیت	دکتر مرجان فرزامی	
	کنترل کیفیت روش های تشخیصی	دکتر بابک ولی زاده	
	کنترل کیفیت آزمون حساسیت ضد میکروبی	دکتر محمد علی برومند	
	کنترل کیفیت در گزارش دهی	دکتر سینا مباشری زاده	
	کنترل کیفیت مرحله پره آنالیتیک در میکروب شناسی	دکتر محمد رهبر	
	پرسش و پاسخ		

چهارشنبه۱۳۹۷/۶/۱۴

زمان	عنوان سخنرانی	سخنرانان	تخصص
۸:۵۰ -۸:۰۰	**هیئت رئیسه: دکتر رجب نیا، دکتر پریسا بدیعی، دکتر مژده حاکمی والا، دکتر مریم پور حاجی باقر، دکتر فرشته جبل عاملی، دکتر هما فروهش تهرانی، دکتر مروارید شفیعی**		
۸:۱۰-۸:۰۰	PREVALENCE OF NONTUBERCLOSIS MYCOBACTERIA IN PATIENTS WITH SUSPECTED PULMONARY TUBERCULOSIS IN TEHRAN, IRAN.	Zahra Nikpour	
۸:۲۰-۸:۱۰	DIAGNOSTIC ACCURACY OF GENEXPERT AND HRM IN COMPARISON WITH PROPORTIONAL METHOD FOR STUDY OF DRUG RESISTANCE IN MYCOBACTERIUM TUBERCULOSIS STRAINS ISOLATED FROM TUBERCULOSIS PATIENTS	Samaneh Arefzadeh	
۸:۳۰-۸:۲۰	MOLECULAR CHARACTERIZATION OF MYCOBACTERIUM TUBERCULOSIS ISOLATES IN ALBORZ PROVINCE	Morassa Farnad	
۸:۴۰-۸:۳۰	CHALLENGE IN DIRECT SPOLIGOTYPING OF MYCOBACTERIUM TUBERCULOSIS	Sharareh Khanipour	
۸:۵۰-۸:۴۰	MYCOBACTERIUM AHVAZICUM SP. NOV., THE NINETEENTH SPECIES OF THE MYCOBACTERIUM SIMIAE COMPLEX	Abodolrazagh Hashemi Shahraki	
۹:۵۰-۸:۵۰	**پانل کنترل عفونت**		
رئیس پانل: دکتر محمدرضا صالحی **اعضاء پانل:** دکتر پیام طبرسی(دانشگاه علوم پزشکی شهید بهشتی)، دکتر آرش سیفی(دانشگاه علوم پزشکی تهران)، دکتر محمدرضا صالحی(دانشگاه علوم پزشکی تهران)، ، دکتر سید علی دهقان منشادی(دانشگاه علوم پزشکی تهران)، دکتر ملیحه حسن نژاد (دانشگاه علوم پزشکی تهران)			
	تاثیر روشهای تشخیصی نوین در بهبود کیفیت کنترل عفونت	دکتر پیام طبرسی	

	الزامات کنترل عفونت در بخشهای مراقبتهای ویژهICU	دکتر آرش سیفی	
	تاثیر برنامه های استواردشیپ آنتی بیوتیکها در بهبود کیفیت کنترل عفونت	دکتر محمدرضا صالحی	
	معرفی بیمار اول و بحث	دکتر سید علی دهقان منشادی	
	معرفی بیمار دوم و بحث	دکتر ملیحه حسن نژاد	
	پرسش و پاسخ		
۱۰:۰۰-۹:۵۰	**یادبود دکتر یلدا**		
۱۰:۳۰-۱۰:۰۰	**پذیرایی و بازدید از پوسترها**		
۱۰:۵۰-۱۰:۳۰	Francisella tularensis in wildlife and ticks in Germany	Dr. Herbert Tomaso	
۱۱:۱۰-۱۰:۵۰	Prevalence, genotyping and risk factors of thermophilic Campylobacter spreading in organic turkey farms in Germany	Dr. Helmut Hotzel	
۱۲:۳۰-۱۱:۱۰	**مجمع فوق العاده انجمن میکروب شناسی و انتخابات هیئت مدیره انجمن**		
۱۴:۰۰-۱۲:۳۰	**نماز ، نهار و استراحت**		
۱۴:۳۰-۱۴:۰۰	**هیئت رئیسه: دکتر سعید اشراقی، دکتر غلامرضا ایراجیان، دکتر مجید زارع بیدکی، دکتر مهرداد آذین، دکتر مروت طاهری کلانی**		
۱۴:۱۰-۱۴:۰۰	MOLECULAR CHARACTERIZATION OF AMINOGLYCOSIDE RESISTANCE AMONG CLINICAL ISOLATES OF STAPHYLOCOCCUS AUREUS	Masoumeh Aslanimehr	
۱۴:۲۰-۱۴:۱۰	SEROTYPES OF LISTERIA MONOCYTOGENES ISOLATED FROM SPONTANEOUS HUMAN ABORTION IN TEHRAN,IRAN	Jalil Vandyousefi	
۱۴:۳۰-۱۴:۲۰	SPA TYPING OF STAPHYLOCOCCUS AUREUS ISOLATES CAUSING NOSOCOMIAL INFECTIONS	Rashid Ramazanzadeh	

۱۶:۰۰-۱۴:۳۰	**پانل بیماری های عفونی نوپدید و باز پدید**		
رئیس پانل: دکتر محمد مهدی گویا (متخصص عفونی، رییس مرکز مدیریت بیماری های واگیر) **اعضاء پانل:** دکتر صفرعلی ماکنعلی (معاون بهداشتی سازمان دامپزشکی کشور)، دکتر بابک عشرتی (رییس برنامه پایش مقاومت میکروبی در وزارت بهداشت)، دکتر احسان مصطفوی (اپیدمیولوژیست، رییس مرکز و پایگاه تحقیقاتی بیماری های نوپدید و بازپدید انستیتو پاستور ایران)، دکتر مصطفی صالحی وزیری (رییس بخش آربوویروس ها و تب های خونریزی دهنده ویروسی انستیتو پاستور ایران)، دکتر سیامک مسعودی (دامپزشکی، کارشناس ارشد سازمان حفاظت محیط زیست)، دکتر محمد حسن پوریای ولی (عضو هیات علمی بخش آربوویروس ها و تب های خونریزی دهنده ویروسی انستیتو پاستور ایران)		
	آخرین وضعیت آنفلوانزای انسانی در ایران	دکتر محمد مهدی گویا	
	امواج ۱۳۹۵-۱۳۹۶ و ۱۳۹۶-۱۳۹۷ آنفلوانزای فوق حاد پرندگان در ایران	دکترعلی صفر ماکنعلی	
	آخرین وضعیت مقاومت میکروبی در ایران	دکتر بابک عشرتی	
	آخرین وضعیت تولارمی در ایران	دکتر احسان مصطفوی	
	تازه های تب خونریزی دهنده کریمه کنگو	دکتر مصطفی صالحی وزیری	
	مروری بر وضعیت بیماری های نوپدید در حیات وحش کشور	دکتر سیامک مسعودی	
	بیماری های جدید آربوویروسی	دکتر محمد حسن پوریای ولی	
	پرسش و پاسخ		
۱۶:۲۰-۱۶:۰۰	**پذیرایی و بازدید از پوسترها**		
۱۶:۵۰ – ۱۶:۲۰	**هیئت رئیسه: دکتر بهمن میرزایی، دکتر صدیقه جوادپور، دکتر فرانک رضایی، دکتر ایرج نیکوکار، دکتر علی مجتهدی، دکتر سید سجاد خرم روز**		
۱۶:۳۰-۱۶:۲۰	DIRECT DETECTION OF STREPTOCOCCUS PNEUMONIAE AND NEISSERIA MENINGITIDES FROM NASOPHARYNGEAL SWAB SPECIMENS IN CHILDREN USING LAMP-PCR	Bahman Mirzaei	
۱۶:۴۰-۱۶:۳۰	RAPID AND SENSITIVE DETECTION OF TICK-BORNE RELAPSING FEVER BORRELIAE IN TICK DNA SAMPLES BY USING LOOP-MEDIATED ISOTHERMAL AMPLIFICATION (LAMP)	Faezeh Houman sadr	

۱۶:۵۰-۱۶:۴۰	THE EVALUATION OF IMMUNITY OF BETA ANTITOXIN OF CLOSTRIDIUM PERFRINGENES BY INDIRECT ELISA AND SERUM NEUTRALIZATION TEST	Lida Abdolmohammadi khiyav	
۱۸:۱۰ - ۱۶:۵۰	**پانل مایکوباکتریوم ها و سل**		
رئیس پانل:دکتر محمد مهدی فیض آبادی **اعضاء پانل:** دکتر پیام طبرسی(دانشگاه علوم پزشکی شهید بهشتی)، دکتر عباسعلی ایمانی فولادی(دانشگاه علوم پزشکی بقیه‌اله (عج)، مهندس سیروس امینی، دکتر کیارش قزوینی (دانشگاه علوم پزشکی مشهد)، دکتر محمد جواد نصیری(دانشگاه علوم پزشکی شهید بهشتی)، دکتر سعید ذاکر بستان آباد(دانشگاه آزاد اسلامی)، دکتر بیژن نعمان‌پور (دانشگاه علوم پزشکی کرمانشاه)			
	اهمیت line probe assay و کاربرد آن در تشخیص و کنترل سل مقاوم به دارو	دکتر محمد مهدی فیض آبادی	
	تازه های درمان سل مقاوم	دکتر پیام طبرسی	
	تکنیکهای جدید در تشخیص مایکوباکتریوم توبرکلوزس	دکتر عباسعلی ایمانی فولادی	
	تکنیک Genexpert معایب و مزایا	دکتر محمد جواد نصیری	
	Epidemiology of Mycobacterium tuberculosis in Northeast border of Iran	دکتر کیارش قزوینی	
	Frequency and prevalence resistance to drug line 1-2 tuberculosis in Mycobacterium tuberculosis isolates from patients	دکتر سعید ذاکر بستان آباد	
	تشخیص فنوتیپی سل مقاوم به پیرازینامید	مهندس سیروس امینی	

پنج شنبه ۱۳۹۷/۶/۱۵

زمان	عنوان سخنرانی	سخنرانان	
۸:۳۰- ۸:۰۰	**هیئت رئیسه: دکتر محمدرضا عربستانی، دکتر پرویز مهاجری، دکتر افسانه کرمستجی، دکتر امین طالبی ، دکتر بهاره حاجی خانی**		
۸:۱۰-۸:۰۰	DETECTION AND SEQUENCING OF TN1546 TRANSPOSON IN TWO VANCOMYCIN-RESISTANT STAPHYLOCOCCUS AUREUS	Davood Kalantar Neyestanaki	
۸:۲۰-۸:۱۰	COMPARISON THE EFFECTS OF DANTROLENE AND 2-AMINOETHYL DIPHENYLBORINATE ON XBP-1 MRNA GENE SPLICING IN C57 MICE TREATED WITH PSEUDOMONAS AEROGINOSA ENDOTOXIN ISOLATED FROM BURNED PATIENT'S LESION	Mojtaba Hedayati ch	
۸:۳۰-۸:۲۰	THE ANTIBIOTIC SUSCEPTIBILITY AND PREVALENCE OF ADHESION GENES IN STREPTOCOCCUS PNEUMONIAE ISOLATES DETECTED IN CARRIER CHILDREN IN TEHRAN	Sara Abdollahi	
۱۰:۰۰ - ۸:۳۰	**پانل میکروبیولوژی دارویی**		
رئیس پانل: دکتر محسن امین (گروه کنترل دارو و غذا، دانشکده داروسازی، دانشگاه علوم پزشکی تهران) **اعضاء پانل:** دکتر محمدرضا فاضلی (گروه کنترل دارو و غذا، دانشکده داروسازی، دانشگاه علوم پزشکی تهران)، دکتر سروش سرداری (گروه بیوتکنولوژی پزشکی، انستیتو پاستور تهران)، دکتر محمد پویا (گروه بیولوژی مولکولی، انستیتو پاستور تهران)			
	پریو وکس۳ بعنوان کاندید واکسن پریودونتیت	دکتر محسن امین	
	یافته های جدید در محصولات پروبیوتیک در ایران	دکتر محمد رضا فاضلی	
	تازه های تحقیق و توسعه مولکول های ضد میکروبی	دکتر سروش سرداری	
	فرصت ها و چالش های واکسن های کشته شده میکروبی	دکتر محمد پویا	
۱۰:۳۰ - ۱۰:۰۰	پرسش و پاسخ		

۱۰:۳۰ - ۱۰:۵۰	Clostridium difficile prevalence in small companion animals and their owners in Germany	Dr. Christian Seyboldt	
۱۰:۵۰ - ۱۱:۱۰	Contagious Bovine Pleuropneumonia (CBPP) OIE Reference Laboratory, role and activities	Dr. Massimo Schacchia	
۱۱:۱۰ -۱۲:۴۵	**پانل مقاومت میکروبی و عفونی**		
رئیس پانل: دکتر فرشته شاهچراغی (عضو هیئت علمی انستیتو پاستور ایران، گروه میکروب شناسی) **اعضاء پانل:** دکتر مرجان فرزامی (متخصص پاتولوژی، آزمایشگاه مرجع سلامت)، دکتر بابک عشرتی (مرکز مدیریت بیماری‌ها)، دکتر محبوبه حاجی عبدالباقی (متخصص عفونی بیمارستان امام خمینی (ره)، دکتر رضا رنجبر (دانشگاه علوم پزشکی بقیه اله (عج)		
	حوزه های تمرکز آزمایشگاه مرجع سلامت در برنامه مهار مقاومت میکروبی دستاوردها و محدودیت ها	دکتر مرجان فرزامی	
	Role Of Carriers Of Antimicrobial Drug Resistant Organisms In Prevention And Development Of Antibiotic Resistance	دکتر فرشته شاهچراغی	
	Antibiotic Stwardship	دکتر محبوبه حاجی عبدالباقی	
	چالشهای تشخیص مولکولی مقاومت ضد میکروبی	دکتر رضارنجبر	
	نقش مرکز مدیریت بیماریهای وزارت بهداشت در کنترل مقاومت میکروبی	دکتر بابک عشرتی	
	پرسش و پاسخ		
۱۲:۴۵ - ۱۴:۰۰	**اختتامیه**		

سالن عزلت

سه شنبه ۱۳۹۷/۶/۱۳

۱۲:۳۰ - ۱۱:۰۰	پانل میکروبیولوژی مواد غذایی و آشامیدنی	
رئیس پانل: دکتر ناهید رحیمی فرد (دانشیار سازمان غذا و دارو، رئیس آزمایشگاه میکروبیولوژی مرکز آزمایشگاه‌های مرجع کنترل غذا و دارو و تجهیزات پزشکی، وزارت بهداشت درمان و آموزش پزشکی) **اعضای پانل:** دکتر مریم تاج آبادی ابراهیمی(رئیس انجمن پروبیوتیک)، دکتر زهره مشاک(عضو هیات علمی و دانشیارگروه بهداشت مواد غذایی دانشگاه آزاد اسلامی کرج)، مژگان حیدرپور (کارشناس ارشد میکروبیولوژی کارشناس مسئول بخش لبنیات سازمان ملی استاندارد)، دکتر امیر رحیمی راد (رئیس آزمایشگاه کنترل غذا و دارو دانشگاه علوم پزشکی و خدمات بهداشتی درمانی ارومیه)، دکتر محمد خضری (استادیار، دکترای تخصصی کنترل کیفیت و بهداشت مواد غذایی، معاونت غذا ودارو دانشگاه علوم پزشکی مشهد)، دکتر شهریار دبیریان(مدیر تضمین کیفیت شرکت صنایع شیر ایران)، دکتر بابک پوراکبری (مرکز تحقیقات بیماریهای عفونی دانشگاه علوم پزشکی و خدمات بهداشتی درمانی تهران، آزمایشگاه مجاز رایمون دایان دانا سازمان غذا و دارو)، دکتر شیلا صفائیان (آزمایشگاه مجاز رازی سازمان غذا و دارو)، دکتر نسرین حاجی سید جوادی(انستیتو تحقیقات تغذیه ای و صنایع غذایی کشور)		
	دکتر محمد خضری	معرفی روش های سریع و پیشرفته در تشخیص عوامل بیماریزای غذازاد Presenting of Rapid & Advanced methods for food borne pathogens detection
	دکتر مریم تاج آبادی	باکتری های اسید لاکتیک راهکاری نو در کاهش مایکوتوکسین های مهم در صنعت خوراک دام
	دکتر مسعود آل بویه	تشخیص باکتری های کد کننده شیگاتوکسین در نمونه های غذایی و نقش آنها در بروز گاستروانتریت و بیماری های خارج روده ای Detection of Shiga-like toxin producing bacteria in foodstuff and human stool samples: Toward next-generation food microbiology techniques
	مژگان حیدرپور	علل بیماری میکروبی در ماهیان پرورشی
	دکتر زهره مشاک	اثرات ضد میکروبی بسته بندیهای زیست تخریب پذیر فعال در امر سلامت و امنیت غذایی The antimicrobial effects of active biodegradable packaging on health and food safety
	دکترامیر رحیمی راد	بررسی میزان آلودگی سالاد فصلی در آزمایشگاه کنترل غذا و داروی ارومیه Evaluation of microbial contamination of Season Salads in URMIA food and drug control lab
	دکتر بابک پوراکبری	مقاومتهای میکروبی در زنجیره غذایی Antimicrobial Resistance in the Food Chain

	دکتر شهریار دبیریان	تاثیر باکتری های سرمادوست در کیفیت محصولات شیری پاستوریزه و استریل The Effect of psychrotrophic bacteria on the Quality of Pasteurized and Sterilized Milk Products
	دکتر سید رضا محبی	مشکلات تکنیکی تشخیص مولکولی آلودگی نورو ویروسی در مواد غذایی
	دکتر ناهید رحیمی فرد	آزمایشگاه میکروبیولوژی در آینده Microbiology Laboratory in the future
	بحث و تبادل نظر	
۱۴-۱۲:۳۰	**نماز ، نهار و استراحت**	
۱۵:۴۰-۱۴	**هیئت رئیسه: دکتر امیرهوشنگ الوندی، دکتر غلامرضا گودرزی، دکتر ارجمند زادگان، دکتر رامین عبیری، دکتر داود کلانتر نیستانکی، دکتر سمیه یسلیانی فر، دکتر محمد نیاکان،دکتر محمود امین مرعشی**	
۱۴:۱۰-۱۴:۰۰	SUB-LETHAL ANTIMICROBIAL PHOTODYNAMIC INACTIVATION AFFECTS QUORUM SENSING-CONTROLLED BIOFILM FORMATION GENE EXPRESSION OF PSEUDOMONAS AERUGINOSA IN-VITRO	Saghar Hendiani
۱۴:۲۰-۱۴:۱۰	EVALUATION OF SILVER NANOPARTICLES EFFECTS ON BLA-PER-1 GENE EXPRESSION FOR BIOFILM FORMATION IN ISOLATES OF ANTIBIOTIC-RESISTANT ACIENTOBACTER BUMANNI BY REAL TIME PCR METHOD	Tohid Piri gharaghie
۱۴:۳۰-۱۴:۲۰	TH1 IMMUNE RESPONSES CONFERRED BY MIXTURE OF NALOXONE, CPG OLIGODEOXYNUCLEOTIDE AND 3-O-DECYLATED MONOPHOSPHORYL LIPID A, AGAINST PLASMODIUM VIVAX RECOMBINANT TRAP AS A SUBUNIT VACCINE IN MOUSE MODEL	Saeed Nazeri
۱۴:۴۰-۱۴:۳۰	FITNESS AND GENOMIC PORTRAIT OF AUSTRALIAN 2008-2012 PERTUSSIS EPIDEMIC	Azadeh Safarchi
۱۴:۵۰-۱۴:۴۰	CAMPYLOBACTER CONCISUS AND ITS EFFECT ON THE EXPRESSION OF CDX1 AND COX2	Behrooz Mozaffari
۱۵:۰۰-۱۴:۵۰	THE FREQUENCY AND VIRAL LOAD OF EPSTEIN-BARR VIRUS IN IRANIAN PATIENTS WITH HEMATOLOGIC MALIGNANCIES	Alireza Tabibzadeh
۱۵:۱۰-۱۵:۰۰	RECOMBINANT ISDE PROTEIN OF STAPHYLOCOCCUS AUREUS: A NOVEL VACCINE CANDIDATE VERSUS MRSA	Yasaman Vahdani
۱۵:۲۰-۱۵:۱۰	EVALUATION OF THE EFFECTS OF DIFFERENT ADJUVANTS ON IMMUNOGENICITY AND PROTECTIVITY OF PASTEURELLA MULTOCIDA VACCINE IN CHICKENS	Rahim Ghadimipour
۱۵:۳۰-۱۵:۲۰	CLONING AND EXPRESSION OF RECOMBINANT LIPL41 ANTIGEN FROM LEPTOSPIRA INTERROGANS IN PROKARYOTIC SYSTEM.	Narges Golab
۱۵:۴۰-۱۵:۳۰	EVALUATION OF REAL TIME PCR FOR DETECTION OF CLINICAL ISOLATES OF STAPHYLOCOCCUS AUREUS AND METHICILLIN-RESISTANCE STRAINS BASED ON MELTING CURVE ANALYSIS METHOD	Narges Heidari

۱۶:۰۰-۱۵:۴۰	**پذیرایی و بازدید از پوسترها**	
۱۸:۰۰-۱۶:۰۰	**پانل پروبیوتیک ها**	
رئیس پانل:دکتر شهریار دبیریان **اعضاء پانل:** دکتر مژگانی، دکتر میردامادی، مژگان حیدرپور، دکتر علیرضا دهناد، دکتر ناهید رحیمی فرد، دکتر مریم تاج آبادی، دکتر سهیل اسکندری، دکتر فاطمه حسینی		
	Physiological and Genetic safety aspects of Enterococcus and Bacillus species intended for Probiotics use	دکتر مژگانی
	The design of bioactive peptides via pro-protease enzyme to produce functional food	دکتر میردامادی
	Protective culture	مژگان حیدرپور
	The effects of Prebiotic, Probiotic and Post probiotic Prevention in Type 2 Diabetes	دکتر دهناد

چهار شنبه ۱۳۹۷/۶/۱۴

۱۲:۳۰-۱۱:۰۰	**مجمع فوق العاده انجمن میکروب شناسی و انتخابات هیئت مدیره انجمن**	
۱۴:۰۰-۱۲:۳۰	**نماز ، نهار و استراحت**	
۱۵ -۱۴:۰۰	**پانل : سیستمهای توکسین -آنتی توکسین و باکتریهای پرسیستر** Toxin- antitoxin systems and bacterial persister	
	رئیس پانل: دکتر ایرج پاکزاد (استاد دانشگاه علوم پزشکی ایلام) **اعضاء پانل:** دکتر سبحان غفوریان(استادیار دانشگاه علوم پزشکی ایلام)، دکتر نورخدا صادقی فرد (استاد دانشگاه علوم پزشکی ایلام)، دکتر افرا خسروی (استاد دانشگاه علوم پزشکی ایلام)، علی همتیان (مرکز تحقیقات میکروب شناسی بالینی-دانشگاه علوم پزشکی ایلام)، حسین کاظمیان (مرکز تحقیقات میکروب شناسی بالینی- دانشگاه علوم پزشکی ایلام)	
	دکتر ایرج پاکزاد	The role of persister cells in biofilm formation
	دکتر سبحان غفوریان	Toxin- antitoxin systems as antimicrobial targets in bacteria
	علی همتیان	Toxin- antitoxin system and bacterial pathogenesis
	حسین کاظمیان	The relationship between persister cells and toxin - antitoxin systems
	پرسش و پاسخ	
۱۶:۲۰- ۱۵	**پانل زئونوز**	
	رئیس پانل: دکتر تقی زهرایی صالحی(استاد دانشگاه تهران) **اعضاء پانل:** دکتر ماکنعلی(معاونت محترم دارو و درمان سازمان دامپزشکی کشور)، دکتر زینلی(رئیس دفتر ملی مبارزه با بیماری‌های زئونوز وزارت بهداشت)، دکتر کریم امیری(مدیر کل دفتر مبارزه با بیماری‌های سازمان دامپزشکی کشور)، دکتر غلامرضا هاشمی تبار(استاد دانشگاه فردوسی مشهد)، دکتر مسعود قربانپور(استاد دانشگاه شهید چمران اهواز)، دکتر اکرم بحرینی پور(مسئول مبارزه با بروسلوز سازمان دامپزشکی کشور)، دکتر علیرضا دهناد (استادیار مرکز تحقیقات جهاد تبریز)	
	دکتر ماکنعلی	Operational policies of zoonoses control
	دکتر زینلی	Epidemiological situation of brucellosis in Iran
	دکتر کریم امیری	Brucellosis Control and eradication programs
	دکتر غلامرضا هاشمی تبار	Leptospirosis and control strategies
	دکتر مسعود قربانپور	Chlamydiosis

	دکتر نادر مصوری	Genetic diversity of Iranian isolates of Burkholderia mallei by PFGE and PCR-MLVA
	دکتر اکرم بحرینی پور	Country Instruction to Combating Animal Brucellosis
	دکتر علیرضا دهناد	بررسی سه جانبه استافیلوکوکوس آریوس در غذا، دام و انسان
	دکتر تقی زهرایی صالحی	Cloning and Expression two recombinant proteins of Mycobacterium bovis
	پرسش و پاسخ	
۱۶:۴۰-۱۶:۲۰	**پذیرایی و بازدید از پوسترها**	
۱۸:۰۰-۱۶:۴۰	**پانل بانک میکروبی**	

رئیس پانل: دکتر سید فضل اله موسوی

اعضا پانل: دکتر سید ابوالحسن شاهزاده فاضلی، دکتر فرزانه عزیز محسنی، دکتر محمدرضا آصف، دکتر شقایق نصر، دکتر مهدی رزاقی ابیانه

	دکتر سید ابوالحسن شاهزاده فاضلی	Role of microorganism banks in development of biotechnology
	دکتر فرزانه عزیز محسن	Distribution and Deposit of Biological Resource in BRCs
	دکتر محمدرضا آصف	اهمیت مجموعه های ذخایر ژنتیکی وتنوع زیستی قارچ ها، با نگاهی به مجموعه قارچهای ایران
	دکتر شقایق نصر	The Iranian Biological Resource Center(IBRC): Repository in bioprospecting of National Microbial Diversity
	پرسش و پاسخ	

پنج شنبه ۱۳۹۷/۶/۱۵

۱۰-۸:۳۰	**پانل عفونت زخم و سوختگی**	
رئیس پانل: دکتر مهنوش مومنی(استادیار جراحی دانشگاه علوم پزشکی ایران) **اعضاء پانل:** دکتر عالی نژاد(متخصص عفونی)، دکتر مریم روهام(متخصص عفونی و استادیار دانشگاه علوم پزشکی ایران)، دکتر مصطفی دهمرده ای(استادیار جراحی پلاستیک دانشگاه علوم پزشکی ایران)		
	دکتر عالی نژاد	نقش پروبیوتیک ها در سوختگی و عفونت های آن
	دکتر مریم روهام	معرفی چند مورد مقاوم به درمان
	دکتر مهنوش مومنی	پانسمان های نوین سوختگی در کنترل عفونت
	دکتر مصطفی دهمرده ای	جراحی سوختگی و کنترل عفونت
	پرسش و پاسخ	
۱۰:۳۰-۱۰	**پذیرایی و بازدید از پوسترها**	
۱۱:۳۰-۱۰:۳۰	**پانل میکروبیولوژی صنعتی و محیط زیست**	
رئیس پانل: دکتر مهرداد آذین **اعضا پانل:** دکتر سید مهدی دستغیب- پژوهشگاه صنعت نفت، آقای دکتر محمدرضا صعودی – دانشگاه الزهراء (س)، فائزه حسامی ذکائی (دانشجوی دکترا) دانشگاه الزهراء (س)، مهندس پیمان سازنده چی- قائم مقام و عضو هیات مدیره شرکت آرین گستر (TAG Biotech)وابسته به شرکت گلرنگ، دکتر پریسا محمدی- دانشگاه الزهراء (س)		
	دکتر سید مهدی دستغیب	کاربردهای صنعتی سامانه های زیستی برای تصفیه جریانهای گازی آلاینده Industrial application of bio-filtration systems for treatment of waste gas streams
	دکتر محمدرضا صعودی	راهبردهای زیست فناورانه در پاکسازی زیستی صنایع تولید الکل Biotechnological approaches in bioremediation of ethanol production industries
	فائزه حسامی ذکائی	بررسی ژنها و آنزیمهای میکروارگانیسمهای دخیل در تجزیه زیستی پلاستیک های پلی اتیلنی Evaluation of genes and enzymes from microorganisms involved in the biodegradation of polyethylene-based plastics
	مهندس پیمان سازنده چی	Microalgal biotechnology
	دکتر پریسا محمدی	میکروبیولوژی آثار باستانی و هنری Microbiology of the ancient and art works
	پرسش و پاسخ	

۱۲:۳۰-۱۱:۳۰	**پانل نقش باکتری‌ها، ویروس‌ها، تک یاخته‌ها و قارچ ها در ایجاد بدخیمی های هماتولوژیک و سالیدتومورها**	
رئیس پانل: دکتر عبدالرحیم حزینی(فوق تخصص خون و انکولوژی و معاونت فنی مراقبت در منزل مرکز پیشگیری سرطان آلاء در تهران **اعضاء پانل:** دکتر رضا ملایری (فوق تخصص خون و انکولوژی و رئیس بخش طب تسکینی مرکز پیشگیری سرطان آلاء در بیمارستان فیروزگر، دکتر وحید کاوه (فوق تخصص خون و انکولوژی و پزشک انکولوژیست بخش طب تسکینی مرکز پیشگیری سرطان آلاء در بیمارستان فیروزگر)، دکتر فقیهی(دانشگاه علوم پزشکی شیراز)، دکتر مجتبی هدایتی چکوسری		
	دکتر عبدالرحیم حزینی	کلیات میکروب شناسی و سرطان
	دکتر رضا ملایری	تازه‌های پاپیلوم ویروس و نقش آن در سرطانها
	دکتر وحید کاوه	نقش ویروسها در ایجاد سرطانها
	دکتر مجتبی هدایتی چکوسری	توکسینهای میکروبی و سرطان
	پرسش و پاسخ	
۱۳-۱۲:۳۰	**اختتامیه**	

سالن A

سه شنبه ۹۷/۶/۱۳

هیات رئیسه: دکتر پروین حیدریه، دکتر عباس عبدالهی، دکتر احمد خورشیدی مال احمدی، دکتر محمد حسین سالاری، دکتر عباس اخوان سپهی، دکتر محمد آهنجان، دکتر مهری هائلی		۱۲:۲۰-۱۰:۳۰
Ali Mohammadi bardbari	CORRELATION BETWEEN ABILITY OF BIOFILM FORMATION WITH THEIR RESPONSIBLE GENES AND MDR PATTERNS IN CLINICAL AND ENVIRONMENTAL ACINETOBACTER BAUMANNII ISOLATES	۱۰:۴۰-۱۰:۳۰
ALKA HASANI	A COMPREHENSIVE STUDY OF ACINETOBACTER BAUMANNII IN VENTILATOR ASSOCIATED PNEUMONIA: A COGITATION CONCEPT	۱۰:۵۰-۱۰:۴۰
Mojdeh Hakemi Vala	COMPARISON OF ROUTINE VS. BACT/ALERT BLOOD CULTURE IN A SAME 6MONTHS OF 2 CONTINUOUS YEARS AMONG PATIENTS WHO REFERRED TO PAYVAND CLINICAL & SPECIALTY LAB	۱۱:۰۰-۱۰:۵۰
Hossein Sadeghi	ISOLATION AND IDENTIFICATION OF HISTAMINE OXIDASE PRODUCING BACTERIA FROM DIVERS IRANIAN HABITATS	۱۱:۱۰-۱۱:۰۰
Atefe Pourdadashi	BROADLY REACTIVE APTAMERS TARGETING DIFFERENT GENERA OF COMMON ORGANISMS RELATED TO ACUTE BACTERIAL MENINGITIS	۱۱:۲۰-۱۱:۱۰
Ramin Bagheri Nejad	IMMUNOGENICITY OF OUTER MEMBRANE VESICLES FROM A BRUCELLA MELITENSIS HUMAN ISOLATE IN BALB/C MICE	۱۱:۳۰-۱۱:۲۰
Maryam Salemi	EVALUATION OF A REAL-TIME PCR ASSAY FOR DETECTION AND QUANTIFICATION OF RUBELLA VIRUS IN MMR VACCINE	۱۱:۴۰-۱۱:۳۰
Maryam Pourhajibagher	GENE EXPRESSION PROFILING OF FIMA FIMBRIAE IN PORPHYROMONAS GINGIVALIS STRAINS IN RESPONSE TO PHOTO-ACTIVATED DISINFECTION THERAPY	۱۱:۵۰-۱۱:۴۰
Mansoureh Sedaghat	MOLECULAR CLONING OF HYALURONAN SYNTHASE GENE AND PRODUCTION OF HYALURONC ACID IN BACILLUS SUBTILIS	۱۲:۰۰-۱۱:۵۰
Shokoofeh Almasi	COMPARISON OF VACCINAL AND REGIONAL CIRCULATING BOVINE EPHEMERAL FEVER VIRUS BASED ON ANTIGENIC RELATIONSHIP AND CROSS-NEUTRALIZATION TEST	۱۲:۱۰-۱۲:۰۰
Arezoo Bozorgomid	MULTILOCUS SEQUENCE TYPING AND GENETIC STRUCTURE OF FASCIOLA ISOLATES FROM LIVESTOCK IN KERMANSHAH, IRAN	۱۲:۲۰-۱۲:۱۰
Khatereh Kabiri	ASSESSMENT OF GENETIC PATTERN MYCOPLASMA AGALACTIAE ISOLATED FROM EAST AZARBAIJAN AND ELAM BY METHOD OF MLST TYPING	۱۲:۳۰-۱۲:۲۰

سالن A

چهارشنبه: ۹۷/۶/۱۴

هیئت رئیسه: دکتر محبوبه نادری نسب، دکتر فرزاد بادمستی، دکتر حمید سلگی، دکتر شیوا میرکلانتری، دکتر نادر شاهرخی، دکتر پرستو احسانی، دکتر فرزانه فیروزی، دکتر محمد حسن شیرازی، دکتر محمد حسن نمایی		۱۶:۰۰-۱۴:۰۰
Mitra Omidi	PHENOTYPIC AND GENOTYPIC CHARACTERIZATION OF ANTIBIOTIC RESISTANCE AMONG METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS ISOLATES IN PATIENTS ADMITTED TO ISFAHAN AND KASHAN HOSPITALS IN2017	۱۴:۱۰-۱۴:۰۰
Masoumeh Aslanimehr	DISSEMINATION OF AMINOGLYCOSIDE-MODIFYING ENZYMES (AME) ENCODING GENES AMONG ESCHERICHIA COLI CLINICAL ISOLATES COLLECTED FROM INTENSIVE CARE UNIT (ICU)	۱۴:۲۰-۱۴:۱۰
Mohammad Savari	DETECTION OF DRUG RESISTANCE GENES RESERVIORES IN TNABARS AND R PLASMIDS AND STUDY OF ADERS AND BAERS REGULATORY SYSTEMS EFFECTS ON ADEABC EFFLUX PUMP AMONG ACINETOBACTER BAUMANNII CLINICAL ISOLATES	۱۴:۳۰-۱۴:۲۰
Sareh Davarzani	PROTOCOL FOR THE VALIDATION OF QUANTITATIVE ALTERNATIVE METHODS OF MICROBIOLOGY	۱۴:۴۰-۱۴:۳۰
Esmaeil Darabpour	HIGHLY EFFICIENT IN VITRO PHOTODYNAMIC INACTIVATION OF P. AERUGINOSA BIOFILM USING GRAPHENE OXIDE QUANTUM DOT-METHYLENE BLUE CONJUGATE	۱۴:۵۰-۱۴:۴۰
Mohsen Marvibaigi	AUTOMATION OF BACTERIAL COLONY COUNTING USING CIS SCANNER AND IMAGE PROCESSING	۱۵:۰۰-۱۴:۵۰
Elnaz Afshari	IN VITRO BIOSYNTHESIS OF HYALURONIC ACID BY RECOMBINANT HYALURONAN SYNTHASE	۱۵:۱۰-۱۵:۰۰
Mehrdad Mohammadi	INFECTIONS AND COINFECTIONS OF HUMAN BOCAVIRUS WITH RSV AND ROTAVIRUS IN ACUTE RESPIRATORY TRACT AND GASTROINTESTINAL INFECTIONS	۱۵:۲۰-۱۵:۱۰
Armina Alagheband Bahrami	DESIGN OF POLYVALENT HEPATITIS VACCINE CANDIDATE AND EVALUATION OF ITS EX VIVO STIMULATION IN HUMAN DENDRITIC CELLS	۱۵:۳۰-۱۵:۲۰
Khatereh Kabiri	CHARACTERIZATION OF SHEEP AND GOAT VACCINE STRAINS OF MYCOPLASMA AGALACTIAE FROM RAZI INSTITUTE BY MOLECULAR TYPING ANALYSIS	۱۵:۴۰-۱۵:۳۰
Maryam Dada	BRUCELLOSIS IN IRAN: IDENTIFICATION OF BRUCELLA SPECIES AND BIOVARS ASSOCIATED WITH ANIMAL AND HUMAN INFECTION	۱۵:۵۰-۱۵:۴۰
Atefeh Noori	SELECTION OF DNA APTAMER WITH SPECIFIC BINDING TO PSEUDOMONAS AERUGINOSA	۱۶:۰۰-۱۵:۵۰

سالن B

چهار شنبه ۱۳۹۷/۶/۱۴

هیئت رئیسه: دکتر شهلا منصوری، دکتر محمدرضا شکیبایی، دکتر اصغر شریفی، دکتر رضا میرنژاد، دکتر احیاء عبدی عالی، دکتر فروغ یوسفی		**۱۴:۵۰-۱۴:۰۰**
Alireza Ebrahimi Mojarad	ISOLATION AND CHARACTERIZATION OF HIGH AFFINITY DNA APTAMERS FOR DETECTION OF VIBRIO CHOLERAE	۱۴:۱۰-۱۴:۰۰
Morvarid Shafiei	DETECTION OF TYPE E CLOSTRIDIUM BOTULINUM NEUROTOXIN IN SERUM AND FECAL SAMPLES BY USING AN AMPLIFIED ENZYME-LINKED IMMUNOSORBENT ASSAY WITH C-MYC TAG ANTIBODIES	۱۴:۲۰-۱۴:۱۰
Zahra Pourramezan	PHYLOGENETIC ANALYSES AND MULTILOCUS SEQUENCE TYPING (MLST) OF E. COLI STRAINS FROM NATIONAL E. COLI REFERENCE LABORATORY	۱۴:۳۰-۱۴:۲۰
Arash Ghalyanchilangeroudi	DESIGNING OF NOVEL SPECIFIC RT-PCR FOR DETECTION OF 793/B GENOTYPE OF AVIAN INFECTIOUS BRONCHITIS VIRUS	۱۴:۴۰-۱۴:۳۰
Sajjad Yazdansetad	DEVELOPMENT OF A NEW IMMUNOBLOTTING TECHNIQUE FOR SERODIAGNOSIS OF BURKHOLDERIA MALLEI INFECTION	۱۴:۵۰-۱۴:۴۰

فهرست پوسترهای

نوزدهمین کنگره بین‌المللی میکروب‌شناسی ایران

جدول زمانبندی ارائه پوسترها

سه شنبه ۱۳ شهریور	چهارشنبه ۱۴ شهریور	پنج شنبه ۱۵ شهریور
ساعت ۱۰:۱۵-۱۲:۱۵ P1-P100	ساعت ۸:۰۰-۱۰:۰۰ P301-P400	ساعت ۸:۰۰-۱۰:۰۰ P501-P600
ساعت ۱۳:۳۰-۱۵:۲۰ P101-P200	ساعت ۱۴:۰۰-۱۶:۰۰ P401-P500	ساعت ۱۰:۱۵-۱۱:۱۵ P601-P658
ساعت ۱۵:۳۰-۱۷:۳۰ P201-P300		

Code	ID	Title	Submission Author	Session
P1-P100				روز اول ساعت ۱۲:۱۵-۱۰:۱۵
P 1	536	OPTIMIZATION OF PHYCOCYANIN EXTRACTION FROM SPIRULINA PLATENSIS	Mina Mousavi	Other related topics
P 2	537	COMPARISON OF DIFFERENT SOLVENTS TO EXTRACT PHYCOCYANIN FROM ARTHROSPIRA PLATENSIS	Mina Mousavi	Other related topics
P 3	1	ANTIBACTERIAL EFFECTS OF METHANOL EXTRACT OF DIFFERENT PARTS OF QUERCUS PERSICA AGAINST MRSA AND MSSA CLINICAL ISOLATES	Behnam Hajizadeh sisakht	Antimicrobial agents and Resistance
P 4	2	OCCURRENCE OF BLA GENES ENCODING CARBAPENEM-RESISTANT ACINETOBACTER BAUMANNII FROM INTENSIVE CARE UNIT	Zahra Moulana	Antimicrobial agents and Resistance
P 5	4	META-ANALYSIS STUDY FOR ANTIBIOTIC RESISTANCE OF CITROBACTER FREUNDII CLINICAL ISOLATES	Abozar Kerami	Antimicrobial agents and Resistance
P 6	7	EVALUATION OF THE PRODUCTION RATE OF EXTENDED-SPECTRUM BETA-LACTAMASE ENZYMES BY GRAM-NEGATIVE BACTERIA IN DIFFERENT CLINICAL SAMPLES ISOLATED FROM PATIENTS	Samaneh Rouhi	Antimicrobial agents and Resistance
P 7	8	DETECTION OF MECA GENE AMONG METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS ISOLATED FROM BLOOD INFECTION	ALI JAVADI	Antimicrobial agents and Resistance
P 8	21	EVALUATION OF DRUG RESISTANCE PATTERN OF CANDIDA ALBICANS ISOLATED FROM DIFFERENT CLINICAL SPECIMENS IN QOM, 1396-1395	ALI JAVADI	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 9	31	EVALUATION OF ANTIBACTERIAL EFFECTS OF NEUTRAL ELECTROLYZED WATER ON MULTI-DRUG RESISTANT PSEUDOMONAS AERUGINOSA STRAINS ISOLATED FROM PATIENTS IN GOLESTAN PROVINCE	Leila Fozouni	Antimicrobial agents and Resistance
P 10	49	PANTON- VALENTIN LEUKOCIDIN AND MECA IN METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS (MRSA) ISOLATES FROM HOSPITALIZED PATIENTS IN RASHT, IRAN	Houra Pourghafar	Antimicrobial agents and Resistance
P 11	52	IDENTIFICATION OF KPC BETA-LACTAMASE GENE IN KLEBSIELLA PNEUMONIA ISOLATES ISOLATED FROM PULMONARY SECRETIONS	Samira Mohammadi	Antimicrobial agents and Resistance
P 12	53	INVESTIGATION OF THE PRESENCE OF EXOTOXIN S IN PSEUDOMONAS AERUGINOSA WITH BROAD-SPECTRUM BETA-LACTAMASE	Samira Mohammadi	Antimicrobial agents and Resistance
P 13	58	EVALUATION OF ANTIBIOTIC RESISTANCE PATTERN AND EFFICACY OF MODIFIED HODGE TEST FOR DETECTION OF CARBAPENEM-RESISTANT KLEBSIELLA PNEUMONIAE STRAINS ISOLATED FROM CLINICAL SAMPLES.	Leila Gheitani	Antimicrobial agents and Resistance
P 14	59	PREVALENCE OF CARBAPENEMASE AND BLAKPC GENE IN KLEBSIELLA PNEUMONIAE STRAINS ISOLATED FROM ISFAHAN HOSPITALS, IRAN	Leila Gheitani	Antimicrobial agents and Resistance
P 15	62	EMERGENCE OF VANCOMYCIN-RESISTANT COAGULASE-NEGATIVE STAPHYLOCOCCI IN AN EDUCATIONAL AND THERAPEUTIC HOSPITAL OF SARI, IRAN	Zahra Norouzibazgir	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 16	63	PREVALENCE OF CITROBACTER FRUNDI BACTERIUM AND ANTIBIOTIC SUSCEPTIBILITY PATTERNS IN ZARREH HOSPITALIZED BURNED PATIENTS SARI, IRAN, 2017.	Zahra Norouzibazgir	Antimicrobial agents and Resistance
P 17	73	INVESTIGATION OF RESISTANCE RATE TO AMINOGLYCOSIDES, BETALACTAM, FLUOROQUINOLONES AND TETRACYCLINES IN ENTEROBACTERIACEAE ISOLATES FROM TABRIZ	Elham Sheykhsaran	Antimicrobial agents and Resistance
P 18	74	RESISTANCE RATE TO TETRACYCLINE AND RELEVANT RESISTANCE GENES, TETA, TETB, TETC AND TETD IN E.COLI ISOLATES FROM AZERBAIJAN	Elham Sheykhsaran	Antimicrobial agents and Resistance
P 19	82	DETECTION OF CLASS 1 INTEGRONS AMONG GRAM NEGATIVE BACILLI ISOLATED FROM SPUTUM CULTURES OF PATIENTS WITH RESPIRATORY SYMPTOMS REFERING TO TEACHING HOSPITALS IN AHVAZ, IRAN	Mahtab Khoshkholgh Sima	Antimicrobial agents and Resistance
P 20	84	MOLECULAR ANALYSIS OF GENES OF ESBL)SHV.TEM.CTX) IN SHIGELLA SONNEI ISOLATED FROM CLINICAL SAMPLES BY PCR	Shadi Mosadegh	Antimicrobial agents and Resistance
P 21	85	IDENTIFICATION OF BLACTX-M, BLASHV, AND BLATEM GENES IN PSEUDOMONAS AERUGINOSA STRAINS ISOLATED FROM HUMAN AND ANIMAL SAMPLES USING MULTIPLEX-PCR METHOD	Farzane Farzali	Antimicrobial agents and Resistance
P 22	86	INVESTIGATION OF PREVALENCE OF TEM GENE AMONG ESCHERICHIA COLI STRAINS ISOLATED FROM ARAK HOSPITALS	Afsoon Shariat	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 23	91	STUDY THE EFFICACY OF ANTIMICROBIAL ACTIVITIES OF EIGHT CLINICALLY APPLIED DISINFECTANTS AGAINST CLINICAL ISOLATED OF ENTEROCOCCI AND PSEUDOMONAS AERUGINOSA	Maryam Hassan	Antimicrobial agents and Resistance
P 24	98	COMPARISON OF VIRULENCE GENES, BIOFILM FORMATION, AND ANTIBIOTIC RESISTANCE PATTERN IN E. FAECALIS AND E. FAECIUM ISOLATED FROM CLINICAL AND COMMENSAL HUMAN SAMPLES IN ISFAHAN, IRAN	Farkhondeh Poursina	Antimicrobial agents and Resistance
P 25	106	IN SILICO IDENTIFICATION AND COMPARATIVE GENOMICS OF CANDIDATE GENES INVOLVED IN BIOSYNTHESIS NATURAL PRODUCTS IN CYANOBACTERIA STRAINS OF IRAN	Bahareh Nowruzi	Antimicrobial agents and Resistance
P 26	113	INVESTIGATION OF ANTIBIOTIC SUSCEPTIBILITY PATTERN OF STAPHYLOCOCCUS AUREUS STRAINS ISOLATED FROM PATIENTS REFERRING TO SOME TREATMENT CENTERS OF QOM CITY, IRAN	Fatemeh Sadat Razavinia	Antimicrobial agents and Resistance
P 27	117	ANTIFUNGAL SUSCEPTIBILITY OF OPPORTUNISTIC MEMBERS OF THE ORDER MUCORALES	Somayeh Dolatabadi	Antimicrobial agents and Resistance
P 28	119	DETECTION OF THE POLYKETIDE SYNTHASE (PKSS) GENES WITH ANTIMICROBIAL ACTIVITY IN SOIL CYANOBACTERIA OF THE LAVASAN	Bahareh Nowruzi	Antimicrobial agents and Resistance
P 29	121	DETERMINATION OF ANTIBIOTIC RESISTANCE AND FREQUENCY EXTENDED-SPECTRUM BETA LACTAMASES IN ACINETOBACTER BAUMANNII STRAINS ISOLATED FROM PATIENTS HOSPITALIZED IN BURNS WARD IN TEHRAN	Farid Tarafdar	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 30	122	THE STUDY MOLECULAR OF OXA-48 AND DETERMINATION OF RESISTANCE PATTERN IN CLINICAL ISOLATE OF PSEUDOMONAS AERUGINOSA IN PATIENTS HOSPITALIZED IN BURNING WARD OF ERFAN HOSPITAL, TEHRAN	Farid Tarafdar	Antimicrobial agents and Resistance
P 31	144	THE FIRST REPORT OF EMERGING MOBILIZED COLISTIN RESISTANCE (MCR) GENES IN E.COLI AND KLEBSIELLA PNEUMONIAE ISOLATES FROM CLINICAL SPECIMENS AND TYPING OF THEM BY ERIC-PCR METHOD IN IRAN	Nasrin Emam	Antimicrobial agents and Resistance
P 32	146	CHARACTERIZATION OF EMBCAB GENE MUTATIONS ASSOCIATED WITH ETHAMBUTOL RESISTANCE IN MYCOBACTERIUM TUBERCULOSIS ISOLATES FROM IRAN	MAHTAB ABDI	Antimicrobial agents and Resistance
P 33	151	PHYLOGENETIC ANALYSIS AND ANTIBIOTIC PATTERN DETERMINATION OF ESCHERICHIA COLI STRAINS ISOLATED FROM THE COAST OF THE GENAVEH REGION	Roya Sardari	Antimicrobial agents and Resistance
P 34	155	THE EFFECT OF THE DEHYDROZINGERONE ON THE BIOFILM FORMATION IN CANDIDA ALBICANS	Sepideh Nejatbakhsh	Antimicrobial agents and Resistance
P 35	157	STUDY OF THE ANTIMICROBIAL EFFECTS OF METHANOLIC EXTRACT OF OLIVE LEAVES ON PATHOGENIC STRAINS UNDER LABORATORY CONDITIONS	Shabnam Torabi	Antimicrobial agents and Resistance
P 36	160	PHENOTYPIC AND GENOTYPIC SCREENING OF ADHESIVE VIRULENCE FACTORS OF ACINTOBACTER BAUMANNII ISOLATED FROM ZANJAN HOSPITALS	Fatemeh Valadkhani	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 37	167	ANTIBIOTIC SUSCEPTIBILITY PATTERN AND PREVALENCE OF MECA GENE AMONG CLINICAL ISOLATES OF STAPHYLOCOCCUS AUREUS FROM SANANDAJ, IRAN	Samira Saedi	Antimicrobial agents and Resistance
P 38	176	EXPRESSION OF AAP AND ICAR GENES INVOLVED IN BIOFILM PRODUCTION IN CLINICAL STRAINS OF STAPHYLOCOCCUS AUREUS RESISTANT TO METHICILLIN AND GENTAMICIN	Narges Heidari	Antimicrobial agents and Resistance
P 39	183	THE EFFECT OF ZN NANOPARTICLES (ZNNPS) ON CIPROFLOXACIN-RESISTANT STAPHYLOCOCCUS AUREUS ISOLATES FROM SKIN INFECTIONS IN QOM PROVINCE	Mohammad hossein Soleimani	Antimicrobial agents and Resistance
P 40	184	INVESTIGATING THE ABILITY OF BIOFILM PRODUCTION IN MULTIDRUG-RESISTANT STAPHYLOCOCCUS AUREUS STRAINS (MDR) ISOLATED FROM SKIN INFECTIONS IN QOM PROVINCE	Mohammad hossein Soleimani	Antimicrobial agents and Resistance
P 41	191	EVALUATION OF ANTIBIOTIC RESISTANCE IN ESCHERICHIA COLI STRAINS ISOLATED FROM URINARY TRACT INFECTIONS IN IMAM REZA HOSPITAL, BOJNURD, IN 1396	Reza Behzadfar	Antimicrobial agents and Resistance
P 42	198	ISOLATING LYTIC COLIPHAGES FROM SEWAGE	Salehe Sabouri	Antimicrobial agents and Resistance
P 43	199	IN VITRO ANTIMICROBIAL ACTIVITY OF CINNAMON, GARLIC, AND GINGER EXTRACTS ON METALLO-B-LACTAMASE-PRODUCING PSEUDOMONAS AERUGINOSA: A POTENTIAL THERAPEUTIC APPROACH	Neda Yousefi	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 44	233	EVALUATION ANTIMICROBIAL SUSCEPTIBILITY PATTERNS AND PRESENCE OF ESBLS AMONG CLINICAL ISOLATES OF P. AERUGINOSA COMPARED TO THE ENVIRONMENTAL AND COCKROACH ISOLATES	Faezeh Kosari	Antimicrobial agents and Resistance
P 45	237	INVESTIGATION OF BETA-LACTAM ANTIBIOTIC RESISTANT E.COLI ISOLATED FROM URINARY TRACT INFECTIONS (UTI) PATIENTS REGARDING SHV, CTX-M AND IMP GENES	Anna Abdolshahi	Antimicrobial agents and Resistance
P 46	240	ANTIMICROBIAL EFFECT OF ATRAGIN HERBAL CREAM ON DIFFERENT MICROBIAL ISOLATES	Narges Golab	Antimicrobial agents and Resistance
P 47	251	STUDY AND MOLECULAR CHARACHTRIZATION OF KLEBSIELLA PNEUMONIAE RESISTANT TO ANTIBIOTIC FROM PATIENTS REFERRING TO HOSPITALS IN TEHRAN BASED ON PER, SHV AND VEB GENES	ZAHRA Kohanrooz bijarpas	Antimicrobial agents and Resistance
P 48	252	ANTIBACTERIAL EFFECT OF GERANIUM OIL ON E. COLI, BACILLUS, STAPHYLOCOCCUS AUREUS, AND PSEUDOMONAS AERUGINOSA	Saeedeh Ghiasvand	Antimicrobial agents and Resistance
P 49	256	EFFECTS OF METHANOLIC EXTRACT OF CALCEOLARIA HERBEOHYBRIDA ON MICROORGANISMS	Vida Tafakori	Antimicrobial agents and Resistance
P 50	270	ANTIBIOTIC RESISTANCE AND FREQUENCY OF CLASS 1 AND 2 INTEGRONS AMONG PSEUDOMONAS AERUGINOSA	Mehrdad Halaji	Antimicrobial agents and Resistance
P 51	288	FREQUENCY OF SEPSIS IN THE NEONATES AND DETERMINATION OF ANTIBIOTIC RESISTANCE OF ISOLATES IN ISFAHAN	Vajihe Karbasizadh	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 52	296	ANTIBIOFILM POTENTIAL OF CURCUMIN AGAINST AEROMONAS HYDROPHILA FISH ISOLATES	Hadi Tanhay	Antimicrobial agents and Resistance
P 53	306	SIX-YEAR EVALUATION OF THE ANTIMICROBIAL SUSCEPTIBILITY PATTERNS OF GRAM-POSITIVE BACTERIA CAUSING BLOODSTREAM INFECTIONS IN IRAN.	Babak Pourakbari	Antimicrobial agents and Resistance
P 54	308	ANTIBACTERIAL ACTIVITY OF NIGELLA SATIVA EXTRACT AGAINST TWO PATHOGENIC BACTERIA	Mohammad Mehdi Attarpour Yazdi	Antimicrobial agents and Resistance
P 55	314	ANTIBIOTIC RESISTANCE PATTERN OF METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS (MRSA) STRAINS ISOLATED OF CLINICAL SPECIMENS IN AHVAZ, IRAN	Simin Ariyarad	Antimicrobial agents and Resistance
P 56	315	OCCURRENCE OF THE METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS (MRSA) AMONG RESPIRATORY TRACT SAMPLES IN PATIENTS ADMITTED IN IMAM REZA HOSPITAL, BOJNURD, IRAN IN 1396	Zahra AliAbadi	Antimicrobial agents and Resistance
P 57	318	FIRST PREVALENCE OF METALLO BETA-LACTAMASES PRODUCING ENTEROBACTERIACEA IN IRANIAN CANCER PATIENTS	Donya Zare	Antimicrobial agents and Resistance
P 58	321	GENETIC ANALYSIS OF STAPHYLOCOCCUS AUREUS STRAINS ISOLATED FROM PATIENTS ADMITTED TOM EMAM REZA HOSPITAL IN BOJNURD	Amir Azimian	Antimicrobial agents and Resistance
P 59	323	EVALUATION OF SOME HEAVY METALS AND ANTIBIOTICS RESISTANCE IN SOME OF PROBIOTIC BACTERIA	Leila Goudarzi	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 60	324	EVALUATING THE SIMULTANEOUS IMPACT OF NANOPARTICLES WITH NETTLE EXTRACT AGAINST KLEBSIELLA THROUGH A CHECKERBOARD METHOD	Mahsa Dadgar	Antimicrobial agents and Resistance
P 61	325	PREVALENCE OF SALMONELLA SEROGROUPS IN CHICKEN MEAT OF ARDABIL, NORTHWEST OF IRAN	Aidin Azizpour	Antimicrobial agents and Resistance
P 62	329	BIODEGRADATION OF TETRACYCLINE BY BASIDIOMYCETE FUNGUS PLEUROTUS OSTREATUS	Ayda Maadani mallak	Antimicrobial agents and Resistance
P 63	339	A COMPARISON STUDY OF PYRAN AND PYRAN NANOPARTICLES INHIBITORY EFFECT ON AMPC BETA-LACTAMASE PRODUCING KLEBSIELLA ISOLATES	Azam Haddadi	Antimicrobial agents and Resistance
P 64	343	ANTIBACTERIAL ACTIVITY OF CINNAMOMUM ZEYLANICUM ETHANOLIC EXTRACT AGAINST ESCHERICHIA COLI ISOLATED FROM URINARY TRACT INFECTIONS	Mohammad Mehdi Attarpour Yazdi	Antimicrobial agents and Resistance
P 65	347	THE STUDY OF EFFECTIVE BACTERIAL FACTORS IN FORMING THE POST BURN INFECTION IN BURN SECTION OF NEKUEI – HEDAYATI HOSPITAL OF QOM	Mohammad Khodadad Motlagh	Antimicrobial agents and Resistance
P 66	350	SEROTYPING AND ANTIBIOTIC RESISTANCE PATTERNS OF ISOLATED SALMONELLA FROM ANIMAL FEED IN ARDABIL, NORTHWEST OF IRAN	Ciamak Ghazaei	Antimicrobial agents and Resistance
P 67	356	MOLECULAR STUDY OF PMRA, PMRB AND MCR-1 GENES IN PSEUDOMONAS AERUGINOSA ISOLATES AMONG BURN PATIENTS IN SHAHID MOTAHARI HOSPITAL, TEHRAN, IRAN	Ghazaleh Talebi	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 68	360	ANTIFUNGAL EFFECT OF ALLIUM CEPA ETHANOLIC EXTRACT AGAINST TRICHOPYTON RUBRUM	Zeynab Mosazadeh	Antimicrobial agents and Resistance
P 69	365	THE PREVALENCE OF GYRA GENE MUTATIONS IN FLUOROQUINOLONES-RESISTANT PSEUDOMONAS AERUGINOSA ISOLATES IN GUILAN PROVINCE	Pouria Sheikhi	Antimicrobial agents and Resistance
P 70	374	EVALUATION OF ANTIMICROBIAL AND HEALING PROPERTIES OF BDELLIUM,DRACOCEPHALUM AND DIANTHUS EXTRACTS ON PSEUDOMONAS AERUGINOSA,STAPHYLOCOCCUS AUREUS,ESCHERCHOA COLI AND ENTREROCOCCUS FEACALIS INFECTIONS IN THE IN_VITRO AND MICE MODEL	Fateme Zayer	Antimicrobial agents and Resistance
P 71	375	ANTIBIOTIC RESISTANCE AMONG ESCHERICHIA COLI, PSEUDOMONAS AERUGINOSA AND ACINETOBACTER BAUMANNII ISOLATES OBTAINED FROM SHIRAZ NAMAZI HOSPITAL ICU WARDS	Reza Khashei	Antimicrobial agents and Resistance
P 72	386	FREQUENCY OF ISOLATION AND ANTIMICROBIAL RESISTANCE PATTERN OF GRAM-POSITIVE BACTERIA ISOLATED FROM PATIENTS REFERRED TO PRIVATE DIAGNOSTIC MEDICAL LABORATORIES IN FARS, SOUTHWEST IRAN	Fatemeh Moradi	Antimicrobial agents and Resistance
P 73	389	ANTIBIOTIC SENSITIVITY PATTERN IN PATIENTS WITH URINARY TRACT INFECTIONS	Zohreh Khazaee	Antimicrobial agents and Resistance
P 74	391	ANTIBIOTIC RESISTANCE PATTERN IN E.COLI ISOLATES IN PATIENTS WITH URINARY TRACT INFECTION IN IMAM REZA HOSPITAL IN MASHHAD	Maryam Hafiz	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 75	398	EVALUATION OF ANTIBACTERIAL EFFECT OF LAVENDER,LAVENDULA ANGUSTIFOLIA,AND MELISSA , MELISSA OFFICIALIS,EXTRACTS ON HUMAN PATHOGENS	NASIM GHORBANI	Antimicrobial agents and Resistance
P 76	399	DETECTION OF METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS (MRSA) IN CLINICAL SAMPLE OF PATIENTS WITH EXTERNAL OCULAR INFECTION	Mohammad reza Kandehkar Ghahraman	Antimicrobial agents and Resistance
P 77	403	NITAZOXANIDE AND DOXYCYCLINE SENSITIVITY AMONG METRONIDAZOLE RESISTANT HELICOBACTER PYLORI ISOLATES FROM PATIENTS WITH GASTRITIS	Ali Baradaran	Antimicrobial agents and Resistance
P 78	405	COMPARISON OF GREEN AND BLACK TEA EXTRACT ON THE DOMINANT PATHOGENS OF ENTERIC	Fatemeh Bazmani	Antimicrobial agents and Resistance
P 79	409	DETECTION OF SGI1 AND ITS VARIANTS IN SALMONELLA SEROVARS ISOLATED FROM DIFFERENT HUMAN AND ANIMAL SOURCES	Arefeh Ghoddusi	Antimicrobial agents and Resistance
P 80	423	EVALUATION AND ENUMERATION OF ANTIBACTERIAL EFFECTS OF XYLITOL AGAINST PNEUMOCOCCAL GROWTH BY MTT ASSAY	Ali Asgari	Antimicrobial agents and Resistance
P 81	425	THE ANTIBACTERIAL ACTIVITY OF ETHANOL EXTRACT OF KHORASANI PROPOLIS ISOLATED FROM BINALOUD MOUNTAINS	Fatemeh Shahab navai	Antimicrobial agents and Resistance
P 82	429	PREVALENCE AND ANTIBIOTIC RESISTANCE PATTERN OF GRAM POSITIVE UROPATHOGENIC BACTERIA ISOLATED FROM URINE SAMPLES IN BANDAR TORKAMAN, IRAN	Mohammad Bartimar	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 83	430	ANTIBIOTIC RESISTANCE PATTERN AND FREQUENCY OF EXTENDED SPECTRUM B-LACTAMASES (ESBLS) IN GRAM NEGATIVE UROPATHOGENIC BACTERIA ISOLATED FROM URINE SAMPLES IN BANDAR TORKAMAN, IRAN	Mohammad Bartimar	Antimicrobial agents and Resistance
P 84	431	EVALUATING THE EFFECT OF HEAT-KILLED PATHOGENS ON ANTIMICROBIAL COMPOUNDS PRODUCTION IN STREPTOMYCES SP.AC117	Hanieh Shakeri moghaddam	Antimicrobial agents and Resistance
P 85	432	ELICITING THE ANTIMICROBIAL COMPOUNDS PRODUCTION IN STREPTOMYCES SP.AC117 BY DIFFERENT INOCULATION AMOUNT OF HEAT-KILLED PSEUDOMONAS AERUGINOSA	Hanieh Shakeri moghaddam	Antimicrobial agents and Resistance
P 86	444	FIRST REPORT OF SOME CLASS 1 INTEGRON-ASSOCIATED GENE CASSETTE ARRAYS AMONG ESCHERICHIA COLI AND KLEBSIELLA PNEUMONIAE ISOLATED FROM PATIENTS WITH URINARY TRACT INFECTION IN SOUTHWEST OF IRAN	Seyed Sajjad Khoramrooz	Antimicrobial agents and Resistance
P 87	445	ANTIMICROBIAL ACTIVITY OF MENTHA PULEGIUM ESSENTIAL OIL	Marzieh Bahramian	Antimicrobial agents and Resistance
P 88	450	ANTIMICROBIAL EFFECTS OF ETHANOL EXTRACTS OF PLANTS MEDICAGO SATIVA AND ECHINOPHORA PLATYLOBA D.C ON ENTEROCOCCUS FAECALIS BACTERIA IN VITRO	Mansoor Khaledi	Antimicrobial agents and Resistance
P 89	466	SYNTHESIS AND EVALUATION OF ANTIBACTERIAL ACTIVITY OF 2,5-DISUBSTITUTED 1,3,4-OXADIAZOLES DERIVATIVES CONTAINING HALOGEN	Elahe Tajbakhsh	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 90	467	EVALUATION OF EFFECTS OF ESSENTIAL OIL OF THREE SPECIES THYMUS ON E.COLI , PESUDOMONAS AERUGINOSA, STAPHYLOCOCCUS AUREUS AND CANDIDA ALBICANS AND COMPARE EFFECT OF ANTIMICROBIAL AGENT	Emad Vahidi manesh	Antimicrobial agents and Resistance
P 91	472	INVESTIGATION OF THE CHARACTERISTICS AND EFFICIENCY OF LYTIC PHAGE MDRACINETOBACTERBAUMANNII SEPARATED FROM THE ICU	Behnam Sisakhtpour	Antimicrobial agents and Resistance
P 92	473	ANTIMICROBIAL EFFECTS OF PHENOXY ETHANOL AND CAPROLYL GLYCOL (VERSTATIL PC) AS PRESERVATIVES IN COSMETIC PRODUCTS	Mojtaba Sade	Antimicrobial agents and Resistance
P 93	485	ASSESSMENT OF COLISTIN SENSITIVITY IN CLINICAL GRAM-NEGATIVE BACTERIA IN THE NORTHWEST OF IRAN	Zahra Aghapour	Antimicrobial agents and Resistance
P 94	493	PRODUCTION OF COML RECOMBINANT AND ITS FUNCTIONAL ROLE IN ANTIBIOTIC RESISTANCE	Elahe Abiri	Antimicrobial agents and Resistance
P 95	496	THE DANGER OF INCREASE MBLS PRODUCTER IN HOSPITAL SAMPLES	Seyede Fateme Daymad	Antimicrobial agents and Resistance
P 96	502	DETECTION OF PLASMID MEDIATED QUINOLONE RESISTANCE GENES AMONG KLEBSIELLA PNEUMONIAE ISOLATES COLLECTED FROM URINARY TRACT INFECTIONS	Mohammad Reza Asadi Karam	Antimicrobial agents and Resistance
P 97	506	ASSESSMENT OF CHEMICAL COMPOSITION AND ANTI-DERMATOPHYTE ACTIVITY OF TREE MEDICINAL PLANT ESSENTIAL OILS.	Rezvan Heidary tabar	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 98	515	ANTIFUNGAL EFFECT OF EUGENOL EXTRACT AGAINST ASPERGILLUS FUMIGATUS	Parvin Aghakhani	Antimicrobial agents and Resistance
P 99	533	AN INVESTIGATION OF ANTIBACTERIAL ACTIVITY OF ZNO NANOPARTICLE ON STAPHYLOCOCCUS AUREUS AND E.COLI	Fatemaeh Akbarzadeh	Antimicrobial agents and Resistance
P 100	541	ANTIBACTERIAL ACTIVITY OF JUNIPERUS POLYCARPUS AND GERANIUM ROBERTIANUM LEAF EXTRACTS AGAINST PATHOGENIC STAPHYLOCCOCAL STRAINS	Abolfazl Shirmohamadi	Antimicrobial agents and Resistance
P101-P200				روز اول ساعت ۱۳:۳۰-۱۵:۲۰
P 101	542	ANTIBACTERIAL PROPERTIES OF THE LEAF AND ROOT EXTRACTS OF EREMOSTACHYS BIOSSERIANA AGAINST STAPHYLOCOCCUS EPIDERMIDIS AND STAPHYLOCOCCUS AUREUS BACTERIA	Abolfazl Shirmohamadi	Antimicrobial agents and Resistance
P 102	554	EGG YOLK IMMUNOGLOBULIN AGAINST PSEUDOMONAS AERUGINOSA OPRF, PREVENTION AND TREATMENT OF INFECTIONS	Fatemeh Noroozi	Antimicrobial agents and Resistance
P 103	562	LINEZOLID, QUINUPRISTIN/DALFOPRISTIN AND DAPTOMYCIN RESISTANCE IN VANCOMYCIN RESISTANT ENTEROCOCCI IN TEHRAN HOSPITALS	Jaber Ghorbani	Antimicrobial agents and Resistance
P 104	566	EVALUATION OF ANTIBACTERIAL ACTIVITY OF MATHANOL,ETHYL ACETATE AND HEXANE EXTRACTS OF CRUCIATA TAURIACA	Behnaz Asadi	Antimicrobial agents and Resistance
P 105	573	BACTERIAL BIOFILM IN VENTILATOR-ASSOCIATED PNEUMONIA	Elnaz Shahrukhi	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 106	580	PREVALENCE OF TEM, CTX-M AND SHV GENES IN KLEBSIELLA PNEUMONIAE ISOLATED FROM PATIENTS WITH VENTILATOR-ASSOCIATED PNEUMONIA	Kamal Ahmadi	Antimicrobial agents and Resistance
P 107	585	THE CORRELATION BETWEEN BIOFILMS FORMATION CAPABILITIES WITH THEIR RELATED GENES AND ANTIBIOTIC RESISTANCE PATTERNS IN CLINICAL AND ENVIRONMENTAL ISOLATES OF PSEUDOMONAS AERUGINOSA	Pezhman Karami	Antimicrobial agents and Resistance
P 108	587	APPLICATION OF MULTIPLEX-PCR IN THE DETECTION OF OXA PLASMID GENES IN CLINICAL ISOLATES OF KLEBSIELLA PNEUMONIAE	Reza Yari	Antimicrobial agents and Resistance
P 109	588	DETERMINATION OF ANTIBIOTIC RESISTANCE PATTERN AND THE PREVALENCE OF BETA-LACTAMASE GENE BLATEM, SHV AND DHA IN PSEUDOMONAS AERUGINOSA CLINICAL SAMPLES	Reza Yari	Antimicrobial agents and Resistance
P 110	593	FREQUENCY OF MULTI-DRUG RESISTANCE IN ENTEROBACTER ISOLATED FROM PATIENTS WITH URINARY TRACT INFECTION IN GORGAN	Hanieh Bagheri	Antimicrobial agents and Resistance
P 111	600	PROPOSING A POTENTIAL SMART DIGITAL NETWORK FOR TREATMENT WITH PROBABLE ANTIBIOTICS	Fateme Elahi	Antimicrobial agents and Resistance
P 112	606	ANTIMICROBIAL PROPERTIES OF CLOVE EXTRACT (SYZYGIUM AROMATICUM)	Hamideh Asayeshtalab	Antimicrobial agents and Resistance
P 113	608	METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS (MRSA) AND STAPHYLOCOCCAL CASSETTE CHROMOSOME MEC GENOTYPES (SCCMEC) IN FASA, FARS	Abbas Abdollahi	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 114	610	EVALUATION OF ANTIBIOTIC RESISTANCE OF ACINETOBACTER BAUMANNII STRAINS ISOLATED FROM CLINICAL SAMPLES OBTAINED IN ZAHEDAN HOSPITALS	Elnaz Arzhang	Antimicrobial agents and Resistance
P 115	611	ANTIMICROBIAL EFFECTS OF THE HYDRO-ALCOHOLIC EXTRACT OF FALCARIA VULGARIS	Azadeh Foroughi	Antimicrobial agents and Resistance
P 116	613	EVALUATION OF ANTIBACTERIAL ACTIVITY OF HYDRO-ALCOHOLIC EXTRACT IN HERBAL PLANT SPECIES, NATIVE OF FASA, FARS	Abbas Abdollahi	Antimicrobial agents and Resistance
P 117	614	ANTIBIOTIC RESISTANCE PATTERN AND FREQUENCY OF ESBL PRODUCING ENTEROBACTERIACEAE ISOLATED FROM LETTUCE AND SPINACH IN GORGAN	Neda Kouroshzadeh	Antimicrobial agents and Resistance
P 118	616	QUINOLONE SUSCEPTIBILITY AND PHYLOGENETIC ANALYSIS OF ESCHERICHIA COLI STRAINS ISOLATED FROM HUMAN AND CALVES	Mojdeh Barzan	Antimicrobial agents and Resistance
P 119	623	TRENDS OF ANTIMICROBIAL RESISTANCE AMONG UROPATHOGENIC ESCHERICHIA COLI ISOLATES IN RUDBAR, NORTH OF IRAN	Susan Khanjani	Antimicrobial agents and Resistance
P 120	628	DETERMINATION OF ANTIBIOTIC RESISTANCE PATTERN IN ENTROBACTERIACEAE ISOLATED FROM HOSPITAL WASTEWATER IN KARAJ	Azam Haddadi	Antimicrobial agents and Resistance
P 121	629	ESBL PREVALENCE IN ENTROBACTERIACEAE ISOLATED FROM HOSPITAL'S WASTEWATER IN KARAJ.	Azam Haddadi	Antimicrobial agents and Resistance
P 122	635	DIFFERENT VIRULENCE CAPABILITY AND PATHOGENIC STRATEGY AMONG CLINICAL ISOLATES OF MULTI-DRUG RESISTANT ACINETOBACTER BAUMANNII	Armaghan Soltani Shirazi	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 123	646	COMPARISON OF DISK DIFFUSION AND E-TEST METHODS TO DETERMINE ANTIMICROBIAL ACTIVITY OF CEFTAZIDIME AND CIPROFLOXACIN ON CLINICAL ISOLATES OF ACINETOBACTER BAUMANNII	Mojtaba Mirshekari Soleimani	Antimicrobial agents and Resistance
P 124	653	MODIFIED CONGO RED AGAR METHOD TO DETECT BIOFILM PRODUCTION BY ENTEROCOCCUS FAECIUM	Saber Soltani	Antimicrobial agents and Resistance
P 125	655	FALSE COMBINED DISCS TEST FOR DETECTION OF EXTENDED-SPECTRUM B-LACTAMASE (ESBL) IN ACINETOBACTER ISOLATES	Nasim Shams	Antimicrobial agents and Resistance
P 126	657	COMPARISON OF METHODS FOR THE DETECTION OF BIOFILM FORMATION BY ENTEROCOCCUS FAECIUM ISOLATED FROM HOSPITALIZED PATIENTS	Saber Soltani	Antimicrobial agents and Resistance
P 127	673	IDENTIFICATION OF A NEW SMALL MOLECULE FROM TAXUS BACCATA PLANT AS A POTENTIAL INHIBITOR OF VIRB8 OF BRUCELLA BACTERIA BY HIGH-THROUGHPUT VIRTUAL SCREENING ON TRADITIONAL CHINESE MEDICINE DATABASE	Seyede Solmaz Moosavi	Antimicrobial agents and Resistance
P 128	680	MOLECULAR ASSESSMENT OF INTEGRONS IN ISOLATES OF ESCHERICHIA COLI OBTAINED FROM CHILDREN WITH URINARY TRACT INFECTIONS IN KERMANSHAH	Nahid Madadigoli	Antimicrobial agents and Resistance
P 129	683	COMPARISON OF ANTIMICROBIAL RESISTANCE PATTERN OF ENTEROCOCCUS FAECALIS NORMAL FLORA AND ENVIRONMENTAL ISOLATES	Saba Asgharzade	Antimicrobial agents and Resistance
P 130	687	ANTIMICROBIAL EFFECT OF ROSEMARY EXTRACT	Faezeh Fallah	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 131	689	THE FREQUENCY OF RESISTANCE TO ANTIFUNGAL DRUGS IN CANDIDA ALBICANS ISOLATES ISOLATED FROM CASES OF VAGINITIS IN TABRIZ ALZAHRA HOSPITAL	Leila Mohammadi	Antimicrobial agents and Resistance
P 132	691	THE PREVALENCE OF PANTON VALENTINE LEUKOCIDIN POSITIVE IN S. AUREUS ISOLATED FROM SKIN AND SOFT TISSUE INFECTION	Zeinab Faghee	Antimicrobial agents and Resistance
P 133	692	PHENOTYPIC AND GENOTYPIC DETECTION OF EXTENDED-SPECTRUM B-LACTAMASE (ESBL)-PRODUCING ESCHERICHIA COLI IN PATIENTS WITH COMMUNITY-ACQUIRED URINARY TRACT INFECTIONS	Meisam Poormaleknia	Antimicrobial agents and Resistance
P 134	696	MULTIPLEX PCR OF QNRB, AAC(6'),16SRRNA METHYL TRANSFERASE GENES AMONG MDR PSEUDOMONAS AERUGINOSA ISOLATES FROM BURN WOUND INFECTIONS OF MOTAHARI HOSPITAL, TEHRAN, IRAN	Atiyeh Shaban Ghahrood	Antimicrobial agents and Resistance
P 135	702	PREVALENCE OF SUL1 IN CLINICAL ISOLATES OF PESUDOMONAS AERUGINOSA	Sahar Alishanni	Antimicrobial agents and Resistance
P 136	706	IDENTIFICATION AND ANTIBIOGRAM ANALYSIS OF VARIOUS BACTERIAL ISOLATES FROM URINE IN ROUTINE DIAGNOSTIC LOBORATORIES OF KERMAN, IRAN	Mohammad Dehvari	Antimicrobial agents and Resistance
P 137	708	FREQUENCY OF FIM GENE IN ESCHERICHIA COLI ISOLATES FROM URINARY TRACT INFECTIONS OF IMAM KHOMAINI HOSPITAL IN TEHRAN	Sepide Ghasemshahi	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 138	714	THE OCCURRENCE OF CTX-M-15 EXTENDED-SPECTRUM B-LACTAMASE AMONG CLINICAL ISOLATES OF KLEBSIELLA PNEUMONIAE IN KHORRAMABAD, IRAN	Gholamreza Goudarzi	Antimicrobial agents and Resistance
P 139	721	EVALUATING THE IN VITRO INHIBITORY EFFECT OF NANOEIZED PARTICLES OF PYRANS ON ESBLS PRODUCING ESCHERICHIA COLI STRAINS ISOLATED FROM CLINICAL SPECIMENS IN KARAJ CITY	Parasto Saadai	Antimicrobial agents and Resistance
P 140	722	COMPARISON OF THE PREVALENCE OF METALLO-B-LACTAMASE RESISTANCE OF PSEUDOMONAS AERUGINOSA BETWEEN 1396 AND 1397 BY DOUBLE DISK SYNERGY TEST AND COMBINE DISK METHODS IN MASHHAD'S HOSPITALS	Kowsar Assad allah pour	Antimicrobial agents and Resistance
P 141	723	FREQUENCY OF INTESTINAL CARRIAGE OF HIGH-LEVEL STREPTOMYCIN RESISTANT ENTEROCOCCAL ISOLATES IN HEALTHY CHILDREN ATTENDING SCHOOLS IN ARDABIL, 2017	Elham Jannati	Antimicrobial agents and Resistance
P 142	733	PHYTOCHEMICAL STUDY AND ANTIBACTERIAL ACTIVITY OF GLYCYRRHIZA GLABRA L. AND ITS COMBINATION WITH GENTAMICIN AGAINST KLEBSIELLA PNEUMONIAE, IN VITRO	Vahid Reisi Vanani	Antimicrobial agents and Resistance
P 143	739	STUDY THE PREVALENCE OF RESISTANCE GENE, QACE TO QUATERNARY AMMONIUM COMPOUNDS IN THE ISOLATED ACINETOBACTER BAUMANNII OF HOSPITAL OF QAZVIN (2015-2016)	Samaneh Keshavarz hedayati	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 144	743	COPPER OXIDE AND TITANIUM DIOXIDE NANOPARTICLES IMPACT ON GROWTH OF ENTEROBACTER AEROGENES IN LIQUID MEDIUMS	Shervin Shabani	Antimicrobial agents and Resistance
P 145	748	STUDY OF ANTIADHISION/ANTIBIOFILM EFFECTS OF RHAMNOLIPID-TYPE BIOSURFACTANT AGAINST CLINICAL ISOLATES OF PSEUDOMONAS AERUGINOSA AND ACINETOBACTER BAUMANNII	Minoo Monzavi	Antimicrobial agents and Resistance
P 146	754	ANTIBIOTIC SUSCEPTIBILITY AND FREQUENCY OF RESISTANCE GENES PENA AND AMPC AMONG L.MONOCYTOGENES ISOLATES WITH CLINICAL, FOOD AND LIVESTOCK ORIGINS	Ali Mohamadi	Antimicrobial agents and Resistance
P 147	755	THE COMPARISON OF ZOUSH OINTMENT WITH SILVER SULFADIAZINE OINTMENT IN BURN WOUND INFECTION	Maryam Meskini	Antimicrobial agents and Resistance
P 148	759	EVALUATION OF SEVERAL PHENOTYPIC METHODS FOR DETECTION OF KPC AND MBL PRODUCTION IN PSEUDOMONAS AERUGINOSA ISOLATES	Masoumeh Beig	Antimicrobial agents and Resistance
P 149	760	THE COMPARISON OF ZOUSH OINTMENT WITH AKBAR 1 OINTMENT IN BURN WOUND INFECTION	Maryam Meskini	Antimicrobial agents and Resistance
P 150	763	RELATIVE FREQUENCY BIOFILM FORMAITON STRAIN AMONG MULTI DRUG RESISTANCE PSEUDOMONAS AERUGINOSA, ISOLATED FROM PATIANT WITH BURN WOUND OF RASHT BURNE CENTER (VALAYET HOSPITA)	Farhad Afrasiabi	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 151	766	ANTIBACTERIAL EFFECTS OF COPPER DIOXIDE AND TITANIUM DIOXIDE NANOPARTICLES ON ENTEROBACTER AEROGENES BACTERIA IN SOLID MEDIUMS	Hamed Charkhian	Antimicrobial agents and Resistance
P 152	767	INVESTIGATION OF THE ANTIBACTERIAL EFFECT OF HUMAN BIOLOGICAL PRODUCTS, PLATELET CONCENTRATE & AMNIOTIC MEMBRANE, AGAINST BETA-LACTAMASE PRODUCER ISOLATES OF PSEUDOMONAS AERUGINOSA AND STAPHYLOCOCCUS AUREUS	Shahrzad Soumeh saraei sabet	Antimicrobial agents and Resistance
P 153	768	HERBAL EXTRACTS ANTIBACTERIAL EFFECT ON STAPHYLOCOCCUS AUREUS – ELECTROCHEMICAL VS DISK DIFFUSION AGAR METHODS	Sarvenaz Esmaeilee	Antimicrobial agents and Resistance
P 154	769	ANTIMICROBIAL ACTIVITY OF LACTIC ACID BACTERIA ISOLATED FROM TRADITIONAL DAIRY PRODUCTS OF VARZEGHAN	Manigheh Hajizadeh Varzeghan	Antimicrobial agents and Resistance
P 155	777	PREVALENCE OF QNR GENES IN EXTENDED-SPECTRUM B-LACTAMASE PRODUCING KLEBSIELLA PNEUMONIAE ISOLATED FROM CLINICAL URINE SPECIMENS IN UNIVERSITY TEACHING HOSPITALS, IRAN	Amin Dehghan banadkouki	Antimicrobial agents and Resistance
P 156	783	PRODIGIOSIN AGAINST SALMONELLA THYPHIMURIUM	Sorayesh Hajian	Antimicrobial agents and Resistance
P 157	795	RELATION OF TOXA AND TOXS GENES AND ANTIMICROBIAL RESISTANCE IN PSEUDOMONAS AERUGINOSA	Niloufar Mohseni	Antimicrobial agents and Resistance
P 158	804	INHIBITORY POTENCY OF HUMAN ANTIMICROBIAL PEPTIDE DCD-1L ON THE BIOFILM FORMATION OF ACINETOBACTER BAUMANNII	Zahra Farshadzadeh	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 159	805	A STUDY OF PREVALENCE OF SHIGELLA SPECIES AND ESBL PRODUCING ISOLATES IN ARDABIL, IRAN	Sahar Sabour	Antimicrobial agents and Resistance
P 160	809	EVALUATION OF ANTIBACTERIAL ACTIVITY OF MATHANOL AND HEXANE EXTRACTS OF CRUCIATA TAURIACA	Behnaz Asadi	Antimicrobial agents and Resistance
P 161	825	ISOLATION AND ANTIMICROBIAL SUSCEPTIBILITY OF METHICILLIN-RESISTANT STAPHYLOCOCCUS PSEUDINTERMEDIUS (MRSP) IN PETS, VETERINARIANS, AND THE ENVIRONMENT	Mahdi Askari Badouei	Antimicrobial agents and Resistance
P 162	826	THE ROLE OF ADEABC, ADEFGH AND ADEIJK EFFLUX PUMPS IN REDUCED SUSCEPTIBILITY TO TIGECYCLINE IN ACINETOBACTER BAUMANNII ISOLATED FROM BURN PATIENTS	Behrouz Taheri	Antimicrobial agents and Resistance
P 163	828	BIOSYNTHESIS OF ZINC OXIDE NANOPARTICLES USING EUCALYPTUS MELLIDORA LEAF EXTRACT AND EVALUATION OF ITS ANTIMICROBIAL EFFECTS	Behnam Rafiee	Antimicrobial agents and Resistance
P 164	829	PHENOTYPIC AND GENETIC BASIS OF BIOFILM FORMATION BY ESCHERICHIA COLI AND PSEUDOMONAS AERUGINOSA IN MECHANICALLY VENTILATED AND VAP DEVELOPED PATIENTS	Elnaz Shahrukhi	Antimicrobial agents and Resistance
P 165	831	EXPERIMENTAL EVALUATION THE EFFECT OF IRON SALT ON THE INHIBITION OF STREPTOCOCCUS MUTANS	Yalda Malekzadegan	Antimicrobial agents and Resistance
P 166	833	INVESTIGATION OF FREQUENCY AND ANTIMICROBIAL RESISTANCE PATTERN OF PSEUDOMONAS AEROGINOSA AND STAPHYLOCOCCUS SPP. ISOLATED FROM CORNEAL ULCER IN SHIRAZ	Yalda Malekzadegan	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 167	835	PHENOTYPIC DETECTION OF ANTIBIOTIC RESISTANCE AND EXTENDED SPECTRUM B-LACTAMASE IN ECOLI STRAIN ISOLATES IN TABRIZ SINA HOSPITAL	Tahereh Eskandari	Antimicrobial agents and Resistance
P 168	839	COMPARISON OF THE ANTIFUNGAL ACTION POTENCY OF TEUCRIUM POLIUM L. AND AMPHOTRICIN B AGAINST CANDIDA PARAPSILOSIS	Elham Rezaei	Antimicrobial agents and Resistance
P 169	840	GREEN SYNTHESIS OF SILVER NANOPARTICLES BY EXTRACT OF JUGLANS REGIA LEAF AND EVALUATION OF ITS ANTIBACTERIAL EFFECTS	Behnam Rafiee	Antimicrobial agents and Resistance
P 170	841	SILVER NANOPARTICLES ECOFRIENDLY SYNTHESIS BY SATUREJA HORTENSIS AND EVALUATION ANTIBACTERIAL PROPERTIES	Behnam Rafiee	Antimicrobial agents and Resistance
P 171	842	COMPARISON OF ANTIFUNGAL EFFECTS OF SPARTIUM JUNCEUM AND MELISSA OFFICINALIS HERBS EXTRACTS ON CANDIDA ALBICANS IN COMPARISON WITH THE ANTIBIOTICAL EFFECT	Razieh Taghavizad	Antimicrobial agents and Resistance
P 172	843	COMPARISON OF THE ANTIFUNGAL EFFECTS OF SPARTIUM JUNCEUM AND MELISSA OFFICINALIS HERBS EXTRACTS ON SAPROLEGNIA SP. IN COMPARISON WITH ANTIBIOTICAL EFFECTS	Razieh Taghavizad	Antimicrobial agents and Resistance
P 173	846	MOLECULAR AND SEROLOGICAL DETECTION OF MYCOPLASMA PNEUMONIAE AND DETERMINE OF THE CIPROFLOXACIN RESISTANCE PATTERN	Zohre Darabi	Antimicrobial agents and Resistance
P 174	855	ANTIMICROBIAL EFFECT OF PISTACIA ATLANTICA (BANEH) FOR CURING INFECTION OF CANDIDA ALBICANS IN MOUTH	Ali Mokhtari	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 175	856	IN VITRO ANTI-BACTERIAL AND ANTI-BIOFILM FORMATION ACTIVITIES OF FOUR MEDICINAL PLANTS OF LAMIACEAE FAMILY AGAINST KLEBSIELLA PNEUMONIAE	Fateme Yazdani	Antimicrobial agents and Resistance
P 176	859	VIRULENCE FACTORS AND ANTIMICROBIAL RESISTANCE IN UROPATHOGENIC ESCHERICHIA COLI STRAINS ISOLATED FROM CYSTITIS AND PYELONEPHRITIS	Shiva Mirkalantari	Antimicrobial agents and Resistance
P 177	862	FREQUENCY OF BACTERIAL INFECTIONS AND ANTIBIOTIC RESISTANCE AMONG CLINICAL SPECIMENS IN SHAHID RAHIMI HOSPITAL, KHORRAMABAD	Gholamreza Goudarzi	Antimicrobial agents and Resistance
P 178	870	FREQUENCY AND SUSCEPTIBILITY PATTERN OF THE NON FERMENTATIVE GRAM NEGATIVE BACTERIA IN TWO EDUCATIONAL HOSPITALS IN SARI.	Zahra Norouzibazgir	Antimicrobial agents and Resistance
P 179	872	URINARY TRACT INFECTION CAUSED BY EXTENDED-SPECTRUM BETA-LACTAMASE–PRODUCING BACTERIA AND INTEGRONS	Zahra Golestani	Antimicrobial agents and Resistance
P 180	877	DETECTION OF B -LACTAMASE ACTIVITY IN VARIOUS CLINICAL COAGULASE NEGATIVE STAPHYLOCOCCI AND ITS CORRELATION WITH DRUG RESISTANCE	Mahsa Ebrahimi	Antimicrobial agents and Resistance
P 181	880	ANTIBACTERIAL EFFECT OF AILANTHUS ALTISSIMA EXTRACT ON SOME BACTERIA IN SWIMMING POOLS IN COMPARISON WITH ANTIBIOTICAL EFFECT	Razieh Taghavizad	Antimicrobial agents and Resistance

Code	ID	Title	Submission Author	Session
P 182	9	WHEAT GROWTH PROMOTING TRAITS OF FREE NITROGEN FIXING BACTERIA OBTAINED FROM A FIELD IN KERMAN DISTRICT	Najmeh Yazdan panah	Applied and Environmental Microbiology
P 183	17	PROBABLE LINK BETWEEN ISOLATION OF NOCARDIA SPP. FROM ENVIRONMENT AND HUMAN NOCARDIOSIS	Masoud Keikha	Applied and Environmental Microbiology
P 184	24	EFFECT OF SYMBIOSIS INTERACTION OF MYCORRHIZAE ARBUSCULAR ON MINERAL UPTAKE IN WHEAT (PISHTAZ CULTIVAR)	Ashraf Esmaeilizadeh	Applied and Environmental Microbiology
P 185	25	APPLICATION OF CARBOXIN THIRAM FUNGICIDE AND AZOSPIRILLUM GENUS ON MINERALS NUTRIENT UPTAKE OF WHEAT PLANT	Ashraf Esmaeilizadeh	Applied and Environmental Microbiology
P 186	32	COMPARING DETERMINISTIC AND PROBABILISTIC METHODS IN RISK ASSESSMENT OF INFECTIVE ENTEROVIRUSES FOR CONSUMPTION OF LETTUCE IRRIGATED WITH WASTEWATER EFFLUENT	Malihe Moazeni	Applied and Environmental Microbiology
P 187	76	USING CONDUCTOMETRY SYSTEM TO FAST DETECTION OF STAPHYLOCOCCUS BACTERIA	Mehrdad Enami	Applied and Environmental Microbiology
P 188	95	IDENTIFICATION AND PURIFICATION OF MODERATE THERMOPHILIC BACTERIA ISOLATED FROM SARCHESHMEH COPPER MINE	REYHANEH TABREZI MOSAFA	Applied and Environmental Microbiology
P 189	96	NEW CULTURE MEDIUM FOR MODERATE THERMOPHILIC BACTERIA ISOLATED FROM SARCHESHMEH COPPER MINE	REYHANEH TABREZI MOSAFA	Applied and Environmental Microbiology
P 190	99	FEASIBILITY STUDY OF PREPARATION OF CO-AGGLUTINATION COMPLEX FOR RAPID DETECTION OF VIBRIO CHOLERA IN VACCINE RESEARCH AND LABORATORY BY USING STAPHYLOCOCCUS AUREUS PROTEIN A	Shahin Hadadian	Applied and Environmental Microbiology

Code	ID	Title	Submission Author	Session
P 191	112	GENETIC ANALYSIS OF NONRIBOSOMAL PEPTIDE SYNTHESIS GENES (NRPSS) IN THE FRESH WATER CYANOBACTERIAL OF THE LAVASAN LAKE	Bahareh Nowruzi	Applied and Environmental Microbiology
P 192	127	MOLECULAR DETECTION OF HUMAN GROUP A ROTAVIRUSES IN URBAN AND HOSPITAL SEWAGE SYSTEMS AND RIVER WATER SAMPLES IN ALBORZ PROVINCE	Zahra Torfeh	Applied and Environmental Microbiology
P 193	129	STUDY OF ANTIBACTERIAL ACTIVITY MEDICINAL PLANTS IN THE TREATMENT OF HELICOBACTER PYLORI INFECTIONS	Nahid Dezvaree	Applied and Environmental Microbiology
P 194	138	SUBMERGED FERMENTATION OF AURICULARIA AURICULA FOR BIOMASS STIMATION	Arghavan Rahimian	Applied and Environmental Microbiology
P 195	139	BIOMASS PRODUCTION OF AURICULARIA AURICULA IN SOLID SUBSTRATE	Arghavan Rahimian	Applied and Environmental Microbiology
P 196	154	ISOLATION OF BLACK YEASTS FROM OIL FIELDS OF AHVAZ; POTENTIAL BIOREMEDIATION CANDIDATES	Somayeh Dolatabadi	Applied and Environmental Microbiology
P 197	182	EFFECT OF ULTRASOUND ON CYANOTOXIN DESTRUCTION	Nima Bahador	Applied and Environmental Microbiology
P 198	202	DECOLORIZATION OF REMAZOL RED B BY HALOMONAS SP. PTCC1417 ISOLATED FROM URMIA LAKE: OPTIMIZATION BY TAGUCHI METHODOLOGY	Nasrin Froedin	Applied and Environmental Microbiology
P 199	208	ISOLATION MOLCULAR AND IDENIFICATION OF MYCOBACTERIUM PORCINUM AND MYCOBACTERIUM CELERIFLAVUM FROM MARKAZI PROVINCE ENVIRONMENTAL RESOURCES AND ANALYSIS OF THEIR POLYCYCLIC AROMATIC HYDROCARBONS' BIODEGRADATION ACTIVITY	Davoud Azadi	Applied and Environmental Microbiology

Code	ID	Title	Submission Author	Session
P 200	227	BIODEGRADATION OF PHENOL USING STAPHYLOCOCCUS SP. ISOLATED FROM HOUSEPLANT POTTING SOIL	Mohsen Shahriari moghadam	Applied and Environmental Microbiology
P201-P300				روز اول ساعت ۱۷:۳۰-۱۵:۳۰
P 201	246	IS THE AIR SAMPLES APPROPRIATE TO ISOLATE THE DENITRIFYING BACTERIA?	Taranom Yarandpour	Applied and Environmental Microbiology
P 202	276	OPTIMIZATION OF TRICHODERMA CULTURE MEDIUM USING DIFFERENT CARBON SOURCES TO INCREASE XYLANASE ENZYME PRODUCTION.	Neda Afzali	Applied and Environmental Microbiology
P 203	281	PERFORMANCE EVALUATION OF BIOFILTER IN REMOVING AMMONIA AND HYDROGEN SULFIDE GASES AT LABORATORY SCALE AS A MODEL IN INDUSTRIAL CATTEL	Sahar Karami rubati	Applied and Environmental Microbiology
P 204	283	INVESTIGATION THE ELIMINATION OF MICROBIAL CONTAMINATION IN GLASS CLEANER FORMULATIONS	Mohammdfazel Abedini	Applied and Environmental Microbiology
P 205	320	ISOLATION OF THERMOPHILIC SULFOBACILLUS THERMOSULFIDOOXIDANS FROM SARCHESHMEH COPPER MINE IN KERMAN, IRAN	Fatemeh Hosseinzadeh Parizi	Applied and Environmental Microbiology
P 206	331	ASSESSMENT THE PHYSICOCHEMICAL PROPERTIES, STRUCTURE AND FUNCTION OF FUNGAL STRAINS LIGNIN PEROXIDASE PHANEROCHAETE CHRYSOSPORIUM	Nasrin Sanayipoor	Applied and Environmental Microbiology
P 207	338	ISOLATION AND CHARACTERIZATION OF POTASSIUM SOLUBILIZING BACTERIA FROM RHIZOSPHERE SOIL AND DIFFERENT PARTS OF SAFFRON	Mansoor Zamanifar	Applied and Environmental Microbiology

Code	ID	Title	Submission Author	Session
P 208	345	ISOLATION OF STREPTOMYCES BY ANTIDERMATOPHYTIC EFFECTS FROM SHORGHALE SOIL	Behin Omidi	Applied and Environmental Microbiology
P 209	359	INVESTIGATING THE MICROFLORA OF IRANIAN TRADITIONAL SOURDOUGH	Maryam Rafiee Damaneh	Applied and Environmental Microbiology
P 210	368	ISOLATION AND IDENTIFICATION OF MERCURY RESISTANT BACTERIA FROM THE HENDIJAN'S BEACHES AND EVALUATION OF THEIR EFFICIENCY IN BIOREMEDIATION OF MERCURY CONTAMINATED ENVIRONMENTS	Zahra Noroozi asl	Applied and Environmental Microbiology
P 211	369	ISOLATION AND IDENTIFICATION OF LEAD RESISTANT BACTERIA FROM WASTEWATER OF THREE PETROCHEMICAL COMPANIES IN BUSHEHR PROVINCE.	Zahra Noroozi asl	Applied and Environmental Microbiology
P 212	376	ISOLATION AND IDENTIFICATION A PROTEASE PRODUCING BACTERIUM FROM THE FLORA OF TERMITES	Reihaneh Assari	Applied and Environmental Microbiology
P 213	392	EFFECT OF DIFFERENT CELL DISRUPTION METHODS ON PROTEIN EXTRACTION OF SPIRULINA	Mina Mehdie shishavane	Applied and Environmental Microbiology
P 214	439	EVALUATION OF MICROBIAL AND PHYSIOCHEMICAL CHARACTERISTICS OF INFLUENT AND EFFLUENT WATER ENTERING TO POINT OF USE WATER TREATMENT SYSTEMS IN GOLSAR COMPLEX, RASHT.	Esmaeil Roohbakhsh	Applied and Environmental Microbiology
P 215	455	EFFECTS OF DIETS SUPPLEMENTED WITH POLYSACCHARIDE EXTRACT FROM ALGAE, PADINA AUSTRALIS ON GROWTH, ANTIOXIDANT AND NONSPECIFIC IMMUNE STATUS OF SHRIMP, LITOPENAEUS VANNAMEI	Zahra Aminikhoei	Applied and Environmental Microbiology

Code	ID	Title	Submission Author	Session
P 216	457	ISOLATION AND CHARACTERIZATION OF PHOSPHORUS SOLUBILIZING BACTERIA	Mansoor Zamanifar	Applied and Environmental Microbiology
P 217	461	EVALUATION OF ENTRAPMENT APPROACH FOR SPORE LACCASE IMMOBILIZATION	Mojtaba Khakshour sini	Applied and Environmental Microbiology
P 218	463	DECOLORIZATION OF INDIGO CARMINE BY THE IMMOBILIZED SPORE LACCASE SYSTEMS	Mojtaba Khakshour sini	Applied and Environmental Microbiology
P 219	464	IDENTIFICATION AND ASSESSMENT OF POTENTIAL BIOLOGICAL CONTROL OF SUGAR BEET RHIZOSPHERIC BACTERIA ON RHIZOCTONIA CROWN AND ROOT ROT DISEASE	Zhaleh Khanibagi	Applied and Environmental Microbiology
P 220	469	OPTIMIZATION OF MEDIA AND CULTURE CONDITION OF PSEUDOMONAS BACTERIA TO INCREASING THE DEGRADATION OF POLYETHYLENE.	Zhale Moradì	Applied and Environmental Microbiology
P 221	471	PRODUCTION OF BACTERIAL CELLULOSE USING SUGARCANE VINASSE	Mehran Ataei	Applied and Environmental Microbiology
P 222	476	ISOLATION AND CHARACTERIZATION OF A BACTERIUM WITH FREE GLUTAMINASE L-ASPARAGINASE II FROM THE PERSIAN GULF	Saloomeh Shoaei Naeeni	Applied and Environmental Microbiology
P 223	481	ALGINATE PRODUCTION USING A NATIVE PSEUDOMONAS SP. ISOLATED FROM SOIL	Marjan Tayyebi	Applied and Environmental Microbiology
P 224	491	CLONING AND EXPRESSION OF L-ASPARAGINASE II GENE EXTRACTED FROM RHIZOBIUM NEPOTUM STRAIN SHN1 IN ESCHERICHIA COLI BL21	Saloomeh Shoaei Naeeni	Applied and Environmental Microbiology
P 225	505	DEGRADATION OF LONG CHAIN ALKANES BY NEWLY ISOLATED BACTERIA	Mohammad javad Mozaffari poor	Applied and Environmental Microbiology

Code	ID	Title	Submission Author	Session
P 226	508	ISOLATION OF PAH DEGRADING BACTERIA FROM OIL CONTAMINATED SOIL OF DARKHOVEYN	Mohammad javad Mozaffari poor	Applied and Environmental Microbiology
P 227	512	DIBUTYL PHTHALATE DEGRADATION USING DEINOCOCCUS SPP. ISOLATED FROM LOUT DESERT OF IRAN	Hosna Abbasi	Applied and Environmental Microbiology
P 228	523	EFFECT OF TEMPERATURE ON GROWTH AND ANTIOXIDANT CONTENT OF THE MICROALGA MONORAPHIDIUM SP.	Asyah Aghababaei	Applied and Environmental Microbiology
P 229	538	INVESTIGATING THE EFFECT OF ANTAGONISTIC BACTERIA ON CONTROL OF PHYTOPHTHORA ROOT ROT OF CUCUMBER IN WEST AZERBAIJAN PROVINCE	Sahel Bange Zare	Applied and Environmental Microbiology
P 230	548	DISTRIBUTION OF FUNGAL CONTAMINATION IN INDOOR BAZAARS- ZANJAN	Arezoo Tavakoli	Applied and Environmental Microbiology
P 231	550	IDENTIFICATION OF APPLE FRUIT BACTERIA AND EVALUATION OF THEIR BIOCONTROL POTENTIAL AGAINST APPLE BLUE MOLD (PENICILLIUM EXPANSUM (IN WEST AZERBAIJAN PROVINCE	Nahideh Sigari	Applied and Environmental Microbiology
P 232	565	ISOLATION OF MAGNETOTACTIC BACTERIA FROM AQUATIC ENVIRONMENTS AND THEIR POTENTIAL IN THE PRODUCTION OF IRON NANOPARTICLES	Nafise Shamsabadi	Applied and Environmental Microbiology
P 233	568	SELECTION A MULTI-METAL RESISTANT BACTERIA FROM ENVIRONMENTAL SAMPLES FOR BIOREMEDIATION PURPOSES	Fatemeh Yaghoobizadeh	Applied and Environmental Microbiology
P 234	590	ISOLATION AND PURIFICATION OF SELENIUM-LEACHING BACTERIA FROM COPPER REFINERY ANODE SLIME	Mobina Bayatian	Applied and Environmental Microbiology

Code	ID	Title	Submission Author	Session
P 235	607	DEVELOPING A NOVEL COST-EFFECTIVE CHROMOGENIC CULTURE MEDIUM FOR DETECTION AND ISOLATION OF SALMONELLA SPECIES	Hassan Salimi	Applied and Environmental Microbiology
P 236	612	ISOLATION OF N2 FIXING AND PHOSPHATE SOLUBILIZING RHIZOBACTERIA FROM DIFFERENT FIELDS IN KERMAN DISTRICT, IRAN	Mahla Farajzadeh Mazandarani	Applied and Environmental Microbiology
P 237	659	INVESTIGATING THE EFFECT OF ENVIRONMENTAL PARAMETERS ON PIGMENTATION OF SOME TALAROMYCES STRAINS.	Parisa Yousefi	Applied and Environmental Microbiology
P 238	661	BIOLOGICAL ACTIVITY AND STRUCTURAL CHARACTERIZATION OF A NOVEL EXOPOLYSACCHARIDE ISOLATED FROM A FOREST FUNGUS IN NORTH OF IRAN	Tayebeh Fooladi	Applied and Environmental Microbiology
P 239	666	EFFECT OF UV RADIATION ON THE SACCHAROMYCES CEREVISIAE FOR IMPROVING ITS TOLERANCE AGAINST 1-BUTANOL	Fatemeh Sheikhi	Applied and Environmental Microbiology
P 240	679	THE STUDY AND IDENTIFICATION OF DETERIORATING FUNGI ON DOCUMENTS IN GOLESTAN PALACE	Melika Hajimoniri	Applied and Environmental Microbiology
P 241	686	STUDY OF PATHOGENIC BACTERIA ISOLATED FROM FLIES IN SARI CITY, NORTH OF IRAN.	Masoumeh Eslamifar	Applied and Environmental Microbiology
P 242	695	ISOLATION OF SALT TOLERANT RHIZOBACTERIA WITH PHOSPHATE SOLUBILIZATION AND NITROGEN FIXATION TRAITS FROM SOME DIFFERENT FIELDS IN KERMAN, IRAN	Marjan Saber	Applied and Environmental Microbiology
P 243	698	MOLECULAR ISOLATION OF RHIZOPUS ORYZAE STRAINS WHICH PRODUCE LIPASE FROM NATURAL SOURCES.	mahdizadeh Zahra	Applied and Environmental Microbiology

Code	ID	Title	Submission Author	Session
P 244	718	ISOLATION AND IDENTIFICATION OF IRON RESISTANT BACTERIA FROM PARDIS MOUNTAIN IN JAM AREA AND FAJR JAM GAS REFINERY COMPANY WASTEWATER AND STUDY OF HEAVY METAL BIOREMEDIATION BY THEM	Maryam Ahmadzadeh	Applied and Environmental Microbiology
P 245	720	ISOLATION AND IDENTIFICATION OF HEAVY METALS RESISTANCE BACTERIA FROM PARDIS MOUNTAIN IN JAM AREA AND STUDY OF LEAD BIOREMEDIATION BY THEM	Maryam Ahmadzadeh	Applied and Environmental Microbiology
P 246	725	A METHOD FOR PREPARATION OF COMPETENT RALSTONIA EUTROPHA CELLS AND GENE TRANSFORMATION	Mohaddeseh Mohsenpour	Applied and Environmental Microbiology
P 247	751	INVESTIGATION OF BIOREMEDIATION POTENTIAL AND BIOPOLYMER PRODUCTION OF PSEUDOMONADS ISOLATED FROM PETROLEUM HYDROCARBON-CONTAMINATED AREAS	Ali Goudarztalejerdi	Applied and Environmental Microbiology
P 248	756	EXAMINATION OF PHYSICOCHEMICAL CHARACTERIZATION OF CELL SURFACES PROPERTIES OF STAPHYLOCOCCUS AUREUS.	Fariba Farniya	Applied and Environmental Microbiology
P 249	761	SCALE UP OF RHAMNOLIPID-TYPE BIOSURFACTANT PRODUCTION BY PSEUDOMONAS AERUGINOSA MA01 IN A 5-L BIOREACTOR	Atefeh Bodagh	Applied and Environmental Microbiology
P 250	762	INVESTIGATING THE BIOPOLYMER CAPACITY OF BACTERIA IN COAGULATION AND FLOCCULATION OF WATER TREATMENT AND SEWAGE TREATMENT	ZABIHOLLAH YOUSEFI	Applied and Environmental Microbiology

Code	ID	Title	Submission Author	Session
P 251	775	BIOREMEDIATION OF AZO DYES BY NEWLY ISOLATED BACTERIA FROM CONTAMINATED SOIL OF NAJAFABAD	Farnaz Kalani	Applied and Environmental Microbiology
P 252	789	QUALITATIVE SCREENING AND LIPID EXAMINATION OF BACTERIAL CELLS BY COLORING USING A NILE RED	Susan Solati	Applied and Environmental Microbiology
P 253	790	EVALUATION OF THE EFFECT OF SOIL BACTERIA AND TEXTILE WASTEWATER BACTERIA ON DECOLORIZATION OF RUBIN DYPRESY AND METHYL RED COLORS	Leila Darvishi	Applied and Environmental Microbiology
P 254	792	QUALITATIVE INVESTIGATION OF CYANOBACTERIA STRAIN OIL PRODUCTION USING IR TECHNIQUE	Susan Solati	Applied and Environmental Microbiology
P 255	799	PRECISION OF HELICOBACTER PYLORI SEROLOGY IN COMPARISON TO STOOL ANTIGEN TEST	ALKA HASANI	Applied and Environmental Microbiology
P 256	813	INVESTIGATION OF FLUORENE BIODEGRADATION USING THE SPRAY PLATE METHOD	Ehteram sadat Rahimi	Applied and Environmental Microbiology
P 257	814	PREVALENCE AND RAPID DIAGNOSIS OF ERYTHRASMA IN A UNIVERSITY DIAGNOSTIC LABORATORY OF NORTH WEST IRAN: ROLE OF CULTURE VS. DIRECT EXAMINATION	Afshin Ghodrati	Applied and Environmental Microbiology
P 258	866	CONSTRUCTION OF AN ALGINATE BASE HYDROGEL AND EVALUATING HEALING ACTIVITIES OF MENTIONED COMPONENT AS LOCAL OINTMENT WERE THE MAIN OBJECTIVES OF THE CURRENT STUDY.	Sanaz Amir gholami	Applied and Environmental Microbiology
P 259	69	ANTI HELICOBACTER ACTIVITY OF AMOXICILLIN CONJUGATED WITH GOLD NANOPARTICLE	Nahid Yarian	Biotechnology and Microbial Nanotechnology

Code	ID	Title	Submission Author	Session
P 260	72	ANTI HELICOBACTER ACTIVITY OF CLARITHROMYCIN CONJUGATED WITH GOLD NANOPARTICLE	Nahid Yarian	Biotechnology and Microbial Nanotechnology
P 261	109	IN SILICO FUSION OF ALPHA AND ALPHA TOXIN GENES OF CLOSTRIDIUM PERFRINGENS TYPE A AND CLOSTRIDIUM SEPTICUM.	Ali Haghroosta	Biotechnology and Microbial Nanotechnology
P 262	210	EFFECTS OF ELECTROMAGNETIC FIELDS EXPOSURE ON THE MAGNETOSOME PRODUCTION, ELIMINATION OF FREE RADICALS AND ANTIOXIDANT DEFENSE SYSTEMS IN MAGNETOSPIRILLUM GRYPHISWALDENSE MSR-1	Leila Hatami giklou	Biotechnology and Microbial Nanotechnology
P 263	213	BACTERIAL MAGNETIC NANOPARTICLES CONJUGATED WITH MONOCLONAL ANTIBODY AS AFFINITY-MAGNETIC MATRIX AND APPLICATION IN AFFINITY MAGNETIC SEPARATION	Leila Hatami giklou	Biotechnology and Microbial Nanotechnology
P 264	254	ENHANCING PROTEOLYTIC ACTIVITY OF LYSOBACTER ENZYMOGENES BY UV MUTAGENESIS	Reyhaneh Jafary Kelahroudi	Biotechnology and Microbial Nanotechnology
P 265	258	DESIGNING A NANOBIOSENSOR FOR DETECTION OF BRUCELLA ABORTUS BASED ON POLYCLONAL ANTIBODY AND SILICA NANOPARTICLES	Arash Shams	Biotechnology and Microbial Nanotechnology
P 266	261	INCREMENT OF LYSOBACTER ENZYMOGENES PROTEASE ACTIVITY BY EMPLOYING COLD ATMOSPHERIC PLASMA	Faranak Faraji Tabar	Biotechnology and Microbial Nanotechnology
P 267	274	THE EXPERIMENTAL MODEL OF NECROTIC ENTERITIS IN CHICKENS INDUCED BY LIVE COCCIDIOSIS VACCINE ALONG WITH CLOSTRIDIUM PERFRINGENS	Mohammad Fatemi Motlagh	Biotechnology and Microbial Nanotechnology

Code	ID	Title	Submission Author	Session
P 268	275	IN SILICO DESIGNING AND ANALYSIS OF A CHIMERIC VACCINE AGAINST CLOSTRIDIUM PERFRINGENS AND EIMERIA SPP	Mohammad Fatemi Motlagh	Biotechnology and Microbial Nanotechnology
P 269	301	GREEN MEDIATED SYNTHESIS AND CHARACTERIZATION OF SILVER NANOPARTICLES USING TEUCRIUM POLIUM LEAF EXTRACT AND EVALUATION OF ITS ANTIFUNGAL POTENTIAL	Solmaz Ghojavand	Biotechnology and Microbial Nanotechnology
P 270	303	ISOLATION AND IDENTIFICATION OF NATIVE XYLITOL PRODUCING YEAST STRAIN AND OPTIMIZATION OF MICROBIAL PRODUCTION	Solmaz Ghojavand	Biotechnology and Microbial Nanotechnology
P 271	304	MYCOSYNTHESIS OF SILVER NANOPARTICLES BY FUSARIUM OXYSPORUM AND ITS APPLICATION AGAINST ASPERGILLUS AND FUSARIUM	Firooze Nasr azadani	Biotechnology and Microbial Nanotechnology
P 272	305	BIOINFORMATICS DESIGN AND PRODUCTION OF RECOMBINANT CHIMERIC ANTIGENS OF E.COLI O157:H7 AND BRUCELLA ABORTUS AND EVALUATION OF ITS STRUCTURE	Nika Aeinechi	Biotechnology and Microbial Nanotechnology
P 273	309	GREEN SYNTHESIS OF SILVER NANOPARTICLES BY STREPTOMYCES SP. OSIP1 AND ITS ANTIBACTERIAL ACTIVITY	Ali Bakhtiari sardari	Biotechnology and Microbial Nanotechnology
P 274	310	SYNTHESIS, CHARACTERIZATION AND ANTIBACTERIAL PROPERTIES OF SILVER NANOPARTICLES BY A PSYCHROTOLERANT STRAIN	Ali Bakhtiari sardari	Biotechnology and Microbial Nanotechnology
P 275	311	BIOSYNTHESIS OF SILVER NANOPARTICLES FROM RUMEX ALVEOLATUS AND INVESTIGATION OF THEIR POTENTIAL IMPACT ON ASPERGLLUS NIGER	Aniseh Defaei	Biotechnology and Microbial Nanotechnology

Code	ID	Title	Submission Author	Session
P 276	317	RANDOM MUTAGENESIS BY NTG TO INCREASE PROTEASE ACTIVITY OF LYSOBACTER ENZYMOGENES	Malihe Amirkhani	Biotechnology and Microbial Nanotechnology
P 277	327	CLONING AND SOLUBLE OVER-EXPRESSION OF HUMAN GROWTH HORMONE(TRX-HIS6-HGH) IN ESCHERICHIA COLI	Seyed mohammad Hasanpour matikolaee	Biotechnology and Microbial Nanotechnology
P 278	330	PURIFICATION OF SOLUBLE OVER-EXPRESSED HUMAN GROWTH HORMONE(TRX-HIS6-HGH) IN ESCHERICHIA COLI WITH NI-NTA CHROMATOGRAPHY SHOWED CLASSI NATIVE PROTEIN CONTAMINANTS.	Seyed mohammad Hasanpour matikolaee	Biotechnology and Microbial Nanotechnology
P 279	332	CLONING AND EXPRESSION OF TRUCATED FORM OF SERRALYSIN ENZYME IN ESCHERICHIA COLI	Atousa Aghai	Biotechnology and Microbial Nanotechnology
P 280	337	PRODUCTION OF ANTIBIOTIC GRISEOFULVIN (GSF) FROM NATIVE NIGROSPORA SP.	Negar Ahmadi	Biotechnology and Microbial Nanotechnology
P 281	340	GREEN SYNTHESIS OF ZINC OXIDE NANOPARTICLES BY LACTOBACILLUS ACIDOPHILUS	Behin Omidi	Biotechnology and Microbial Nanotechnology
P 282	358	INVESTIGATING THE ANTIMICROBIAL EFFECTS OF NANOPARTICLES BACTERIA ISOLATED FROM AGRICULTURAL TERRITORYS OF URMIYE , IRAN	Asadi Mohammad	Biotechnology and Microbial Nanotechnology
P 283	361	LACTIC ACID PRODUCTION BY LACTOBACILLUS DELBRUECKII FROM AGRICULTURAL WASTE: ROLE OF C:N RATIO AND DIFFERENT CARBON AND NITROGEN SOURCES	Amirhossein Ghadiri	Biotechnology and Microbial Nanotechnology
P 284	364	PRODUCTION AND OPTIMIZATION OF PHYTASE IN THE SOLID-STATE FERMENTATION BY ASPERGILLUS NIGER	Shahab Nazari Shad	Biotechnology and Microbial Nanotechnology

Code	ID	Title	Submission Author	Session
P 285	370	CHITOSAN GEL-EMBEDDED SIMVASTATIN NIOSOMES AN EFFICIENT ANTIMICROBIAL SYSTEM FOR WOUND INFECTIONS	Iman Akbarzadeh	Biotechnology and Microbial Nanotechnology
P 286	397	PROPIONIC ACID: METHODS OF PRODUCTION AND CURRENT STATE	Zahra Pilevar	Biotechnology and Microbial Nanotechnology
P 287	421	ANTIFUNGAL EFFECTS OF GREEN SYNTHESISED SILVER NANOPARTICLES AGAINST CANDIDA GLABRATA AND CANDIDA DOUBLINIENSIS	Marzieh Jahangiri	Biotechnology and Microbial Nanotechnology
P 288	433	EXPRESSION OF CONSERVED DOMAIN OF P1 PROTEIN OF M. PNEUMONIAE IN E.COLI	Mahdieh Mahmoodi	Biotechnology and Microbial Nanotechnology
P 289	440	EXPRESSION OF RECOMBINANT P48 PROTEIN OF MYCOPLASMA BOVIS IN E. COLI, APPLICABLE TO ELISA TEST	Saeideh Khakpour oqani	Biotechnology and Microbial Nanotechnology
P 290	488	ASAIA BACTERIUM AS A POTENTIAL TOOL TO COMBAT AGAINST MALARIA AND OTHER VECTOR BORNE DISEASES	Majid Asgari	Biotechnology and Microbial Nanotechnology
P 291	518	CLONING OF PHBC GENE, ENCODING PHB POLYMERASE ENZYME, IN ALCALIGENES EUTROPHUS PTCC 1615	Farzaneh Barati	Biotechnology and Microbial Nanotechnology
P 292	530	INVESTIGATION THE EFFECT OF SELENATE ON PHYCOCYANIN CONTENT OF SPIRULINA PLATENSIS	Fatemeh Yaghoobizadeh	Biotechnology and Microbial Nanotechnology
P 293	531	ANALYSIS OF ALPHA AMYLASE ENZYME IN IRANIAN THERMOPHILIC STRAINS	Narges Soleimani tabar	Biotechnology and Microbial Nanotechnology
P 294	534	TREATING KLEBSIELLA PNEUMONIAE -MEDIATED LOBAR PNEUMONIA IN MICE BY A SPECIFIC BACTERIOPHAGE	Mahboubeh Soleimani sasani	Biotechnology and Microbial Nanotechnology

Code	ID	Title	Submission Author	Session
P 295	539	APPLICATION OF CORN STEEP LIQUOR AS FACTORY OVERPLUS PRODUCTS AND NITROGEN SOURCE FOR OPTIMIZATION PROCESS OF BACTERIAL CELLULOSE PRODUCTION USING RESPONSE SURFACE METHODOLOGY	Ali Abdollahi	Biotechnology and Microbial Nanotechnology
P 296	544	SEQUENCING OF A LACCASE GENE FROM POLYETHYLENE-DEGRADING BACTERIUM	Marzieh Partozadeh	Biotechnology and Microbial Nanotechnology
P 297	552	HYALURONIC ACID PRODUCTION BY CORYNEBACTERIUM GLUTAMICUM	Mahshid Yousefian shahabeddini	Biotechnology and Microbial Nanotechnology
P 298	553	AUGMENTATION OF BACTERIAL CELLULOSE PRODUCTION BY VARIOUS TREATMENTS AND DENSITY ALTERATION OF CORN STEEP LIQUOR AND BEET MOLASSES	Ali Abdollahi	Biotechnology and Microbial Nanotechnology
P 299	591	THE EFFECT OF ANTIBACTERIAL POLYVINYL ALCOHOL/FE3O4@CARBON NANOTUBES NANOCOMPOSITE AGAINST PSEUDOMONAS AERUGINOSA	Hadis Hassanvand	Biotechnology and Microbial Nanotechnology
P 300	592	THE EFFECT OF ANTIBACTERIAL ZN4NO3 NANOPARTICLE AGAINST PSEUDOMONAS AERUGINOSA	Farzaneh Fassihi	Biotechnology and Microbial Nanotechnology
P301-P400				روز دوم ساعت ۱۰:۰۰-۸:۰۰
P 301	597	ISOLATION, IDENTIFICATION AND OPTIMIZATION OF MICROBIAL OIL PRODUCTION AND EVALUATION OF THE ANTIBACTERIAL EFFECT	Fatemeh Khosravani por	Biotechnology and Microbial Nanotechnology
P 302	602	SONOCHEMICAL INCORPORATED OF CYTOSINE IN CU-H2BPDC AS AN ANTIBACTERIAL AGENT AGAINST STANDARD AND CLINICAL STRAINS OF PROTEUS MIRABILIS WITH RSBA GENE	Vahid Pezeshkpour	Biotechnology and Microbial Nanotechnology

Code	ID	Title	Submission Author	Session
P 303	633	CLONING THE MUTATED PYRAZINAMIDE ENZYME OF MYCOBACTERIUM TUBERCULOSIS IN ESCHERICHIA COLI BL21	Farahnoosh Doustdar	Biotechnology and Microbial Nanotechnology
P 304	642	SOLID LIPID NANOPARTICLES OF KHORASANI PROPOLIS EXTRACT: PREPARATION, CHARACTERIZATION, AND ANTIBACTERIAL ACTIVITY	Fatemeh Shahab navai	Biotechnology and Microbial Nanotechnology
P 305	664	GRAPHITIC CARBON NITRIDE NANOPARTICLE AS A SAFE AND EFFICIENT PHOTOSENSITIZER FOR PHOTODYNAMIC THERAPY OF METHICILLIN RESISTANT-STAPHYLOCOCCUS AUREUS	Esmaeil Darabpour	Biotechnology and Microbial Nanotechnology
P 306	667	ISOLATION AND IDENTIFICATION OF PHENOL DEGRADING YEASTS FROM CONTAMINATED SAMPLES	Kimiya Ghavami langroudi	Biotechnology and Microbial Nanotechnology
P 307	688	ANTIBACTERIAL EFFECTS OF CEFTIZOXIME COMBINED WITH METAL NANOPARTICLES AGAINST NEISSERIA GONORRHOEAE	Pouria Sheikhi	Biotechnology and Microbial Nanotechnology
P 308	728	STUDYING THE ANTIBACTERIAL PROPERTIES OF CHITOSAN NANOPARTICLES ALONG WITH ORIGANUM ESSENTIAL OIL TO INCRESE THE NEPHROPIDAE SHELF LIFE AT REFRIGERATOR TEMPERATURE	Zohre Saeidi	Biotechnology and Microbial Nanotechnology
P 309	765	IRANIAN NATIVE HONEY AS A ROBUST AGENT IN GREEN SYNTHESIS OF SILVER NANOPARTICLES WITH ANTIBACTERIAL FEATURES	Sadegh Khorrami	Biotechnology and Microbial Nanotechnology
P 310	781	OPTIMIZATION OF CARBON AND NITROGEN SOURCES FOR THE PRODUCTION OF LYSINE IN CORYNEBACTERIUM GLUTAMICUM BY COLORIMETRIC METHOD	Hadis Akbarian	Biotechnology and Microbial Nanotechnology

Code	ID	Title	Submission Author	Session
P 311	807	THE EFFECT OF MAGNETIC NANOPARTICLES ON THE GROWTH OF LUMINESCENT BACTERIA	Shadab Jabbarzadeh	Biotechnology and Microbial Nanotechnology
P 312	815	STUDY OF THE EFFECT OF SILVER NANOPARTICLES ON GRAM NEGATIVE BACTERIA ISOLATED FROM RESISTANT URINARY TRACT INFECTION	Armaghan Azimi	Biotechnology and Microbial Nanotechnology
P 313	847	COMPARISON OF ANTIBACTERIAL ACTIVITY OF GRAPHEN OXIDE-SILVER NANOCOMPOSITE SYNTHESIZED BY TWO DIFFERENT GREEN APPROACHES	Sadegh Khorrami	Biotechnology and Microbial Nanotechnology
P 314	869	DESIGNING AND EXPRESSION OF THE ENGINEERED SERRALYSIN ENZYME	Sogol Pourasghar	Biotechnology and Microbial Nanotechnology
P 315	35	PREVALENCE OF BLOOD INFECTION BY GRAM NEGATIVE BACTERIA IN PATIENTS ADMITTED TO SHAHID RAJAEE HOSPITAL OF KARAJ	Sara Ghozati	Clinical Infection and Vaccine
P 316	83	OPRI MODIFIED GENE CLONING FROM PSEUDOMONAS AERUGINOSA BACTERIA IN E.COLI	TINA SADRI	Clinical Infection and Vaccine
P 317	87	EVALUATION OF ANTI-VARICELLA ANTIBODY IN YOUNG WOMEN BEFORE THEIR MARRIAGE: A SERO-EPIDEMIOLOGIC STUDY IN SOUTH OF IRAN	Abdolreza Sotoodeh	Clinical Infection and Vaccine
P 318	89	ENDOBRONCHIAL TUBERCULOSIS AND BRONCHIAL ANTHRACOFIBROSIS: A CASE REPORT	Fatemeh Abbasi	Clinical Infection and Vaccine
P 319	90	EVALUATION OF NLRP1 GENE EXPRESSION IN PATIENT WITH SEPTICEMIA AND CONTROLS	Hamid Mosahasankhani	Clinical Infection and Vaccine
P 320	116	STUDY OF URINARY TRACT INFECTION IN DIABETIC PATIENTS AND THEIR ANTIBIOTIC RESISTANCE PATTERN IN THE ABBAS ABAD	Maryam Shahrdami	Clinical Infection and Vaccine

Code	ID	Title	Submission Author	Session
P 321	128	THE IMPACT OF THE HELICOBACTER PYLORI TREATMENT ON THE QUALITY OF LIFE IN THE PATIENTS WITH CHRONIC IDIOPATHIC URTICARIA	Maryam Taburak	Clinical Infection and Vaccine
P 322	135	OPRM CLONING OF PSEUDOMONAS AERUGINOSA BACTERIA IN ESCHERICHIA COLI AFTER BIOINFORMATICS CONFIRMATION AS A CANDIDATE FOR VACCINE.	Hamidreza Kalantari	Clinical Infection and Vaccine
P 323	189	EVALUATION OF TNF-A CYTOKINE PRODUCTION IN PATIENTS WITH TUBERCULOSIS COMPARED TO HEALTHY PEOPLE	Hassan Mahmoudi	Clinical Infection and Vaccine
P 324	195	MOLECULAR DETECTION AND SEROTYPING OF STREPTOCOCCUS PNEUMONIAE IN MENINGITIS SUSPECTED CHILDREN IN 2014-2018, BOJNURD, IRAN. WHICH TYPE OF VACCINE IS MORE SUITABLE FOR THIS REGION?	Sepideh Abdoli	Clinical Infection and Vaccine
P 325	196	PREVALENCE OF URINARY TRACT INFECTIONS AND ITS CAUSATIVE AGENTS IN IMAM REZA HOSPITAL, BOJNURD, IN 1396	Amirreza Khoshniat	Clinical Infection and Vaccine
P 326	197	A CASE OF HUMAN WRIST SYNOVIAL INFECTION CAUSED BY ACCIDENTAL INJECTION OF ANIMAL VACCINE	SEYYED AHMAD HASHEMI	Clinical Infection and Vaccine
P 327	215	INVESTIGATION THE SENSITIZATION OF ASTHMATIC PATIENTS TO A.ALTERNATA, BY IGE-IMMUNOBLOTTING	Azar Sabokbar	Clinical Infection and Vaccine
P 328	248	IDENTIFICATION OF CAPSULAR TYPES K1 AND K2 IN CLINICAL ISOLATES OF KLEBSIELLA PNEUMONIAE PRODUCING BIOFILM AND NON-PRODUCING BIOFILM	Parisa Roshani Asl	Clinical Infection and Vaccine

Code	ID	Title	Submission Author	Session
P 329	255	ASSESSMENT OF ORNITHOBACTERIUM RHINOTRACHEALE INFECTION IN COMMERCIAL CHICKENS SUBMITTED TO POULTRY CLINIC OF RAZI INSTITUTE AND SLAUGHTERHOUSES OF KARAJ CITY	Seyedgholamreza Mirzaei	Clinical Infection and Vaccine
P 330	269	PREVALENCE OF UREAPLASMA UREALYTICUM IN VAGINAL SWAB SAMPLES OF INFERTILE FEMALES REFERRED TO MAHDIEH HOSPITAL OF TEHRAN	Fatemeh Sameni	Clinical Infection and Vaccine
P 331	292	EVALUATION OF THE INCIDENCE OF BRUCELLOSIS IN A 10-YEAR PERIOD IN ASADABAD CITY, HAMEDAN PROVINCE	Fatemeh Darabi	Clinical Infection and Vaccine
P 332	313	PATTERN OF STAPHYLOCOCCUS SIMULANS ANTIBACTERIAL RESISTANCE IN A REFERRAL TEACHING HOSPITAL IN NORTHEAST OF IRAN	Ayda Tafazoli	Clinical Infection and Vaccine
P 333	371	BACTERIAL PATTERN AMONG PATIENTS WITH WOUND INFECTIONS AT GHAEM HOSPITAL, MASHHAD, IRAN	Sepideh Hasanzade	Clinical Infection and Vaccine
P 334	379	EPIDEMIOLOGY OF HUMAN BRUCELLOSIS IN KANGAVAR CITY, KERMANSHAH PROVINCE, IRAN	Naser Nazari	Clinical Infection and Vaccine
P 335	448	FLUOROQUINOLONE RESISTANCE OF E.COLI ISOLATED FROM PATIENTS WITH URINARY TRACT INFECTION IN INTENSIVE CARE UNIT IN IMAM KHOMEINI HOSPITAL, SARAB, IRAN	Ali Sadighi	Clinical Infection and Vaccine
P 336	451	PREVALENCE OF HELICOBACTER PYLORI INFECTION IN PEDIATRIC PATIENTS WITH FAMILIAL MEDITERRANEAN FEVER (FMF) AT SOTH OF TURKEY	Ali Sadighi	Clinical Infection and Vaccine

Code	ID	Title	Submission Author	Session
P 337	460	EVALUATION OF CAUSATIVE BACTERIAL AGENTS IN URINARY TRACT INFECTIONS AND DETERMINATION OF ANTIBIOTIC RESISTANCE PATTERNS IN IMAM KHOMEINI HOSPITAL, SARAB, IRAN	Ali Sadighi	Clinical Infection and Vaccine
P 338	563	EXPRESSION AND PURIFICATION OF AN IRON SCAVENGER RECEPTOR OF PROTEUS MIRABILIS AS A NEW TARGET AGAINST URINARY TRACT INFECTIONS	Mohammad Reza Asadi Karam	Clinical Infection and Vaccine
P 339	576	FREQUENCY OF BACTERIA ISOLATED FROM ASCETIC AND PLEURAL FLUIDS IN BUSHEHR PERSIAN GULF HOSPITAL IN 1396	Zeynab Gharadaghi	Clinical Infection and Vaccine
P 340	577	BLOOD AND PERICARDIAL FLUID CULTURE IN CARDIAC PATIENTS IN BENTOLHODA HOSPITAL OF BUSHEHR	Shaghayegh Rostami yasuj	Clinical Infection and Vaccine
P 341	609	THE RELATION BETWEEN PREVALENCE OF POSITIVE ANTI-CHLAMYDIA PNEUMONIA ANTIBODY TITERS AND ATHEROSCLEROTIC DISEASES	Abbas Abdollahi	Clinical Infection and Vaccine
P 342	643	PREVALENCE OF SHIGELLA IN CHILDREN WITH DIARRHEA IN TEHRAN CHILDREN'S MEDICAL CENTER HOSPITAL	Melisa Eghbal	Clinical Infection and Vaccine
P 343	701	PREVALENCE OF CRYPTOSPORIDIUM PARASITE IN CHILDREN OF LARESTAN IN 2017	Mohammadreza Foroutani	Clinical Infection and Vaccine
P 344	716	IN SILICO DESIGN OF A CHIMERIC HIGH IMMUNOGENIC OUTER MEMBRANE PROTEIN AS A NEW VACCINE CANDIDATE AGAINST SALMONELLA TYPHI	Ehsan Esmailnia	Clinical Infection and Vaccine
P 345	730	RECENT ADVANCES IN BRUCELLA PATHOGENESIS AND IMMUNE RESPONSE IN HUMANS	Ali Nemati	Clinical Infection and Vaccine

Code	ID	Title	Submission Author	Session
P 346	731	STUDY OF THE ABILITY OF BIOFILM FORMATION IN ESCHERICHIA COLI ISOLATES FROM URINARY TRACT INFECTIONS (UPEC) BY MICROTITER PLATE	Ali Dadvar	Clinical Infection and Vaccine
P 347	732	THE SEARCH FOR FIMA AND CSGA GENES IN ESCHERICHIA COLI ISOLATES FROM URINARY TRACT INFECTIONS (UPEC) BY MULTIPLEX PCR	Ali Dadvar	Clinical Infection and Vaccine
P 348	56	ANAEROBIC INFECTION:	Ali Ghorbanipour	Emerging and Reemerging Infectious Diseases
P 349	204	PREVALENCE OF BACTERIAL CONJUNCTIVITIS IN PATIENTS REFERRED TO EYE SPECIALIST HOSPITALS IN KASHAN, IRAN	Ali Nazari Alam	Emerging and Reemerging Infectious Diseases
P 350	214	THE EXPRESSION OF RECOMBINANT HYDI PROTEIN OF ECHINOCOCCUS GRANULOSUS IN E. COLI BL21 (DE3) STRAIN	Minoo Dasehmahmanesh	Emerging and Reemerging Infectious Diseases
P 351	230	DETECTION OF FOWL ADENOVIRUS E IN BROILER FLOCK IN GOLESTAN PROVINCE , 2018.	Leila Aghaiyan	Emerging and Reemerging Infectious Diseases
P 352	333	MODELING THE POPULATION DYNAMICS OF ACQUIRED IMMUNITY TO PARASITE INFECTION	Ashkan Dehghan	Emerging and Reemerging Infectious Diseases
P 353	351	ASSESSMENT OF CATALASE AND GLIOTOXIN CYTOTOXICITY IN ASPERGILLUS FLAVUS FUNGAL	Sara Roeen	Emerging and Reemerging Infectious Diseases
P 354	632	ISOLATION OF CLOSTRIDIUM DIFFICILE FROM CDI SUSPECTED PATIENTS IN KERMAN HOSPITALS, IRAN	Mojtaba Alimolaei	Emerging and Reemerging Infectious Diseases

Code	ID	Title	Submission Author	Session
P 355	719	FREQUENCY OF CHLAMYDIA TRACHOMATIS, MYCOPLASMA GENITALIUM, UREAPLASMA UREALYTICUM AND LISTERIA MONOCYTOGENES ISOLATED FROM VAGINAL SAMPLES OF WOMEN IN KERMAN, IRAN	Zahra Zahirnia	Emerging and Reemerging Infectious Diseases
P 356	740	A COMPARATIVE ANALYSIS ON PREVALENCE OF INTESTINAL PARASITES AMONG CANCER PATIENTS WITH A CONTROL GROUP IN HEALTH CARE CENTERS OF RASHT CITY (2017)	Mohammad Reza Mahmoudi	Emerging and Reemerging Infectious Diseases
P 357	742	TOXOPLASMA GONDII INFECTION IN CANCER PATIENTS IN GUILAN	Mohammad Reza Mahmoudi	Emerging and Reemerging Infectious Diseases
P 358	800	MICROSCOPY STUDY AND NESTED PCR FOR DETECTION OF CRYPTOSPORIDIUM SPP. AND MICROSPORIDIA IN REFERRED TUBERCULOSIS INDIVIDUALS AND THEIR FAMILY TO THE MASIH-DANESHVARI HOSPITAL, TEHRAN, 2016-2017	Taher Azimi	Emerging and Reemerging Infectious Diseases
P 359	850	PHYLOGENIC ANALYSIS OF HUMAN BOCAVIRUS IN CHILDREN WITH ACUTE RESPIRATORY INFECTION IN IRAN	Mehrdad Mohammadi	Emerging and Reemerging Infectious Diseases
P 360	3	THE INHIBITORY EFFECTS OF 3 IRANIAN HONEYS IN PREVENTING TISSUE DAMAGE CAUSED BY ASPERGILLUS FUMIGATUS IN BALB/C MICE.	Tina Hasankhani	Food and Water Microbiology
P 361	13	EMERGENCE AND STABILITY OF HIGH-PRESSURE RESISTANCE IN DIFFERENT FOOD-BORNE PATHOGENS	Amin Khalili	Food and Water Microbiology
P 362	114	ANTIBACTERIAL EFFECTS OF KUMQUAT(CITRUS JAPONICA) ESSENTIAL OIL AGAINST SOME PATHOGENIC BACTERIA AND COMPARISON WITH SOME STANDARD ANTIBIOTICS	Sara Moosazad	Food and Water Microbiology

Code	ID	Title	Submission Author	Session
P 363	136	STUDY OF THE ANTIMICROBIAL EFFECTS OF METHANOLIC EXTRACT OF OLIVE LEAVES ON PATHOGENIC STRAINS UNDER LABORATORY CONDITIONS	Shabnam Torabi	Food and Water Microbiology
P 364	168	INFLUENCE OF CUMINUM CYMINUM ESSENTIAL OIL ON LISTERIA MONOCYTOGENES AND ASPERGILLUS FLAVUS IN FETA CHEESE	Ali Heshmati	Food and Water Microbiology
P 365	171	ENTROCINS PRODUCED BY THE STRAIN ENTEROCOCCUS FAECALIS T23	Tannaz Mirhadizadi	Food and Water Microbiology
P 366	187	THE EFFECT OF AJOWAN OIL ON THE PHYSICOCHEMICAL, SENSORY AND MICROBIAL PARAMETERS OF YOGURT (LOW-FAT WITH MOLD)	Fatemeh Dadmarzi	Food and Water Microbiology
P 367	201	ANTIBACTERIAL AND ANTICANCER ACTIVITY OF A BIOFLAVONOID FRACTIONATED FROM ALLIUM ASCALONICUM	Razieh Aliyan	Food and Water Microbiology
P 368	236	ENTEROCOCCUS SPP. IN TRADITIONAL CHEESE: VIRULENCE TRAITS	Jalal Mardaneh	Food and Water Microbiology
P 369	238	EFFECT OF FERULA ASSAFOETIDA FRUITS ESSENTIAL OIL ON GROWTH OF ESCHERICHIA COLI 7H: 157O AND SHIGOTOXIN 2 PRODUCTION	Anna Abdolshahi	Food and Water Microbiology
P 370	280	SHELF LIFE EXTENSION OF SILVER CARP DURING STORAGE USING NATURAL PRESERVATIVE	Mohamadreza Ghazizadeh	Food and Water Microbiology
P 371	286	OPTIMIZATION OF BIOLUMINESCENCE OF VIBRIO FISCHERI	Zeinab Majidzadeh moghadam	Food and Water Microbiology
P 372	299	MUTAGENIC,ANTI MUTAGENIC ACTIVITIES AND ANTIBACTERIAL EFFECTS OF 3 JUNIPERUS BY AMES METHOD USING SALMONELLA TYPHIMURIUM STRAIN	Milad Mehralizadeh	Food and Water Microbiology

Code	ID	Title	Submission Author	Session
P 373	300	PROTOCOL FOR THE VALIDATION OF QUALITATIVE ALTERNATIVE METHODS OF MICROBIOLOGY	Sareh Davarzani	Food and Water Microbiology
P 374	312	AN EVALUATION OF LISTERIA MONOCYTOGENES PREVALENCE IN FRESH VEGETABLES COLLECTED FROM GREENGROCERS IN BIRJAND IN 1396	Majid Zare Bidaki	Food and Water Microbiology
P 375	328	RAPID IDENTIFICATION OF SALMONELLA ENTERITIDIS IN CHICKEN SKIN USING INVA MOLECULAR MARKER	Najmeh Sodagar	Food and Water Microbiology
P 376	334	SYNTHESIS OF ISOXAZOLE DRIVATIVES ON DISINFECTION OF FICAL COLIFORM BACTERIA	Fatemeh Nazemi	Food and Water Microbiology
P 377	382	SURVEY AND IDENTIFICATION OF ENTEROVIRUSES IN BOTTLED WATER BY PCR-RT METHOD	Giti Kashi	Food and Water Microbiology
P 378	385	AMYLASE PRODUCTION UNDER SUBMERGED CULTURE OF MONASCUS PURPUREUS	Najme Gord Noshahri	Food and Water Microbiology
P 379	388	EXPERIMENTAL STUDY OF THE SURVIVAL AND GROWTH OF PSEUDOMONAS AERUGINOSA IN WATER AFFECTED BY TEMPERATURE, STORAGE TIME AND TYPE OF WATER	Azin Takalloo	Food and Water Microbiology
P 380	395	INVESTIGATION OF MUTAGENIC AND ANTI MUTAGENIC EFFECTS OF PORTULACA OLERACEA ON SALMONELLA TYPHIMORIUM TA100 USING AMES METHOD	Tina Sadeghi nasr	Food and Water Microbiology
P 381	411	EFFECTS OF ZIZIPHORA CLINOPODIOIDES ESSENTIAL OIL AND APPLE PEEL EXTRACT ON SHELF LIFE EXTENSION OF CAMEL MEAT DURING REFRIGERATED STORAGE	Yasser Shahbazi	Food and Water Microbiology
P 382	412	ANTIMICROBIAL EFFECTS OF MENTHA PULEGIUM ESSENTIAL OIL AND NISIN AGAINST STAPHYLOCOCCUS AUREUS IN COMMERCIAL BARLEY SOUP	Yasser Shahbazi	Food and Water Microbiology

Code	ID	Title	Submission Author	Session
P 383	415	DETERMINATION OF ANTIMICROBIAL EFFECTS OF NISIN AND MENTHA SPICATA ESSENTIAL OIL AGAINST SALMONELLA TYPHIMURIUM UNDER VARIOUS CONDITIONS	Nassim Shavisi	Food and Water Microbiology
P 384	416	CHEMICAL COMPOSITION AND IN VITRO ANTIBACTERIAL ACTIVITY OF FERULAGO GLAREOSA ESSENTIAL OIL	Nassim Shavisi	Food and Water Microbiology
P 385	442	INVESTIGATION OF REMOVAL AMOUNT OF HEAVY METALS CADMIUM AND LEAD FROM AQUEOUS SOLUTION BY PSEUDOMONAS AERUGINOSA BACTERIA	Esmaeil Roohbakhsh	Food and Water Microbiology
P 386	452	ANTIBIOTIC RESISTANCE AMONG STAPHYLOCOCCUS AUREUS AND ESCHERICHIA COLI ISOLATED FROM TRADITIONAL AND INDUSTRIAL FOOD SAMPLES	Mojtaba Sade	Food and Water Microbiology
P 387	490	INVESTIGATION OF FREQUENCY AND VIRULENCE GENES OF TYPICAL AND ATYPICAL ENTEROPATHOGENIC ESCHERICHIA COLI (EPEC) AND SHIGA TOXIN –PRODUCING ESCHERICHIA COLI (STEC) IN BIOLOGICAL SAMPLES.	Mahdie Jafarian	Food and Water Microbiology
P 388	504	BIOFILM-PRODUCING ABILITY OF STAPHYLOCOCCAL SPP ISOLATED FROM DIFFERENT FOODSTUFFS PRODUCTS	Laleh Hoveida	Food and Water Microbiology
P 389	522	EVALUATION OF CONTAMINATION OF TRADITIONAL LACTIC CHEESES TO ESCHERICHIA COLI, STAPHYLOCOCCUS AUREUS AND LISTERIA MONOCYTOGENES	Fatemeh Rabinejd	Food and Water Microbiology
P 390	529	ASSESSMENT OF THE MICROBIOLOGICAL QUALITY OF HERBAL HAIR COLORS IN YAZD, IRAN	Somayeh Mousavi nodoushan	Food and Water Microbiology

Code	ID	Title	Submission Author	Session
P 391	532	EFFECT OF POLYLYSINE AND CARRAGEENAN COATING ON MICROBIAL PROPERTIES OF RAINBOW TROUT (ONCHORYNCHUS MYKYSS) DURING CHILLED STORAGE AT 4°C	Maryam Abbasvali	Food and Water Microbiology
P 392	546	EFFECT OF ACTIVE EDIBLE COATING ON MICROBIAL PROPERTIES OF RAINBOW TROUT (ONCHORYNCHUS MYKYSS) DURING CHILLED STORAGE	Maryam Abbasvali	Food and Water Microbiology
P 393	549	EVALUATION OF MICROBIAL QUALITY OF SIAHMAZGI CHEESE PRODUCED IN NORTHWESTERN IRAN	Adel Mirza Alizadeh	Food and Water Microbiology
P 394	557	EFFECT OF E-POLY-LYSINE TO EXTEND THE SHELF LIFE OF READY-TO-EAT TURKEY BREAST	Maryam Abbasvali	Food and Water Microbiology
P 395	560	DETERMINATION OF MICROBIAL CONTAMINATION IN VEGETABLE CONSUMPTION IN YAZD PROVINCE	Somayeh Mousavi nodoushan	Food and Water Microbiology
P 396	572	EVALUATION OF MICROBIAL CONTAMINATION OF PACKAGED SPICES IN YAZD	Somayeh Mousavi nodoushan	Food and Water Microbiology
P 397	619	AZADIRACHTA INDICA EXTRACT EFFECT AGANIST APPLE BLUE MOLD CAUSED BY PENICILLIUM EXPANSUM	Jalal Gholamnejad	Food and Water Microbiology
P 398	620	THE EFFECT OF THYMUS DAENENSIS EXTRACT AGAINST APPLE BLUE MOLD CAUSED BY PENICILLIUM EXPANSUM	Jalal Gholamnejad	Food and Water Microbiology
P 399	638	EFFECT OF CHITOSAN AND CINAMON ESSENTIAL OIL ON FOOD-BORNE PATHOGEN AND ANTIOXIDANT ACTIVITY IN FROZEN RAINBOW TROUT (ONCORHYNCHUS MYKISS)	Afsaneh Mohajer	Food and Water Microbiology

Code	ID	Title	Submission Author	Session
P 400	639	DETECTION OF MYCOBACTERIUM AVIUM SUBSP. PARATUBERCULOSIS IN COWS' RAW MILK BY POLYMERASE CHAIN REACTION (PCR) IN SHIRAZ, IRAN	Shirin Safaeian	Food and Water Microbiology
P401-P500				روز دوم ساعت ۱۶:۰۰-۱۴:۰۰
P 401	678	THE ANTIBACTERIAL PROPERTIES OF THE ALLIUM ATROVIOLACEUM (VERCOAZ) PLANT	Behzad Hafeznia	Food and Water Microbiology
P 402	726	SURVEY ON THE MICROBIAL AND QUALITY CHARACTERISTICS OF ORANGE JUICE PROCESSED WITH ULTRASONICATION	Roghieh Ashrafi yourghanloo	Food and Water Microbiology
P 403	729	INVESTIGATING THE EFFECT OF HYDROCOLLOIDS ON SURVIVAL BIFIDOBACTERIUM BIFIDUM IN YOGURT	Roghieh Ashrafi yourghanloo	Food and Water Microbiology
P 404	745	FREQUENCY AND ANTIBACTERIAL SENSITIVITY OF LISTERIA SPP. AND LISTERIA MONOCYTOGENES ISOLATED FROM FOOD AND ENVIRONMENTAL SAMPLES IN URMIA	Lida Lotfollahi	Food and Water Microbiology
P 405	746	DETECTION OF ACTA GENE IN LISTERIA MONOCYTOGENES ISOLATED FROM DAIRY PRODUCT	Marzieh Shafiei	Food and Water Microbiology
P 406	750	THE CARVACROL AND P-CYMENE INHIBITORY EFFECTS ON FUNGAL GROWTH AND AFLATOXIN PRODUCTION BY AFLATOXINOGEN STRAINS	Aref Rahimi	Food and Water Microbiology
P 407	757	PURIFICATION OF A PROTEASE FROM AN ORGANIC-SOLVENT TOLERANT ALKALOPHILIC BACILLUS SP.	Shohreh Mohamadi	Food and Water Microbiology

Code	ID	Title	Submission Author	Session
P 408	758	SCREENING AND ISOLATION OF AN ORGANIC-SOLVENT TOLERANT ALKALOPHILIC PROTEASE PRODUCER BACILLUS SP.	Shohreh Mohamadi	Food and Water Microbiology
P 409	773	IDENTIFYCOMMON BACTERIA AND ANTIMICROBIAL SUSCETIBILITY IN ZARANDIEH POPULATION SINCE MARCH TO DECEMBER 2017	Aliakbar Bakhtiari	Food and Water Microbiology
P 410	801	DETECTION OF ENTEROTOXIGENIC BACILLUS CEREUS ISOLATED FROM MEAT PRODUCTS IN ZANJAN BY PCR	Zahra Deilami Khiabani	Food and Water Microbiology
P 411	820	OPTIMIZATION OF AMYLASE ACTIVITY FROM MONASCUS PURPUREUS	Najme Gord Noshahri	Food and Water Microbiology
P 412	827	PREVALENCE OF AFLATOXIN BIOSYNTHESIS GENES ACCORDING TO AFLATOXIN LEVELS IN FEEDSTUFF SAMPLES	Nooshin Sohrabi	Food and Water Microbiology
P 413	838	STUDY THE PREVALENCE OF HBL AND NHE COMPLEXES IN ISOLATED BACILLUS CEREUS FROM SOME PASTEURIZED MILK AND CHEESE SAMPLES OF IRAN	Zahra Deilami Khiabani	Food and Water Microbiology
P 414	861	EFFECTS OF CONTINUOUS WAVE LASER RADIATION AGAINST PATHOGENIC BACTERIA ESCHERICHIA COLI O157: H7 IN IRANIAN PROBIOTIC DOOGH	Ahmad Nasrollahzadeh	Food and Water Microbiology
P 415	868	APPLICATION OF OPTAMER IN THE DETECTION OF AFLATOXIN B1	Saeedeh Shahbazizadeh	Food and Water Microbiology
P 416	43	HELICOBACTER PYLORI INFECTION ASSOCIATION WITH COLON POLYP AND COLORECTAL CANCER	Mohammad Hadi Karbalaie niya	Microbial Infection and Cancer
P 417	162	INVESTIGATING EXACERBATING FACTORS HERPES VIRUS INFECTION (HSV1 AND HSV2)	Sina Moradi yeganmahale	Microbial Infection and Cancer

Code	ID	Title	Submission Author	Session
P 418	186	PREVALENCE OF HELICOBACTER PYLORI IN PATIENTS WHIT COLORECTAL CANCER	Parisa Abedi elkhichi	Microbial Infection and Cancer
P 419	221	REPORTING TWO CASES OF STOMACH CARCINOMA WITH HELICOBACTER PYLORI RESISTANT TO CLARITHROMYCIN AND METRONIDAZOLE	Fatemaeh Akbarzadeh	Microbial Infection and Cancer
P 420	404	CORRELATION OF BLOOD MIRNA-221 EXPRESSION WITH DIFFERENT PATHOLOGIC LEVELS OF HELICOBACTER PYLORI INFECTION	Mona Noohi	Microbial Infection and Cancer
P 421	437	MOLECULAR DIAGNOSIS OF MOBILUNCUS CURTISII AND MEGASPHAERA TYPE1 ASSOCIATED WITH BACTERIAL VAGINOSIS IN IRANIAN WOMEN, THE FIRST REPORT	Esmaeil Roohbakhsh	Microbial Infection and Cancer
P 422	438	DETECTION OF HELICOBACTER PYLORI IN THE PATIENTS WITH GASTRIC CANCER BASE ON VARIOUS VIRULENCE GENES USING MULTIPLEX PCR	Mojtaba Sade	Microbial Infection and Cancer
P 423	443	MOLECULAR IDENTIFICATION OF PAPILLOMAVIRUS TYPE 16 AND 18 ISOLATED FROM WOMEN WITH CERVICAL CANCER	Mojtaba Sade	Microbial Infection and Cancer
P 424	527	STUDY OF SIRT3 EXPRESSION IN PATIENTS SUFFERING FROM GASTRIC CANCER AND HELICOBACTER PYLORI INFECTION SIMULTANEOUSLY.	Leila Montazeri	Microbial Infection and Cancer
P 425	547	HUMAN PAPILOMA VIRUS STUDY IN PATIENTS WITH BREAST CANCER IN ISFAHAN, 1396	Ahmadreza Shahniani	Microbial Infection and Cancer
P 426	624	DEMOGRAPHIC DISTRIBUTION OF URINARY TRACT INFECTION AMONG REFERENTS TO A MEDICAL LABORATORY IN KERMANSHAH	Azadeh Foroughi	Microbial Infection and Cancer

Code	ID	Title	Submission Author	Session
P 427	671	DETERMINATION OF 16 AND 18 GENOTYPES OF THE HUMAN PAPILLOMAVIRUS (HPV) IN CERVICAL CYTOLOGICAL SAMPLES FROM AHVAZ	Raziyeh Kashisaz	Microbial Infection and Cancer
P 428	837	THE EFFECT OF HELICOBACTER PYLORI ON THE PATTERN OF METHYLATION OF GENE	Hamed Charkhian	Microbial Infection and Cancer
P 429	120	CYTOTOXIC EFFECT OF SAPONINS EXTRACTED FROM SPIRULINA PLATENSIS ON THREE CANCER CELL LINES	Mahboobeh Akbarizare	Microbial Metabolites and Cancer Treatment
P 430	130	STUDY THE ANTI-CANCER EFFECT OF BACTERIOCINS ISOLATED FROM LACTOBACILLUS-RHAMNOSUS ON CANCER CELL LINE AND ITS TOXICITY EFFECT ON NORMAL CELLS BY THE TRYPAN BLUE	Meysam Khodayari	Microbial Metabolites and Cancer Treatment
P 431	571	SCREENING HEMOLYTIC ACTIVITY OF LUMINESCENT VIBRIOS WITH FURTHER HEMOLYSIN EXTRACTION AND MOLECULAR WEIGHT DETERMINATION	Shokufeh Ghasemian	Microbial Metabolites and Cancer Treatment
P 432	700	STRUCTURAL AND FUNCTIONAL DESIGN AND EVALUATION OF NEW IMMUNOTOXIN STRUCTURES AFFECTING LIVER CANCER IN QUASI-PHYSIOLOGICAL CONDITIONS	Leyli Mir	Microbial Metabolites and Cancer Treatment
P 433	738	IDENTIFICATION AND EXTRACTION OF ANTICANCEROUS ENZYMES FROM E.COLI AND A NEW METHOD TO STUDY ITS ACTIVITY	Melika Farzin	Microbial Metabolites and Cancer Treatment
P 434	26	APPROPRIATE CIRCADIAN DARKNESS MAY HELP RECOVERY OF SEPTIC SHOCK PRODUCED BY BACTERIAL LIPOPOLYSACCHARIDE	Mojtaba Hedayati ch	Microbial Metabolites and Diseases

Code	ID	Title	Submission Author	Session
P 435	27	EVALUATION ONE MOLECULAR EFFECT OF NEISSERIA GONORRHOEAE LIPOOLIGOSACHARIDE TOXICITY IN MICE SPLEEN, BASED ON ACTIVATION OF UNFOLDED PROTEIN RESPONSE THROUGH INOSITOL REQUIRING ENZYME-1A	Mojtaba Hedayati ch	Microbial Metabolites and Diseases
P 436	61	STUDY OF EPSTEIN-BARR VIRUS (EBV) IN CHILDREN UNDER 5 YEARS SUSPECTED TO INFECTIOUS MONONUCLEOUS	Pezhman Sharifi	Microbial Metabolites and Diseases
P 437	107	FIRST REPORT OF MICROCYSTIN PRODUCING BY TWO TERRESTRIAL CYANOBACTERIA OF THE GENERA FISCHERELLA SP. F29 AND NOSTOC SP. N27 FROM IRAN	Bahareh Nowruzi	Microbial Metabolites and Diseases
P 438	156	COMPARATIVE STUDY OF PROTEINASE ACTIVITY IN CANDIDA ISOLATES	Mohsen Ilkhani zadeh Ghomi	Microbial Metabolites and Diseases
P 439	203	DETECTION OF BIOFILM DEVELOPMENT IN CLINICAL ENTEROCOCCUS FAECIUM AND ENTEROCOCCUS FAECALIS ISOLATES FROM KASHAN	Ali Nazari Alam	Microbial Metabolites and Diseases
P 440	225	STUDY PREVALENCE OF AGR IN STAPHYLOCOCCUS AUREUS	Abotaleb Nikpour	Microbial Metabolites and Diseases
P 441	349	MOLECULAR ANALYSIS OF INFLUENZA VIRUS A/H1N1 NON-STRUCTURAL GENE ISOLATED FROM IRANIAN PATIENTS WITH SEVERE SYMPTOMS	Zahra Asadollahi	Microbial Metabolites and Diseases
P 442	393	THE EFFECT OF UV MUTAGENESIS TO PRODUCE MORE CLAVULANIC ACID BY FACTORS SUCH AS THE PRODUCTION OF ENZYMES, THE CONSUMPTION OF CARBON AND NITROGEN, AND ENZYMES AND SUGARS. STREPTOMYCES CLAVULIGERUS	AMIR HOSSIEN ArabVand	Microbial Metabolites and Diseases

Code	ID	Title	Submission Author	Session
P 443	630	ANALYSIS OF QUORUM SENSING RELATED GENES IN PSEUDOMONAS AEUROGINOSA ISOLATES FROM CYSTIC FIBROSIS PATIENTS	Farahnoosh Doustdar	Microbial Metabolites and Diseases
P 444	634	PREVALENCE OF THE CLOSTRIDIUM DIFFICILE TOXINS IN TEHRAN HOSPITALS	Fatemeh Savaheli moghadam	Microbial Metabolites and Diseases
P 445	704	EVALUATION OF HERPES SIMPLEX VIRUS I&II IN SUSCEPTIBLE PSEUDOMONAS AERUGINOSA KERATITS BY PCR MOLECULAR METHOD	Milad Zarini	Microbial Metabolites and Diseases
P 446	764	PREVALENCE OF MYCOPLASMA HOMINIS AND UREAPLASMA UREALYTICUM INFECTIONS IN PATIENTS REFERRED TO SHAHID MOTAHARI HOSPITAL IN URMIA BY PCR	Azam Mokhtari	Microbial Metabolites and Diseases
P 447	821	VIRTUAL MODELING OF INHIBITING THE HELICOBACTER PYLORI ACID RESISTANCE SYSTEM	Shadab Jabbarzadeh	Microbial Metabolites and Diseases
P 448	878	PRODUCTION AND FAST PARTIAL PURIFICATION OF STAPHYLOCOCCUS AUREUS SUPER ANTIGEN C	Mohammad reza Ataie kachoee	Microbial Metabolites and Diseases
P 449	38	CHITOSAN-BASED NANOVACCINE CANDIDATE AGAINST ESCHERICHIA COLI O157:H7	Jaleh Khanifar	Microbial vaccines
P 450	39	IMMUNIZATION WITH NANOPARTICLED CHITOSAN CONTAINING OF RECOMBINANT EIT AND STX2B ANTIGENS AGAINST E. COLI O157:H7 IN	Jaleh Khanifar	Microbial vaccines
P 451	101	CHARACHTRIZATION OF ASAIA SP. ISOLATED FROM MALARIA VECTORS IN SOUTHWEST OF IRAN	Masoomeh Bagheri	Microbial vaccines

Code	ID	Title	Submission Author	Session
P 452	102	THE EFFECT OF BCG ON IRON METABOLISM IN THE EARLY NEONATAL PERIOD: A CONTROLLED TRIAL IN IRANIAN NEONATES.	Seyed ehsan Asadi	Microbial vaccines
P 453	133	IMMUNOGENICITY STUDY OF RECOMBINANT AUTOLYSIN OF STAPHYLOCOCCUS IN BALB/C MICE	Mandana Bagherzadeh mogaddam	Microbial vaccines
P 454	161	B CELL EPITOPE-BASED VACCINE CANDIDATE AGAINST BACTEROIDES FRAGILIS BY IMMUNOINFORMATICS APPROACH	Shirin Dashtbin	Microbial vaccines
P 455	229	APPLICATION OF MINITAB SOFTWARE ON THE OPTIMIZATION OF INACTIVATION CONDITIONS OF RABIES VIRUS USED IN VET RABIES VACCINE BY BETA-PROPIOLACTONE	Zohre Eftekhari	Microbial vaccines
P 456	232	NEW GENERATION OF ADJUVANTS IN VACCINE DELIVERY	Zohreh Fasihi	Microbial vaccines
P 457	298	IDENTIFICATION OF NOVEL VACCINE CANDIDATES AGAINST SHIGELLA SPP. THROUGH REVERSE VACCINOLOGY METHODS	Abolfazl Hajialibeighi	Microbial vaccines
P 458	316	POLYTOPE VACCINE DESIGN AGAINST STREPTOCOCCUS PNEUMONIAE AND INFLUENZA VIRUS: AN IN SILICO APPROACH	Sahar Sadeghi	Microbial vaccines
P 459	354	OPRL CLONING OF PSEUDOMONAS AERUGINOSA IN ESCHERICHIA COLI BL21 AFTER BIOINFORMATICS VERIFICATION AS A CANDIDATE FOR VACCINE.	Omid Shirmohammadi	Microbial vaccines
P 460	418	IDENTIFICATION OF NOVEL OUTER MEMBRANE PROTEINS OF SALMONELLA TYPHI AS VACCINE CANDIDATE BY REVERSE VACCINOLOGY APPROACH	Ehsan Esmailnia	Microbial vaccines

Code	ID	Title	Submission Author	Session
P 461	446	DETECTION AND SEQUENCE EVALUATION OF UPAH GENE AMONG UROPATHOGENIC ESCHERICHIA COLI ISOLATED FROM URINARY TRACT INFECTIONS AS A NEW VACCINE CANDIDATE	Mohammad Reza Asadi Karam	Microbial vaccines
P 462	503	ASSESSMENT OF FREQUENCY AND NUCLEOTIDE SEQUENCE OF IRON RECEPTOR PMI0842 IN PROTEUS MIRABILIS COLLECTED FROM URINARY TRACT INFECTIONS CASES IN TEHRAN, IRAN	Mohammad Reza Asadi Karam	Microbial vaccines
P 463	650	ISOLATION AND CHARACTERIZATION OF OUTER MEMBRANE VESICLES (OMVS) FROM BORDETELLA PERTUSSIS TOHAMA STRAIN	Mohammad Sekhavati	Microbial vaccines
P 464	693	ISOLATION AND IDENTIFICATION OF BRUCELLA ABORTUS BIOVAR 3 IN A DAIRY CATTLE HERD VACCINATED WITH BRUCELLA ABORTUS RB51 VACCINE IN IRAN	Maryam Dadar	Microbial vaccines
P 465	30	STUDY OF CCR5-59353C/T POLYMORPHISM IN THE IRANIAN PATIENTS WITH CHRONIC HBV INFECTION	Farahnaz Bineshian	Microbiomes
P 466	94	THE MICROBIOTA OF FEMALE REPRODUCTIVE TRACT AND ITS RELATION TO FERTILITY AND ASSISTED REPRODUCTIVE TECHNOLOGY	Zahra Golestani	Microbiomes
P 467	525	FREQUENCY AND RISK OF ATOPOBIUM VAGINAE IN PRETERM DELIVERY	Sedigheh Livani	Microbiomes
P 468	823	COMPARED PROTEIN PROFILES OF THE OUTER MEMBRANE VESICLES (OMV) AND OUTER MEMBRANE PROTEINS (OMP) STANDARD STRAINS OF AKKERMANSIA MUCINIPHILA	Arefeh Shahriary	Microbiomes

Code	ID	Title	Submission Author	Session
P 469	10	ECOR PHYLOTYPING AND DETERMINATION OF VIRULENCE GENES IN ESCHERICHIA COLI ISOLATES FROM PATHOLOGICAL CONDITIONS OF BROILER CHICKENS IN POULTRY SLAUGHTERHOUSES OF SOUTHEAST OF IRAN.	Akbar Asadi	Molecular Diagnosis and Typing
P 470	42	IL-28B POLYMORPHISM IN HCV PATIENTS OF TEHRAN FIROOZGAR HOSPITAL	Mohammad Hadi Karbalaie niya	Molecular Diagnosis and Typing
P 471	44	RESISTANT ASSOCIATED VARIANTS (RAVS) INVESTIGATION IN THE NAÏVE HCV PATIENT CANDIDATE FOR DAA THERAPY	Mohammad Hadi Karbalaie niya	Molecular Diagnosis and Typing
P 472	45	IDIOPATHIC PULMONARY FIBROSIS INVESTIGATION FOR VIRAL INFECTION	Mohammad Hadi Karbalaie niya	Molecular Diagnosis and Typing
P 473	64	DETECTION OF TICK-BORNE RELAPSING FEVER BORRELIAE IN TICK DNA SAMPLES BY USING PCR	Faezeh Houman sadr	Molecular Diagnosis and Typing
P 474	68	COMPARISON OF GENOMIC POLYMORPHISM OF ENTEROCOCCUS FAECALIS ISOLATED FROM CLINICAL SAMPLES USING ERIC-PCR AND BOX-PCR METHODS	Fateme Ahmadi	Molecular Diagnosis and Typing
P 475	77	IDENTIFICATION OF MYCOPLASMA MURIS ISOLATED FROM VAGINAL SAMPLES OF NIH MICE	Mohammad Reza Zinatizadeh	Molecular Diagnosis and Typing
P 476	110	PREVALENCE OF RESISTANCE TO FLUOROQUINOLONES ESCHERCHIA COLI QNR GENES ISOLATED FROM PATIENTS ADMITTED TO JAHROM´S HOSPITALS BY PHENOTYPIC AND MOLECULAR METHODS, 2016-2017	Abdolreza Sotoodeh	Molecular Diagnosis and Typing

Code	ID	Title	Submission Author	Session
P 477	123	DETECTION OF STREPTOCOCCUS AGALACTIAE SURFACE PROTEIN ANTIGEN GENES ISOLATED FROM URINARY TRACT INFECTION IN TEACHING HOSPITALS OF ISFAHAN BY MULTIPLEX PCR.	Saba Jalalifar	Molecular Diagnosis and Typing
P 478	142	HIGH INCIDENCE OF TOXIN AND BIOFILM GENES AMONG METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS STRAINS	Mitra Motallebi	Molecular Diagnosis and Typing
P 479	143	PREVALENCE OF THE 4 GENES ENCODING FIMBRIAE IN UROPATHOGENIC ESCHERICHIA COLI CLINICAL ISOLATES AND STATISTICAL ANALYSIS OF RELATIONSHIP BETWEEN THE ABUNDANCE OF THIS VIRULENCE FACTORS AND PHYLOGENETIC GROUPS	Mahsa Mirzarazi Dehaghi	Molecular Diagnosis and Typing
P 480	173	ISOLATION AND MOLECULAR IDENTIFICATION OF BIOFILM PRODUCING PSEUDOMONAS AERUGINOSA BACTERIA FROM LIQUID STORAGE OF CONTACT LENS AND COSMETIC IN JAHROM PROVINCE	Manoochehr Shabani	Molecular Diagnosis and Typing
P 481	175	PREVALENCE OF PAPA, FIMH, MALX AND ISS GENES IN ESCHERICHIA COLI ISOLATES FROM PATIENTS WITH COMMUNITY-ACQUIRED UTIS	Arash Soltani Borchaloee	Molecular Diagnosis and Typing
P 482	178	MOLECULAR DIAGNOSIS OF HELICOBACTER PYLORI IN SEMEN OF INFERTILE MEN	Mostafa Khoshbin	Molecular Diagnosis and Typing
P 483	179	DETECTION OF SOME ADHESIVE GENES IN ESCHERICHIA COLI ISOLATES FROM PATIENTS WITH URINARY TRACT INFECTIONS IN MASHHAD BY MULTIPLEX PCR	Mahnaz Najafi	Molecular Diagnosis and Typing

Code	ID	Title	Submission Author	Session
P 484	190	DIAGNOSTIC OF VBNC BACTERIA IN SYNOVIAL FLUID OF RHEUMATOID ARTHRITIS PATIENTS	Seyyed reza Hashemi miyan abad	Molecular Diagnosis and Typing
P 485	194	ISOLATION OF PORCINE BOCAVIRUS FROM NASOPHARYNGEAL SWAB OF A CHILD WITH ACUTE RESPIRATORY TRACT INFECTION IN NORTHEASTERN IRAN	Saghar Safamanesh	Molecular Diagnosis and Typing
P 486	205	PREVALENCE OF PAPC GENE IN UROPATHOGENIC E.COLI ISOLATES FROM URINARY TRACT INFECTIONS IN RASHT AND THEIR ANTIBIOTIC RESISTANCE PATTERN	Zahra Askari	Molecular Diagnosis and Typing
P 487	207	INVESTIGATION OF SFA/FOC GENE IN UROPATHOGENIC E.COLI ISOLATES FROM URINARY TRACT INFECTIONS IN RASHT	Zahra Askari	Molecular Diagnosis and Typing
P 488	223	PREVALENCE OF EBP B AND EBP C GENES IN ENTEROCOCCUS FAECALIS PRODUCING BIOFILM ISOLATED FROM MEAT	Elahe Tajbakhsh	Molecular Diagnosis and Typing
P 489	241	PSEUDOMONAS AERUGINOSA VIRULENCE MARKERS	Jalal Mardaneh	Molecular Diagnosis and Typing
P 490	257	ENHANCMENT OF CD22 EXPRESSION PROFILE IN ESCHERICHIA COLI ROSSETA (DE3) BY EXPOSURE TO EXTREMELY LOW FREQUENCY MAGNETIC FIELDS	Behnaz Rashidieh	Molecular Diagnosis and Typing
P 491	262	ANTIBIOTIC RESISTANCE GENES CODING OF EFFLUX PUMP (ADEA AND ADES GENES) IN ACINETOBACTER BAUMANNII ISOLATED FROM PATIENTS BY MOLECULAR METHODS	Mohammad Niakan	Molecular Diagnosis and Typing

Code	ID	Title	Submission Author	Session
P 492	273	STUDY PHYLOGENETIC GROUPS OF PATHOGENIC E.COLI STRAINS ISOLATED FROM PATIENTS IN IMAM REZA HOSPITAL, KERMANSHAH	Arezoo Asadi	Molecular Diagnosis and Typing
P 493	282	PLASMID-MEDIATED QUINOLONE RESISTANCE GENES IN ESBL PRODUCING KLEBSIELLA PNEUMONIAE ISOLATED FROM URINARY TRACT INFECTIONS IN TEHRAN HOSPITALS	Zahra Khodabandelo	Molecular Diagnosis and Typing
P 494	319	MOLECULAR ANALYSIS OF PSEUDOMONAS AERUGINOSA ISOLATED FROM CLINICAL, ENVIRONMENTAL AND COCKROACH SOURCES BY ERIC-PCR	Hadi Hossainpour	Molecular Diagnosis and Typing
P 495	341	MOLECULAR DETECTION OF YELLOW FEVER AND RIFT VALLEY FEVER VIRUS USING MULTIPLEX PCR	Afshin Samimi nemati	Molecular Diagnosis and Typing
P 496	342	SIMPLE DETECTION OF YERSINIA AND FRANCISELLA USING POLYMERASE CHAIN REACTION (PCR)	Nafiseh Pourmahdi	Molecular Diagnosis and Typing
P 497	344	DETECTION OF TETRACYCLINE AND FLUOROQUINOLONES RESISTANCE AMONG CAMPYLOBACTERS ISOLATED FROM DIARRHEA PATIENTS IN MARKAZI PROVINCE - 2015	Elnaz Abbasi	Molecular Diagnosis and Typing
P 498	355	COMPARISON OF PCR AND CULTURE METHODS TO DETECT LISTERIA MONOCYTOGENES IN VAGINAL SPECIMENS	Zahra Sadeghi	Molecular Diagnosis and Typing
P 499	378	A RELIABLE COMBINATION METHOD TO IDENTIFICATION AND TYPING OF EPIDEMIC AND ENDEMIC CLONES AMONG CLINICAL ISOLATES OF ACINETOBACTER BAUMANNII	Arezoo Piran	Molecular Diagnosis and Typing

Code	ID	Title	Submission Author	Session
P 500	387	ISOLATION AND SUDY OF DRUG-RESISTANT GENE (EFFLUX PUMP) IN PSEUDOMONAS AERUGINOSA ISOLATED FROM CLINICAL SAMPLES AND MILK FOOD BY MPCR AND DETERMINE ANTIBIOTIC SUSCEPTIBILITY PATTERN	Narges Olya	Molecular Diagnosis and Typing
P501-P600				روز سوم کنگره ساعت ۸:۰۰-۱۰:۰۰
P 501	390	DETECTION OF MIXED STRAIN INFECTIONS OF MYCOBACTERIUM TUBERCULOSIS IN RESOURCE-LIMITED SETTINGS	Mansour Kargarpour Kamakoli	Molecular Diagnosis and Typing
P 502	400	ASSOCIATION OF INDUCIBLE NITRIC OXIDE SYNTHASE (INOS) GENE POLYMORPHISMS WITH SUSCEPTIBILITY TO VISCERAL LEISHMANIASIS IN THE IRANIAN POPULATION	Akram Pourkazem	Molecular Diagnosis and Typing
P 503	401	EVALUATING THE RELATIONSHIP BETWEEN SERUM IMMUNOGLOBULIN G (IGG) AND A (IGA) ANTI-CAGA ANTIBODY AND THE CAGA GENE IN PATIENTS WITH DYSPEPSIA	Ali Baradaran	Molecular Diagnosis and Typing
P 504	402	DILEMMA OF DIRECT MIRU-VNTR GENOTYPING OF CLINICAL SAMPLES OF TUBERCULOSIS	Ghazaleh Farmanfarmaei	Molecular Diagnosis and Typing
P 505	410	MOLECULAR IDENTIFICATION OF WHIB7 EXPRESSION IN DRUG RESISTANT MYCOBACTERIUM TUBERCULOSIS	Fahimeh Morteza	Molecular Diagnosis and Typing
P 506	428	DETERMIND VIRULENCE FACTORAND ANTIBIOTICS RESISTANCE AMONG CLINICAL ISOLATES OF UROPATHOGENIC E.COLI IN NORTHEAST OF IRAN	Mahdis Ghavidel	Molecular Diagnosis and Typing

Code	ID	Title	Submission Author	Session
P 507	435	TNFA GENE POLYMORPHISMS IN PEDIATRICS WITH AUTOIMMUNE HEPATITIS IN CHILDREN'S MEDICAL CENTER	Sarvenaz Falsafi	Molecular Diagnosis and Typing
P 508	479	ISOLATION, MOLECULAR IDENTIFICATION AND GENOMIC DNA FINGERPRINTING OF MYCOBACTERIUM STRAINS FROM TUBERCULIN POSITIVE CATTLE IN KERMAN PROVINCE	Mahfam Sadri	Molecular Diagnosis and Typing
P 509	540	ISOLATION AND IDENTIFICATION OF MYCOBACTERIUM FROM RAW MILK AND TRADITIONAL CHEESE SAMPLES COLLECTED FROM DAIRY STORES IN KARAJ, IRAN	Tahereh Tafreshi	Molecular Diagnosis and Typing
P 510	545	THE FREQUENCY OF REVERSE TRANSCRIPTASE'S (RT) GENES IN ESCHERICHIA COLI ISOLATED OF URINARY TRACT INFECTIONS	Fatemeh Jokar	Molecular Diagnosis and Typing
P 511	561	THE NUCLEOTIDE ANALYSIS OF REVERSE TRANSCRIPTASE (RT) ENZYME GENE IN ESCHERICHIA COLI ISOLATED OF URINARY TRACT INFECTIONS	Shabnam Pourmohammadian	Molecular Diagnosis and Typing
P 512	586	MOLECULAR CHARACTERIZATION OF CLINICAL AND ENVIRONMENTAL PSEUDOMONAS AERUGINOSA ISOLATED IN A BURN CENTER	Pezhman Karami	Molecular Diagnosis and Typing
P 513	595	THE PREVALENCE OF RESPIRATORY VIRUSES IN IRANIAN CHILDREN WITH ASTHMA	Farhad Babaei	Molecular Diagnosis and Typing
P 514	596	DIAGNOSIS OF CRYPTOSPORIDIUM IN BRONCHOALVEOLAR LAVAGE SPECIMENS OF IMMUNOCOMPROMISED PATIENTS BY TWO METHODS, ARAK CITY, IRAN	Zahra Eslamirad	Molecular Diagnosis and Typing

Code	ID	Title	Submission Author	Session
P 515	711	GENOTYPING OF MYCOPLASMA AGALACTIAE ISOLATED FROM SHEEP IN ARDABIL AND GOLESTAN PROVINCES OF IRAN COUNTRY	Khatereh Kabiri	Molecular Diagnosis and Typing
P 516	715	UTILIZATION OF MLST GENOTYPING IN PHYLOGENIC STUDY OF MYCOPLASMA AGALACTIAE IN SEMANAN	Khatereh Kabiri	Molecular Diagnosis and Typing
P 517	717	PREGNANCY- RELATED LISTERIOSIS: FREQUENCY AND GENOTYPIC CHARACTERISTICS OF L. MONOCYTOGENES FROM HUMAN SPECIMENS, KERMAN-IRAN	Zahra Zahirnia	Molecular Diagnosis and Typing
P 518	734	SPECIFIC AND ACCURATE IDENTIFICATION OF MYCOBACTERIUM TUBERCULOSIS IN CLINICAL SAMPLES BY PCR-ELISA TECHNIQUE	Reihaneh Ramezani	Molecular Diagnosis and Typing
P 519	778	INVESTIGATING THE FREQUENCY OF BLAZ GENE AND MECA GENE IN STAPHYLOCOCCUS AUREUS ISOLATED FROM CLINICAL SAMPLES IN GORGAN	Yasaman Rahnama	Molecular Diagnosis and Typing
P 520	794	PREVALENCE OF CAGA GENE AND RELATION WITH DIFFERENT CLINICAL FORMS OF HELICOBACTER PYLORI INFECTIONS IN ISOLATED STRAINS OF AHVAZ-SOUTHWEST OF IRAN	Amirarsalan Serajian	Molecular Diagnosis and Typing
P 521	830	MOLECULAR CHARACTERIZATION OF THE CHICKEN ANAEMIA VIRUSES ISOLATED FROM BROILER FARMS OF EAST AZERBAIJAN, IRAN	Masoud Ezami razliqi	Molecular Diagnosis and Typing
P 522	226	EVALUATION OF ANTIMICROBIAL SUSCEPTIBILITY OATTERN STREPTOCOCCUS MUTANS ISOLATED FROM DENTAL PLAQUES TO CHLORHEXIDINE, NANOSIL AND COMMON ANTIBIOTICS	Abotaleb Nikpour	Oral Microbiology

Code	ID	Title	Submission Author	Session
P 523	263	THE ANTIMICROBIAL AND CLINICAL EFFECTS OF OZONIZED WATER, CHLORHEXIDINE, AMOXICILLIN -METRONIDAZOLE, ON PORPHYROMONAS GINGIVALIS	Mohammad Niakan	Oral Microbiology
P 524	289	PREVALENCE AND RISK FACTORS OF ENTAMOEBA GINGIVALIS AND TRICHOMONAS TENAX IN PATIENTS WITH PERIODONTITIS IN LORESTAN PROVINCE, IRAN	Setare Azade	Oral Microbiology
P 525	291	PREVALENCE AND ASSOCIATED RISK FACTORS OF ORAL CAVITY PROTOZOA (ENTAMOEBA GINGIVALIS & TRICHOMONAS TENAX) IN THE PATIENTS WITH DENTAL CAVITY CARIES IN LORESTAN PROVINCE, IRAN	Zahra Mehri	Oral Microbiology
P 526	817	THE EFFECT OF SILICON DIOXIDE AND ZEOLITE-ZINC NANOPARTICLES AGAINST STREPTOCOCCUS MUTANS BIOFILMS	Zahra Hosseinali hakim gheshlaghi	Oral Microbiology
P 527	834	QUORUM SENSING INHIBITION POTENTIAL OF RUBUS ULMIFOLIUS BLOSSOM EXTRACT IN VITRO AGROBACTERIUM TUMEFACIENS NTL/PZLR4	Elham Pishgar	Oral Microbiology
P 528	29	ANTI-CANDIDA ACTIVITIES OF SEEDS HYDROALCOHLIC EXTRACT OF RUMEX OBTUSIFOLIUS	Farahnaz Bineshian	Pharmaceutical Microbiology
P 529	36	INVESTIGATION OF BACITRACIN FUNGICIDAL EFFECTS PRODUCED BY BACILLUS SP. ISOLATED FROM SOIL OF FOREST PARKS IN TEHRAN	Ali Sayyah Varg	Pharmaceutical Microbiology
P 530	111	COMPARISON OF ERME GENE EXPRESSION IN SACCHAROPOLYSPORA ERYTHRAEA WILD TYPE AND OVERPRODUCTION MUTANTS	Hossein Rassi	Pharmaceutical Microbiology

Code	ID	Title	Submission Author	Session
P 531	118	EVALUATION OF THE SYNERGISTIC EFFECTS OF THE ALCOHOLIC EXTRACT OF STACHYS BYZANTINA IN COMPARISON WITH GENTAMYCIN, ERYTHROMYCIN AND PENICILLIN ANTIBIOTICS	Roya Safarkar	Pharmaceutical Microbiology
P 532	181	ISOLATION OF SCLEROGLUCAN ORIGINATED FROM SCLEROTINIA SCLEROTIORUM AND INVESTIGATION OF ITS BIOLOGICAL PROPERTIES	Mahboobeh Heidari	Pharmaceutical Microbiology
P 533	265	SYNTHESIS, PREPARATION, CHARACTRIZATION AND ANTIBACTERIAL PROPERTIES OF AG/PLA NANOFIBER	Mohammad Hassan Moshafi	Pharmaceutical Microbiology
P 534	266	SYNTHESIS, PREPARATION, CHARACTRIZATION AND ANTIBACTERIAL EFFECT OF AG NPS LOADED ON CHITOSAN/PLA NANOFIBER	Mohammad Hassan Moshafi	Pharmaceutical Microbiology
P 535	277	EVALUATION OF THE ANTIMICROBIAL EFFECT OF THE ALCOHOLIC EXTRACT OF FLOWER, LEAVES BEFORE AND DURING FLOWERING OF CLERODENDRUM BUNGEI ON THE CLINICAL ISOLATES OF KLEBSIELLA SPP. , PSEUDOMONAS SPP. AND SHIGELLA SPP.	Zahra Azmoudeh kasmaei	Pharmaceutical Microbiology
P 536	302	CHEMICAL COMPOSITION AND ANTI-DERMATOPHYTE ACTIVITY OF CUMINUM CYMINUM ESSENTIAL OILS	Rezvan Heidary tabar	Pharmaceutical Microbiology
P 537	352	ANTIFUNGAL ACTIVITY OF ROSEMARY OIL EXTRACT AGAINST AND ITS EFFECT ON THE AFL.1 GENE EXPRESSION IN THE ASPERGILLUS FLAVUS BY RT-PCR	Mojtaba Mohammadi	Pharmaceutical Microbiology

Code	ID	Title	Submission Author	Session
P 538	413	ANTIMICROBIAL EFFECT OF AQUEOUS AND HYDROALCOHOLIC EXTRACTS OF PLANTAGO PSYLLIUM AGAINST EXPERIMENTAL INFECTION OF HELICOBACTER PYLORI IN FEMALE RAT.	Shima Keshavarzi	Pharmaceutical Microbiology
P 539	458	ANTIMYCOTIC EFFECT OF MENTHOL ON EXPRESSION OF SAP1-ENCODING GENE IN CANDIDA ALBICANS	Shahrzad Shayegan	Pharmaceutical Microbiology
P 540	495	LETHAL EFFECTS OF VARIOUS EXTRACTS OF NIGELLA SATIVA SEED ON PROTOSCOLECES OF ECHINOCOCCUS GRANULOSUS	Saghar Modaresi	Pharmaceutical Microbiology
P 541	497	LEISHMANICIDAL EFFECTS OF BIOGENIC SELENIUM NANOPARTICLES AGAINST SENSITIVE AND GLUCAN-TIME-RESISTANT LEISHMANIA TROPICA STRAINS	Kianmehr Kianmehr	Pharmaceutical Microbiology
P 542	499	IN VITRO SCOLICIDAL EFFECT OF BERBERIS VULGARIS EXTRACT AND BERBERINE ECHINOCOCCUS GRANULOSUS PROTOSCOLECES	Zahra Chegeni	Pharmaceutical Microbiology
P 543	582	PHOTOCHEMICAL EFFECTS OF ECHIUM AMOENUM EXTRACT AGAINST STREPTOCOCCUS MUTANS	Jaber Ghorbani	Pharmaceutical Microbiology
P 544	662	ANTIMICROBIAL POTENTIAL OF TIO2 NANOPARTICLES AGAINST MDR PSEUDOMONAS AERUGINOSA	SADiDi SADiDi	Pharmaceutical Microbiology
P 545	669	ANTIFUNGAL ACTIVITY OF ROSEMARY OIL EXTRACT AGAINST AND ITS EFFECT ON THE AFL.1 GENE EXPRESSION IN THE ASPERGILLUS FLAVUS BY RT-PCR	Mojtaba Mohammadi	Pharmaceutical Microbiology
P 546	741	PREVALENCE OF ANTI-HELICOBACTER PYLORI ANTIBODIES IN PATIENTS WITH MULTIPLE SCLEROSIS IN TABRIZ	Aytak Farhangazar	Pharmaceutical Microbiology

Code	ID	Title	Submission Author	Session
P 547	776	ETHANOL EXTRACT MECHANISM OF RUMEX ALVEOLATUS ON CANDIDA ALBICANS	Nasim Ghayour	Pharmaceutical Microbiology
P 548	803	ANTIFUNGAL PROPERTIES OF CLOVE ETHANOLIC EXTRACT ON ASPERGILLUS NIGER	Zohreh Gholizadeh siahmazgi	Pharmaceutical Microbiology
P 549	5	ISOLATION AND IDENTIFICATION OF PATHOGENIC BACTERIA OF RAINBOW TROUT FISH IN KERMAN PROVINCE.	Laleh Yazdanpanah	Zonosis and Veterinary Microbiology
P 550	18	A SEROLOGICAL SURVEY ON COXIELLA BURNETII IN PREGNANT WOMEN WHO WERE HISTORICAL ABORTION IN KHORRAMABAD, WESTERN IRAN	Eiman Azizyari ghobadi	Zonosis and Veterinary Microbiology
P 551	54	STUDY OF BACTERIAL CONTAMINATION IN GALLBLADDER OF SHEEP SLAUGHTERED IN SHIRAZ ABATTOIR	Arash Soltani Borchaloee	Zonosis and Veterinary Microbiology
P 552	67	AMPLIFICATION AND CLONING OF A OUTER MEMBRANE PROTEIN (OMPL37) OF LEPTOSPIRA INTERROGANS SEROVAR CANICOLA, SERJOE HARDJO, GRIPPOTYPHOSA	Elaheh Rezaei	Zonosis and Veterinary Microbiology
P 553	70	THE ROLE OF THE AEROMONAS HYDROPHILA IN THE SAFETY OF FISHERY PRODUCTS	Laleh Yazdanpanah	Zonosis and Veterinary Microbiology
P 554	78	MOLECULAR DETECTION OF TOXOPLASMA GONDII FROM LIVESTOCK IN KASHAN	Sima Rasti	Zonosis and Veterinary Microbiology
P 555	79	COMPARISON PREVALENCE OF TOXOPLASMA GONDII IN KIDNEY TRANSPLANTATION REGIMES	Sima Rasti	Zonosis and Veterinary Microbiology
P 556	104	THE EVALUATION OF IMMUNITY OF INACTIVATED RAZI BLACKLEG VACCINE BY AN INDIRECT ELISA AND COMPARISON OF THE METHOD WITH CHALLENGE TEST.	Ali Haghroosta	Zonosis and Veterinary Microbiology

Code	ID	Title	Submission Author	Session
P 557	153	ALTERATION IN GST ACTIVITY IN LIVER, KIDNEY AND SPLEEN TISSUE OF IMMUNIZATION RAINBOW TROUT (ONCORHYNCHUS MYKISS) AGAINST ICHTHYOPHTHIRIUS MULTIFILIIS	Marzieh Heidarieh	Zonosis and Veterinary Microbiology
P 558	164	SURVEY OF HYDATID CYST SURGERIES IN PATIENTS REFERRED TO SHAHID BEHESHTI HOSPITAL OF KASHAN DURING 2012-2017	Sima Rasti	Zonosis and Veterinary Microbiology
P 559	180	SEARCHING FOR MYCOBACTERIUM AVIUM SUBSPECIES PARATUBERCULOSIS FROM BREAST MILK OF TWO CROHN'S DISEASE PATIENTS AND THEIR INFANTS BY NESTED-PCR: CASE REPORT	Saba Faeli	Zonosis and Veterinary Microbiology
P 560	209	DETECTION OF NOVEL PICORNAVIRUS IN BROILER FLOCKS ,IRAN, 2018 : THE FIRST REPORT	Arash Ghalyanchilangeroudi	Zonosis and Veterinary Microbiology
P 561	216	GENOMIC DETECTION OF CHLAMYDOPHILA ABORTUS IN SHEEP VAGINAL SWAB SAMPLES WITH ABORTION HISTORY IN LORESTAN PROVINCE USING NESTED-PCR METHOD	Homa Shamshiri	Zonosis and Veterinary Microbiology
P 562	231	GENOMIC DETECTION OF MYCOPLASMA AGALACTIAE IN SHEEP VAGINAL SWAB SAMPLES WITH ABORTION HISTORY IN LORESTAN PROVINCE BY PCR	Masoumeh Bairanvand	Zonosis and Veterinary Microbiology
P 563	243	THE EFFECT OF PROBIOTICS CELL FREE SUPERNATANT ON GROWTH AND VIABILITY OF IRANIAN ISOLATE OF PAENIBACILLUS LARVAE, THE ETIOLOGICAL AGENT OF AMERICA FOULBROOD DISEASE	Ramsina Betesho babrud	Zonosis and Veterinary Microbiology

Code	ID	Title	Submission Author	Session
P 564	267	REEMERGENCE OF VELOGENIC NEWCASTLE VIRUS GENOTYPE 7D (7L) IN GILAN PROVINCE 2018	Reyhaneh Khezrdoust	Zonosis and Veterinary Microbiology
P 565	362	EVALUATION OF NEUTRALIZING ANTIBODY ON VACCINATED CHICKEN BY GAMMA IRRADIATED AVIAN INFLUENZA VACCINE SUBTYPE H9N2	Saba Mesbah	Zonosis and Veterinary Microbiology
P 566	363	EFFECTS OF GAMMA IRRADIATED AVIAN INFLUENZA VACCINE SUBTYPE H9N2 ON VACCINATED CHICKEN'S SPLENIC CELL PROLIFERATION	Saba Mesbah	Zonosis and Veterinary Microbiology
P 567	447	DETERMINATION OF ANTIBIOTIC RESISTANCE 1 PATTERN AND VIRULENCE GENES IN 2 ESCHERICHIA COLI ISOLATED FROM BOVINE WITH MASTITIS IN SOUTHWEST OF IRAN	Seyed Sajjad Khoramrooz	Zonosis and Veterinary Microbiology
P 568	449	USING THE MULTIPLEX-PCR METHOD FOR DETECTION FOUR VENEREAL BACTERIA (TAYLORELLA EQUIGENITALIS ، KLEBSIELLA PNEUMONIAE ، PSEUDOMONAS AERUGINOSA AND STREPTOCOCCUS ZOOEPIDEMICUS) FROM THE MARE'S CLITORAL SAMPLES	Rasoul Imanian Njaf Abadi	Zonosis and Veterinary Microbiology
P 569	453	USING THE MULTIPLEX-PCR METHOD FOR DISCOVERY FOUR VENEREAL BACTERIA (TAYLORELLA EQUIGENITALIS ، KLEBSIELLA PNEUMONIAE ، PSEUDOMONAS AERUGINOSA AND STREPTOCOCCUS ZOOEPIDEMICUS) FROM THE MARE'S CLITORAL SAMPLES	Rasoul Imanian Njaf Abadi	Zonosis and Veterinary Microbiology
P 570	454	CLONING AND EXPRESSION OF RECOMBINANT LIPL32 ANTIGEN FROM LEPTOSPIRA INTERROGANS IN PROKARYOTIC SYSTEM.	Nina Bakhshandeh	Zonosis and Veterinary Microbiology

Code	ID	Title	Submission Author	Session
P 571	456	EPIDEMIOLOGICAL STATUS OF HUMAN CCHF IN DIFFERENT REGION OF IRAN FROM 1999 TO 2017	Simin Nayebi moghaddam	Zonosis and Veterinary Microbiology
P 572	468	PREVALENCE OF BRUCELLOSIS IN MILK AND BLOOD OF MARES OF YAZD PROVINCE IN 1396	Ladan Reisimotlagh	Zonosis and Veterinary Microbiology
P 573	477	THE INFORMATION SOURCES OF STUDENTS NON-MEDICAL UNIVERSITIES IN KERMANSHAH PROVINCE, IRAN ABOUT SALMONELLOSIS	Amir Amiri paryan	Zonosis and Veterinary Microbiology
P 574	483	STUDYING THE KNOWLEDGE OF NON-MEDICAL STUDENTS IN KERMANSHAH PROVINCE ABOUT VETERINARIANS' PERSPECTIVES ON THE PREDICTION OF THE CRIMEAN-CONGO HEMORRHAGIC FEVER (CCHF) AS A NECESSITY IN BIOSAFETY	Mona Mohammad zaheri	Zonosis and Veterinary Microbiology
P 575	487	STUDYING THE KNOWLEDGE OF NON-MEDICAL STUDENTS IN KERMANSHAH PROVINCE ABOUT VETERINARIANS' PERSPECTIVES ON THE PREDICTION OF THE SALMONELLOSIS (TYPHOID) DISEASE AS A NECESSITY IN BIOSAFETY	Mona Mohammad zaheri	Zonosis and Veterinary Microbiology
P 576	492	SEROPREVALENCE OF TOXOPLASMA GONDII INFECTION AMONG CHILDBEARING AGE WOMEN IN KERMAN CITY, SOUTHEASTERN IRAN	Fatemeh Akbarpour	Zonosis and Veterinary Microbiology
P 577	494	STUDY OF THE KNOWLEDGE OF STUDENTS RELATED TO BIOLOGICAL SCIENCES IN UNIVERSITIES AND FACULTY OF KERMANSHAH PROVINCE ABOUT THE EFFECTS OF GENETICALLY MODIFIED SUBSTANCES ON ECOSYSTEM AND HEALTH	Ghazal Keyvanfard	Zonosis and Veterinary Microbiology

Code	ID	Title	Submission Author	Session
P 578	509	PREVALENCE OF COAGULASE POSITIVE STAPHYLOCOCCUS AUREUS IN SOME DOMESTIC ANIMALS.	Bahar Malek ghaini	Zonosis and Veterinary Microbiology
P 579	510	CLONING AND EXPRESSION TWO RECOMBINANT PROTEIN OF MYCOBACTERIUM BOVIS	Reza Arefpajoohi	Zonosis and Veterinary Microbiology
P 580	511	EFFECT OF PROTECTION VACCINE TS11 IN CILINICAL SAMPLES FROM COMMERCIAL AND DOMESTIC POULTRY WITH PCR ASSAYE	Fatemeh Babaahmadi	Zonosis and Veterinary Microbiology
P 581	519	STRUCTURAL ANALYSIS OF THE EFFECT OF MUTATIONS OCCURRED IN A PARTIAL SEQUENCED RDRP GENE OF BOVINE PICOBIRNAVIRUSES.	Ahmad Nazaktabar	Zonosis and Veterinary Microbiology
P 582	520	PREVALENCE OF MYCOBACTERIUM AVIUM SUBSPECIES PARATUBERCULOSIS IS 900 DNA IN BIOPSY TISSUES FROM PATIENTS WITH CROHN'S DISEASE: HISTOPATHOLOGICAL AND MOLECULAR COMPARISON WITH JOHNE'S DISEASE IN FARS, IRAN	Forough Zarei Kordshouli	Zonosis and Veterinary Microbiology
P 583	528	COMPARISION OF SEROLOGICAL TESTS AND ELISA FOR DIAGNOSIS OF BRUCELLOSIS IN SHEEP AND GOATS	Rasa Sheini Mehrabzadeh	Zonosis and Veterinary Microbiology
P 584	559	THE PREVALENCE OF BRUCELLOSIS IN PATIENTS ADMITTED TO IMAM KHOMEINI HOSPITAL IN ARDABIL	Sahar Sabour	Zonosis and Veterinary Microbiology
P 585	603	ANALYSIS RISK FACTORS FOR HUMAN CYSTIC ECHINOCOCCOSIS IN MOGHAN PLAIN, AN ENDEMIC REGION OF ARDABIL PROVINCE, IRAN	Hafez MirzanezhadAsl	Zonosis and Veterinary Microbiology
P 586	604	SUBTYPE DETECTION OF AVIAN INFLUENZA NEURAMINIDASE WITH NEURAMINIDASE INHIBITION TEST	Najmeh Motamed	Zonosis and Veterinary Microbiology

Code	ID	Title	Submission Author	Session
P 587	615	MOLECULAR DETECTION OF PATHOGENIC AND NON-PATHOGENIC LEPTOSPIRA BASED ON MULTIPLEX PCR	Fatemeh Rahimi zarchi	Zonosis and Veterinary Microbiology
P 588	621	STREPTOCOCCOSIS AND ANTIBIOTIC RESISTANCE IN INFECTED RAINBOW TROUT (ONCORHYNCHUS MYKISS) FARMS IN GUILAN PROVINCE	Monireh Faeed	Zonosis and Veterinary Microbiology
P 589	626	COMPARISON OF IFA AND ELISA TECHNIQUES FOR DIAGNOSIS OF COXIELLA BURNETII	Amin Jaydari	Zonosis and Veterinary Microbiology
P 590	627	A SEROEPIDEMIOLOGICAL SURVEY OF Q FEVER AMONG SHEEP AND GOAT BY ELISA METHOD IN ALASHTAR, LORESTAN PROVINCE	Amin Jaydari	Zonosis and Veterinary Microbiology
P 591	631	MOLECULAR IDENTIFICATION OF SHEEPPOX VIRUS (SPV) IN YAZD PROVINCE OF IRAN	Mojtaba Alimolaei	Zonosis and Veterinary Microbiology
P 592	641	FIRST REPORT OF ANONCOTAENIA INFESTATION OF ALECTORIS CHUKAR FROM NORTHEAST OF IRAN	Somayeh Namroodi	Zonosis and Veterinary Microbiology
P 593	644	DTECTION OF ZOONOTIC SALMONELLA SPP IN ROAD-KILLED RURAL DOGS	Somayeh Namroodi	Zonosis and Veterinary Microbiology
P 594	648	DETERMINATION OF TOTAL PROTEIN CONTENT IN BACTERIAL SUSPENSION CONTAINING CLOSTRIDIUM PERFRINGENS TYPE D	Mehrdad Shamsaddini Bafti	Zonosis and Veterinary Microbiology
P 595	649	THE MORTALITY RATE OF EPSILON TOXIN CLOSTRIDIUM PERFRINGENS TYPE D	Mehrdad Shamsaddini Bafti	Zonosis and Veterinary Microbiology
P 596	654	SURVEY ON SALMONELLA CONTAMIATION OF WILD RODENTS IN MAZANDARAN PROVINCE	Somayeh Namroodi	Zonosis and Veterinary Microbiology
P 597	660	ISOLATION AND IDENTIFICATION OF MYCOBACTERIUM CAPTURED FROM MICE FROM INFECTED FARM BY TUBERCULOSIS	Khashaiar Mansouri	Zonosis and Veterinary Microbiology

Code	ID	Title	Submission Author	Session
P 598	685	PHENOTYPIC AND GENOTYPIC CHARACTERISTICS OF THE FIRST ESCHERICHIA COLI FECAL ISOLATES REPORTED FOR SEROGROUPS O55, O104 AND O118 ISOLATED FROM LIVESTOCK IN KHUZESTAN, IRAN	Mojdeh Barzan	Zonosis and Veterinary Microbiology
P 599	699	ISOLATION AND MOLECULAR IDENTIFICATION OF MYCOBACTERIUM FROM RAINBOW FISHES IN SABZEVAR	Faezeh Sedighi	Zonosis and Veterinary Microbiology
P 600	705	SEROEPIDEMIOLOGY OF LEPTOSPIRA INFECTION IN STRAY DOGS BY MAT DURING A ONE-YEAR PERIOD FROM RURAL COMMUNITIES OF KOOHSAR, ALBORZ, IRAN	Afrooz Fahimipour	Zonosis and Veterinary Microbiology
P601-P658				روز سوم کنگره ساعت ۱۰:۱۵-۱۱:۱۵
P 601	713	OPTIMIZATION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNP) ANALYSIS IN THE CLASSICAL PCR MACHINES FOR TYPING OF MYCOPLASMA AGALACTIAE	Khatereh Kabiri	Zonosis and Veterinary Microbiology
P 602	771	GENOMIC DETECTION OF CHICKEN ANEMIA VIRUS IN LAYING HENS IN ISFAHAN PROVINCE	Azam Mokhtari	Zonosis and Veterinary Microbiology
P 603	772	THE FIRST SEROLOGICAL STUDY OF COXIELLA BURNETII IN PREGNANT WOMEN WHO WERE REFERRED TO HOSPITAL IN KHORRAMABAD CITY FOR ABORTION	Eiman Azizyari ghobadi	Zonosis and Veterinary Microbiology
P 604	780	FIRST REPORT ON ISOLATION OF CHLAMYDIA FELIS FROM IRAN	Masoud Ghorbanpoor	Zonosis and Veterinary Microbiology
P 605	796	SEROLOGICAL SURVEY OF AVIAN INFLUENZA (H9N2) IN INDUSTRIAL POULTRY IN GOLESTAN PROVINCE DURING 2017-2018	Naser Sadri	Zonosis and Veterinary Microbiology

Code	ID	Title	Submission Author	Session
P 606	810	RESISTANT MOTILE SALMONELLOSIS TREATMENT USING TRACHYSPERMUM EXTRACTS WITH YOGHURT IN PEAFOWL'S	Abdolreza Nabinejad	Zonosis and Veterinary Microbiology
P 607	816	COMPARISON OF CLASSICAL AND ALTERNATIVE PATHWAYS OF SERUM COMPLEMENT OF KHAZAK AGAINST AVIAN PATHOGENIC ESCHERICHIA COLI	Hamed Heidari Mokarar	Zonosis and Veterinary Microbiology
P 608	832	THE EFFECT OF COMPLEMENT SYSTEM OF KHAZAK AND BROILER SERUM AGAINST AVIAN PATHOGENIC ESCHERICHIA COLI: AN INVITRO EXPERIMENTAL STUDY	Hamed Heidari Mokarar	Zonosis and Veterinary Microbiology
P 609	853	FIELD INVESTIGATION OF MYCOPLASMA GALLISEPTICUM INFECTION IN BACKYARD AND COMMERCIAL CHICKEN IN URMIA USING PCR METHOD	Fatemeh Babaahmadi	Zonosis and Veterinary Microbiology
P 610	860	IMMUNOLOGICAL AND PATHOLOGICAL CHANGES IN MICE TOWARDS INFECTION BY PASTEURELLA MULTOCIDA CULTURED IN HIGH AND LOW IRON MEDIA	Elham Hosseini	Zonosis and Veterinary Microbiology
P 611	34	PREPARATION OF PROBIOTIC MILK USING LACTOBACILLUS BIFIDOBACTERIUM ANGULTUM PTCC 1366 AND ITS EFFECTS ON THE PREVENTION AND TREATMENT OF IBD	Nafiseh Farazandehnia	پروبیوتیک ها و پربیوتیک ها
P 612	124	STUDY OF THE SURVIVAL RATE OF BIFIDOBACTERIUM BIFIDUM IN DOUGH BY POWDER AND ESSENTIAL OIL OF MENTHA LONGIFOLIA	HAMED KHATAMI	پروبیوتیک ها و پربیوتیک ها
P 613	149	GROWTH OPTIMIZATION OF LACTOBACILLUS PLANTARUM T5JQ301796.1, AN IRANIAN INDIGENOUS PROBIOTIC IN LAB SCALE FERMENTER	Faranak Noori	پروبیوتیک ها و پربیوتیک ها

Code	ID	Title	Submission Author	Session
P 614	152	IMPROVEMENT OF PROBIOTIC VIABILITY IN YOGURTS CONTAINING CEREAL BRAN	Ali Heshmati	پروبیوتیک ها و پربیوتیک ها
P 615	169	EFFECT OF HYPOLIPIDEMIC SUPERNATANT LACTOBACILLUS GASSERI IN HEALTHY AND DIABETIC LABORATORY MICE	Anoosheh Soleimani Rahim Abadi	پروبیوتیک ها و پربیوتیک ها
P 616	170	EVALUATING THE OF THE EXTRACTED SUPERNATANT OF LACTOBACILLUS GASSERI CONTAIN MEDIUM ON THYROID CANCEROUS CELL LINES; USING MTT METHOD	Anoosheh Soleimani Rahim Abadi	پروبیوتیک ها و پربیوتیک ها
P 617	172	MOLECULAR SEPARATION, PROBIOTIC PROPERTIES AND ANTILISTRIOSTIC BACTERIOCIN PRODUCTION OF ENTEROCOCCUS FAECIUM AND LACTOBACILLUS CURVATUS	Tannaz Mirhadizadi	پروبیوتیک ها و پربیوتیک ها
P 618	220	THE EFFECT OF ARTEMIA URMIANA POWDER ON INCREASING THE GROWTH OF PROBIOTIC LACTOBACILLUS ACIDOPHILUS AND BIFID BACTERIUM BIFIDIUM ON PROBIOTICS MILK	Fatemaeh Akbarzadeh	پروبیوتیک ها و پربیوتیک ها
P 619	228	FAST AND SIMPLE METHOD FOR DETERMINATION OF CALCIUM PROPIONATE AS PREVENTION OF FORMATION OF MYCOTOXINS IN BREAD SAMPLES BY HPLC	Freshteh Mehri	پروبیوتیک ها و پربیوتیک ها
P 620	242	ASSESSMENT OF VIABILITY OF BIFIDOBACTERIUM LACTIS(BB12), IN PROBIOTIC SUGAR-FREE CHOCOLATE DAIRY DESSERT	Seyede maryam Noorbakhsh	پروبیوتیک ها و پربیوتیک ها
P 621	294	PROBIOTIC APPLICATION IN HONEYBEE BREEDING	Niloufar Soleymani	پروبیوتیک ها و پربیوتیک ها
P 622	372	INVESTIGATION OF THE PRESENCE OF BIOACTIVE PEPTIDES IN TARKHINEH AND THEIR ANTIOXIDANT ACTIVITY	Zohreh Nematollahi	پروبیوتیک ها و پربیوتیک ها

Code	ID	Title	Submission Author	Session
P 623	373	INVESTIGATION OF THE PRESENCE OF BIOACTIVE PEPTIDES IN TARKHINEH AND THEIR ANTIBACTERIAL ACTIVITY AGAINST FOOD BORNE PATHOGENS	Zohreh Nematollahi	پروبیوتیک ها و پربیوتیک ها
P 624	381	THE EFFECT OF LACTOBACILLUS CASEI.ON SKIN WOUND HEALING IN WISTAR DIABETIC RATS BY GAVAGE METHOD ON DAYS 1,3,7,14,21	Atena Bazjo	پروبیوتیک ها و پربیوتیک ها
P 625	384	EFFECT OF BIFIDOBACTERIUM BIFIDUM ON REDUCING BLOOD SUGAR AND CHOLESTEROLE IN DIABETIC RATS	Shahab Jamaran	پروبیوتیک ها و پربیوتیک ها
P 626	414	EFFECT OF LIVE OR HEAT-KILLED L. ACIDOPHILUS ON FREE AFLATOXIN M1 IN DOOGH	Zahra Sarlak	پروبیوتیک ها و پربیوتیک ها
P 627	424	THE EFFECT OF PROBIOTIC BACTERIA AND PREBIOTICS ON THE GROWTH OF E.COLI ATCC23922 AND ENTEROCOCCUS FAECALIS ATCC 29212	Akram Asadi	پروبیوتیک ها و پربیوتیک ها
P 628	426	COMPARISON OF PROBIOTIC PROPERTIES OF LACTOBACILLUS PARACASEI AND LACTOBACILLUS PLANTARUM ISOLATED FROM TRADITIONAL SEMNAN CHEESE	Mahnoosh Parsaeimehr	پروبیوتیک ها و پربیوتیک ها
P 629	434	THE EFFECT OF LACTOBACILLUS PLANTARUM AND HONEY-DERIVED LACTOBACILLUS RHAMNOSUS ON GASTRITIS CAUSED BY HELICOBACTER PYLORI IN C57BL/6 MOUSE MODEL	Behnoush Asgari	پروبیوتیک ها و پربیوتیک ها
P 630	462	EFFECT OF PROBIOTIC STRAINS OF LACTOBACILLUS SP. ON ENTEROPATHOGENIC ESCHERICHIA COLI O SEROGROUPS ISOLATED FROM CLINICAL SPECIMENS	Morteza Mohajeri Amiri	پروبیوتیک ها و پربیوتیک ها

Code	ID	Title	Submission Author	Session
P 631	482	THE EFFECT OF NATIVE IRANIAN PROBIOTIC BACILLUS COAGULANS 6068 AND MEDICAGO SATIVA EXTRACT ON LOWERING BLOOD SUGAR AND HEPATIC ENZYMES ACTIVITY IN DIABETIC RATS	Parisa Mohammadi Hezaveh	پروبیوتیک ها و پربیوتیک ها
P 632	513	THE SPORE-FORMER PROBIOTICS REDUCE THE EFFECTS OF SALMONELLA ON THE GUT MICROFLORA POPULATION	Somaye Mazkour	پروبیوتیک ها و پربیوتیک ها
P 633	516	THE EFFECT OF BACILLUS SUBTILIS AND BACILLUS COAGULANS SPORES AS PROBIOTIC ON SALMONELLA CONCENTRATION IN THE INTESTINE AND ORGANS	Somaye Mazkour	پروبیوتیک ها و پربیوتیک ها
P 634	524	EVALUATION ANTIMICROBIAL EFFECTS OF PROBIOTIC EXTRACT OF LACTOBACILLUS FOR TREATMENT OF INFECTIONS CAUSED BY SALMONELLA	Zahra moghimi	پروبیوتیک ها و پربیوتیک ها
P 635	526	EFFECT OF OLIGOFRUCTOSE ON VIABILITY OF BIFIDOBACTERIUM LACTIS AND SENSORY PROPERTIES IN SYNBIOTIC YOGURT	Motahare Broughani	پروبیوتیک ها و پربیوتیک ها
P 636	543	PRIMARY EVIDENCE ON THE POTENTIAL OF THREE IRANIAN ENDEMIC PROBIOTICS IN TREATMENT OF HEPATOCELLULAR CARCINOMA	Fatemeh Karami	پروبیوتیک ها و پربیوتیک ها
P 637	564	STUDY ON ANTAGONIST ACTIVITY OF LACTOBACILLI ISOLATED FROM BUFFALO MILK AND YOGHURT AGAINST SOME BACTERIAL PATHOGENS	Neda Kouroshzadeh	پروبیوتیک ها و پربیوتیک ها
P 638	570	EFFECT OF SACCHAROMYCES CEREVISIAE ON EXPRESSION TOXIN GENE STX1 IN ENTEROHAEMORRHAGIC ESCHERICHIA COLI EHEC	Maryam Kopayee	پروبیوتیک ها و پربیوتیک ها

Code	ID	Title	Submission Author	Session
P 639	578	THE PRELIMINARY EFFECT OF DAIRY PRODUCTS' PROBIOTIC LACTOBACILLI ON THE CELL VIABILITY OF U937 CELLS	Nadia Karimi	پروبیوتیک ها و پربیوتیک ها
P 640	579	MOLECULAR IDENTIFICATION AND ISOLATION OF DAIRY PRODUCTS' PROBIOTIC LACTOBACILLI FROM FARS, IRAN	Nadia Karimi	پروبیوتیک ها و پربیوتیک ها
P 641	589	ANALYSIS OF STREPTOCOCCUS THERMOPHILUS COMMUNITY PROFILES OF DAIRY PRODUCTS FROM FARS, IRAN	Sara Sadeghi	پروبیوتیک ها و پربیوتیک ها
P 642	622	IDENTIFICATION OF LACTOBACILLUS GASTROINTESTINAL WHITE PERCH FISH (SANDER LUCIPERCA)	Monireh Faeed	پروبیوتیک ها و پربیوتیک ها
P 643	637	DISCRIMINATION OF LACTOBACILLUS SPECIES EXTRACTED FROM TRADITIONAL DAIRY PRODUCTS USING RAPD-PCR MOLECULAR MARKER	Seyed mostafa Hosseini	پروبیوتیک ها و پربیوتیک ها
P 644	640	ISOLATION, CHARACTERIZATION AND PRESERVATION OF LACTIC ACID BACTERIA (LAB) FROM MAZANDARAN PROVINCE TRADITIONAL FOODS AND SURVEY OF THEIR IN-VITRO PROBIOTIC ACTIVITY	Shahrzad Tavanania	پروبیوتیک ها و پربیوتیک ها
P 645	703	IMMUNOLOGICAL EFFECT OF LACTOBACIILUS CASEI IN RAT WITH CANDIDA ALBICANS INFECTION	Behnazsadat High-tech zavareh	پروبیوتیک ها و پربیوتیک ها
P 646	724	SURVEY AND COMPARISON OF THE EFFECT OF MULTIPLE LACTOBACILLUS ON THE FUNCTION OF LIVER ENZYMES IN THE VISTAR MATURE NAFLD RATS	Mohammadjafar Begoo	پروبیوتیک ها و پربیوتیک ها

Code	ID	Title	Submission Author	Session
P 647	735	STUDY OF THE SURVIVAL RATE OF LACTOBACILLUS ACIDOPHILUS IN DOUGH BY POWDER AND ESSENTIAL OIL OF MINT	Hesam Eskandari	پروبیوتیک ها و پربیوتیک ها
P 648	784	ANTIBIOTIC SUSCEPTIBILITY OF YOGURT`S PROBIOTICS	Narges Aghajanian	پروبیوتیک ها و پربیوتیک ها
P 649	785	EVALUATION OF THE PERFORMANCE OF PLANTAGO PSYLLIUM, PLANTAGO MAJOR AND LALLEMANTIA IBRICA LOCAL PREBIOTICS ON LACTIC ACID BACTERIA	Shima Babaei	پروبیوتیک ها و پربیوتیک ها
P 650	793	CYTOTOXICITY EFFECT OF BACTERIOCIN LIKE INHIBITORY SUBSTANCE (BLIS) PRODUCED BY PROBIOTIC LACTOBACILLUS CASEI TA0021 ON COLORECTAL CANCER CELL LINES (HT-29	Elham Norouzi	پروبیوتیک ها و پربیوتیک ها
P 651	798	ANTIMICROBIAL ACTIVITY AND ANTIBIOTIC SUSCEPTIBILITY OF BIFIDOBACTERIUM SPP ISOLATE FROM HUMAN MILK AGAINST HOSPITAL , ENTEROPATHOGENIC AND FOOD-BORNE PATHOGENS	Soda Amini	پروبیوتیک ها و پربیوتیک ها
P 652	811	ANTIMICROBIAL ACTIVITY AND ANTIBIOTIC SUSCEPTIBILITY OF BIFIDOBACTERIUM SPP ISOLATE FROM THE FECES OF HEALTHY INFANT AGAINST HOSPITAL , ENTEROPATHOGENIC AND FOOD-BORNE PATHOGENS	Soda Amini	پروبیوتیک ها و پربیوتیک ها
P 653	818	ISOLATION AND IDENTIFICATION OF PROBIOTICS FROM MARAGHEH LOCAL YOGURT	Mona Kordloo	پروبیوتیک ها و پربیوتیک ها
P 654	836	DETECTION OF A BENZOAT DEGRADATION GENE (BOX-B) IN L. CASEI ISOLATED STRAIN IN CHEESE	Narges Dadfarma	پروبیوتیک ها و پربیوتیک ها
P 655	854	ISOLATION AND IDENTIFICATION OF PROBIOTICS FROM LOCAL WHEY WATER IN MARAGHEH	Mona Kordloo	پروبیوتیک ها و پربیوتیک ها

Code	ID	Title	Submission Author	Session
P 656	863	ISOLATION AND IDENTIFICATION OF LACTIC ACID BACTERIA FROM CARP FISH SPECIES IN GUILAN	Hosein Alipour	پروبیوتیک ها و پربیوتیک ها
P 657		ANTIMICROBIAL EFFECT OF SILVER-NANOPARTICLES ON BACITRACIN-POLYMIXIN-GENTAMYCIN-CLINDAMYCIN AND ERYTHROMYCIN AGAINST BACILLUS SUBTILIS- BACILLUS CEREUS- PSEUDOMONAS AERUGINOSA- E-COLI	Nastaran Ghobadi	Antimicrobial agents and Resistance
P 658		SIGNIFICANT HEMOLYTIC ACTIVITY OF A BACILLUS STRAIN ISOLATED FROM AQUACULTURE WATER OF SHRIMPS FARM	Shukufeh Ghasemian	Microbial Metabolites and Cancer Treatment

یادداشت:

مقالات سخنرانی

نوزدهمین کنگره بین‌المللی میکروب‌شناسی ایران

Oral

Antimicrobial agents and Resistance

O1 - 47: SUB-LETHAL ANTIMICROBIAL PHOTODYNAMIC INACTIVATION AFFECTS QUORUM SENSING-CONTROLLED BIOFILM FORMATION GENE EXPRESSION OF PSEUDOMONAS AERUGINOSA IN-VITRO

Saghar Hendiani[1], Nasim Kashef [2], Majid Pornour [3]

1. Department of Microbiology, School of Biology, College of Science, University of Tehran, Tehran, Iran, Email: hendiani.s@ut.ac.ir
2. Department of Microbiology, School of Biology, College of Science, University of Tehran, Tehran, Iran, Email: kashefn@ut.ac.ir
3. Photo Healing and Regeneration Research Group, Medical Laser Research Center, Academic Center for Education, Culture and Research (ACECR), Tehran, Iran, Email: ma_pornour@yahoo.com

Background and Aim: The worldwide rise in antibiotic resistance made it mandatory to search for new alternative therapies that are able to eliminate resistant microorganisms and impair the development of new forms of resistance. In this context, antimicrobial photodynamic inactivation (APDI) is highlighted for the treatment of localized infections. During treatment, bacteria may expose to sub-lethal doses of APDI (sAPDI). Although sAPDI cannot kill microorganisms, it can significantly affect microbial virulence. In this study, we evaluated the effect of sAPDI using methylene blue (MB) on the expression of genes belonging to two quorum sensing (QS) operons (rhl and las systems) and two genes necessary for biofilm formation (pelF and pslA) under QS control in Pseudomonas aeruginosa ATCC 27853.

Methods: Planktonic cells exposed to sAPDI (MB at 0.012 mM and red light dose of 23 J/cm2) were allowed to form biofilm for 24 h. Biofilm formation was evaluated using triphenyl tetrazolium chloride (TTC) assay and scanning electron microscopy (SEM). Gene expression of sAPDI-treated cells was evaluated by quantitative real-time polymerase chain reaction.

Results: Quantitative assay (TTC) results and morphological observations (SEM) indicated that a single sAPDI treatment resulted in a significant decrease in biofilm formation ability of P. aeruginosa ATCC 27853 compared to their non-treated controls (P=0.012). sAPDI down-regulated the expression of QS-controlled biofilm formation genes (pslA and pelF) and QS genes (lasI, lasR, rhlI and rhlR) in P. aeruginosa ATCC 27853.

Conclusion: Our results indicated that the transcriptional decreases caused by MB-sAPDI did lead to phenotypic changes.

Keywords:sub-lethal antimicrobial photodynamic inactivation, biofilm formation, quorum sensing, Pseudomonas aeruginosa

O2 - 105: EVALUATION OF SILVER NANOPARTICLES EFFECTS ON BLA-PER-1 GENE EXPRESSION FOR BIOFILM FORMATION IN ISOLATES OF ANTIBIOTIC-RESISTANT ACIENTOBACTER BUMANNI BY REAL TIME PCR METHOD

Tohid Piri gharaghie[1], Seyed Ataollah Sadat Shandiz2[2], Neda banae[3], Somaye moulaei yenki kand[4]

1. Dr.Ebrahimi microbiology Labratoar
2. Supervisor
3. Co-Worker
4. Co-Worker

Background and Aim:: Acinetobacter bomanni is one of the most common opportunistic pathogen in hospital that is resistant to many antibiotics due to the production of biofilm. This study aimed to evaluate an anti-biofilm activity of silver nanoparticles (AgNPs) on clinical antibiotic resistant Acientobacter bumanni.

Methods: In this experimental study, Acientobacter bumanni were isolates from 100 clinical samples. After identification of Acientobacter bummani strains and determination of antibiotic resistant profiles, biofilm producer isolates were determined using PCR method. The Minimum inhibitory concentration (MIC) of strains against AgNPs was determined. After 24 hours exposure of strains with subMIC concentration of AgNPs, RNA extraction and cDNA synthesis was performed. Finally, evaluation of Bla-per-1gene expression was measured using real time PCR method.

Results:out of 100 clinical isolates, 12 isolates were belonged to Acientobacter bummani and all of strains were resistant to antibiotics except colistin. PCR results show that 12 isolates have Bla-per-1gene and they were biofilm positive. Real Time PCR results show that after treatment of isolates with subMIC concentration of AgNPs, all of strains had a significant reduction in Bla-per-1gene expression ($P<0.05$).

Conclusion: According to anti-biofilm effects of AgNPs, it seems that AgNPs can be used as drug candidate in pharmaceutical industries

Keywords: Acientobacter bummani, Silver nanoparticle, Biofilm.

O3 - 249: DETECTION AND SEQUENCING OF TN1546 TRANSPOSON IN TWO VANCOMYCIN-RESISTANT STAPHYLOCOCCUS AUREUS

Davood Kalantar Neyestanaki[1], Mahsa Ziasistani[2], Mohammad Reza Shakibaie[3], Davood Kalantar-Neyestanaki[4]

1. -
2. Pathology and Stem Cell Research Center، School of Medicine, Kerman University of Medical Sciences, Kerman, Iran.
3. Department of Microbiology and Virology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran.
4. Department of Microbiology and Virology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran.

Background and Aim: Tn1546 is a Tn3-related transposon conferring vancomycin resistance, consists of a cluster of seven genes including vanS, vanR, vanH, vanA, vanX, vanY, and vanZ.The aim of this study was detection and sequencing of Tn1546 transposon in two vancomycin-resistant Staphylococcus aureus.

Methods: During 2015-2016, two vancomycin resistant S. aureus were isolated from two hospitalized patient in Kerman, Iran. The Tn1546 transposon was amplified and sequenced by primer walking method using primers designed by Primer designing tool in NCBI (https://www.ncbi.nlm.nih.gov/tools/primer-blast) for different regions of Tn1546. The sequences were assembled by Lasergene 6 software (DNASTAR) and analyzed by the basic local alignment search tool (BLAST) in NCBI (https://blast.ncbi.nlm.nih.gov/Blast.cgi). Open reading frames (ORF) were determined from contiguous sequences tag obtained using open reading frame finder software (https://www.ncbi.nlm.nih.gov/orffinder).

Results: The amplification and sequencing of Tn1546 showed that, this transposon contain 9 genes, a transposase (tnp) and resolvase (rev) genes connected via ORF2 to vanR, vanS, vanH, vanA, vanX, vanY and vanZ, respectively. Analysis of the sequence of Tn1546 indicated closely related to Tn1546 in Enterococci spp. The sequence of Tn1546 was submitted in GenBank under accession number MG592387.

Conclusion: By sequencing of Tn1546, we found its closed phylogenetic relationship with ancestral Enterococci spp. which can probably confirmed that the Tn1546 was transferred from Enterococci spp. to S. aureus in our hospital settings.

Keywords: Vancomycin resistance, S. aureus, Tn1546

O4 - 394: PREVALENCE OF NONTUBERCLOSIS MYCOBACTERIA IN PATIENTS WITH SUSPECTED PULMONARY TUBERCULOSIS IN TEHRAN,IRAN.

Zahra Nikpour[1], Mohammad javad nasiri[2], Hossein dabiri[3], maryam ghane[4], masoud dadashi[5]

1. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences Department of Microbiology, Faculty of Basic Sciences, Islamic Azad University, Islamshahr Branch, Islamshahr, Iran
2. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences
3. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences
4. Department of Microbiology, Faculty of Basic Sciences, Islamic Azad University, Islamshahr Branch, Islamshahr, Iran
5. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences

Background and Aim: Nontuberculous mycobacteria(NTM) can be a cause of a variety of diseases that can not be distinguished from tuberculosis (TB) and is a diagnostic and therapeutic challenge. The purpose of this study was to isolate Nontuberculous mycobacteria from patients suspected to having pulmonary tuberculosis referring to Tehran regional tuberculosis laboratory.

Methods: To identify NTM isolated from patients suspected of pulmonary tuberculosis at the species level, phenotypic tests including the method of Petroff method (NaOH 2%) as well as biochemical test were applied on the Loon Stein Johnson media. Also from colonies the DNA was extracted and PCR was performed for interested genes.

Results: Overall 62 NTM strains were isolated from studied clinical samples were taken from TB suspected patients. Mycobacterium simiae(22.5%) was the most common isolated NTM followed by Mycobacterium fortuitum (16.1%), Mycobacterium kansasii (12.9%) and M. avium complex (6.4%).

Conclusion: Our data showed that a significant number of tuberculosis cases were caused by NTM strains, among which Mycobacterium simiae has the highest prevalence. M. simiae can cause the same illness as tuberculosis, which is a serious problem for public health and attracts the attention of health officials, physicians and microbiologists.

Keywords: Nontuberculous mycobacteria / phenotypic method / molecular method / prevalence rate

O5 - 441: CORRELATION BETWEEN ABILITY OF BIOFILM FORMATION WITH THEIR RESPONSIBLE GENES AND MDR PATTERNS IN CLINICAL AND ENVIRONMENTAL ACINETOBACTER BAUMANNII ISOLATES

Ali Mohammadi bardbari[1], Mohammad Yousef Alikhani [2], Mohammad Reza Arabestani[3]

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: Acinetobacter baumannii potential to form biofilm and exhibit multiple antibiotic resistances may be responsible in its survival in hospital environment. Accordingly, our study was aimed to determine the correlation between ability of biofilm formation and the frequency of biofilm related genes with antibiotic resistance phenotypes in clinical and environmental isolates.

Methods:A total of 75 clinical and 32 environmental strains of the A. baumannii were collected and identified via API 20NE. Antibiotic susceptibility was evaluated by disk diffusion and microdilution broth methods. Biofilm formation assay was performed by microtiter plate method. OXA types and biofilm related genes including BlaOXA-51, BlaOXA-23, BlaOXA-24, BlaOXA-58, bap, blaPER-1, and ompA were amplified by PCR.

Results: The rate of MDR A. baumannii in clinical isolates (100%) was higher than environmental (81.2%) isolates ($P<0.05$). Analysis of the frequency of blaOXA-23 gene revealed a statistically significant difference between clinical (85.3%) and environmental (68.7%) isolates ($P < 0.05$). The prevalence of strong biofilm producers in clinical and environmental isolates were 58.7% to 31.2%, respectively. In the clinical and environmental isolates, the frequencies of ompA, blaRER-1 and bap genes were 100%, 53.3%, 82.7% and 100%, 37.5%, 84.4% respectively. Statistical analysis revealed a significant correlation between the frequency of MDR isolates and biofilm formation ability ($P = 0.008$).

Conclusion: One dominant resistance pattern has shown among clinical and environmental isolates. There was a significant correlation between multiple drug resistance and biofilm formation and clinical isolates had a higher ability to form strong biofilms compared to the environmental samples

Keywords:A. baumannii, biofilm formation, biofilm-related genes, MDR, OXA type genes

O6 - 672: PHENOTYPIC AND GENOTYPIC CHARACTERIZATION OF ANTIBIOTIC RESISTANCE AMONG METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS ISOLATES IN PATIENTS ADMITTED TO ISFAHAN AND KASHAN HOSPITALS IN2017

Mitra Omidi[1], Farzaneh Firoozeh[2], Mahmood Saffari[3], Hossein Sedaghat[4]

1. Ms student, Department of Microbiolog, School of Medicine, Kashan University of Medical Sciences, Kashan, I.R. Iran
2. Associated professor, Department of Microbiology, School of Medicine, Alborz University of Medical Sciences, Karaj, I.R. Iran.
3. Professor, Department of Microbiology, School of Medicine, Alborz University of Medical Sciences, Karaj, I.R. Iran.
4. Assistant Professor, Department of Microbiology, School of Medicine, Alborz University of Medical Sciences, Karaj, I.R. Iran.

Background and Aim: Background and Aim: Staphylococcus aureus is the most important human pathogen, which has become a concern as a result of its increasing resistance to various antimicrobials. The aim of this investigation was characterization of antimicrobial resistance pattern among methicillin-resistant Staphylococcus aureus isolated from patients' clinical specimens in Isfahan and Kashan hospitals.

Methods: This cross-sectional study was conducted on 140 patients hospitalized in ICU, surgical, heart, infectious and emergency departments in Isfahan and Kashan hospitals. The resistance pattern of isolates was determined using disc diffusion and D- test methods according to CLSI guidelines. The antibiotics used included cefoxitin, cefazolin, erythromycin, clindamycin, linzolid, and trimethoprim-sulfamethoxazole. All isolates were screened for the presence of femA and mecA genes by PCR assay.

Results: All methicillin-resistant Staphylococcus aureus isolates were confirmed by PCR method using femA and mecA genes. The results showed of all isolates, 24, 13, 3 and 11 methicillin-resistant Staphylococcus aureus isolates were cefoxitin, cefazolin linzolid and trimethoprim-sulfamethoxazole –resistant respectively. Phenotypic and genotypic characterization of antibiotic resistance among methicillin-resistant Staphylococcus aureus isolates in patients admitted to Isfahan and Kashan hospitals. 7 isolates D_shaped clear zone around CLSI disk proximal erythromycin disk,13 isolates D_shaped zone around CLSI disk proximal to the erythromycin disk and small colonies, growing to CLSI in otherwise clear zone.

Conclusion: The increasing resistance in methicillin-resistant Staphylococcus aureus isolates even to last resort antibiotics, such as linzolide, can be a serious threat to human health and society.

Keywords: Staphylococcus aureus, antibiotic resistance, D- test, femA, mecA

O7 - 707: DISSEMINATION OF AMINOGLYCOSIDE-MODIFYING ENZYMES (AME) ENCODING GENES AMONG ESCHERICHIA COLI CLINICAL ISOLATES COLLECTED FROM INTENSIVE CARE UNIT (ICU)

Masoumeh Aslanimehr[1], Azadeh Rahmani[2], Ammeneh Barikani[3], Daruish Hamedi-Asl[4]

1. Qazvin Uni of Med Sci
2. Qazvin Uni of Med Sci
3. Qazvin Uni of Med Sci
4. Qazvin Uni of Med Sci

Background and Aim:E. coli is one of the most common (HCI) agents. The aim of this study was investigation of phenotypic and molecular charachterization of aminoglycoside resistance among clinical isolates of E. coli of ICU.

Methods:A total of 254 E. coli isolates were collected from ICU of 16 hospitals in Qazvin, Karaj and Tehran. The antibiotic susceptibility test was conducted according to the Clinical and Laboratory Standards Institute (CLSI) guideline using seven aminoglycosides antibiotics (MAST, UK). The gentamicin (Sigma Co) MIC was determined with agar dilution using a range between 0.5-256 µg/ml. Aminoglycoside Modifying Enzyme genes (ant(2″)-Ia, aac(3)-IIa,aac(6′)-lb, aac(3)-Ia, ant(4′)-IIb) was performed by PCR and sequencing.

Results: Of total 254 E. coli isolates, 237 (93.3%) isolates were non- susceptible against at least one of the aminoglycosides tested among those gentamicin 136 (53.5%), and streptomycin 134(52.8%) showed the highest rates of resistance whereas amikacin and netilmicin revealed high susceptibility rates of 93.3% and 78.7%, respectively. MIC result showed that 53.2% of isolates were resistant to gentamicin. The lowest level of MIC for gentamicin was 0.5mg/mL, and the highest level was over 256 mg/mL The MIC50 was 64 µg/ml and MIC90 was 128 µg/m. Of 254 isolates 78.3% were positive for the presence of aac(3)-IIa as the dominant gene followed by aac(6′)-lb(50%), aac(3)-Ia(4.7%), ant(4′)-IIb(3.6%).

Conclusion: The result of this study showed that here was a high rate of aminoglycoside resistance and AME genes among E. coli isolates from ICU.

Keywords: Escherichia coli, aminoglycosides resistance, aminoglycoside modifying enzymes

O8 - 737: DETECTION OF DRUG RESISTANCE GENES RESERVIORES IN TNABARS AND R PLASMIDS AND STUDY OF ADERS AND BAERS REGULATORY SYSTEMS EFFECTS ON ADEABC EFFLUX PUMP AMONG ACINETOBACTER BAUMANNII CLINICAL ISOLATES

Mohammad Savari[1], Abbas Bahador[2]

1. Department of Microbiology, School of medicine, Ahvaz Jundishapur uinversity of medical sciences
2. Department of Microbiology, School of medicine,Tehran university of medical sciences, Tehran, Iran

Background and Aim: The aim of this study was to detecttion of drug resistance genes reserviores in TnAbaRs and R plasmids and study of AdeRS and BaeRS regulatory systems on AdeABC efflux pump among Acinetobacter baumannii clinical isolates with decreased susceptibility to tigecycline.

Methods: By using PCR, more than 20 antibiotics resistance genes were tested in term of chromosomal location on AbaRs or R plasmids and the isolates were AbaR mapped. By using Real time PCR, adeB gene expression was evaluated in isolates with decreased susceptibility to tigecycline and were compared with a sensitive strain. The expression levels of adeRS and baeSR genes and their sequence in isolates with decreased susceptibility to tigecycline was evaluated and compared with a sensitive strains.

Results: Genes associated with drug resistance were distributed between AbaR and R plasmid. All the isolates in this study were horboring new variants of AbaR. The adeB, adeS, adeR, baeS and baeR genes were overexpressed, in all isolates with decreased susceptibility to tigecycline in compare with the sensitive strain. Sequencing of adeS, adeR, baeS and baeR genes in isolates with decreased susceptibility in compare to the reference strains revealed that all of them suffered multiple amino acid substitutions.

Conclusion: The majority of A. baumannii isolates with decreased susceptibility to tigecycline reserve the resistance gene reservoirs in AbaR and R plasmid. Both AdeRS and BaeSR two components systems in A. baumannii isolates with decreased susceptibility to tigecycline were overexpressed.

Keywords: Acinetobacter baumannii, Tigecycline, AbaR, R plasmid, AdeABCefflux pumps, AdeSR two components system, BaeSR two components system

O9 - 753: MOLECULAR DETERMINANTS OF ACQUIRED COLISTIN RESISTANCE AMONG CLINICAL ISOLATES OF KLEBSIELLA PNEUMONIAE

Mehri Haeili[1]

1. Department of Biology, Faculty of Natural Sciences, University of Tabriz, Tabriz, Iran

Background and Aim: Colistin is among the few antimicrobial agents that retain activity against problematic Gram negative bacilli (GNB) and often considered as the last-line defense against infections caused by these superbugs. Recently, increased use of colistin has resulted in development of resistance to this last hope antibiotic. The most common mechanism of bacterial resistance includes covalent modification of LPS through incorporation of positively charged groups which neutralize the negative charges of LPS and reduce binding affinity of colistin to its target. LPS modifications are mediated by genetic alterations in the PmrA-PmrB or PhoP-PhoQ two component regulatory systems or their regulators (MgrB). Recently a plasmid mediated resistance mechanism (mcr genes) has been identified among GNB

Methods: We explored the underlying mechanisms of colistin resistance among 20 colistin resistant clinical isolates of Klebsiella pneumoniae. The presence of mcr-1, mcr-2, mcr-3, and mcr-4 genes were examined by PCR and nucleotide sequences of pmrA, pmrB, phoP, phoQ, and mgrB genes were determine. The expression levels of LPS modifying enzymes PmrK and PmrC was evaluated by RT-qPCR method.

Results: All col-R isolates lacked mcr genes or any genetic alterations in the pmrA, phoP, and phoQ genes and substitutions identified in the pmrB were not found to be involved in resistance conferring .Inactivation of MgrB due to nonsense mutations and insertion of IS elements was found in 15 isolates (75%) which was associated with overproduction of LPS modifying enzymes.

Conclusion: MgrB alterations was found to be the main mechanism of colistin resistance among the studied K. pneumoniae isolates.

Keywords:colistin, Klebsiella pneumoniae, MgrB, PmrAB, PhoPQ

O10 - 779: DIAGNOSTIC ACCURACY OF GENEXPERT AND HRM IN COMPARISON WITH PROPORTIONAL METHOD FOR STUDY OF DRUG RESISTANCE IN MYCOBACTERIUM TUBERCULOSIS STRAINS ISOLATED FROM TUBERCULOSIS PATIENTS

Samaneh Arefzadeh[1], Hossein Dabiri[2], Mohammad Javad Nasiri[3]

1. Department of Medical Microbiology, Shahid Beheshti University of Medeical Sciences, Tehran, Iran
2. Department of Medical Microbiology, Shahid Beheshti University of Medeical Sciences, Tehran, Iran
3. Department of Medical Microbiology, Shahid Beheshti University of Medeical Sciences, Tehran, Iran

Background and Aim: Nowadays Tuberculosis is one of the most serious public health problems worldwide. The emergence of multidrug-resistant TB, (MDR)-TB, has had a significant negative effect on TB control. Despite the fact that the proportional method is the gold standard test to diagnose TB in Iran, but it is a time consuming process that takes up to several weeks to show result. Molecular TB diagnostic methods are designed to target specific genes harboring mutations that are associated with resistance to specific anti-TB drugs. High-resolution melting curve analysis(HRM) is a relatively new molecular method that can be used for detection of MDR-TB directly from clinical isolates.

Methods:A total of 81 sputum specimens were collected from patients suspected of having multidrug resistant tuberculosis. DNA from sputum samples was extracted. Real-time PCR and HRM were done by the Corbett machine in succession. Briefly, HRM components was prepared in 20 µl reaction mixtures.

Results: The HRM assay categorized 74 patient samples of 82 sputum samples as MDR-TB. The sensitivities of detection of mutations in genes responsible for RIF for rpoB was 90.5%.

Conclusion: According to previous studies, single-drug resistance to Rifampicin is rare. In fact, resistance to Rifampicin is also a marker of resistance to Isoniazid. In general, tuberculosis is more prevalent in developing countries, and diagnosis and treatment costs a lot for patients. Therefore, given that the specificity and sensitivity of the HRM test are the same with the GeneXpert technique, it is concluded that HRM is an appropriate choice in these communities.

Keywords: Tuberculosis, MDR-TB, HRM, Resistance

O11 - 786: MOLECULAR CHARACTERIZATION OF AMINOGLYCOSIDE RESISTANCE AMONG CLINICAL ISOLATES OF STAPHYLOCOCCUS AUREUS

Masoumeh Aslanimehr[1], valli Abasi[2], Amir Peymani[3], Amir Javadi[4]

1. Qazvin Uni of Med Sci
2. Qazvin Uni of Med Sci
3. Qazvin Uni of Med Sci
4. Qazvin Uni of Med Sci

Background and Aim: Aminoglycosides are potent bactericidal agents that often used in combination with either a β -lactam or a glycopeptide, especially in the treatment of staphylococcal. Enzymatic inactivation of this antibiotic by cellular enzymes that modify aminoglycosides is the major mode of mechanisms for bacterial resistance to this drug. The aim of Present study was to determine the frequency of aminoglycoside-modifying enzymes (AME) encoding genes in clinical isolates of S. aureus.

Methods: Two hundred thirty clinical isolates of S. aureus were collected from patients in Qazvin and Tehran educational hospitals. Antibiotic susceptibility determined by disk diffusion method according to the CLSI guideline. The gentamicin (Sigma Co) MIC was determined with agar dilution method using a range between 0.5-256 µg/ml. Aminoglycoside Modifying Enzyme ([aac(6')-Ie-aph(2")] ‘ ant(4')-Ia and aph(3')-IIIa)genes ()was performed by PCR and sequencing.

Results: Aminoglycosides resistance were detected to Kanamycin (43/8 %), Gentamicin (47 %), Tobramycin (47%), Amikacin (46/1 %), Netilmicin (26/1 %) Doxycycline (50/5 %), Ciprofloxacin (50 %), Rifampin (36/5 %), Mupirocin (9/1 %) and Teicoplanin (4/3 %). Forty four percent of strains were resistant to Gentamicin on agar dilution method. The frequency of [aac(6')-Ie-aph(2")] ‘ant(4')-Ia and aph(3')-IIIa genes in the isolates was determined by PCR method that 39.1 %, 6.5 % and 18.3 % reported, respectively.

Conclusion: The result of this study showed that here was a high rate of aminoglycoside resistance and AME genes among S.aureus clinical isolates.

Keywords: Staphylococcus aureus, AME, [aac(6')-Ie-aph(2")] ‘ant(4')-Ia ‘aph(3')-III

O12 - 797: A COMPREHENSIVE STUDY OF ACINETOBACTER BAUMANNII IN VENTILATOR ASSOCIATED PNEUMONIA: A COGITATION CONCEPT

ALKA HASANI[1], Elnaz Shahrokhi[2], Khalili Ansarin[3], Halah Mikaili[4], Akbar Hasani[5], Mohammad Aghazadeh[6], Saeed Mosavi[7], Akbar Sharifi [8]

1. Tabriz University of Medical Sciences, Tabriz, I.R.Iran
2. Tabriz University of Medical Sciences, Tabriz, I.R.Iran
3. Tabriz University of Medical Sciences, Tabriz, I.R.Iran
4. Tabriz University of Medical Sciences, Tabriz, I.R.Iran
5. Tabriz University of Medical Sciences, Tabriz, I.R.Iran
6. Tabriz University of Medical Sciences, Tabriz, I.R.Iran
7. Tabriz University of Medical Sciences, Tabriz, I.R.Iran
8. Tabriz University of Medical Sciences, Tabriz, I.R.Iran

Background and Aim: Ventilator-associated pneumonia (VAP) due to a multidrug-resistant microorganism is a clinical concern. Acinetobacter baumannii is one of the appalling nosocomial organism featured by high antibiotic resistance and virulence capacity rendering the therapeutic modalities difficult. We aimed to characterize Acinetobacter baumannii isolated from mechanically ventilated patients in terms of epidemiological characteristics, antibiotic susceptibility, and presence of carbapenemase genes, sequence typing and their involvement in biofilm formation.

Methods: Endotracheal secretions collected from 40 adults mechanically ventilated patients for bacterial culture. Antibiotic susceptibility was performed by disc diffusion test. Medical records were retrieved and analyzed to search out the risk factors of patient. Sequence group (SG) of isolates were identified by trilocus sequence-based typing (3LST). Presence of carbapenemase genes was assessed by PCR.

Results: The incidence of VAP was 12.5% among patients on mechanical ventilation. The tracheostomy was found as an increased risk of VAP followed by a heart attack and chronic heart disease. A very high frequency of resistance was exhibited towards traditional antibiotics; none were resistant to colistin. Among all isolates, 55.9% belonged to SG1 and 8.8% to SG2 while others were grouped in novel epidemiological types. Oxacillinase genes showed their involvement in carbapenemase resistance. Presence of VIM and NDM was obvious in 26.2%, and 39.7% of isolates while 57.4% of them possessed bap gene.

Conclusion:A. baumannii is a prevalent nosocomial pathogen, especially in patients who undergo mechanical ventilation. Finding risk factors and other characteristic features involved helps to discriminate real pathogen with commensal and opt accurate therapeutic agents.

Keywords: Acinetobacter baumannii; Ventilator associated pneumonia; Antibiotic resistance; Biofilm

Applied and Environmental Microbiology

O13 - 478: COMPARISON OF ROUTINE VS. BACT/ALERT BLOOD CULTURE IN A SAME 6MONTHS OF 2 CONTINUOUS YEARS AMONG PATIENTS WHO REFERRED TO PAYVAND CLINICAL & SPECIALTY LAB

Mojdeh Hakemi Vala[1], Naser Omidi[2], Sepideh Ghasemshahi[3], Behzad Poopak[4], Masood Parsania[5]

1. Shahid Beheshti Uni of Med Sci
2. Payvand Clinical & Specialty Lab
3. Payvand Clinical & Specialty Lab
4. Islamic azad university of medical sciences branch- Payvand Clinical & Specialty Lab
5. Islamic azad university of medical sciences branch- Payvand Clinical & Specialty Lab

Background and Aim: The results of blood culture in critical patients is important for treatment.In routine blood culture at least 3 weeks of incubation for special bacteria is needed. In comparison, in automated systems such as BacTech or Bact/Alerts by using special blood bottles with antibacterial inhibitors only incubation for 3-5 days even for fastidious bacteria is recommended. So, the aim of this study was comparison of routine Vs. automated blood culture methods in a same 6 months during 2 continuous years among patients who referred to Payvand Clinical & Specialty Lab in Tehran.

Methods: The manual blood culture was routine in this Lab until December 2016. At this time, the microbiology section was armed to automated Bact/ Alert system. To evaluate the effect of automated system Vs. manual method at the same 6 months in 2 continuous years(Nov-Jun 2016-2017), all blood cultures which were submitted in this private laboratory, were grabbed to comparison.

Results:9 blood culture submitted in 2016 and all were negative by manual method vs. to 19 blood cultures which were submitted in the same selected time in 2017 . Of them, 15 were negative and 4 were positive of both gram negative and positive bacteria .

Conclusion: However. different conditions may effect on the results including the number of patients who refered to this laboratory but all positive results were detected by Bact/Alert during a couple days. So, using this system in all clinical laboratories is recommended.

Keywords:blood culture, critical illness,clinical laboratory techniques

O14 - 567: ISOLATION AND IDENTIFICATION OF HISTAMINE OXIDASE PRODUCING BACTERIA FROM DIVERS IRANIAN HABITATS

Hossein Sadeghi[1], gholamhossein ebrahimipour[2], Seyyed omid Ranaee siadat[3], jamshid Fooladi[4]

1. Department of microbiology and microbial biotechnology, faculty of Biological Sciences and Technologies, shahid beheshti university
2. Department of microbiology and microbial biotechnology, faculty of Biological Sciences and Technologies, shahid beheshti university
3. Protein Research Center, shahid beheshti university
4. department of biotechnology, Faculty of Biological Sciences, alzahra university

Background and Aim: Histamine poisoning, an allergy like food poisoning, caused by ingesting scombroid fishes such as mackerel and tuna which have high amount of histidine in their muscle. histamine is formed by decarboxylation from histidine through the activity of microorganisms. Though it is not present in fresh fish, Histamine in fish is a good indicator of hygienic food quality. Current methods used for histamine determination (HPLC) are complicated, time-consuming and expensive to use for many food plant. Therefore it is essential to implement rapid and portable procedures for field analysis of fishery products. The main purpose of this study was the isolation of bacteria producing histamine oxidizing enzyme for development an enzymatic methods for histamine determination.

Methods: For isolation bacteria with potent histamine oxidase several soil samples collected at different places in Iran. we used histamine as main nitrogen and carbon source in culture media. Then we designed primer sets for histamine oxidase gene and amplified by PCR. The histamine oxidase-producing bacteria were chosen from histamine-utilizing strains

Results: From the samples of soil, about 100 histamine-utilizing bacteria were isolated that 4 strain had histamine oxidase gene revealed by PCR amplification and gene sequencing. One strain, N1L4 was selected and used for further experiments. HPLC analysis of histamine degradation activity showed that N1L4 strain degrading up to 90 % of the histamine with 12 h of incubation at 37 oC

Conclusion:by optimization of the cultivation condition and purification, the N1L4 enzyme can be used for development of a test kit for histamine determination in fishery products.

Keywords:histamine degrading bacteria, soil, Histamine oxidase enzyme, enzymatic determination

O15 - 865: DIRECT DETECTION OF STREPTOCOCCUS PNEUMONIAE AND NEISSERIA MENINGITIDES FROM NASOPHARYNGEAL SWAB SPECIMENS IN CHILDREN USING LAMP-PCR

Bahman Mirzaei[1], Seyed Fazlollah Mousavi[2], Sara Bahonar[3]

1. Department of Medical Microbiology and Virology, Faculty of Medicine, Mazandaran University of Medical Sciences, Sari, Iran.
2. Department of Bacteriology, Pasteur Institute of Iran, Tehran, Iran
3. Department of Medical Microbiology and Virology, Faculty of Medicine, Mazandaran University of Medical Sciences, Sari, Iran.

Background and Aim: Streptococcus pneumoniae and Neisseria meningitides, two main causative agents of meningitis have been assigned as overall concerns in children hospital wards. Since the importance of rapid detection of these bacterial agents in Cerebro-spinal Floods specimen's, standardization and suitability of loop mediated isothermal amplification (LAMP) technique on nasopharyngeal swabs of mentioned bacteria were targeted in this research.

Methods: Following the collection of fifty inserted nasopharyngeal swabs into skimmed milk– tryptone–glucose–glycerol (STGG) transport medium, crude bacterial DNA was extracted. S. pneumoniae and N. meningitidis gene determinants (lytA and ctrA) were targeted taking advantage of LAMP technique successively. A comparison was performed between the results of culture technique in detection of S. pneumoniae and those of LAMP technique as well as.

Results: Twenty nine (58%) and 3 (6%) of fifty collected swabs were reported as positive for S. pneumoniae N. meningitidis respectively. Positive swabs were among those of S. pneumoniae positive swabs therefore, a positive correlation between the S. pneumoniae and N. meningitidis colonization was observed. Comparison between LAMP assay and culture technique showed that, LAMP assay is more sensitive since LAMP assay declared 29 swabs S. pneumoniae positive, while culture technique showed 25 swabs positive for S. pneumoniae.

Conclusion: This study has revealed LAMP assay to be sensitive and suitable for direct detection of S. pneumonia and N. meningitidis from nasopharyngeal swabs.

Keywords:S. pneumoniae, N. meningitidis, LAMP technique

Biotechnology and Microbial Nanotechnology

O16 - 80: SELECTION OF DNA APTAMER WITH SPECIFIC BINDING TO PSEUDOMONAS AERUGINOSA

Atefeh Noori[1], Seyed Latif Mousavi Gargari[2]

1. Department of Biology, Shahed University, Tehran, Iran
2. Department of Biology, Shahed University, Tehran, Iran

Background and Aim: Pseudomonas aeruginosa, remains a serious cause of infection and septic mortality in burn patients, particularly when nosocomially acquired and cystic fibrosis patients. The bacteriology of Pseudomonas is reviewed to increase the burn care providers understanding of the behaviour of this very common and serious pathogen in the burn care setting, before reviewing the approach to detection of the organism and treatment both medically and surgically.

Methods: To improve the early detection of P. aeruginosa, several culture, PCR and serology based approaches have been compared. In recent years its mortality has increased by 15% which in part could be due to lack of a rapid and sensitive diagnostic test. In this work we introduced a new detection test for Pseudomonas aeruginosa with highly specific aptamer molecules. High binding affinity DNA oligonucleotide aptamers toward P. aeruginosa were selected through 12 rounds of whole cell System Evolution of Ligands by Exponential enrichment process (SELEX). The SELEX procedures was monitored by flow cytometry.

Results: The amount of FITC-labeled aptamer pool bound to the target was increased from 12.5% in the third round to 65% in the twelfth round of SELEX.

Conclusion: The sensitivity of test toward the clinical isolates reveal that aptamers are sensitive and specific enough for the rapid detection of P. aeruginosa from clinical isolates.

Keywords:pseudomonas aeruginosa- aptamer- cell SELEX

O17 - 278: ISOLATION AND CHARACTERIZATION OF HIGH AFFINITY DNA APTAMERS FOR DETECTION OF VIBRIO CHOLERAE

Alireza Ebrahimi Mojarad[1], Seyed Latif Mousavi Gargari[2]

1. Department of Biology, Shahed University, Tehran, Iran.
2. Department of Biology, Shahed University, Tehran, Iran.

Background and Aim: In recent years, the prevalence diseases caused by cholera spp is increasing in the world and among these species, Vibrio cholerae is the most important Vibrio associated with pandemic and epidemic cholera outbreaks. Therefore, the development of a reliable method for early and accurate detection of V.cholerae for management of diseases is a real need. Aptamers with the ability to detect targets with high specificity and accuracy can be one of the candidates used for whole cell and there by V. Cholerae detection.

Methods: In this research high affinity DNA aptamers against V. cholerae O1 with two major serotypes of Inaba and Ogawa were selected from DNA aptamer library through 12 rounds of Systematic Evolution of Ligands by Exponential (SELEX) enrichment procedure using live cells as a target. The aptamer pool of 12th round was cloned and transferred into the E. coli DH5α cells. A total of 67 aptamer transformants were attained and were approved as positive clones with colony PCR. Thirteen positive clones were analyzed by flow cytometry and three clones with the highest fluorescent intensity were chosen for additional analysis.

Results: During the SELEX rounds, the binding efficiency showed a significant growth from the second round (4.44%) to the twelfth round (50.9%). Our results showed descending affinity toward counter cells.

Conclusion: In conclusion, the isolated aptamers can be used in any tool like biosensor for detection of V. cholerae.

Keywords: Aptamer, V. cholerae O1, Cell-SELEX, Flow Cytometry

O18 - 377: BROADLY REACTIVE APTAMERS TARGETING DIFFERENT GENERA OF COMMON ORGANISMS RELATED TO ACUTE BACTERIAL MENINGITIS

Atefe Pourdadashi[1], Seyed Latif Mousavi Gargari[2]

1. M.Sc student of microbial biotechnology, Faculty of Basic Science, Department of Biology, Shahed University
2. Professor in Biotechnology , Faculty of Basic Science, Shahed University

Background and Aim: Meningitis is one of the ten death leading cause of worldwide infectious diseases. Neisseria meningitides, Haemophilus influenza, and Streptococcus pneumoniae are the most common cause of bacterial meningitis (BM) and finding a new method for detection of BM is an urgent need for clinical treatment.

Methods: We applied a new method to isolate single-stranded DNA aptamers that have broad affinity for different bacterial genera. The key point of this method is that targets of interest are changed sequentially at each SELEX cycle. The main plan of SELEX was screening of DNA library for three groups of bacteria containing H. influenza type B, N. meningitides serogroups A, B, C, Y and S. pneumonia serotypes 19A, 6A, 6B. The amplicons were sequentially separated through incubation with each group and combinational cell mixtures as complete SELEX cycle repeated four times. The binding efficiency of the ssDNA pools shows progressive increment estimated by flow cytometry up to 45%. The aptamer pool of round 20th was cloned and transferred in to E.coli Dh5α cells.

Results:A total of 93 aptamer transformants were achieved. These aptamers showed the highest affinity and specificity for superior cause of BM and the lowest affinity to other groups of bacteria.

Conclusion: These results demonstrate the potential to isolate aptamers with broad affinity to bacterial taxa in different genera and development of diagnostic tools for multiple targets with similar or different structures.

Keywords:DNA aptamer library,Selection of DNA aptamers,Affinity binding and recognition,Cell SELEX for bioanalytical assays,Detection of bacterial meningitis

O19 - 663: HIGHLY EFFICIENT IN VITRO PHOTODYNAMIC INACTIVATION OF P. AERUGINOSA BIOFILM USING GRAPHENE OXIDE QUANTUM DOT-METHYLENE BLUE CONJUGATE

Esmaeil Darabpour[1], Nasim Kashef[2], Behzad Karimi[3]

1. Department of Biology-Faculty of Science-Shahid Chamran University of Ahvaz-Ahvaz-Iran
2. Department of Microbiology, School of Biology, College of Science, University of Tehran, Tehran, Iran
3. Department of Inorganic Pigment and Glazes, Institute for Color Science and Technology, Tehran, Iran

Background and Aim: Recently, nanotechnology-based approaches have been directed toward developing novel nanotechnology platforms to combat biofilms. Here we aimed to evaluate PDT of Pseudomonas aeruginosa biofilms using graphene oxide quantum dot-methylene blue conjugate.

Methods: At first, graphene oxide quantum dot (GOQD) was synthesized and characterized by several techniques. Methylene blue (MB) was immoblized on to the negatively charged graphene oxide quantum dot (GOQD) through electrostatic interaction. In the next step, in vitro phototoxic effect of the above photosensitizer system (GOQD-MB conjugate) on 24 h-old biofilms was assessed using laser light (650 nm). Also, in vitro cytotoxicity and photo toxicity of the conjugated product was assessed on human dermal fibroblast. Finally, we used atomic force microscopy (AFM) to determine the effect of GOQD-MB-mediated PDT on P. aeruginosa biofilm structure.

Results: The successful conjugation of MB to the GOQDs surface was mainly confirmed by FT-IR spectroscopy. The metabolic activity of P. aeruginosa biofilm following GOQD-MB-mediated PDT was significantly lower than MB-mediated PDT. Also, only 28.5% of the fibroblasts were photo-inactivated in the presence of GOQD-MB conjugate. AFM confirmed severe alternations in the biofilm structure and cell morphology of P. aeruginosa after GOQD-MB-mediated PDT treatment.

Conclusion: In summary, the photo-activated MB-GOQD particles resulted in complete elimination of the biofilm structure of P. aeruginosa, this finding suggest that the MB-GODQ has great potential as sensitizer for PDT of burn wound infections.

Keywords: Nano-PDT, Biofilm, Wound infection

O20 - 736: AUTOMATION OF BACTERIAL COLONY COUNTING USING CIS SCANNER AND IMAGE PROCESSING

Mohsen Marvibaigi[1], Maryam Aminaee[2], Alireza Jahangiri[3], Fatemeh Karami[4]

1. Department of Medical Genetics, Applied Biophotonics Research Center, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. Department of Medical Genetics, Applied Biophotonics Research Center, Science and Research Branch, Islamic Azad University, Tehran, Iran
3. Department of Medical Genetics, Applied Biophotonics Research Center, Science and Research Branch, Islamic Azad University, Tehran, Iran
4. Department of Medical Genetics, Applied Biophotonics Research Center, Science and Research Branch, Islamic Azad University, Tehran, Iran

Background and Aim: Although it seems simple, bacteria colony counting is still the critical primary step of most of the microbiologic researches and technologies which is laborious and time consuming. Herein, we aimed to introduce a simple and fast protocol for colony counting using Contact Image Scanner (CIS).

Methods: Lactibacillus Paracasei strain TD3 was cultured in de Man Rogosa Sharpe (MRS) broth medium and then was subjected to agar plating following making serial dilution up to 9 times. Imaging of appeared bacterial colonies was performed using Contact Image Scanner (CIS) and the picked up images were compared to Android cellphone Charged Coupled Device (CCD) results. Moreover, obtained quantitative data from all the three processes have been modified with our developed modified imaging software.

Results: The obtained images by CIS through our suggested protocol had demonstrated considerably higher quality than CCD and Andriod images in determining the exact number of bacterial colony. Besides, suggested protocol was able to take the two dimensional pictures and high quality cross sections from bacterial colony counts in a fraction of seconds.

Conclusion: In the present study, it was demonstrated that using CIS though suggested protocol not only could achieved best quality colony counting images but also it was considerably cheaper and faster than traditional methods as well as CCDs.

Keywords: Contact Image Scanner (CIS), bacterial colony counting, software

O21 - 787: IN VITRO BIOSYNTHESIS OF HYALURONIC ACID BY RECOMBINANT HYALURONAN SYNTHASE

Elnaz Afshari[1], Reza Ahangari Cohan[2], Parsa Parsian[3], Roshanak Ahani[4], Dariush Norouzian Shamassebi[5], *Malihe Keramati[6]

1. Nano-biotechnology Department, Pasteur Institute of Iran
2. Nano-biotechnology Department, Pasteur Institute of Iran
3. Nano-biotechnology Department, Pasteur Institute of Iran
4. Nano-biotechnology Department, Pasteur Institute of Iran
5. Nano-biotechnology Department, Pasteur Institute of Iran
6. *Nano-biotechnology Department, Pasteur Institute of Iran

Background and Aim: Hyaluronic acid (HA) has many applications in the pharmaceutical and cosmetic industries. Hyaluronan synthase (HAS) is the enzyme responsible for the synthesis of HA by coupling of β1-3D-N-acetylglucosamine and β1-4D-glucuronic acid. Since obtaining the fully active recombinant form of enzyme allows a safe and controllable way for HA production, therefore, the aim of the current study is expression and enzymatic assessment of recombinant HAS in E.coli.

Methods:has gene was amplified using PCR from S.equisimilis genomic DNA and cloned into pET21a expression vector using NdeI and XhoI restriction enzymes. The recombinant enzyme was expressed in E.coli BL21 strain and analyzed using SDS-PAGE and western blot. The enzyme was purified using nickel affinity chromatography form the host membrane. The polymeric activity of the recombinant enzyme was assessed using Carbazole method according to the USP pharmacopeia.

Results: The cloning procedure was confirmed by restriction map analysis and sequencing. 12% gel SDS-PAGE and western blot showed a band around 45 kDa with respect to the recombinant enzyme. The enzyme was isolated from the host membrane with high purity. Activity test showed that the recombinant enzyme has the ability to polymerize monomeric substrates to hyaluronic acid.

Conclusion: The results showed successful expression of fully active recombinant HAS in E.coli BL21 strain. This project allows in vitro biosynthesis of HA in a safe manner.

Keywords: Hyaluronan Synthase, S.equisimilis, Hyaluronic acid

Clinical Infection and Vaccine

O22 - 15: TH1 IMMUNE RESPONSES CONFERRED BY MIXTURE OF NALOXONE, CPG OLIGODEOXYNUCLEOTIDE AND 3-O-DECYLATED MONOPHOSPHORYL LIPID A, AGAINST PLASMODIUM VIVAX RECOMBINANT TRAP AS A SUBUNIT VACCINE IN MOUSE MODEL

Saeed Nazeri[1], Sedigheh Zakeri[2], Akram Abuie Mehrizi[3], Navid Dinparast Jadid[4]

1. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran, Tehran, Iran
2. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran, Tehran, Iran
3. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran, Tehran, Iran
4. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran, Tehran, Iran

Background and Aim:A key tool for the control, elimination, and eradication of Plasmodium vivax is the development of an effective vaccine; however, there is no available effective vaccine against P. vivax. The thrombospondin-related adhesion protein (TRAP) is one of the major sporozoite antigens that plays an important role in the invasion of hepatocytes by sporozoites and it is a promising malaria vaccine candidate. The goal of this study was to investigate the role of antibodies and cellular immune responses induced by purified recombinant PvTRAP delivered in mixture of three adjuvants, naloxone (NLX), CpG oligodeoxy nucleotides ODN 1826 (CpG ODN) and 3-O-decylated monophosphoryl lipid A (MPL), was evaluated in immunized C57BL/6 mice.

Methods: For this purpose, the rPvTRAP alone or combined with a mixture of NLX-MPL-CpG adjuvants and Freund's Complete Adjuvant (CFA) were applied for immunization of mice. Antibody-dependent immune mechanisms (IgG, IgG1, IgG2b, IgG2c, and IgG3 responses) as well as the IFN-γ, IL-4, and IL-10 cytokines were determined in post-immunized mouse plasma.

Results: The highest level of anti-rPvTRAP IgG (mean OD490nm = 2.55), IgG2b (mean OD490nm = 1.68), and IgG2c (mean OD490nm = 1.466) were identified in the group received rPvTRA/NLX-MPL-CpG. Also, mice receiving rPvTRAP/NLX-MPL-CpG induced significantly the higher levels of interferon gamma (IFN-γ) ($P < 0.05$, independent sample t-test), low level of detectable IL-10, and no detectable IL-4 production.

Conclusion: In general, the results exhibited that rPvTRAP is immunogenic and its administration with mixture of CPG-MPL-NLX in mice induced Th1 immune response and had more potential to increase the level and persistence of anti-TRAP antibodies.

Keywords: Plasmodium vivax, TRAP, MPL, CpG, NLX, Vaccine

O23 - 245: SEROTYPES OF LISTERIA MONOCYTOGENES ISOLATED FROM SPONTANEOUS HUMAN ABORTION IN TEHRAN,IRAN

Jalil Vandyousefi[1], Maryam Rezaei[2], Nadia Kazemipour[3], Farrokh RokhbahkshZamin[4], Gholamreza Irajian[5]

1. Professor of Microbiology Shila Medical Diagnostic Laboratory Tehran, Iran
2. - Division of Microbiology Dental Azad Islamic University Tehran,Iran
3. Department of Microbiology Kerman branch IslamicAzad University Kerman, Iran
4. Department of Microbiology Kerman branch IslamicAzad University Kerman, Iran
5. Department of Microbiology Iran University of Medical Science Tehran, Iran

Background and Aim: Listeria monocytogenes as a foodborne, sapronotic, zoonotic microorganism which is reported in many kinds of food stuffs, including, processed foods, milk and dairy products, vegetables, as well as row or ready- to-eat meat products. Surveys have indicated that Listeria monocytogenes may be present in approximately 4% of row milk samples examined in the USA. Listeria monocytogenes has also been recovered from unpasteurized dairy products.

Methods:258 samples from 123 patients with spontaneous abortion were collected based on patient,s profile, age, second or third abortion trimester with biochemical and bacteriological methods, isolation comprised of 28 cases (18.8%) of Listeria monocytogenes from 118 (45.7%) placental bits, 53(20.5%) patient,s blood and 87(33.7%) from vaginal secretion. All samples were collected in complete sterilized condition and transformed into the laboratory on the same day of sampling. The samples after cold enrichment, were cultured on specific media

Results: In this study 28(18.8%) Listeria monocytogenes with various serovars from 123 patients including 118(47.5%) placental bits, 54(20.5%) patients blood and 87(33.7%) vaginal swabs were isolated

Conclusion: The correlation between the dominant serovars in spontaneous abortion in this research, indicated that total serovars with multiplex PCR method were confirmed, all serovars are kept in collection in order to detection of dominant genes, mostly “hly” and “Iap”.

Keywords:: Humans, Listeria monocytogenes, spontaneous abortion, dominant serovars

O24 - 253: THE ANTIBIOTIC SUSCEPTIBILITY AND PREVALENCE OF ADHESION GENES IN STREPTOCOCCUS PNEUMONIAE ISOLATES DETECTED IN CARRIER CHILDREN IN TEHRAN

Sara Abdollahi[1], Seyed Davar Siadat[2], Reza Shapouri[3], Seyed Fazlollah Mousavi[4], Vajihe Sadat Nikbin[5]

1. Department of Microbiology, Pasteur Institute of Iran, Tehran, Iran.
2. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran.
3. Department of Microbiology, Islamic Azad University, Zanjan Branch, Zanjan, Iran.
4. Department of Microbiology, Pasteur Institute of Iran, Tehran, Iran.
5. Department of Microbiology, Pasteur Institute of Iran, Tehran, Iran.

Background and Aim: Pharyngeal carriers are the source and a transitional vector of invasive. Attachment is the first step of the pathogenicity. Strains of Streptococcus as normal flora can cause the diseases in certain circumstances. Adhesin proteins of these bacteria play a fundamental role in attachment and colonization .In the present study, 5genes which encode surface proteins include phtD, pspC, phtE, lytA , rrgA were evaluated in Streptococcus pneumoniae isolates collected from 4 main care centers and Children's Medical Center of Tehran

Methods:308 nasopharyngeal swabs specimens were collected from children under 6 years old. Identification of S.pneumoniae isolates was performed using biochemical tests and were confirmed by PCR to have cpsA gene. The excistance of phtD, phtE, pspC, lytA and rrgA genes were studied by PCR amplification assays

Results: From 308 nasopharyngeal swabs, 102 isolates of S.pneumoniae were confirmed after identification tests. Among these isolates, 87 (85.2%), 54 (%52.9), 51 (%50), 43 (%42.1) and 31 (30.3%) were positive for lytA, rrgA, phtE, pspC and phtD genes respectively

Conclusion: Our studies showed that cpsA of S. pneumoniae is one of the major characteristic genetic markers for diagnostic purposes. Among five adhesin genes, lytA was the most frequent gene and the strain have the both combination of rrgA and lytA was predominant pattern. These findings could be very useful for design of further studies about vaccine against S. pneumoniae in our country.

Keywords:S.pneumoniae, Nasopharynx,Adhesion genes, PCR.

Emerging and Reemerging Infectious Diseases

O25 - 108: FITNESS AND GENOMIC PORTRAIT OF AUSTRALIAN 2008-2012 PERTUSSIS EPIDEMIC

Azadeh Safarchi[1], Ruiting Lan[2], Sophie Octavia[3]

1. University Of New South Wales
2. University Of New South Wales
3. University Of New South Wales

Background and Aim: The resurgence of pertussis has been reported worldwide including Australia. Strain variation and pathogen adaptation have been reported in many countries in response to acellular pertussis vaccine. Single Nucleotide Polymorphism (SNP) typing separated Australian B. pertussis isolates into five clusters, known as SNP cluster I to V with the current predominant cluster I strains, also known as the ptxP3 strains worldwide.

Methods: Whole genome sequencing was used to investigate the microevolution of 22 B. pertussis isolates from the latest Australian pertussis epidemic (2008-2012), all belonged to SNP profile 13 of cluster I including ten pertactin (Prn) negative. Five Australian pre-epidemic isolates were also included for analyses. Lastly, a mixed infection competition assay in a mouse model study was used to determine the differential fitness between Prn negative and Prn positive strains as well as between cluster I and cluster II strains.

Results: Five SNPs differentiated epidemic isolates from pre-epidemic isolates. Phylogenetic analysis separated the 22 epidemic isolates into 5 lineages, EL1 to EL5. There were spatial and temporal clustering for the isolates analysed. However, there were also some isolates from different locality and time of isolation that were grouped together suggesting clonal spread of B. pertussis across Australia. The results revealed that cluster I strains colonised better in mice respiratory tract regardless of immunisation status and Prn negative strains have better fitness in ACV-immunised mice.

Conclusion: Ongoing genomic microevolution and better fitness of ptxp3 and prn negative strains are consistent with reports of selective advantage of currently circulating B. pertussis strains.

Keywords:B. pertussis , whole genome sequencing, mixed infection competition assey

O26 - 849: INFECTIONS AND COINFECTIONS OF HUMAN BOCAVIRUS WITH RSV AND ROTAVIRUS IN ACUTE RESPIRATORY TRACT AND GASTROINTESTINAL INFECTIONS

Mehrdad Mohammadi[1], Sharareh Moghim[2], Jila Yavarian[3], Bahram Nasr Esfahani[4], Vajihe karbasizadeh[5], Nafiseh Sadat Hosseini[6]

1. MSc student, Department of Microbiology, Isfahan University of Medical Sciences, Isfahan, Iran
2. Associate professor, Department of Microbiology, Isfahan University of Medical Sciences, Isfahan, Iran
3. Associate Professor, Department of Virology, School of Public Health, Tehran University of Medical Sciences.
4. Professor, Department of Microbiology, Isfahan University of Medical Sciences, Isfahan, Iran
5. Assistant Professor, Department of Microbiology, Isfahan University of Medical Sciences, Isfahan, Iran
6. PhD candidate, Isfahan University of Medical Sciences, Isfahan, Iran

Background and Aim: Human bocavirus reported in the respiratory secretions of children with respiratory infection. The main objectives of the study were: to determine the relative frequency of HBoV in hospitalized children with acute gastrointestinal and acute respiratory infections; and to compare the data with those from other respiratory and gastrointestinal viral infections (RSV and Rotavirus) in the same population; and Indication of the seasonal outbreak of relative infections.

Methods: This cross-sectional has done in the period 2016–2017 that involved children less than 3 years old, who were admitted to central pediatric Imam Hossein hospital in Isfahan, Iran. At first, The respiratory samples was tested for the RSV virus by direct immunofluorescence test and, the stool samples are tested for the Rotavirus virus by ELISA test and then all samples tested for the NP-1 gene of HBoV by PCR. .

Results:ten out of 75 respiratory samples (13.3%) and eleven out of 75 fecal samples (14.7%) were positive for HboV. The twenty (26.7%) and twenty-five (33.3) specimens were positive for RSV and Rotavirus respectively. the 40% of respiratory samples have coinfection between HBoV and RSV ($P < 0.05$) and 36.4% of samples have coinfection HBoV and Rotavirus ($P < 0.05$). In seasonal distribution, the winter has upmost extent outbreak ($P < 0.05$).

Conclusion: The HBoV is a major causes acute respiratory infections and coinfections of other viral causes must be investigated and explain their roles in dual infections, but in gastrointestinal infections of HBoV we need extended studies in our country and other geographical areas.

Keywords:human bocavirus; Acute respiratory infections; viral infections; coinfections; gastrointestinal infections

Food and Water Microbiology

O27 - 103: FFECTS OF A FOOD ENRICHED WITH PROBIOTICS ON STREPTOCOCCUS MUTANS AND LACTOBACILLUS SPP. SALIVARY COUNTS IN PRESCHOOL CHILDREN: A CLUSTER RANDOMIZED TRIAL.

Seyed ehsan Asadi[1], raha latifi[2], elahe mohtasham[3]

1. phd in Nursing, Esfahan Medical University, Esfahan, Iran.
2. msc in Nursing, ahwaz Medical University, ahwaz, Iran.
3. Midwifery Student OF shahrekord University ,shahrekord .Iran

Background and Aim: This study aimed to evaluate milk supplemented with probiotic bacteria and standard milk, measured by levels of Streptococcus mutans (S. mutans) and Lactobacillus spp., in 3-4-year-old children after 9 months of intervention.

Methods: The study was a triple-blind, placebo-controlled, randomized trial. The sample was composed of 400 preschoolers attending five child development centers in isfahan, Colombiairan. They were randomized to two groups: children in the intervention group drank 200 mL of milk with Lactobacillus rhamnosus 5x106 and Bifidobacteruim longum 3x106, and children in the control group drank 200 mL of standard milk. Interventions occurred on weekdays and information was gathered through scheduled clinical examination.

Results: The primary result was the number of colony forming units (CFU) of S. mutans and Lactobacillus spp. in the saliva. Secondary results were dental caries, rated by the International Caries Detection and Assessment System (ICDAS), dental plaque, pH, and salivary buffer capacity. The proportion of S. mutans was lower in the intervention group compared with the control group after 9 months; however, the differences did not reach statistical significance (p=0.191); on the other hand, statistically significant differences between groups were found in the CFU/mL of Lactobacillus spp. (p=0.003). There was not statistically significant difference in the prevalence of dental caries for both groups (p=0.753). Differences between groups were found in the salivary buffering capacity (p=0.000).

Conclusion: Regular consumption of milk containing probiotics bacteria reduced CFU/mL of Lactobacillus spp. and increased salivary buffering capacity at 9 months of consumption.

Keywords:probiotics,Streptococcus mutans,Lactobacillus spp,preschool children

O28 - 295: DETECTION OF TYPE E CLOSTRIDIUM BOTULINUM NEUROTOXIN IN SERUM AND FECAL SAMPLES BY USING AN AMPLIFIED ENZYME-LINKED IMMUNOSORBENT ASSAY WITH C-MYC TAG ANTIBODIES

Morvarid Shafiei[1]

1. Department of Bacteriology, Pasteur Institute of Iran

Background and Aim: Clostridium botulinum is an anaerobic, gram-positive, spore-forming rod that produces a potent neurotoxin. There are seven types of botulinum toxin designated by the letters A through G. Types A, B, and E are most commonly associated with illness in humans. The current “gold standard” for detection of BoNTs is the mouse bioassay. However, the assay requires several days to complete, large numbers of animals and can only be performed at a select number of laboratories. The objective of this study was to investigate the presence of botulinum toxin type E in serum and stool samples using Enzyme-Linked Immunosorbent Assay with c-myc tag antibodies.

Methods:96-well microtitre plates were coated with 100 serum and 156 fecal specimens. c-Myc tag C.botulinum type E monoclonal antibody was used to detect C. botulinum type E toxin.

Results:ELISA method is able to detect Clostridium botulinum type E toxin to a value of 2 ng in less than 6 hours. The sensitivity and specificity of ELISA technique was 97.7% and 99.9%, respectively.

Conclusion: The ELISA method is very precise and fast in detecting Clostridium botulinum type E. This method can be used for determining specific antigen in unknown samples.

Keywords:ELISA method, Clostridium botulinum type E toxin, Mouse bioassay

O29 - 335: PROTOCOL FOR THE VALIDATION OF QUANTITATIVE ALTERNATIVE METHODS OF MICROBIOLOGY

Sareh Davarzani[1], Reza Soltani[2]

1. Faculty of Food Industry and Agriculture, Department of Microbiology, Standard Research Institute (SRI), Karaj, Iran
2. Faculty of Food Industry and Agriculture, Department of Microbiology, Standard Research Institute (SRI), Karaj, Iran

Background and Aim: Today, many alternative, mostly proprietary, methods exist that are used to assess the microbiological quality of raw materials and finished products and the microbiological status of manufacturing procedures. These methods are often faster and easier to perform than the corresponding standardized method.

Methods: It consists of four parts. — A comparative study of the results of the reference method to the results of the alternative method in a variety of different items (naturally and/or artificially) contaminated samples. — A comparative study of the results of the reference method to the results of the alternative method in artificially contaminated samples using replicates of a single item per category. — A limit of quantification (LOQ) study of the results of the alternative method in artificially contaminated samples using replicates of a single item per category. The data are used to calculate the LOQ of the alternative method. This study is only done for instrumentally-based methods — An inclusivity/exclusivity study of the alternative method.

Results: The results obtained are analysed using the Bland-Altman method.Plot the data for each sample per category and for each sample in all categories and draw the line of identity on which all points would lie if the two methods gave identical results for each sample analysed.The alternative method is accepted as being equivalent to the reference method if it is equivalent for all individual and combined categories.

Conclusion: This article determines general principle and the technical protocol for the validation of quantitative alternative methods for microbiology in the food chain.

Keywords: Validation, Alternative methods, Refrence method, Quantitative methods

Microbial Infection and Cancer

O30 - 23: CAMPYLOBACTER CONCISUS AND ITS EFFECT ON THE EXPRESSION OF CDX1 AND COX2

Behrooz Mozaffari[1], Behrooz Mozaffari namin[2], Mohammad Mehdi Soltan Ddallal,[3]

1. -
2. Behrooz Mozaffari namin ,1. Department of Microbiology of Pathobiology, School of Public Health, Tehran University of Medical Sciences, International Campus (TUMS-IC), Tehran, Iran. , 2. Microbiology and Gut Biology Group, University of Dundee, Ninewells Hospital Medical School, Dundee, UK.
3. 3. Division of Food Microbiology, Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran., 4. Food Microbiology Research Center, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: Barrett's oesophagus (BE) is a pre-malignant condition in which normal squamous epithelium of the lower oesophagus and gastroesophageal junction is replaced by columnar cells and progress to oesophageal adenocarcinoma. The increase burden of oesophagus cancer morbidity and mortality worldwide make study of factors involved in the pathogenesis of BE essential. However, most of studies that examine the environmental risk factors associated with increased incidence and prevalence of BE have largely ignored the potential role of bacteria in disease aetiology. This study examined the role of Campylobacter concisus isolated from Barrett's and adenocarcinoma patient samples as one of possible environmental factors in the progression of Barrett's oesophagus to oesophagus adenocarcinoma.

Methods: We focused on the effect of C. concisus on the expression caudal type homeobox 1 gene (CDX1) and cyclooxygenase-2 (COX-2) in three BE cell lines using quantitative real-time PCR. In addition, the attachment and invasion characteristics of C. concisus were also tested.

Results: Results showed that C. concisus had a strong attachment to the cell lines and induce the expression of CDX1 in Barrett's cell lines in a time-dependent manner.

Conclusion: Findings indicate that C. concisus could be as a new challenge in the progression of BE to adenocarcinoma.

Keywords: Campylobacter concisus, Barrett's oesophagus, COX2, CDX1

O31 - 132: THE FREQUENCY AND VIRAL LOAD OF EPSTEIN-BARR VIRUS IN IRANIAN PATIENTS WITH HEMATOLOGIC MALIGNANCIES

Alireza Tabibzadeh[1], Mohammad Hadi Karbalaie Niya[2], Maryam Esghaie[3], Farah Bokharaei-Salim[4], Angila Ataei-Pirkooh[5], Seyed Jalal Kiani[6]

1. Department of Virology, Iran University of Medical Sciences, Tehran, Iran,
2. Research center of pediatric infectious diseases, Institute of immunology and infectious diseases, Iran University of medical sciences, Tehran, Iran.
3. Department of Virology, Iran University of Medical Sciences, Tehran, Iran,
4. Department of Virology, Iran University of Medical Sciences, Tehran, Iran,
5. Department of Virology, Iran University of Medical Sciences, Tehran, Iran,
6. Department of Virology, Iran University of Medical Sciences, Tehran, Iran,

Background and Aim: Epstein-Barr virus (EBV) has been associated with different malignancies, including Hodgkin lymphoma (HL), non-Hodgkin lymphoma (NHL) nasopharyngeal carcinoma and lymphoproliferative disorders. Patients with hematologic malignancies, chronic blood disorders could be infected with different types of this virus. This study reported the frequency and viral load of Epstein-Barr virus in Iranian patients with hematologic malignancies for estimation of possible factors affecting malignancy.

Methods: Peripheral blood mononuclear cell (PBMC) of patients diagnosed with hematological malignancies obtained from individuals who referred to hospitals affiliated to Iran University of Medical Sciences, Tehran, Iran, from Sep 2016 to Sep 2017. A real-time PCR assay performed for detection and viral load evaluation of EBV by EBNA-3C gene. The quantitative real-time PCR SYBER Green method used by standard curve analysis. Standard was cloned into pTZ57R/T plasmid.

Results: Of 79 subjects, 28 were NHL, 19 were HL, 20 were acute myeloblastic leukemia (AML), 11 were chronic lymphocytic leukemia (CLL), by the mean age ± Std. Deviation 59.64±19, 54±18.52, 55±18.72, 63.55±19.77, respectively. EBV EBNA-3C was detected in 43% (34/79) of all patients. The mean viral load ± std. deviation was 275148±1201944 and lower and higher viral loads were 280, 6622998 that detected in NHL group. Majority of EBV infection was in NHL group.

Conclusion:there is not a clear relation between EBV infection and hematologic malignancies and EBV viral load cannot be significantly considered as one of the predisposing factors of hematologic malignancy in these patients. Further prospective studies by broader sample size and included interventions need to get comprehensive results.

Keywords: Epstein-Barr virus (EBV); hematologic malignancies; EBNA3C; tumorigenesis; genotyping

Microbial Metabolites and Diseases

O32 - 28: COMPARISON THE EFFECTS OF DANTROLENE AND 2-AMINOETHYL DIPHENYLBORINATE ON XBP-1 MRNA GENE SPLICING IN C57 MICE TREATED WITH PSEUDOMONAS AEROGINOSA ENDOTOXIN ISOLATED FROM BURNED PATIENT'S LESION

Mojtaba Hedayati ch[1], Mahla Shariyari[2], Atabak Nagheli[3], mahmood Abedinzade[4]

1. Cellular and molecular research center, Faculty of medicine (Department of Microbiology), Guilan University of Medical Sciences, Rasht, , IRAN
2. Cellular and molecular research center, Faculty of medicine (Department of Microbiology), Guilan University of Medical Sciences, Rasht, , IRAN
3. Cellular and molecular research center, Faculty of medicine (Department of Microbiology), Guilan University of Medical Sciences, Rasht, , IRAN
4. Medical Biotechnology Research Center, Department of Physiology, Faculty of Paramedicine, Guilan University of Medical Sciences, Rasht, Iran

Background and Aim: Pseudomonas aeruginosa is an opportunistic pathogen isolated from burn wounds which is the fourth cause of trauma and death in the world beside HIV and other fatal infectious disease. Research related to mortality in burn patients indicate that Pseudomonas aeruginosa endotoxin (LPS) might be start apoptotic cell death as a result of excessive calcium ions overload through the calcium channels (Like L type channels and mitochondrial IP3 channels). That's why we select to different specific calcium channels blockers (dantrolene and 2-Aminoethyl diphenylborinate) to investigate their probable supportive role due to vital unfolded protein response (UPR) activation beside LPS inducing endotoxicity in burned patients.

Methods:lipopolysacharide was extracted using specific extraction kit. Intraperitoneally (IP) injected C57BL/6 male mice were ethically sacrificed and their spleen removed after 2, 8 and 24 hours after treatment.Considering aseptic-RNase free condition, Extracted RNA from removed spleen was applied for. cDNA synthesis After Reverse Transcriptase Polymerase Chain Reaction (RT-PCR), the unfolded protein response pathway through IRE-1 stress sensor activation was evaluated via agarose gel electrophoretic pattern.
Results: Evidence shows co-administration of dantrolene and 2-Aminoethyl diphenylborinate along with LPS, may be a potent activator of IRE-1 route activation of UPR (XBP-) and calcium channel blockers, seems to be a useful supportive treatment in burned patients.
Conclusion: This is a pilot study on susceptible animal model and more studies seems to be necessary for final order of burned lesions treatment

Keywords:burned lesions; Pseudomonas aeroginosa; endotoxin; calcium channel blockers; unfolded protein response; XBP-1

Microbial vaccines

O33 - 134: RECOMBINANT ISDE PROTEIN OF STAPHYLOCOCCUS AUREUS: A NOVEL VACCINE CANDIDATE VERSUS MRSA

Yasaman Vahdani[1], Setareh Haghighat [2], Mehdi Mahdavi[3]

1. 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. Recombinant Vaccine Research Center, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: Staphylococcus aureus is one of the dangerous pathogens with resistance against antibiotics especially β-lactams. With raising methicillin resistance Staphylococcus aureus (MRSA) in the world, immunotherapy approach was developed to eradicate such infections. Herein, immunogenicity of IsdE antigen was evaluated as a vaccine candidate in Balb/C mouse model.

Methods: Recombinant IsdE protein was produced and evaluated by SDS-page and western blot and then formulated in Freund s' and MF59 adjuvants to immunize Balb/C mice. Cytokines IFN-γ, IL-2, IL-4, IL-17 and TNF-α level and total IgG, IgG1 and IgG2a antibodies were assessed by ELISA.

Results: Result of IFN-γ cytokine showed a significant increase in IsdE/MF59 group versus mere IsdE and PBS groups. Results of IL-2 demonstrated a remarkable increase in IsdE/Freund s' group versus PBS group. Also, IL-17 cytokine cause significantly increases in IsdE/Freund s' versus IsdE/MF59 group. Result of IL-4 cytokine showed that there was a remarkable increase in IsdE/MF59 versus mere IsdE antigen group. Result of TNF-α cytokine showed significantly increase in IsdE/MF59 group versus PBS group. Results of total IgG showed remarkable increase in IsdE /MF59 group versus mere IsdE group at dilutions of 1/00 and 1/200. Also a significant increase in IgG1 and IgG2a levels in experimental vaccine group which received IsdE /MF59 group as compared to the mere IsdE antigen and PBS group.

Conclusion: These results may indicate the capacity of IsdE in the induction of cellular and humoral immune responses and also as a candidate vaccine to control the MRSA infections.

Keywords: IsdE protein;Vaccine;MRSA

O34 - 163: EVALUATION OF THE EFFECTS OF DIFFERENT ADJUVANTS ON IMMUNOGENICITY AND PROTECTIVITY OF PASTEURELLA MULTOCIDA VACCINE IN CHICKENS

Rahim Ghadimipour[1], Masoud Ghorbanpoor[2], Dariush Gharibi[3], Mansoor Mayahi[4], Ahmad Reza Jabbary[5]

1. Department of Research and Development, Razi Vaccine and Serum Research Institute, Agricultural Research Education and Extension Organization, Ahvaz, Iran
2. Department of Pathobiology, Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz, Ahvaz, Iran
3. Department of Pathobiology, Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz, Ahvaz, Iran
4. Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz, Ahvaz, Iran
5. Pasteurella Research Laboratory, Razi Vaccine and Serum Research Institute, Agricultural Research Education and Extension Organization (AREEO), Karaj, Iran

Background and Aim: The aim of the current study was to investigate selected adjuvants on immunogenicity and protectivity of Pasteurella multocida bacterin in chickens in comparison with an Iranian commercial vaccine.

Methods: Different groups of 8-week-old laying chicken pullets were immunized with vaccines for two times, 3 weeks apart. Vaccine immunogenicity was assessed by measuring serum antibody titers at days 7, 14 and 21 post-primary and day 14 post-secondary immunization, by an in-house indirect ELISA, and their probable side effects were monitored by a poultry specialist. To evaluate the protectivity of vaccines, the immunized chickens were challenged with 2 × LD50 of a virulent P. multocida strain, 2 weeks post-secondary immunization, and the protection level was expressed as the percentage of live and healthy animals at day 7 post-challenge.

Results: The results showed that the vaccines formulated with oil adjuvant Montanide ISA71 (with or without saponin), aluminum adjuvanted vaccine and commercial vaccine induced a strong immune responses as compared to others ($P < 0.05$). Only the oil adjuvanted vaccines without saponin and the commercial vaccine could induce an acceptable protection against challenge (100%). In most tested chickens, the injection sites were inflamed and had a yellow appearance during the experiment.

Conclusion: In general, it seems that ISA70- and ISA71- containing vaccines, as two new and efficient inactivated vaccines, can induce significant protection against fowl cholera disease.

Keywords: Vaccine, Chicken, Adjuvants, Pasteurella multocida

O35 - 247: A NOVEL MULTI-EPITOPE SUBUNIT VACCINE AGAINST BRUCELLA ABORTUS AND MELITENSIS

Zohre Sadeghi[1], Mahdi Fasihi-Ramandi[2], Saeid Bouzari[3]

1. Department of Molecular Biology, Pasteur Institute of Iran, Tehran,Iran
2. Molecular Biology Research Center, System biology and poisonings institute, Baqiyatallah University of Medical Sciences, Tehran, Iran
3. Department of Molecular Biology, Pasteur Institute of Iran, Tehran,Iran

Background and Aim: Brucellosis is a zoonotic disease that can cause abortion in domestic animals and severe disease in humans. Brucellosisis exhibited as an endemic disease in iran. Live attenuated Brucella vaccines have several drawbacks. Peptide-based vaccines have been advocated as an attractive approach for prevention or treatment of infectious diseases. The reverse vaccinology has introduced new candidates for Brucella such as BhuA, FliC, 7α- HSDH through computer analysis.

Methods:B cell and CD4+ and CD8+T cell epitopes from BhuA, FliC, 7α-HSDH antigens were selected and arranged in different patterns. The two and three-dimensional structure of the constructs were evaluated. Then, expression of the synthetic constructs were performed using pET28a expression vector in E. coli BL21(DE3). The proteins were purified with Ni-NTA column. SDS-PAGE and Western blot was used for confirmation of purified proteins. After expression of multi-epitopes, we evaluated mice humoral and cellular immune responses.

Results: Antigenic regions of BhuA, FliC, 7α-HSDH were found and assembled in construct for stimulating humoral and cellular immunity. SDS-PAGE and Western blotting results indicated the similarity of in silico designing and in vitro expression. Vaccination of BALB/c mice with the recombinant proteins provided the significant protection level against B. melitensis and B. abortus challenge.

Conclusion: In the present study, we designed the novel multi-epitope proteins from brucella antigens.The present study suggests that the peptide based vaccine as potential candidates for protection against Brucella.

Keywords: Brucella, multi-epitope vaccine, new candidate, in-silico

O36 - 297: CONSTRUCTION OF PTX-DEFICIENT BORDETELLA PERTUSSIS VACCINE STRAIN 134 BY ALLELIC EXCHANGE

Vajihe Sadat Nikbin[1], Maliheh Keramati[2], Mojtaba Nofeli[3], Fereshteh Shahcheraghi[4]

1. Pasteur Institute of Iran
2. Pasteur Institute of Iran
3. Razi Vaccine and Serum Research Institue
4. Pasteur Institute of Iran

Background and Aim: Vaccination of whooping cough (pertussis) caused by Bordetella pertussis is still major concern all over the world. Resurgence of pertussis has been observed globally even after replacement of second generation of vaccine (Acellular) with whole cell vaccine in many countries. The third generation of vaccines against B. pertussis has focused on the genetically manipulation of virulence genes in this bacteria. The aim of this project was to construct the B. pertussis vaccine strain 134 lacking S1 subunit of pertussis toxin (PTXA) by homologous recombination.

Methods:B. pertussis 134 was obtained from Razi Vaccine and Serum Research Institute. First of all chloramphenicol resistance gene (cat) was cloned into pss1129 vector between upstream and downstream sequences of ptxA gene and the recombinant DNA was transferred to E. coli SM10 host cell. Then this donor bacterium was mated with B. pertussis 134. Finally ptxA-deficient B. pertussis was selected using chloramphenicol in the selective media.

Results:B. pertussis 134 lacking S1 subunit of ptx gene should be resistant to chloramphenicol by allelic exchange. This bacterium was confirmed by PCR of ptxA, cat, upstream and downstream regions and by western blot to verify lack of S1 subunit of toxin in this target cells.

Conclusion: We constructed vaccine strain 134 which S1 subunit of pertussis toxin was deleted in its genome. This strain will be very useful to further studies of manufacture of a new formula of vaccines as the third generation vaccines like live-attenuated vaccines.

Keywords:pertussis, vaccine, ptx, homologous recombination

O37 - 417: IMMUNOGENICITY OF OUTER MEMBRANE VESICLES FROM A BRUCELLA MELITENSIS HUMAN ISOLATE IN BALB/C MICE

Ramin Bagheri Nejad[1], Taghi Zahraei Salehi[2], Ramak Yahyaraeyat[3], Ali Es'haghi[4], Bahar Nayeri Fasayi[5]

1. Microbiology & Immunology Department, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran and Razi Vaccine & Serum Research Institute, Agricultural Research, Education and Extension Organization, Karaj, Iran
2. Microbiology & Immunology Department, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
3. Microbiology & Immunology Department, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
4. Razi Vaccine & Serum Research Institute, Agricultural Research, Education and Extension Organization, Karaj, Iran
5. Microbiology & Immunology Department, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran

Background and Aim: Brucellosis is a bacterial zoonosis with worldwide importance caused by members of the genus Brucella. Human infection occurs mainly by contact with infected animals and their products. Animal vaccination is the key for the disease control and prevention. However, live vaccines used for animal immunization have drawbacks which limit their application. Moreover, no approved vaccine is available for human use. Outer membrane vesicles (OMVs) are interesting tools for vaccine development against Gram-negative bacteria.

Methods: In this study, OMVs from a B. melitensis human isolate were extracted by ultracentrifugation and characterized. BALB/c mice (n=12) were immunized with OMVs intramuscularly by 2 injections with a 2-week interval. Another 12 mice were used as controls. Two weeks after the last vaccination, 6 mice of each group were sacrificed to evaluate splenocyte proliferation and interferon gamma (IFNγ) production following in vitro stimulation. Concomitantly, other mice were challenge with the B. melitensis isolate. Two weeks later, all mice were killed and spleens were cultured for colony forming units (CFU) determination of challenge strain.

Results: The results showed proliferative response and IFNγ production of splenocytes in vaccinated mice were significantly higher than those in control mice (2.18±0.57 stimulation index (SI) (mean±SD) vs 1.03±0.03 SI; 1519.35±10.7 pg/ml vs 210.01±17.58 pg/ml, respectively). Logarithms of challenge strain numbers in spleens of vaccinated mice were significantly less than those of controls (5.1±0.86 and 6.7±0.15, respectively).

Conclusion: Our study revealed vaccination with OMVs of the B. melitensis isolate could induce specific immune responses and protection against its challenge in the mouse model.

Keywords: Brucellosis, Vaccine, Outer Membrane Vesicles

O38 - 419: EVALUATION OF A REAL-TIME PCR ASSAY FOR DETECTION AND QUANTIFICATION OF RUBELLA VIRUS IN MMR VACCINE

Maryam Salemi[1], Khosrow Aghaiypour Kolyani[2], Ashraf Mohammadi[3]

1. Genomics and Genetic Engineering Department, Razi Vaccine and Serum Research Institute (RVSRI), Agricultural Research, Education and Extension Organization (AREEO), Karaj Iran
2. Genomics and Genetic Engineering Department, Razi Vaccine and Serum Research Institute (RVSRI), Agricultural Research, Education and Extension Organization (AREEO), Karaj Iran
3. Human Viral Vaccines Department, Razi Vaccine and Serum Research Institute (RVSRI), Agricultural Research, Education and Extension Organization (AREEO), Karaj Iran

Background and Aim: Rubella virus is the causative agent of rubella, a mild illness that may lead to fetal death or congenital defects when the virus infects pregnant women in early pregnancy. Rubella vaccination has been safe and really effective. Potency of rubella-containing vaccine (MMR) is conventionally measured by two assays: CCID50 and plaque forming unit (pfu). These two are labor intensive and time consuming. Quantitative Real-time PCR has been introduced as an easily available and fast method to estimate the potency of live-attenuated viral vaccines.

Methods: Primers and probe were designed for RT-qPCR system. A 400-base pair fragment was amplified using another set of primers. The fragment was then cloned into pTZ57R/T plasmid by T/A cloning technique. Serial 10-fold and 2-fold dilutions of recombinant plasmids were used to generate standard curves. RK-13 cells were inoculated with vaccine virus. After 2 days of virus inoculation, rubella virus RNA was extracted and RT-qPCR was performed. The results of Real-Time PCR were compared with those of CCID50.

Results: Standard curves were evaluated for parameters such as linearity and precision. Inter-assay CV and intra-assay CV were determined to be below 2%. Moreover, limit of detection was defined as 35 copies/reaction and quantification as 70 copies/reaction for the test. The results indicated that the titers estimated by RT-qPCR were comparable to CCID50 and statistical analysis showed promising results with p-value>0.05.

Conclusion: Real-Time PCR has the ability to estimate virus titer in vaccine preparations. It is relatively inexpensive, rapid and repeatable.

Keywords: Rubella virus, MMR vaccine, Real-Time PCR

O39 - 651: DESIGN OF POLYVALENT HEPATITIS VACCINE CANDIDATE AND EVALUATION OF ITS EX VIVO STIMULATION IN HUMAN DENDRITIC CELLS

Armina Alagheband Bahrami[1], Mojgan Bandehpour[2], Bahram Kazemi[3], Mahmood bozorgmehr[4]

1. Department of Biotechnology, School of Advanced Technologies in Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran
2. Cellular and Molecular Biology Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. Department of Biotechnology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran
4. Oncopathology Research Center, Iran University of Medical Sciences, Tehran, Iran

Background and Aim: Hepatitis C Virus (HCV) the main cause of chronic hepatitis; Annually, about 185 million people are infected with HCV and despite many efforts, it remains a serious burden to global public health. Thus, vaccine design based on the new approach is an appropriate alternative for this problem. In this study, besides the immunodominant epitopes of HCV core, in order to enhance the efficiency of designed polyvalent vaccine and induce a robust immune response, Hepatitis B surface antigen (HBsAg) and polio virus VP antigen were used as antigenic determinants.

Methods: Epitopes identification carried out for each antigen using various immunoinformatics tools and analysis. The selected epitopes were fused together by proper linkers. The entire features of final protein were evaluated by different servers and downstream analyses were performed subsequently. Polyepitope vaccine construct was chemically synthesized in pET28a expression vector. Protein expression in E.Coli was induced by adding IPTG 1mM. Purification was performed using affinity chromatography. In the next step, the immune stimulation of the desired vaccine evaluated in dendritic cells derived from human peripheral blood mononuclear cells and its effect on the activation and proliferation of T cells and cytokines secretion were assessed by flow cytometry and Elisa.

Results: The results indicated that the designed polyepitope has better or in some cases at least equal effect in comparison to the monovalent vaccine to induce T-cell activation and proliferation.

Conclusion: Our designed vaccine candidate has a capacity for simultaneous immunization against three viral diseases and induction of proper immune response.

Keywords: Hepatitis C Virus, PolyEpitope, Polyvalent Vaccine, Dendritic Cells, Flow Cytometry

O40 - 710: CHARACTERIZATION OF SHEEP AND GOAT VACCINE STRAINS OF MYCOPLASMA AGALACTIAE FROM RAZI INSTITUTE BY MOLECULAR TYPING ANALYSIS

Khatereh Kabiri[1], Keyvan Tadayon[2], Seiyed Ali Pourbakhsh[3], Jamile Norouzi[4]

1. Department of Microbiology, North Tehran Branch, Islamic Azad University, Tehran, Iran.
2. Department of Veterinary Aerobic Bacteria Razi Institute Karaj
3. Mycoplasma reference laboratory, Razi vaccine and serum research institute, Karaj, Iran
4. Department of Microbiology, North Tehran Branch, Islamic Azad University, Tehran, Iran.

Background and Aim: Agalactia is a contagious disease in small ruminants. In 1968 the sheep and goat strains of M. agalactiae were collected respectively from Iranian diseased animals. These strains have been used ever since for preparation of Contagious agalactia vaccine at Razi institute. Multi Locus Sequence Typing (MLST) and multiple locus variable number of tandem repeat analysis (MLVA) analysis are standard methods of genotyping for M.agalactiae. This is was conducted to assess genomic structure of the vaccine M. agalactiae strains at Razi institute.

Methods: In the present study, Genes were chose for MLST and MLVA based on the sequenced genome of M.agalactiae type strain PG2. PCR amplicons were sequenced and results were comparatively scrutinized against those already registered with the M.agalactiae MLST databases. The diversity of repeated sequences in M.agalactiae was conducted using polymerase chain reaction.

Results: In order to investigate the genomic relations between these strains, MLVA and MLST strategies concentrating on Target genes was employed. Results analysis by both methods showed identical genetic pattern between all the three vaccine strains. The result of this study indicated that three vaccine strains belonged to the closed clonal complex.

Conclusion: If using these strains as vaccine for all the past consecutive decades has had major impacts in population and epidemiology of M.agalactiae in this country, much more work is required. Extending this study to include larger number of local isolates will help to better assess this observation.

Keywords:MLST, Agalactia, MLVA

Microbiomes

O41 - 60: CLONING AND EXPRESSION OF RECOMBINANT LIPL41 ANTIGEN FROM LEPTOSPIRA INTERROGANS IN PROKARYOTIC SYSTEM.

Narges Golab[1], Naser[2], Pejvak[3], Majid[4], Majid[5], Soheila[6]

1. Islamic Azad Uni, karaj
2. Harzandi
3. Khaki
4. Esmaelizad
5. Tebyanian
6. Moradibidhendi

Background and Aim: Leptospirosis is a worldwide zoonosis caused by pathogenic Leptospira spp. Outer membrane proteins of leptospire are among the most effective antigens which can stimulate remarkable immune responses during the infection processes. LipL41 is the third most abundant lipoprotein found in the outer membranes of pathogenic leptospires and has been considered a putative virulence factor. The objective of the present study was Cloning and expression of recombinant LipL41 antigen from Leptospira interrogans in prokaryotic system.

Methods: LipL41 was clonned in E. coli strain BL21 using pET32 + plasmid as a vector and induced with 25 µM IPTG at 22 °C for 16 hours. The bacterial pellet was obtained by centrifugation (5,000 rpm). The resuspended cells were disrupted by sonication. The cell lysate was centrifuged at 15,000 rpm at 4 °C for 20 min. Samples were solubilized in sample buffer plus mercaptoenthaol , Proteins were separated on 10% sodium dodecyl sulfate (SDS) and followed by Coomassie Brilliant Blue staining.

Results: The protein was successfully expressed in Escherichia coli BL21 and purified. SDS-PAGE results showed that the full-length 47kD protein was induced by IPTG

Conclusion: Leptospirosis is considered as a reemerging infectious disease, not only for the increase in its incidence during the past recent years but also for the increased severity of the illness. The cloned gene could be further used for expression of recombinant protein for serodiagnosis and leading candidate vaccine antigens of leptospirosis. .

Keywords: Leptospira, LipL41cloning , expression

Molecular Diagnosis and Typing

O42 - 48: SPA TYPING OF STAPHYLOCOCCUS AUREUS ISOLATES CAUSING NOSOCOMIAL INFECTIONS

Rashid Ramazanzadeh[1], Mohammad Hosein Darehshiri,[2], Mehdi Mirzaii,[3]

1. Cellular & Molecular Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran.
2. Department of Microbiology, Kurdistan University of Medical Sciences, Sanandaj, Iran.
3. Department of Microbiology, Shahroud University of medical sciences

Background and Aim: Spa-typing, is a typing method based on the DNA sequence analysis of the protein A gene. The purpose of this study was to molecular typing of Staphylococcus aureus isolated from patients in Toohid and Besat hospitals Sanandaj (2014).

Methods: The clinical specimens from hospitalized patients were collected over a period of 1 year. Staphylococcus aureus isolates were identified by culture and biochemical standard methods based on CLSI guideline. Spa gene patterns in Staphylococcus aureus isolates were identified spa-typing techniques.

Results: In total, 20 different patterns of Spa gene in staphylococcus aureus isolates were obtained in this study, which includes 6 type t030, 3 type (t230, t459 & t701), 2 type (t11332 & t304) and types t325, t012, t1149, t1810, t197, t325, t7789, t808, t871, t937, t14896, t14913, t14928 and t14929. The highest prevalence was belong to types t030 (18.18%), type t230, t459 and t701 (9.09%). New types t14896, t14913, t14928 & t14929 were identified during this study.

Conclusion: In conclusion there was a well-known pattern of Spa types and also we identified new types that require more studies to qualify. Analysis of these patterns can improve insight to design nosocomial infection control programs.

Keywords: Staphylococcus aureus, Spa Typing, Sanandaj, Epidemiology

O43 - 65: RAPID AND SENSITIVE DETECTION OF TICK-BORNE RELAPSING FEVER BORRELIAE IN TICK DNA SAMPLES BY USING LOOP-MEDIATED ISOTHERMAL AMPLIFICATION (LAMP)

Faezeh Houman sadr[1], Mohammad Soleimani[2]

1. Tasnim Biotechnology Research Center (TBRC), 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: Tick Borne Relapsing Fever (TBRF) caused by Borreliae spp. is transmitted via bites of the soft tick Ornithodoros spp. that primarily inhabits burrows, nests, caves, and cavities. TBRF is an endemic disease in Iran, with more 100 annual cases. In the study, the glpQ-LAMP assay was used to detect of TBRF Borreliae in DNA of Ornithodoros ticks collected from the endemic area from Iran during 2017.

Methods: Sixty Ornithodoros spp. ticks were collected from endemic areas of Iran and subjected to DNA extraction. The specific glpQ primers were used for amplification of a specific conserved fragment of glycerophosphodiester phosphodiesterase gene (glpQ). So the extracted DNA samples were examined by the glpQ-LAMP assay at 60 °C for 60 minutes.

Results: Visual analysis of the reaction tubes showed a white turbidity corresponds to glpQ gene amplification in 19 DNA thick samples. Comparing to positive and negative control reactions, the other samples did not show positive signal.

Conclusion: For the first time, we used the glpQ-LAMP assay to detect TBRF Borreliae in ticks successfully. The glpQ-LAMP assay can be used as a sensitive, specific and rapid method in epidemiologic and field studies. Despite the improvement in health conditions, significant rates of ticks are still contaminated with TBRF Borreliae in Iran.

Keywords: Borreliae- Tick- TBRF - LAMP - GlpQ

O44 - 115: MULTILOCUS SEQUENCE TYPING OF PENICILLIN NON-SUSCEPTIBLE S. PNEUMONIAE ISOLATES FROM INVASIVE INFECTIONS

Mohammad Azarsa[1], Mohammad Reza Pourmand[2]

1. Khoy University of Medical Sciences, Khoy, Iran
2. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: Worldwide spread of penicillin non-susceptible pneumococci (PNSSP) has created a serious problem in the treatment of pneumococcal infections. Monitoring of resistant clones is essential to antibiotic resistance surveillance. In this study, PNSSP isolates were typed using the Multilocus Sequence Typing (MLST) method.

Methods: Various clinical samples were collected from patients with suspected pneumococcal disease and were cultured on sheep blood agar with 5% sheep blood. Suspected colonies were identified by biochemical and molecular assays. The penicillin susceptibility test was performed by serial broth microdilution method. MLST protocol was used to determine the molecular type of PNSSP isolates.

Results:A total of 46 strains of S. pneumoniae were isolated from suspected clinical samples. Penicillin nonsusceptibility was detected in 12 (12/46) isolates. Molecular analysis showed that pneumococcus isolates clustered into five major clonal complexes and 42% (5/12) of the STs were novel.

Conclusion: Our results showed that the majority of isolates (74%) are penicillin susceptible according to the recently revised S .pneumoniae breakpoints for penicillin. MLST analysis indicates that the high genetic diversity is among PNSP isolates.

Keywords:penicillin non-susceptible pneumococci, molecular typing, multi locus sequence typing (MLST), sequence type (ST), clonal complex (CC)

O45 - 177: EVALUATION OF REAL TIME PCR FOR DETECTION OF CLINICAL ISOLATES OF STAPHYLOCOCCUS AUREUS AND METHICILLIN-RESISTANCE STRAINS BASED ON MELTING CURVE ANALYSIS METHOD

Narges Heidari[1], Mohammad Yousef Alikhani[2], Mohammad Reza Arabestani[3], Arezoo bozorgomid[4]

1. Asadabad school of medical sciences. asadabad. Iran
2. Hamedan university of medical sciences
3. Hamedan university of medical sciences
4. Asadabad school of medical sciences. asadabad. Iran

Background and Aim: Rapid and timely detection of Staphylococcus aureus can play a significant role in the treatment of staphylococcal infections.Impresingly, by precise designing methods which have acceptable sensitivity and specificity, can identify species and even antibiotic-resistant strains. The purpose of this study was to evaluate the real time PCR diagnostic method based on the melting curve analysis for the detection of clinical isolates of S. aureus and the methicilin resistance gene.

Methods: In this experimental study, clinical isolated of S. aureus was used from the Microbiology Bank of Hamadan University of Medical Sciences. The primer design was done by selecting (ITS) target for S. aureus and the mecA gene for methicillin-resistant strains. Real-time PCR and DNA melting curves analysis were used to determine the analytical specificity and sensitivity of the designed primers.

Results: The analytical specificity of the primers was 83.79 ° C for S. aureus and 76.6 ° C for methicillin resistant Staphylococcus aureus respectively. The analytical sensitivity of the primers was 15 CFU/ml bacteria for ITS gene and 25 CFU/ml bacteria for mecA gene.

Conclusion: By selecting appropriate primers and using sensitive molecular techniques, which could be the main factors for designing of both quick and accurate method, it is possible to identify invasive bacteria such as S. aureus.

Keywords: Staphylococcus Aureus, Methicillin-Resistant, Real Time PCR, Drug Resistance

O46 - 192: MOLECULAR EPIDEMIOLOGY OF PVL HARBORING HOSPITAL-ASSOCIATED METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS IN SEPTICEMIC CHILDREN, NORTHEASTERN IRAN, BOJNURD

Amir Azimian[1], Saghar Safamanesh[2], Mahsa Khosrojerdi[3], Reza Besharati[4]

1. ph.D of Medical Bacteriology, Faculty of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
2. M.Sc of Medical Virology, Faculty of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
3. Specialist in Peditrics, Faculty of Medicine, Semnan University of Medical Sciences and Health services, Semnan, Iran.
4. M.Sc of Microbiology, Faculty 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 in adults and children. Sepsis caused by Staphylococcus aureus is one of the major health problems associated with treatment failure in adults, but its clinical outcomes, rate of treatment failure and its molecular epidemiology is poorly understood.

Methods: We focused on Staphylococcus aureus strains isolated from children blood cultures in Bojnurd, Northeastern Iran. Totally, 58 S. aureus strains were isolated from blood cultures in major teaching hospital in Bojnurd. After primary verification of Methicillin resistance by agar screening method, the isolated MRSA strains were confirmed with detection of mecA gene. mecA positive strains evaluated for SCCmec, agr, and toxin profile. PVL positive isolates were subjected to evaluation of spa and Sequence Type.

Results: Our data indicate 53.4% (31) of isolates were MRSA. 38.7% (12) of these isolates had PVL gene that 25% (3) of them had tsst-1 gene and 58.3% (7) had etb gene. 3.2% (1), 64.5% (20) and 32.2% (10) of these isolates belonged to SCCmec I, III and IV respectively. Predominant Sequence Type (ST) and spa types among PVL positive isolates were ST6 and t304 respectively.

Conclusion: We had an uncommon finding, because PVL was routinely found in Community- Associated MRSA, but in this study we found PVL harboring Hospital-Associated MRSAs. A notable point about these isolates is that most of them belonged to Asian Endemic clones.

Keywords: Staphylococcus aureus, Methicillin, Resistance, PVL, MLST, spa type, SCCmec, agr, Children.

O47 - 211: DETECTION OF LEGIONELLA PNEUMOPHILA IN THE SPUTUM SPECIMENS OF PATIENT WITH RESPIRATORY SYMPTOMS BY CULTURE, PCR AND LOOP-MEDIATED ISOTHERMAL AMPLIFICATION METHODS

Mojtaba Moosavian[1], Fatemeh Shahi[2], Sakineh Seyed-Mohammadi[3], Morteza Saki[4], Davoud Afshahr[5], Mahtab Khoshkholgh Sima[6], Sara Barati[7]

1. 1Infectious and Tropical Diseases Research Center, Health Research Institute, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran 2Department 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. 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 and Virology, School of Medicine, Zanjan University of Medical Sciences, Zanjan, Iran
6. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
7. Department of Bacteriology, School of Veterinary, University of Shahid Chamran, Ahvaz, Iran

Background and Aim: Legionellosis is an important public health problem that can cause substantial mortality and morbidity. This bacterial infection is caused primarily by the Legionella pneumophila found in freshwater environments throughout the world. However, legionellosis risk estimation may be compromised by uncertainties in Legionella detection methods. So the aim of current study was detection of L. pneumophila in patients with respiratory symptoms by culture, polymerase chain reaction (PCR) and loop-mediated isothermal amplification (LAMP) methods.
Methods: Sputum samples were obtained from patients with respiratory symptoms admitted to the teaching hospitals in Ahvaz, Iran from June 2016 to March 2017. Identification of Legionella spp. was done by culture the sputum directly onto Buffered Charcoal Yeast Extract (BCYE) Agar medium. Then the PCR and LAMP assay were performed to detect the Legionella pneumophila via its Macrophage Infectivity Potentiator (mip) gene in the sputum Specimens.
Results:A total of 94 sputum samples were collected. Our results showed that 1 of the sputum samples (1.04%) were culture positive for Legionella spp., 3 (3.12%) and 7 samples (7.28%) of samples were positive for L. pneumophila using the mip gene PCR and LAMP assay, respectively.
Conclusion: This study showed that legionellosis should be considered in the diagnosis of respiratory infectious diseases. We also concluded that the LAMP assay is a faster method with high sensitivity and specificity than conventional methods such as PCR and culture for laboratory diagnosis of legionellosis. The LAMP assay can be employed in medical centers with limited equipment without the need of a thermocycling apparatus.

Keywords: Legionella pneumophila, Loop-mediated isothermal amplification (LAMP), mip gene, Sputum

O48 - 217: DIAGNOSTIC ACCURACY OF MONOCYTE CHEMOTACTIC PROTEIN (MCP)-2 AS BIOMARKER FOR THE DISCRIMINATION BETWEEN ACTIVE AND LATENT TUBERCULOSIS

Shima Mahmoudi[1], Babak Pourakbari[2], Reihaneh Hosseinpour Sadeghi[3], Majid Marjani[4], Setareh Mamishi[5]

1. Pediatric Infectious Disease Research Center, Tehran University of Medical Sciences, Tehran, Iran
2. Pediatric Infectious Disease Research Center, Tehran University of Medical Sciences, Tehran, Iran
3. Pediatric Infectious Disease Research Center, Tehran University of Medical Sciences, Tehran, Iran
4. Clinical Tuberculosis and Epidemiology Research Center, National Research Institute of Tuberculosis and Lung Diseases (NRITLD), Shahid Beheshti University of Medical Sciences, Tehran, Iran
5. Pediatric Infectious Disease Research Center, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: Several studies have been conducted to find new biomarkers for the discrimination of latent tuberculosis infection (LTBI) from active TB (ATB); however, their findings are inconsistent. The aim of the current study was to evaluate the potential of in vitro antigen-specific expression of Monocyte chemotactic protein (MCP)-2 for discrimination of PTB and LTBI after stimulation of whole blood with PE35 and PPE68 recombinant proteins.

Methods: The recombinant PE35 and PPE68 proteins were evaluated at a final concentration of 5 µg/ml by a 3-day whole blood assay. Secreted MCP-2 from the culture supernatants were measured by commercially available Human MCP2 ELISA Kit. The diagnostic performance of MCP-2 was ascertained by Receiver operator characteristic (ROC) curve and measuring the area under the curve (AUC) and their 95% confidence intervals (CI). Cut-offs was estimated at various sensitivities and specificities and at the maximum Youden's index (YI), i.e. sensitivity specificity–1.

Results: The median MCP-2 response to both PE35 and PPE68 in those with LTBI was significantly higher than patients with pulmonary TB (PTB). The discrimination performance of MCP-2 response following stimulation of PE35 (assessed by AUC) between LTBI and patients with PTB was 0.98 (95%CI: 0.94-1.00). Maximum discrimination was reached at a cut-off of 86pg/mL with 100% sensitivity and 97% specificity. The highest sensitivity and specificity was obtained using cut off 58 pg/mL following stimulation with PPE68 (100% and 90%, respectively; AUC: 0.94, 95%CI: 0.85-1.00).

Conclusion:MCP-2 induced by PE35 and PPE68 shows good discriminatory power for discrimination of PTB and LTBI.

Keywords:MCP-2, discrimination, active tuberculosis, latent tuberculosis

O49 - 293: PHYLOGENETIC ANALYSES AND MULTILOCUS SEQUENCE TYPING (MLST) OF E. COLI STRAINS FROM NATIONAL E. COLI REFERENCE LABORATORY

Zahra Pourramezan[1], Fatemeh Akhavan Attar [2], Mana Oloomi[3], Saeed Bouzari[4], Saeed Mostan [5]

1. Molecular Biology Department, Pasteur Institute of Iran, Tehran
2. Molecular Biology Department, Pasteur Institute of Iran, Tehran
3. Molecular Biology Department, Pasteur Institute of Iran, Tehran
4. Molecular Biology Department, Pasteur Institute of Iran, Tehran
5. Molecular Biology Department, Pasteur Institute of Iran, Tehran

Background and Aim: Bacteremia represents one of the significant causes of death in the developed countries and among Gram-negative bacteria. Escherichia coli represent the first cause of bacteremia, with 30% of the total number of bacteremia due to this pathogen. Phylogenetic analysis suggested that E. coli can be divided into four major groups (A, B1, B2 and D). Multilocus Sequence Typing (MLST), in which internal portions of multiple housekeeping genes are sequenced to define clonal diversity, has emerged as a powerful tool to describe the genetic structure of bacterial populations.

Methods:50 E. coli strains from National E. coli Reference Laboratory were used. Total DNA was isolated from overnight culture strains. Primer pairs were designed for PCR amplification and sequencing of internal portions of eight housekeeping genes (dinB, icdA, pabB, polB, putP, trpA, and trpB). All PCR products were thus sequenced using the same two sequencing primers. Bionumerics software version 7.6 was used for MLST analysis of 5 selected strains.

Results: The internal portions of eight selected housekeeping genes were sequenced in defined isolates; the results highlighted the strong phylogenetic clustering of E. coli strains into five separated branches. PCR results show that STEC (Shiga-toxin-producing E. coli) strains were PCR-negative for some housekeeping genes and these strains were also PCR-negative for put primer.

Conclusion: In conclusion, MLST and defined Sequence Type (ST) of each group can be used for clonal diversity determination of E. coli clinical isolates.

Keywords: Multilocus Sequence Typing, E. coli strains, Phylogenetic analysis

O50 - 380: MOLECULAR CHARACTERIZATION OF MYCOBACTERIUM TUBERCULOSIS ISOLATES IN ALBORZ PROVINCE

Morassa Farnad[1], Keyvan Tadayon[2], Nader Mosavari[3], Hassan Momtaz[4]

1. Razi Vaccine and Serum Research Institute, Islamic Azad University, Shahre Kord branch
2. Razi Vaccine and Serum Research Institute
3. Razi Vaccine and Serum Research Institute
4. Islamic Azad University, Shahre Kord branch

Background and Aim: Tuberculosis (TB), caused by the Mycobacterium tuberculosis complex (MTBC), is a serious infection in humans and animals. Iran is one of the countries with the highest burden of TB. However, limited information is available on the genotypic characteristics of M. tuberculosis strains infecting humans. The objective of the present study was to characterize the mycobacterial species isolated from pulmonary TB patients using molecular typing.

Methods:A cross-sectional study was conducted on 20 patients with smear-positive pulmonary TB, using Ziehl Neelsen staining and bacteriological culturing. DNA was extracted from the isolates by the van Solingen method. Molecular characterizations of the mycobacterial isolates were performed by polymerase chain reaction (PCR)-16SrRNA, PCR-IS6110, and RD-typing with primers RD1, RD4, RD9, and RD12, respectively.

Results: The proportion of culture positivity was 100% (20/20). Out of 20 isolates, only one isolate appeared negative in IS6110-PCR and was considered nontuberculosis complex. All isolates except one from Alborz Province appeared positive for Mycobacterium tuberculosis. Based on the obtained results, all isolates except one were identified as M. tuberculosis. The only negative isolate appeared 97% similar to Mycobacterium sp. (Mycobacterium neoaurum).

Conclusion: This study confirmed the presence of known M. tuberculosis strains and revealed new strains circulating in Alborz province of Iran.Accurate identification of Mycobacterium isolates has great importance for proper and immediate treatment of TB patients.

Keywords: 16S rRNA; IS6110, Mycobacterium tuberculosis complex; RD typing

O51 - 396: CHALLENGE IN DIRECT SPOLIGOTYPING OF MYCOBACTERIUM TUBERCULOSIS

Sharareh Khanipour [1], Mansour Kargarpour Kamakoli [2], Shima Hadifar [3], Hasan Ghajavand[4], Ghazaleh Farmanfarmaei [5], Abolfazl Fateh [6], Seyed Davar Siadat [7], Farzam Vaziri [8]

1. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran 2-Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
2. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran 2-Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
3. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran 2-Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
4. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran. 2-Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
5. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran. 2-Microbiology Research Center (MRC), 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. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran. 2-Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
8. 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: Based on our recent studies the prevalence of polyclonal infection in tuberculosis clinical specimens is more than 50 percent in Tehran, Iran. Multiple strain infections may cause false Spoligotypes that have been reported previously. The aim of the present study was comparing the direct and indirect Spoligotyping on clinical specimens and their respective cultures, respectively. We also examined whether mixed infections interfere with the results or not.

Methods: Spoligotyping was performed on clinical specimens and their respective cultures with a commercially available kit (Mapmygenome Genomics company, India).

Results: Based on the Spoligotyping pattern, among the fourteen patients, 57.1% had different genotypes in clinical samples and their respective cultures. These discrepant patterns were suggestive of polyclonal infections in clinical samples with possible overlapping Spoligotype patterns.

Conclusion: In conclusion, direct Spoligotyping is very efficient in regions where mixed infections are little in their clinical specimens. On the other hand, in societies with high mixed infections (e.g. Iran) in clinical specimens, we recommend to rule out mixed infection by the MIRU-VNTR method in the first step and after that direct Spoligotyping can be performed more accurately.

Keywords: Direct Spoligotyping; Tuberculosis; Polyclonal infection; MANU2 genotype

O52 - 752: MYCOBACTERIUM AHVAZICUM SP. NOV., THE NINETEENTH SPECIES OF THE MYCOBACTERIUM SIMIAE COMPLEX

Abodolrazagh Hashemi Shahraki[1], Mohammad Hashemzadeh[2], Parvin Heidarieh[3], Amar Bouam[4], Michel Drancourt[5]

1. Department of Epidemiology, Pasteur Institute of Iran, Tehran, Iran. 5School of Veterinary Medicine
2. Dept of Microbiology, Faculty of medicine, Ahvaz Jundishapur University of Medical Science, Ahvaz, Iran
3. Department of Microbiology, School of Medicine, Alborz University of Medical Science, Alborz, Iran
4. Unité des Rickettsies, CNRS UMR 7278 Faculté de Médecine, Aix-Marseille-Université, Marseille, France
5. Unité des Rickettsies, CNRS UMR 7278 Faculté de Médecine, Aix-Marseille-Université, Marseille, France

Background and Aim: Four strains isolated in Iran from pulmonary and soft tissue specimens are proposed as representative a novel mycobacterium species.

Methods: Four slowly growing mycobacteria isolates were isolated from the respiratory tract and soft tissue biopsies collected in four unrelated patients in Iran. Conventional phenotypic tests indicated that these four isolates were identical to Mycobacterium lentiflavum while 16S rRNA gene sequencing yielded a unique sequence separated from that of M. lentiflavum. One representative strain AFP-003T was characterized as comprising a 6,121,237-bp chromosome (66.24% guanosine-cytosine content) encoding for 5,758 protein-coding genes, 50 tRNA and one complete rRNA operon.

Results:total of 2,876 proteins were found to be associated with the mobilome, including 195 phage proteins. A total of 1,235 proteins were found to be associated with virulence and 96 with toxin/antitoxin systems. The genome of AFP-003T has the genetic potential to produce secondary metabolites, with 39 genes found to be associated with polyketide synthases and non-ribosomal peptide syntases and 11 genes encoding for bacteriocins. Two regions encoding putative prophages and three OriC regions separated by the dnaA gene were predicted. Strain AFP-003T genome exhibits 86% average nucleotide identity with Mycobacterium genavense genome.

Conclusion: Genetic and genomic data indicate that strain AFP-003T is representative of a novel Mycobacterium species that we named Mycobacterium ahvazicum, the nineteenth species of the expanding Mycobacterium simiae complex.

Keywords: Novel species, Mycobacterium ahvazicum, dnaA gene, 16SrRNA

Oral Microbiology

O53 - 647: GENE EXPRESSION PROFILING OF FIMA FIMBRIAE IN PORPHYROMONAS GINGIVALIS STRAINS IN RESPONSE TO PHOTO-ACTIVATED DISINFECTION THERAPY

Maryam Pourhajibagher[1], Abbas Bahador[2]

1. Dental Research Center, Dentistry Research Institute, Tehran University of Medical Sciences, Tehran, Iran
2. Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: The endodontic infection therapy majorly aims to eradicate the microbial pathogens. Photo-activated disinfection (PAD), also known as antimicrobial photodynamic therapy, is an alternative antimicrobial modality used to control the microorganisms causing endodontic infections. The present study assessed the effects of PAD on expression profiling of the gene associated with the biofilm formation being the most essential virulence factor in Porphyromonas gingivalis strain cells.

Methods: Sixteen clinical strains of P. gingivalis that were isolated in vivo, were further photosensitized with toluidine blue O (TBO), methylene blue (MB), and indocyanine green (ICG) as the photosensitizing agents, which were excited with specific wavelength of light based on the photosensitizer. After evaluating sub-lethal dose of PAD (sPAD), its effects on the fimA gene expression were assessed using real-time quantitative reverse transcription PCR (qRT-PCR).

Results: In this study, maximum values of sPAD against P. gingivalis were 6.25 µg/mL TBO at a fluency of 171.87 J/cm2, 15.6 µg/mL ICG at fluency of 15.6 J/cm2, and 25 µg/mL MB at fluency of 93.75 J/cm2. MB-, TBO-, and ICG-sPAD could cause about 4.6-, 14.4-, and 17.3-fold suppression of fimA expression, respectively. P. gingivalis strains expressed less virulence in cells surviving PAD.

Conclusion: The gene expression profiling reduced in the bacterial cells, wherein greater reduction was observed for ICG-sPAD than TBO- and MB-sPAD.

Keywords:gene expression; indocyanine green; methylene blue; photo-activated disinfection; Porphyromonas gingivalis; toluidine blue O

Pharmaceutical Microbiology

O54 - 556: MOLECULAR CLONING OF HYALURONAN SYNTHASE GENE AND PRODUCTION OF HYALURONC ACID IN BACILLUS SUBTILIS

Mansoureh Sedaghat[1], mohammad Barshan tashnizi[2], Gholamreza Ahmadian[3]

1. Department of Life Science Engineering (LSE), Faculty of New Sciences & Technologies (FNST), University of Tehran, Tehran, Iran.
2. Department of Life Science Engineering (LSE), Faculty of New Sciences & Technologies (FNST), University of Tehran, Tehran, Iran.
3. National Institute of Genetic Engineering and Biotechnology, Tehran, Iran.

Background and Aim: Hyaluronic acid (HA) plays important roles in human tissue system, thus it is highly desirable for various applications, such as in medical, clinic and cosmetic fields. Expressing hyaluronan synthase alone could make B. subtilis produce HA. The hasA gene from Streptococcus equisimilis (sehasA), which encodes the enzyme hyaluronan synthase, has been expressed in Bacillus subtilis, resulting in the production of hyaluronic acid. In addition, the B. subtilis-derived material was shown to be secreted and of high quality, comparable to commercially available sources of HA.

Methods: The sehasA gene encoding hyaluronan synthase was artificially synthesized with codon preference of B. subtilis with the restriction sites HindIII/BamHI. The B. subtilis WASD was used as the host for HA synthesis and E. coli DH5α was used for cloning of the shuttle plasmid. B. subtilis cells were made competent by the method of Anagnostopoulos and Spizizen. For the expression of HA synthase in B. subtilis to produce HA, MMG medium was employed. Presence of HA in broth was demonstrated by a modified cetyltrimethylammonium bromide (CTAB) turbidity method.

Results: Codon analysis showed that the rare codon numbers in sehasA for host B. subtilis dropped to zero. Electrophoresis of digested Recombinant shuttle plasmid, showed a 1290 bp band of Hyaluronan synthase gene. Presence of HA in broth was demonsted by CTAB method.

Conclusion:B. subtilis has proven to be a superior expression host for producing HA. Analysis by CTAB turbidity and FTIR have revealed that HA produced in B. subtilis.

Keywords:hyaluronan synthase, Hyaluronic acid, Bacillus subtilis

Zonosis and Veterinary Microbiology

O55 - 100: THE EVALUATION OF IMMUNITY OF BETA ANTITOXIN OF CLOSTRIDIUM PERFRINGENES BY INDIRECT ELISA AND SERUM NEUTRALIZATION TEST

Lida Abdolmohammadi khiyav[1], Reza Pilehchian Langeroodi[2], Ali Haghroosta[3], Mona Hasanzadeh[4]

1. Department anaerobic bacterial vaccine Production and Research, Clostridia Research laboratory, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Tehran, Iran
2. Department anaerobic bacterial vaccine Production and Research, Clostridia Research laboratory, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Tehran, Iran
3. Department anaerobic bacterial vaccine Production and Research, Clostridia Research laboratory, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Tehran, Iran
4. Department anaerobic bacterial vaccine Production and Research, Clostridia Research laboratory, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Tehran, Iran.

Background and Aim: Clostridium perfringens is the etiology agents of enterotoxaemia, which has severe economic losses. The evaluation of immunity of beta antitoxin, that which prevents against the disease in animals, are measured in vivo using serum neutralization test (SN) (conventional method) that has disadvantages. So the purpose of this plan was using Enzyme linked Immuno Sorbent Assay (ELISA) as an alternative to measure beta antitoxin.

Methods: In this research, beta toxin was concentrated and purified. Then MLD and amount of protein were measured using Lowry method. After that positive (hyper immune), negative control and test antiserum specimens (polyvalent enterotoxaemia vaccine were produced in fermenter) were prepared. Then, we were measured beta antitoxin by ELISA and SN simultaneously and the results were analyzed by SPSS software.
Results: The results of this study showed that there is a significant agreement between in vivo and in vitro tests in serum samples of vaccinated rabbits by polyvalent vaccine. Linear regression analysis showed a correlation coefficients of 0.84 and $P<0.01$. Sensitivity, positive and negative predictive value of ELISA in these samples were 100%, 84.21% and 100%, respectively. In this group, the cut off of 10 IU /ml for beta antitoxin was calculated in 95% of the cases ELISA test.
Conclusion:ELISA systems are as a suitable alternative to measure beta antitoxin of enterotoxaemia vaccine. It contributes to reducing the use of rabbit and mouse and which is also faster and more inexpensive than serum neutralization test. There are also no disadvantages of conventional method.

Keywords: Clostridium perfringens, beta antitoxin, SN, ELISA, MLD, polyvalent vaccine

O56 - 268: DESIGNING OF NOVEL SPECIFIC RT-PCR FOR DETECTION OF 793/B GENOTYPE OF AVIAN INFECTIOUS BRONCHITIS VIRUS

Arash Ghalyanchilangeroudi[1], Zahra Ziafati[2], Reza Khaltabadi Farahani[3], Leila Aghaeean[4], Reyhaneh Khezrdoust[5], Amir Hossein Mohseni[6], Masoumeh Jabbarifakhr[7]

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. Iranian Veterinary Organization, 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
6. Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
7. Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran

Background and Aim: Avian Infectious Bronchitis is a severely contagious, acute viral respiratory disease of chickens caused by infectious bronchitis virus (IBV), which leads to substantial economic losses in the poultry industry. So far, many serotypes have been detected but Massachusetts and 793/B are among the most important and prevalent serotypes of IBV worldwide. The S gene of IBV carries virus-neutralizing, serotype-specific, and genotyping determinants.

Methods:RNA of virus has been isolated from chicken by respiratory clinical sign and commercial 4/91 vaccine. A set of primer was designed based on sequences in the Gene Bank for amplified Spike gene. The sensitivity of the RT-PCR primers was established by different amount IBV strains. To evaluate the specificity of the method, the following RNA viruses were used NDV and AI and other IBV strains. RT-PCR product was sent to sequence.

Results: To carry out IBV of 793/B was achieved by using primers specific for this types (S gene) in two-step RT-PCR. Product size was ~200 bp. The specificity pairs of each specific primers were examined by another genotype. Pairs of each specific primers identified specific genotypes. The samples were confirmed by de-deoxi Sanger sequencing.

Conclusion:IBV has a significant effect in poultry industry including drops in egg production, poor eggshell quality, drops in hatchability, nephritis, sometimes false layers, poor weight gain and feed efficiency in commercial broiler. Currently, 793/B type viruses have been detected in several other Asian countries, including IRAN. So it was needed to detect this strain with a quick and accurate test in the flocks.

Keywords: Infectious bronchitis virus (IBV), 793/B, RT-PCR

O57 - 346: DEVELOPMENT OF A NEW IMMUNOBLOTTING TECHNIQUE FOR SERODIAGNOSIS OF BURKHOLDERIA MALLEI INFECTION

Sajjad Yazdansetad[1], Nader Mosavari[2], Keyvan Tadayon[3], Iraj Mehregan[4]

1. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran.
2. PPD Tuberculin Department, Razi Vaccine & Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran.
3. Veterinary Aerobic Bacteria Vaccines Department, Razi Vaccine & Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran.
4. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran.

Background and Aim: Burkholderia mallei is a causative agent of glanders, a highly contagious disease in equines which is notifiable to the World Organisation of Animal Health (OIE). The disease is still endemic in our country, Iran. The present study was conducted to develop a new immunoblotting method based on lipopolysaccharide (LPS) antigen of B. mallei for glanders serodiagnosis.

Methods: One horse was immunized subcutaneously using a mixture of crude suspensions of heat inactivated B. mallei adjuvanted with aluminium hydroxide gel to prepare a panel of positive sera. Immunizations were performed weekly for seven weeks with 7 doses of 1.5 ml antigen containing increasing cell concentrations. The sera was confirmed by ELISA. Antigen from B. mallei was prepared by formaldehyde 12% and a typical LPS ladder was proofed by SDS-PAGE. A partly purified LPS of B. mallei was assayed by Western blot using HRP-conjugated rabbit anti-horse IgG. A comprehensive set of positive and negative sera obtained from horses validated the test.

Results:A ladder pattern of the B. mallei LPS was seen within the region of 20 to 60 kDa clearly and the immunoblot was scored positive, while no reaction was seen for the negative sera. Western blot assay indicated a noticeably higher diagnostic specificity for positive or negative sera of glanders.

Conclusion: The developed immunoblot technique based on LPS-preparation testified is highly practicable in our study. The prepared antigen demonstrated to be suitable for its use in immunoblotting. The developed method is a sensitive and specific for glanders serodiagnosis in endemic areas in less developed countries.

Keywords: Burkholderia mallei, immunoblotting, glanders, LPS

O58 - 353: COMPARISON OF VACCINAL AND REGIONAL CIRCULATING BOVINE EPHEMERAL FEVER VIRUS BASED ON ANTIGENIC RELATIONSHIP AND CROSS-NEUTRALIZATION TEST

Shokoofeh Almasi[1], Dr. Mehran Bakhshesh[2], Dr. Shahla Shahsavandi[3]

1. Razi vaccine and serum research institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
2. 1. Department of viral animal disease research and diagnosis, 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

Background and Aim: Bovine Ephemeral fever is an arthropod-born and disabling disease of cattle and water buffaloes. The BEFV is classified as a -ssRNA in the genus Ephemerovirus, of the family Rhabdoviridae. We have analyzed and compared the whole glycoprotein G encoding gene and its 4 antigenic sites in BEFV isolate isolated during 2012 in Iran and commercially available vaccinal strain applied in Iran.

Methods: The One-Step RT-PCR reactions were carried out and entire G gene sequences were analyzed. Hyperimmune sera against vaccinal and Iranian isolate were raised in rabbit. Then cross-neutralization test was performed and R value was calculated in according to Archetti formula.

Results: The analysis of the Iranian isolate and vaccinal strain showed 95.6% identity, with 17 amino acids substitutions that 4 of them occurred in antigenic epitope sites. The antiserum against vaccinal strain neutralized the Iranian isolate 4 times lower than of the homologous strain. The R value among two viruses was 34.8% , so classified into distinct subtypes.

Conclusion: Residue 218 (R) in G3 epitope is more important substitution than other amino acid variations, and we find that it has been changed to K in Iran isolate. Other substitution occurred at positions 223, 277and 503 in known epitopes. These amino acid substitutions between iranian and vaccinal strain have affected the immunity induced by commercial vaccine against field strains. Relatively low R value indicates on insufficient efficiency of commercial used vaccine and implying on revision of how to use the vaccine, or developing a vaccine from the native isolate of the country.

Keywords:bovine ephemeral fever, R value, antigenic variation

O59 - 535: MULTILOCUS SEQUENCE TYPING AND GENETIC STRUCTURE OF FASCIOLA ISOLATES FROM LIVESTOCK IN KERMANSHAH, IRAN

Arezoo Bozorgomid[1], Mohamad Bagher Rokni[2], Naser Nazari[3], Eshrat Beigom Kia[4], Homa Hajjaran[5], Medi Mohebali[6]

1. Department of Microbiolgy, Asadabad School of Medical Sciences, Asadabad, Iran
2. Department of Medical Parasitology and Mycology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
3. Department of Medical Parasitology and Mycology, School of Medicine, Kermanshah University of Medical Sciences, Kermanshah, Iran
4. Department of Medical Parasitology and Mycology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
5. Department of Medical Parasitology and Mycology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
6. Department of Medical Parasitology and Mycology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim:asciolosis is a parasitic disease caused by liver fluke species of the genus Fasciola, Fasciola hepatica and Fasciola gigantica. There is limited information aboutthe diversity of the genus Fasciola in Iran.Implementation of molecular strategies for parasite typing,particularly multilocus sequence typing (MLST)represents an improved approach for genetic variabilityand population dynamics analyses. For the first time, we introduce a Multilocus Sequence Typing (MLST) method to genetically characterize Fasciola species.

Methods: Thirty-fourFasciola species isolated from livestock and from Kermanshah province were characterized using MLST approach. DNA fragments (500-800 bp) from 5 housekeeping genes were sequenced. A MLST analysis was developed based on the genes Cyt b, ND1, HSP 70, Pold, Pepck.Phylogeny analysis was conducted both on concatenated MLST loci and on each individual locus

Results:A total of 3154 bp were analyzed for each isolate. In all,52 and 72 polymorphic sites were identified for Fasciola hepatica and Fasciola gigantica, respectively. The neutrality hypothesis could not be rejected. The overall MLSTscheme exhibited a high level of discrimination (Simpson Index = 0.9929) for Fasciola hepatica and Fasciola gigantica.

Conclusion: We suggest that MLST will have a strongimpact on molecular epidemiological studies of fasciolosis disease and the phylogenetics of its causative agent.

Keywords: Fasciola, genotyping, livestock, MLST, Iran

O60 - 658: GENETIC DIVERSITY OF IRANIAN ISOLATES OF BURKHOLDERIA MALLEI BY PFGE AND PCR-MLVA

Nader Mosavari[1], Rouhollah Keshavarz[2], Shojaat Dashtipour[3]

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

Background and Aim: Glanders is a contagious and fatal zoonotic disease seen more often in equines. Causative agent of the disease is Burkholderia mallei. In last couple of years, researchers have been looking for raising awareness of the epidemiology of the disease by using modern and sophisticated molecular biology techniques.

Methods: In order to analysis genetic diversity in Iranian isolates of B. mallei, five wild isolates (Tiger, Semirum, Kordan, Oshnavieh and Tehran) and one product strain (B. mallei 325) were comparatively examined by PFGE and PCR-MLVA. For MLVA two Variable Number of Tandem Repeats (VNTR) loci of VNTR1217 and VNTR13 were employed. The amplification products of MLVA PCRs were sequenced to guaranty accuracy of sizing and nucleotide structure.

Results: Consequently, in PFGE three profiles were detected with the first specific to B. mallei 325 and the second represented by B. mallei Semirum. The other three strains shared the third type. The PFGE pattern of the 325 strain was characteristically different to those of the Iranian isolates. In MLVA, at VNTR13 three alleles were detected where B. mallei 325 appered to be clearly different to other four examined strains. Furthermore, at VNTR1217 two allels were observed leading to a total of 4 combinational VNTR profiles between the five straines.

Conclusion: Findings of this study back the assumption that if an appropriate panel of VNTR loci are sleceted, MLVA typing can provide the capability required for epidemiologic investigations. This is a much needed requirement specifically in the Iranian environment where mini outbreaks of glanders take place every year.

Keywords: Glanders, Burkholderia mallei, REA, VNTR

O61 - 690: BRUCELLOSIS IN IRAN: IDENTIFICATION OF BRUCELLA SPECIES AND BIOVARS ASSOCIATED WITH ANIMAL AND HUMAN INFECTION

Maryam Dadar [1], Saeed Alamian[2], Ali Mohammad Behrozikhah[3], Freshteh Yazdani[4], Armin Kalantari[5], Afshar Etemadi[6]

1. Brucellosis Department, Razi Vaccine and Serum Research Institute (RVSRI); Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
2. Brucellosis Department, Razi Vaccine and Serum Research Institute (RVSRI); Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
3. Brucellosis Department, Razi Vaccine and Serum Research Institute (RVSRI); Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
4. Brucellosis Department, Razi Vaccine and Serum Research Institute (RVSRI); Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
5. Brucellosis Department, Razi Vaccine and Serum Research Institute (RVSRI); Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
6. Brucellosis Department, Razi Vaccine and Serum Research Institute (RVSRI); Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran

Background and Aim: Brucellosis is a costly contagious disease of domestic and wild animals that also infects humans. It is a serious health problem in Iran causing significant economic losses and control approaches to prevent its spread are of overwhelming importance. In Iran, the species and biovars of virulent Brucella species are still underreported due to inadequate diagnostic protocols and insufficient laboratory facilities.

Methods:A total of 419 samples from 65 cases/case series were examined bacteriologically and resulting Brucella isolates were further characterized by phenotypic and molecular approaches.

Results: All recovered isolates were either B. abortus or B. melitensis – infection in sheep appeared to be exclusively associated with B. melitensis, but both B. abortus and B. melitensis were common in bovine samples. A small number of ovine cases were confirmed to be caused by the B. melitensis vaccine strain Rev1. In spite of the B. abortus burden in animals infection in humans was predominantly associated with B. melitensis. Results confirmed that B. melitensis biovar 1 and B. abortus biovar 3 remain the most prevalent biovars in Iran

Conclusion: These data, and the techniques implemented in the course of the study, begin to build a picture of the significance of different Brucella species in different hosts in Iran currently, knowledge required to ultimately design and implement any future control program.

Keywords: Brucellosis; Bruce ladder; AMOS-PCR

O62 - 712: ASSESSMENT OF GENETIC PATTERN MYCOPLASMA AGALACTIAE ISOLATED FROM EAST AZARBAIJAN AND ELAM BY METHOD OF MLST TYPING

Khatereh Kabiri[1], Keyvan Tadayon[2], Seiyed Ali Pourbakhsh[3], Jamile Norouzi[4]

1. Department of Microbiology, North Tehran Branch, Islamic Azad University, Tehran, Iran.
2. Department of Veterinary Aerobic Bacteria Razi Institute Karaj
3. Mycoplasma reference laboratory, Razi vaccine and serum research institute, Karaj, Iran
4. Department of Microbiology, North Tehran Branch, Islamic Azad University, Tehran, Iran.

Background and Aim: Mycoplasma agalactiae is the main etiologic agent of contagious agalactia, a serious syndrome affecting sheep and goat associated with several clinical signs, including mastitis, arthritis, keratoconjunctivitis, pneumonia and septicaemia. The aim of this study was conducted to genotype M.agalactiae strains isolated from East Azarbaijan and Elam in milk samples using Multi Locus Sequence Typing (MLST) method.

Methods: To perform MLST analysis bacterial DNA was extracted by simple boiling method, then primers were designed based on the sequence proposed by the MLST database (https://pubmlst.org/magalactiae/). The PCR products obtained from amplification of five housekeeping genes (dnaA, gltX , gyrB , metS, tufA) were sequenced. The nucleotide sequences of five genes in Target isolate were analyzed in the MLST database, then by using characterization of the alleles specific to each gene, the sequence types (ST) of all isolates were determined.

Results: In consequence, at dnaA, gltX, gyrB, metS and tufA loci of all the target strains alleles 1, 21, 2, 2 and 1 were identified, respectively. A new sequence type 34 (ST34) was identified from archived target isolates at Razi institute for the first time in Iran.

Conclusion:MLST method is portable, rapid, and very stable and is useful tool for epidemiological studies. We recommend using MLST for genotyping the isolates of other endemic areas of the country.

Keywords: Mycoplasma agalactiae, MLST, PCR, strain

پروبیوتیک ها و پربیوتیک ها

O63 - 259: COMPARISON OF PROBIOTIC THERAPEUTIC EFFECTS IN ERADICATION OF HELICOBACTER PYLORI INFECTION

Yasamin zahra Asadi[1], sasan saki[2], mohammad taher[3], zahedin kheiri[4], saeed alizade[5], hamidreza mohajerani[6]

1. department of biology faculty of basic scince/ Islamic azad university arak/ iran
2. department of scince faculty of medical scince /Islamic azad university arak /iran
3. (MD), Assistant Proffesor at School of Medicine, Tehran University of medical sciences
4. (MD), Assistant Proffesor at School of Medicine, Tehran University of medical sciences
5. Medicine Student, school of medicine, semnan university of medical sciences, semnan, Iran.
6. department of biology faculty of basic scince/ Islamic azad university arak/ iran

Background and Aim: Helicobacter pylori (H-pylori) antibiotic resistance is a growing problem which needs an alternative treatment with acceptable eradication effect. Several studies have been done in relation to effect of probiotics in different infectious diseases, therefore the aim of this study is evaluating the effect of adding probiotic to the Helicobacter pylori's standard eradication regimen.

Methods: In this clinical trial, we studied 120 patients with H. pylori infection in two groups (60 subjects in each probiotic and control groups). Both groups were treated with quadruple regimen of omeprazole, bismuth, clarithromycin, and amoxicillin for two weeks. In addition, the intervention group, received protexin (restore). After 4 weeks of treatment, outcome and eradication success rates were measured in both groups.

Results: Eradication success rate based on pathological and carbon-14 breath test assessment was significantly higher in the intervention group as compared to control group ($p < 0.05$). Moreover, the complication rates did not differ between both groups. (P>0.05(

Conclusion: Adding probiotic to the Helicobacter pylori's standard treatment regimen will increase eradication success rate without causing significant complications.

Keywords: Helicobacter pylori, Probiotic, Eradication

پانل زئونوز

Leptospirosis and control strategies

Hashemi Tabar, GH. R.,

Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.

Introduction and Objectives: The worldwide incidence of leptospirosis is increasing year on year, from an initial estimate of 500,000 cases in 1999 to over one million cases and 60,000 fatalities in 2015. Leptospirosis is caused by numerous distinct serovars of a spiral-shaped bacterium known as *Leptospira interrogans* and it is a disease of animals and humans. These serovars are harbored by a wide range of animals, and all of them are capable of causing illness in humans. Inactivated whole-cell vaccines (bacterins) are routinely used in livestock and domestic animals, however, protection is serovar-restricted and short-term only. To overcome these limitations, efforts have focused on the development of recombinant vaccines, with partial success and recently, reverse vaccinology (RV) has been successfully applied to Leptospirosis for prospective vaccine antigens.

Materials and Methods: The most abundant protein in the entire leptospiral proteome is an outer membrane lipoprotein of 32 kDa, LipL32, accounting for 75% of the outer membrane proteome. 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. The most promising results regarding protection against leptospirosis were achieved using the leptospiral immunoglobulin-like (Lig) B, A proteins. Reverse vaccinology (RV) has been widely used for screening of surface-exposed proteins (PSEs) of important pathogens, including outer membrane proteins (OMPs), and extracellular proteins (ECPs) as potential vaccine candidates.

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.While there are reports that LigB can induce protection in animal models, LigA induced an unequivocal immune protection in the hamster model using recombinant protein immunization. However, the *ligA* gene is present only in three *Leptospira* spp. (*L. interrogans*, *L. kirschneri* and *L. alstonii*), making it difficult for a LigA vaccine to broadly protect against leptospirosis. As hundreds of draft genomes of all known *Leptospira* species are now available, this should aid novel target discovery through reverse vaccinology (RV) and pangenomic studies. The identification of surface-exposed vaccine candidates that are highly conserved among infectious *Leptospira* spp. is a requirement for the development of a cross-protective universal vaccine.

Conclusions: The urgent need for a new vaccine has motivated several research groups to evaluate the protective immune response induced by recombinant vaccines. Significant protection has been reported with several promising outer membrane proteins, including LipL32 and the leptospiral immunoglobulin-like proteins. However, efficacy was variable and failed to induce a cross-protective response or sterile immunity among vaccinated animals. As a large number of annotated proteins in Leptospira genomes does not have any known orthologues, RV represents the most promising approach for the discovery of a recombinant vaccine, thereby reducing the burden of leptospirosis.

Key words: Leptospirosis, Recombinant vaccine, Reverse vaccinology.

Cloning and Expression two recombinant proteins of *Mycobacterium bovis*

Reza Arefpajoohi[1], Ramak yahyaraeyat[2], Zahra Salehi-Najafabadi[1], Nader Mosavari[1], Taghi Zahraei Salehi[2]

1-Bovine Reference Laboratory, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran

2- Department of Microbiology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran.

Introduction: *Mycobacterium bovis* is agent of bovine tuberculosis that mainly separated from bovidae. The consequences of disease are widely spread including decrease in production, early death and economic losses. Primary diagnosis based on tuberculin skin test that may have false positive. ESAT-6 and CFP-10 are important proteins that secreted in early stage of disease. Also these proteins are eliminated in process of bovine PPD (PPD-B) production. To investigate the functions of that, two genes esat-6 and CFP-10 are cloned and expressed.

Material and method: Sequence of esat6 & cfp10 of *Mycobacterium bovis* obtained from bovilst. First, primers designed with restriction enzymes BamHI and EcoRI and after that synthetize at Macrogen co. After that, Polymerase Chain Reaction(PCR) was performed to amplify these genes. In parallel DH5α-pET23a (+) replicated and then isolated the vector. Both vector and PCR product are digested, ligation was done at 16˚C then cloned vector transform to DH5α. After being identified with sequencing, cloned vector transformed to BL21. Expressed proteins optimized and analyzed with sodium dodecyl sulfate-polyacrylamide gel electrophoresis(SDS-PAGE) and Western Blotting (WB).

Results: The esat6 and cfp10 genes were amplified successfully. Both of them were cloned into expression vector. After identified by sequencing, genes were expressed. Analyzed of proteins expressed showed the molecular weight about 10 KDa and identified by WB technique

Conclusion: The esat6 and cfp10 genes were successfully cloned and expressed in *E. coli*.

Epidemiological situation of brucellosis in Iran

Mohammad Zeinali1,Mahbobeh Khaton Ghanbari

1. Department of National programs of zoonotic diseases

2. Department of National programs of zoonotic diseases

Background and Aim: Brucellosis is one of the most common infectious diseases in Iran, Middle East and the vast areas worldwide. As Brucellosis is transmitted from animals to humans (Zoonoses), in addition to debility of patients and complications from disease and also economic losses caused by the disease control strategies in human population, leads to a reduction in food resources due to reduced animal population because of abortion in livestock and economic burden inflicted on the population

Methods: The required information has been gathering from the summary of patient information forms which are sent monthly through provincial health centers. In Our country Epidemiological care strategies done by probable case definition, monthly case reports and if necessary, sentinel surveillance of high-risk groups, and annual and current reports indicate the disease process during several years and its influencing factors affects the increasing or decreasing disease trend.

Results: By studing the disease over the past 17 years, since2001 till 2017, It can be seen that the cases since2001 till 2009 from25 cases in hundred thousand people have been decreased to 18cases in hundred thousand people. Following the success of increasing vaccine coverage for livestock, the disease has been declining.

From 2010 till 2014 from 17 cases in hundred thousand people has increased to 26 cases in hundred thousand people. The main reason for this increase is improving patient care and reporting, in addition to implemented policy

changes in Animal vaccination during these years in order to raise vaccine coverage in population of mature and immature animals (Cattle, calves, sheep, goats, lambs and kids).

The incidence of disease has been reduced from years of 2015to 2017 so that from 23 cases in hundred thousand people to 19 cases in hundred thousand people Which is in accordance with the brucellosis control program that includes developing and improving cross-sectoral coordination as the most important way of preventing and controlling human-animal transmissible diseases, the public education and high-risk groups using new educational methods such as the Shep model, training of doctors, veterinarians and staff as other strategies for the program over the past years. It has been seriously considered. Latest information on the disease shows that Hamedan, Lorestan , Kurdistan, Zanjan , Razavi Khorasan, Northern Khorasan West Azerbaijan, Ardebil, Kermanshah provinces had the highest incidence rate(incidence rate between 41-77 per 100,000)

Conclusion: Increasing vaccination coverage in veterinary livestock sector and widespread deployment of pasteurization factories and producing pasteurized milk and products during these years has been the most important factors in reducing the incidence of the disease. Identify infected livestock foci - eligible animals vaccination - training at risk groups (farmers, herders, shepherds, slaughterhouse workers, butchers, housewives women in rural areas and laboratory staff) , using or not using pasteurized dairy products, development of pasteurized dairy production factories, are the main factors that will reduce or increase brucellosis.

Keywords: Brucellosis - Iran-Epidemiology

Brucellosis Control and eradication programs

Dr Karim Amiri

An important problem encountered by the veterinary authorities in countries affected by brucellosis is to select the sanitary strategy to be applied against the disease. Adequate organization of veterinary services is, without any doubt, the most important element to be taken into consideration by decision-makers previous to any potential selection of a sanitary programme.

The economic costs of eradication programs are very important, and financial resources should be allocated to support the programs as an essential requisite prior to the selection of any eradication strategy.

The adequate organization and involvement of shepherds is also another essential requisite for success in the implementation of even the simplest control strategy based on mass vaccination.

Once the professional organization and the economic resources are fully adequate, the epidemiological unit of intervention should be defined. Whenever the collective prevalence (percentage of infected flocks) in this unit be uniformly very low (always less than 1% of flocks infected), a strategy based on a *test and slaughter* programme and a ban on vaccination could be applied to eradicate the disease in the short to medium term in that particular epidemiological unit. In the case where prevalence is uniformly moderate, a *combined eradication* programme based on the simultaneous application of vaccination in young replacements and a test and slaughter in adult animals could be recommended to eradicate the disease in the medium to long term. However, when the disease is highly prevalent (more than 10% of flocks are infected), even though the professional organization and the economic resources be fully adequate, the *mass vaccination* of all animals is the only reasonable strategy that can be applied to control the disease.

Country Instruction to Combating Animal Brucellosis

Dr Akram Bahreinipoor

Brucellosis is a family of infectious and contagious gram negative coccobacilli that causes disease in animals and humans. It is one of diseases that can be transmitted from animal to humans (zoonoses). The disease primarily affects cattle and sheep, goats, pigs, horses, dogs and humans. Because of its large economic impacts and possible human health implications, an eradication program was begun in 1346 in Iran.
Cattle and sheep are the major farm species infected by this disease.

On the whole, the control strategy for brucellosis in cattle and Sheep and goat is as follows:

1. Education and promotion
2. Health regulations and quarantine rules
3. Vaccination
4. Testing and slaughter

A. Combat Brucellosis in the Cattle
In cattle, brucellosis is generally identified by late term abortions and inflammatory lesion in the male reproductive tract. The bacteria are an intracellular pathogen that survives and replicates in the white blood cells. In the female, the organism localizes in the udder, uterus and lymph nodes next to the reproductive tract causing degeneration of the placenta leading to abortion or the birth of weak calves. In bulls, the organism localized in the testicles. Transmission is most often through ingestion although there are reports of venereal transmission.

B. Combat Brucellosis in the Sheep and goat

Sheep and goat brucellosis, is caused by the bacterium Brucella melitensis, B. melitensis is very important for common health, and causes disease in most human cases in the world. The disease is also due to extensive abortion in sheep and goats, and economic damage to the economy.

Zonosis and Veterinary Microbiology

Masoud Ghorbanpoor[1], Bahman Mosalanejad[1], Sara barati[1], Babak Barimani[1], Saleh Esmailzadeh[5], Naghmeh Moori Bakhtiari[1]

1- Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz

Chlamydiae are gram-negative obligate intracellular bacteria that affects both human and animal health. According to the latest classifications, the order Chlamydiales consists of one family, the Chlamydiaceae, containing one genus, the Chlamydia, which consists of 12 different species that are responsible for a wide range of diseases. Feline chlamydiosis is one of the most important upper respiratory tract diseases of cats. In this paper the successful isolation of C. felis from a cats affected with conjunctivitis is reported.

Several conjunctival swabs were taken from both eyes of a 2-month-old female kitten with a history of severe bilateral conjunctivitis. The samples were used for direct microscopic examination, microbial cultures, and molecular diagnosis of C. felis infection and the case was treated ophthalmic tetracycline ointment twice daily for 1 week.

Microbiological cultures of swabs did not yielded the growth of extra-cellular pathogenic bacteria or fungi. Molecular diagnosis of C. felis infection by conventional PCR with C. felis specific primers revealed the presence of targeted gene. The Gimsa and imunoperoxidase staining of smears also showed the specific intra-cytoplasmic chlamydial inclusions. Chlamydia felis was isolated from samples by inoculation to cycloheximide-treated L 929 cells. The symptoms and clinical signs of affected kitten disappeared after treatment.

To the best of our knowledge, this is the first reports on isolation of C. felis from Iran. The use of an effective C. felis vaccine for preventing infections in cat populations seem to be necessary and should be recommended.

Chlamydia felis, kitten, Conjunctivitis, Isolation, Iran

Operational policies of zoonoses control

Dr Alisafar Makenali

Increasing importance of zoonoses is the result of many different factors as follows:

- The technologies available for their diagnosis have been improved;
- Control techniques have been further developed;
- Zoonoses influence not only health and economic aspects of human society, but also factors related to agriculture and trade;
- The prevalence of many zoonoses, and also their social and economic relevance, are changing as a result of actions by man on his environment, e.g. urbanisation, land reclamation, changes in agriculture;
- Some zoonoses are emerging as problems because of conditions provided by environmental changes (e.g. infection by Microsporum canis in urbanised areas) or food-processing systems (e.g. presence of Listeria monocytogenes in cold-preserved foods);
- Zoonoses are also emerging as a problem for immunodepressed persons and other groups at special risk;

These and other factors have led to an increase in the number of infections which are considered as zoonoses, and their importance as public health problems has become greater. As a result, national and international budgetary allotments have been increased in spite of competition with other programs (in public health and agriculture, and elsewhere) which also demand financial support. Owing to the specific nature of infections which are primarily animal-dependent, zoonoses cannot be controlled without a veterinary contribution. Veterinary Services generally possess the knowledge and capabilities for performing zoonoses control.

پانل بانک میکروبی

Role of microorganism banks in development of biotechnology

Seyed Abolhassan Shahzadeh Fazeli, MD, Ph.D[1,2]

1- Iranian Biological Resource Center, 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

Microbes constitute the largest biomass on the earth and comprise of three domains of life (bacteria, archaea and eukaryotes). Almost 90 % of this diversity is still unexplored. Microorganisms are not only of value for the production of useful substances; they also play unique roles in element cycles with plants and animals. Microorganisms are widely used for biological studies, and new advances in biochemistry, genetics, and molecular biology are essentially due to the studies of microorganisms as a model of life. A new era will be opened in biotechnology in parallel with the development of science and technology relevant to microorganisms. Microorganisms are also significant gene pools, and these gene pools must not be lost. Microorganism banks have more than a century old history and play a vital role in the conservation and sustainable use of microbial resources. There are 758 culture collections in 76 countries with 2963913 microorganisms. They also provide the authentic biological material for high quality research and teaching in the form of reference strains, reagents for quality control. The advances in molecular biology have resulted in the continued discovery of new microbial taxa and strains and there is a need to preserve these so as to make them accessible to other researchers for research, teaching and for biotechnological exploitation. Recently, a survey was made on the application of microorganisms in the production of foods, food additives, enzymes, and related materials, with the exception of antibiotics, in applied microbiology. Thus improvement of culture collections is critical and crucial for the further development of microbiology, microbial industry, and biotechnology.

Keyword: Microorganism, Bank, Biotechnology

پانل پروبیوتیک ها

Prevention and treatment of Prebiotic, Probiotic and Postbiotic in Type 2 Diabetes

Alireza Dehnad

1- Assistant Professor of Microbial biotechnology , Biotechnology Department, East Azerbaijan Research and Education Center Agricultural and Natural Resources, AREEO, Tabriz- IRAN. a.dehnad@areeo.ac.ir
2-Higher education institute of Rab-Rashid, Tabriz, IRAN
3- Infectious and Tropical Diseases Research Center,Tabriz University of Medical Sciences, Tabriz,Iran

Millions of bacteria, viruses, fungi and other microscopic organisms living in the intestines are known as germs. Many of these germs, which are part of a large gut called cecum, are beneficial to the overall health of the body and are therefore known to be known bacteria.

prebiotics and probiotics are the best-known bacteria, although they have been discovered to date, but biotic posts have attracted attention due to the growing health benefits they provide.

Prebiotics are non-digestible carbohydrates by the human body. Their goal is to provide probiotics with energy through role play as a food source. Probiotics are good bacteria that help maintain the health of the digestive system by controlling the growth of harmful bacteria and feeding on the Prebiotic during a fermentation process that post-biopsies are a byproduct of this.

Postbiotics are compounds that are produced during the fermentation of probiotic bacteria. When probiotics are fed with certain types of fiber molecules, they leave waste materials that are generally called postbiotic. There are several types of postbiotic drugs, including lipopolysaccharide, moramyl dipeptide, indole ... .They provide a significant source of energy for the large intestine and, in addition to their effects on several metabolic processes, contribute to the growth and intestinal differentiation.

Although research on Postbiotics is still relatively new, antimicrobial properties appear to be one of their benefits. Postbiotics can reduce harmful bacteria and thus help prevent infections and diseases. Studies have shown that Postbiotics is useful for reducing inflammation, which helps to treat intestinal problems such as irritable bowel syndrome or inflammatory bowel disease.

In the new study, found that post Antibiotics may prevent diabetes in people with pre-diabetes perfect assist. When bacteria are chronically out of balance, the possibility of the formation of insulin resistance or pre-diabetes there in person. This imbalance of intestinal bacteria is common among obese people.

In fact, postbiotics, which are useful parts of the bacterial wall, can increase insulin absorption by the cells of the body.

A specific Postbiotics (MDP) has been able to reduce insulin resistance, regardless of conditions such as weight loss or changes in the microbiota of the intestine during obesity.

Since Postbiotics have recently been discovered and research has not matured in this area, access to them is not easy for probiotics. If you are looking for Postbiotics supplements, choose products that include various types of post-biotic, especially short-chain fatty acids.

Researchers are clinical trials in humans to investigate the effects of Postbiotics on the prevention of type 2 diabetes in obese people with the goal of producing drugs based on this part of the bacteria.

For example the scientists developed genetic manipulation of obese mice, it was discovered that post-biotic drugs increase insulin's effect.

Key words: Prebiotic, Probiotic , Postbiotic, Diabetes

Proteolytic activity of Lactic Acid Bacteria as a tool for development of novel functional food

Saeed Mirdamadi[1], Mahta Mirzaei[2], Nazila Soleymanzadeh[1]

[1]Biotechnology department, Iranian Research Organization for science and Technology (IROST), Tehran, Iran.

2.Department of food science and technology, Shahr-e-Qods branch, Islamic azad university, Tehran, Iran.

Modification of the molecular structure of food proteins with enzymes is an attractive way of improving the functional and nutritional properties of these proteins. Today various enzymes are applied to food proteins for the manufacture of new and valuable products. Protein structure is modified to improve solubility, emulsification, gelling and foaming properties.

Proteolytic activities of lactic acid bacteria (LAB) are responsible for producing biologically active peptides in different fermented food products. Proteolytic system of LAB is consisted of a cell wall-bound proteinase and a number of distinct intracellular peptidases. Our studies focused on potential of probiotic bacteria such as LAB for producing bioactive substances.

Several strains of LAB isolated from fermented dairy products were investigated for their proteolysis activity Our studies showed the release of ACE-inhibitory, antioxidant and antimicrobial peptides during the fermentation of dairy products. The results indicated a good correlation between degree of hydrolysis and biological activity. LAB have the potential to be used as a starter culture in the manufacture of functional food products.

One of the other applications of proteases is to decrease the risk of allergenicity when cow's milk is used as a substitute for human milk. Hydrolyzing of ß-Lactoglobulin by enzymatic activities during fermentation can reduce allergenicity. Also our future studies will focus on enzymatic activity of isolated LAB to decrease the allergenicity of gluten in sour dough.

Keywords: LAB, Proteolytic activity , Bioactive peptide, Allergenicity, Functional Food

پانل تشخیص و تایپینگ

Mycobacterium tuberculosis Typing: A Molecular Epidemiologic Tool to Control and Manage Tuberculosis

Mina Ebrahimi-Rad (Ph.D.)

Biochemistry Department Pasteur Institute Tehran.Iran

Mycobacterium tuberculosis (*M. tuberculosis*), the causative agent of tuberculosis is still a major health threatening problem worldwide. It is considered as the top infectious killer, with a figure of 4500 lives a day, all over the world. According to the CDC report, in 2016, 10.4 million people had tuberculosis of which 1.7 million died. By the emergence of MDR and XDR strains of *M. tuberculosis*, even the treatment and control of the disease have been more sophisticated.Molecular typing of *M. tuberculosis* has been widely used for different epidemiologic purposes, including outbreak studies, misdiagnosis and mixed infections detections, identifications of strain lineage, and their correlations with drug resistance, and discrimination of the related strains from un-related ones, to name a few. The data obtained from typing of the bacteria can potentially be used to control, manage and monitor the disease.

Among the several techniques proposed for typing of Mycobacterium, the method of choice is based on different geographical conditions and the laboratory facilities. Although restriction fragment length polymorphism (RFLP) is considered the gold standard method of *M.tuberculosis* typing, because of its limitations, other methods have often been replaced. Spacer oligonucleotide typing (Spoligotyping), variable number of tandem repeats (VNTR), mycobacterial interspersed repetitive units-variable number tandem repeats (MIRU-VNTR), whole genome sequencing (WGS), MLST (multilocus sequence typing) and several alternative methods are the other typing procedures, frequently used. Spoligotyping is more sensitive than RFLP and the demanded DNA for the former is less than that used in RFLP. Spoligotyping might be the technique of choice in screening test followed by other methods of typing.

Different molecular methods for typing of *Staphylococcus aureus*; A special focus on *spa*typing

Davood Darban-Sarokhalil

Associate Professor, Department of Microbiology, School of Medicine, Iran University of Medical Sciences

Staphylococcus aureus, as leading cause of community-acquired and nosocomial infections, remains a major health problem around the world. Molecularcharacterization is used for the rapid identification of prevalent strains and will contribute to the control and prevention of *S. aureus*in healthcare settings. Pulsedfield gel electrophoresis (PFGE) is the most recent gold standard method for the typing of *S. aureus* isolates. However, due to its laborious character and difficulties in exchanging data between laboratories, and the requirement for inter-laboratory standardization, PFGE was replaced by multi-locus sequence typing (MLST) and staphylococcal protein A (*spa*) typing. MLST is a great tool for evolutionary investigations and differentiates isolates according to nucleotide variations in 7 housekeeping genes. *Spa* typing, which relies only on the assessment of the number of and sequence variation in repeats at the x region of the spa gene, exhibits excellent discriminatory power and has become a useful typing tool in terms of ease of performance, cheaper procedure, andstandardized nomenclature. According to the literature, the prevalence of *spa* types among *S. aureus* isolates varies in different areas worldwide. The most prevalent *spa* types are t032, t008 and t002 in Europe; t037 and t002 in Asia; t008, t002, and t242 in America; t037, t084, and t064 in Africa; and
t020 in Australia. In Europe, all the isolates related to *spa* type t032 were MRSA. In addition, *spa* type t037 in Africa and t037and t437 in Australia also consisted exclusively of MRSA isolates.

Loop-Mediated Isothermal Amplification as a Reliable Technique for Diagnosis of Microbial Infections

Ramin Abiri 1, Amirhooshang Alvandi1, Somaye Bakhtiari 2, Sara Kashani 2, Elahe Ghasemian 2

1 Associate Professor of Microbiology, Kermanshah University of Medical Science

2- Master of Microbiology, Kermanshah University of Medical Sciences

Rapid detection of pathogens and on-time treatment decrease the mortality and morbidity of the infections. Therefore, one method that can diagnose the infection faster and more accurate is desirable. Although there are several microbiologic, immunologic and molecular methods for diagnosis of bacterial infections like gram staining and culture, all the techniques have several drawbacks.

Due to cross-reactivity, inability to recognize low concentration of antigen in clinical samples and low sensitivity, immunological methods are not satisfactory. New technologies such as DNA or protein microarray, gas- liquid chromatography, MOLDI-TOF are not applicable in routine diagnostic laboratories due to the high cost of the instruments and requirement to skilled personnel. Gene amplification methods, like Polymerase Chain Reaction (PCR) and Real-Time PCR, are developed to diagnose all kinds of bacterial infections without requiring to culture. These methods are very sensitive and specific and have been widely used in clinical settings. However, PCR requires expensive instrument and experienced technician and is time- consuming (nearly two hour per reaction)

An alternative method for gene amplification, the Loop-Mediated Isothermal Amplification (LAMP) assay has the potential to overcome the limitations of PCR In 2000, Notomi and colleagues invented the LAMP method for amplification of target DNA to 10^{10} copies in less than one hour in high-temperature conditions (65 ° C) with high specificity and sensitivity.

Hereby, We present the diagnostic accuracy of LAMP for diagnosis of Helicobacter pylori , Streptococcus pneumonia, Neisseria meingitidis, MRSA in non clinical samples.

Update on Helicobacter pylori Epidemiology, Diagnosis and Treatment in Iran

Hossein Dabiri

Department of Clinical Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Helicobacter pylori infection contributes to the development of diverse gastrointestinal and extra- gastrointestinal manifestation while many are asymptotic.It is estimated that more than half of world population are infected with H. pylori. Iran is a country with a high rate of H. pylori infection and different parts of Iran have different prevalence rates of *H. pylori* infection ranging from 35% to 90% based on health status, age, ethnic and location of studied population. Effective management of H. pylori infections in term of diagnosis and treatment is a very important issue,as any failure in patient management may leads to acatastrophic outcome such as gastric cancer. There are several diagnostic tools for detection of H. pylori infection which each offers different sensitivity and specificity considering type of specimens and patient condition. Thereby selection of appropriate laboratory test is very important in diagnosis or follow up of H. pylori infected patients. There are many articles published over the last decade on H. pylori treatment and antibiotic susceptibility in Iran and region. the most ideal option for effective treatment of H. pylori is to treat according to the results of culture and susceptibility tests. However, culture is not easily available.Empirically, there are several treatment regimens for H. pylori infection, however, unfortunately, there is an ascending trend in H. pylori resistance rate against commonly used antibioticsmainly due to overuse of these antibiotics which has made the treatment of H. pylori infection very sophisticate and challenging. Thereby beside to appropriate use of antibiotics, seeking for alternative treatment options is very crucial. Since the prevalence, appropriate diagnostic tools, and antibiotic susceptibility status of H. pylori variesin different region based on socioeconomicalconditions, public health and host factors, as well as microbial factors, thereby collection and analysis of regularly updated information regarding to epidemiology, diagnosis and treatment of H. pylori is required for any infection control policy and managementapproach either at local or national level.

Keywords : Helicobacter pylori, Epidemiology, Diagnosis, Treatment, Iran

Staphylococci: identification methods

Mohammad Emaneini, PhD.

Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran.

Staphylococci, including *Staphylococcus aureus* and Coagulase Negative *Staphylococci* (CoNS) are Gram positive cocci that form irregular grape-like clusters. They arenormal commensals of the skin and mucus membranes and are increasingly being known as opportunistic pathogens causing hospital and community acquired infections. *S. aureus* is the most common cause ofwound infections, whereas CoNSis the most common in nosocomial blood streaminfections.

Rapid and efficient identification of *Staphylococci* is important for correct management of patients with staphylococcal infections. The development of reliable, simple, and low-cost procedures is essential for identifying outbreaks and new strains of *Staphylococci*.

In recent years, the research toolbox has significantly expanded, providing a large collection of different commercial systems for the identification of *Staphylococci* as an alternative to biochemical identification methods. Automated systems and phenotypic tests are widely used today both, in microbiology laboratories. However, these diagnostic systems have some disadvantages such as their high cost. In addition, they are unable to reliably distinguish between different staphylococcal species due to the variable expression of phenotypic characteristics.

In the present discussion, the different identification methods of *Staphylococci* are reviewed.

پانل میکروبیولوژی صنعتی و محیط زیست

Evaluation of Genes and Enzymes from Microorganisms Involved in The Biodegradation Of Polyethylene-based Plastics

Faeze Hesami Zokai[1], Zahra Soleimani Dorche[1] and Sara Gharavi[2]

1. PhD Candidates in Microbial Biotechnology and 2. Associate Professor, Department of Biotechnology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran

One of the most ubiquitous and long-lasting challenges of plastic waste management is polyethylene (PE) accumulation, posing a major ecological threat to our planet. The aim of this study is to find microorganisms and enzymes involved in polyethylene biodegradation as well as the genes (and operons) from the metagenomes of these degraders.

For this purpose, soil sample from three areas with accumulation of plastic waste with different climates (dry-desert, semi-arid and temperate) were sampled. Two approaches were used: culture-based screening and functional metagenomics.

In the culture-based approach, 20 bacterial and 3 fungal isolates were identified by sequencing of 16S rDNA from bacterial genomes and ITS from fungal genomes. The presence of laccase and peroxidase enzymes in these isolates have been assayed with ABTS and Guaiacol as substrates. All isolates have shown appropriate enzyme activity for polyethylene biodegradation.

In the metagenomics-based approach, soil DNA was extracted; construction and screening of metagenomic fosmid libraries were carried out as a source of potential polyethylene degrader genes/operons and 750 out of 2600 clones tested positive through hexadecane biodegradation screening (as a model substrate). The viability and degradability potential of positive clones are presently being verified using polyethylene as the sole carbon source.

Industrial application of bio-filteration systems for treatment of waste gas streams

Seyed Mohammad Mehdi Dastgheib

Research Institute of Petroleum Industry(RIPI),West side of Azadi Complex,Tehran, Iran 1485733111

Bioprocesses for waste gas treatment have been developed as more economical alternatives to conventional, physico-chemical technologies. Major bioprocesses used nowadays for the treatment of polluted air could be categorized as biofilters, biotrickling filters, and bioscrubbers. Conventional biofilter based on an organic packed bed, has been used for several decades for the removal of odors, mainly at wastewater treatment plants and composting facilities. Due to some drawbacks, research on biotrickling filters (BTFs) using artificial packings and circulating nutrient solution, started in the 1980s, mainly in Central-Western European countries. Nowadays, BTFs have become quite popular for removal of VOC and sulfur-containing pollutants from industrial waste gases.
In a recent project in Iran, a bio-filtration process was exploited to treat soil vapors extracted from an industrial contaminated underground-water. Reactor working volume was 5000 liter packed with Polypropylene Pall-ring (2 inch) Packing with a nutrient tank capacity of 500 liter. The maximum inlet air flow rate was 150 m3 /h with 1000 ppm ethylbenzene as the main pollutant, and following the biofilm formation removal efficiency of around 90 % was achieved. The results showed good and robust performance of the biotrickling filters and promise operational applications of these systems in various industries.
New researches are now focused on operational problems of BTFs such as clogging problems, due to excess biomass or elemental sulfur accumulation on the packing material.

KEYWORDS: *Biotrickling filter, Biofilter, Pall ring, Biofilm, Compost, VOC*

Microbiology of Ancient and Art Works

Parisa Mohammadi, Associate Professor

Department of Microbiology, Faculty of Biological Sciences, Alzahra University, I.R.Iran

The microorganisms are ubiquitous and can be found on many natural or synthetic materials which was used in field of art works, ancient monuments and cultural heritage subjects. In the last forty years, our understanding of the interaction between microorganism and different materials has significantly advanced because of increasing developments in scientific methodologies and awareness of a requirement for systematic research strategies via multidisciplinary groups. Thereinafter, the word of biodeterioration was entered into the scientific literary in 1965 which defined as the attack on natural and manmade materials through the growth and activities of living organisms by Hueck. A wide variety of microorganisms, including bacteria, archaea, fungi, algae, lichens as well as other macroorganisms such as mosses, liverworts, insects, invertebrates, bird, mammals, and plants through different physico-chemical mechanisms involve in the biodeterioration phenomenon. The part of the science which pays to discovery the involved microorganisms in the biodeterioration and to know their deteriorative mechanisms named “Microbiology of Ancient and Art Works”, which is a novel branch of the microbiology. This innovative aspect of microbiology placed their hands into the restorators and conservators of ancient monuments and art works to carry out more efficient and prolonged restoration and conservation. The consequence of this interdisciplinary collaborative activities help the restorators and conservators to mitigate, not only the cost of prevention, restoration and renovation significantly, but they organize more efficient works.

پانل میکروبیولوژی غذایی

Detection of Shiga-like toxin producing bacteria in foodstuff and human stool samples: Toward next-generation food microbiology techniques

Dr. Masoud Alebouyeh

Foodborne and Waterborne Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Shiga toxin-producing bacteria are considered as main cause of bloody or non-bloody diarrhea. They can produce a life threatening disease known as hemolytic-uremic syndrome (HUS). While *Shigella dysenteriae* serotype 1 is the most notable bacteria that produce this toxin, other members of Enterobacteriacea, such as Shiga toxin-producing *Escherichia coli* (STEC), and enterohemorrhagic *E. coli* (EHEC), as well as *Citrobacter*, *Enterobacter*, *Acinetobacter*, *Aeromonas, and Campylobacter spp., also could carry different stx genes and their variants* (*stx1* and/or *stx2*). Cooperation of Shiga toxins (Stx) with other virulence factors, such as aggregative adhesin and intimin (EAE), could induce more severe diseases in the infected patients. The *stx* genes are encoded in the genome of heterogeneous lambdoid bacteriophages and can inherit in other bacteria during horizontal gene transfer. High distribution of *stx* genes in farm or wild animals, wastewater and the terrestrial and aquatic environments proposes possible involvement of different bacterial species carrying these genes in the occurrence of *stx*-related diseases during water- and food-borne diseases and outbreaks. Prompt laboratory diagnosis of these pathogens could be effective in outbreak responses and control measures. In this presentation, we review prevalence of *stx*-encoding bacteria and methods of their detection in foodstuff and diarrheal stool samples.

Microbiology Laboratory in the future

Nahid Rahimifard, *Department of Microbiology, Food and Drug Control Laboratories(FDCL), Food And Drug Laboratories Research Center(FDLRC); Ministry of Health(MOH), Iran.*

Corresponding author: Nahid Rahimifard ;PhD*

Associate Professor in Microbiology;

Doctorate in Medical Diagnostic Laboratory Sciences

ABSTRACT

During the last decades, the prevalence of foodborne diseases due to contaminated food as well as demand for natural and healthy foods has increased. Standard methods or Gold standard methods in Microbiology laboratory are still the routine culture methods. Rapid diagnostic in food microbiological control laboratories for this purpose and for inhibiting growth of food pathogens is an interesting topic.

Some instrumental new methods such as TEMPO, Scan RDI AES, Mycometer, 3M molecular detection assay, BAX, Bio Tecon Diagnostics (Real time PCR), Solus, Gene Quence, VIDAS(Vitec2), Duopath Merck, Sylab's, Riboflow, Neogen,Remel.have been replaced with the routine methods due to having high analytical characteristics of assays such as sensitivity, specificity, precision, accuracy and uncertainty beside of the feasibility and time consuming.So Microbiology laboratory major changes won't be avoidable in the near future and we should accept this real necessity.

Keywords: Microbiology laboratory, food control, future

The effect of psychrotrophic bacteria on the quality of raw milk and pasteurized and sterilized dairy products

Shahriar Dabirian[1], Najmeh Sabahi Mohammadi[2], Zahra Iranmanesh[3], Azam Asgarpour[4]

1- Ph.D. of food hygienic and quality assurance of Iran Dairy Industries
2- Ph.D. candidate of food microbiology and quality control manager of West azarbayjan Pegah Dairy Company
3- Quality control manager of Kerman Pegah Dairy Company
4- Quality control expert of Kerman Pegah Dairy Company

Abstract

In the past, microorganisms that could grow at refrigerater temperatures were located in the group of Psychrophils, and this term was used for organisms that grow from minus temperatures to 20 ° Celsius, and the optimum growth temperature was considered 15 ° Celsius. By accepting this definition, a large number of microorganisms that were able to grow at a temperature higher than 20 ° C but actually caused food spoilage at a refrigerator temperature (0 ° C to 7 ° C) were effectively abandoned. Therefore, the word "psychrotroph" was suggested for microorganisms that could grow at 0 to 7° Celsius and create visible colonies within 7 to 10 days. In our country, pscycrotrophic bacteria have become an important challenge in the dairy industries, and by producing heatresistant lipolytic and proteolytic enzymes, they play an important role in reducing the quality and degradation of pasteurized and sterilized products. Also pathogenic bacteria such as Listeria and Bacillus cereus are also included in this category. There are several reasons for increasing the number of pscycrotrophic colonies in raw milk, most notably, the rinsing lack of equipment, completely, after each use or neglecting the disinfection of equipment before use in livestock farms. Also Long-term storage at temperatures above 4 ° C due to the absence of a tank cooling system or it's inadequacy, the low speed of reducing the raw milk temperature in the bulk tank of the livestock or keeping the raw milk in inappropriate conditions in the storage tanks of the plants, can increase the number of psychrotrophic bacteria. In a study conducted in Kerman province (May 2018), on the rate of bacterial growth in industrial livestock, it was determined that the average number of psychrotrophic bacteria in the livestocks which deliver the raw milk to the plant immediately after milking and cooling was less than 100 cfu/ml while in the livestocks which keep the raw milk cold and then transfer to the plant the average number of psychrotrophic bacteria was more than 15000 cfu/ml. The aim of this study was to determine the importance of the number of psychrotrophic bacteria in raw milk and its effect on the quality of pasteurized and sterilized products.

Key words

Psychrotrophic bacteria, raw milk, pasteurized and sterilized products

Evaluation of microbial contamination of Season Salads in URMIA food and drug control lab (during years of 2017-2018)

Dr. Amir Rahimirad*[1], Dr. Gallal Ghaffarzadeh[2] and Maryam Abbasi ghaznag[1]1- Urmia food and drug control lab, Food and Drug Assistance, Urmia Medical University
2- Food and Drug Assistance, Urmia Medical University

For this purpose, in this article has been evaluated microbial quality of Season Salads which are distributed in restaurants of Western Azarbaijan province of Iran.
Aim of this paper is of Checking of food products safety level consumed by population and Improving of food products safety level by assumption of true solutions.

Samples were collected in completely sterile condition from this province's restaurants and transferred to the microbiological laboratory of Urmia food and drug control lab. All microbiological analyses were performed based on microbiological order of food and drug organization and in the mentioned manners of ISIRI (Iranian National Standards Organization).
Samples were evaluated from the point of contamination by Escherichia, Enterococcus, Molds, Listeria monocytogenes, Salmonella species, Staphylococcus aureus, Yersinia enterocolitica and determination of Total count contamination levels.

From 52 of Salads samples, 33 cases of them were not in accordance with national microbiological order of Iranian Food and Drug Organization from point of view of contamination by Escherichia, Enterococcus, Molds and high levels of Total count contamination.

From inspection of results, we can conclude the situation in case of restaurant salads in Western Azarbaijan province of Iran from point of microbial contamination needs much attention of producers and food authorities for obtaining better results.

Keywords: Microbial contamination, Season salads and West Azarbaijan Province.

Early Detection of Diagnostic Markers Of Measles For Better Management And Control Of Infection

G. Fatima, Shahana Urooj Kazmi
Civil Hospital and Dadabhoy Institute of Higher Education ., Karachi, Pakistan

Abstract
Measles is a highly infectious and contagious viral disease which affects the respiratory system caused by a single-stranded, enveloped RNA paramyxovirus of the genus Morbillivirus. Measles is an endemic disease in many countries of the world including Pakistan, mostly affecting children under 14 years of age. Measles is a droplet infection so the disease is spread to others through contact with fluids from an infected person's nose and mouth, either directly or through aerosol transmission. Overcrowding and improper ventilation are major predisposing factors in its spread, 90% of people without immunity sharing a house with an infected person will catch it. The classical symptoms of measles include four day fevers, the three Cs—cough, coryza (runny nose) and conjunctivitis (red eyes). The fever may reach up to 40C (1040F). Koplik's spots seen inside the mouth are diagnostic, they are transient and may disappear within a day of arising. The characteristic measles rash is classically described as a generalized, maculopapular, erythematous rash that begins several days after the fever starts. It starts on the head before spreading to cover most of the body, often causing itching. The rash is said to "stain", changing colour from red to dark brown, before disappearing. The consequences of infection with measles virus are recovery, chronicity or death. Although most patients survive, but approximately 15 percent of patients experience complications, mild, or severe such as subacute sclerosing panencephalitis (SSPE) which is fatal. Laboratory diagnosis of measles can be done with confirmation of positive measles IgM antibodies, or detection of Measles virus RNA by PCR from respiratory specimens. Fortunately the vaccine against measles is available and is included in the EPI (expanded program of immunization. This study was designed to know the best laboratory diagnostic test for early diagnosis of measles virus infection to facilitate better management of disease and prevention of its complications like Pneumonia and fever and typical symptoms of measles (running nose, conjunctivitis and rashes), between the age of 2-12 years, visiting Pediatric units of Civil Hospital, Karachi, were included in this study. Demographic data including age, gender, socioeconomic status, especially vaccination against measles and duration of fever were recorded. A total of 106 clinically diagnosed cases of measles were included. Out of 106 blood samples of patients , 48 (45.3%) children exhibited measles specific IgM antibodies . Among measles positive children, 18 children had received measles vaccination. Among the vaccinated group of 18 children, only 6 (33.3%) were positive for measles IgM, while among the unvaccinated group 42(47.7%) tested positive for measles specific IgM, All measles specific IgM positive children (N=48) had history of fever for three days and more while others had fever of less than three days. Females (52%) were affected slightly more than males .Measles virus RNA was detected in all 106 samples of nasal secretions. Genotype analysis indicated Measles virus genotype B2 as the most prominent causative strain. In conclusion we can say that Anti-Measles IgM test can be used for early diagnosis of measles after three days of onset of fever for better management , negative test does not exclude measles. Measles virus RNA can be detected in nasal secretion irrespective of duration of fever. Measles infection in vaccinated children reflects on the efficacy of vaccines in Pakistan. The poor quality of routine vaccination program plus lack of proper surveillance system are some of the factors responsible for the rise in measles cases in Pakistan

خلاصه مقالات پوستر
نوزدهمین کنگره بین‌المللی میکروب‌شناسی ایران

Poster

P1 - 536: OPTIMIZATION OF PHYCOCYANIN EXTRACTION FROM SPIRULINA PLATENSIS

Mina Mousavi[1], Dr Jamshid Mehrzad[2], Dr Hossain Mehrani[3]

1. Department of biochemistry Neyshabur Branch, Islamic Azad University, Neyshabur, Iran.
2. Department of biochemistry Neyshabur Branch, Islamic Azad University, Neyshabur, Iran.
3. Department of biochemistry Neyshabur Branch, Islamic Azad University, Neyshabur, Iran.

Background and Aim: Phycocyanin is a blue pigment from Arthrospira platensis which is considered as a good replacement for artificial blue pigment. It is widely used in European countries and in China in different ways as additives in food, cosmetic, therapeutic and as fluorescent pigment. Since Phycocyanin is as intracellular pigment, it should be extracted from cells.

Methods: To find the best method for breaking cell wall, we surveyed various methods such as the ultrasonic bath, probe ultrasonic, and freezing in two temperatures (-20˚C and -80˚C) and thawing in room temperature. Furthermore, we analyzed the effect of the number of repeated freeze-thaw cycles under -20˚C, followed by evaluating the ratio of biomass to buffer (Britton Robinson Buffer, pH 5) in 1:6, 1:8, 1:10, 1:12 and 1:14

Results: The results show that probe ultrasonic can significantly lysis the cell wall so chlorophyll which is placed in the membrane release in crude extract, leading to the reduction of Phycocyanin purity. The most purity is observed in freeze thaw method by freezing at -20˚C. While fifth times freeze- thaw increase the yield of the phycocyanin production, the purity ratio (A620/A280) decreases after the forth times. The best ratio of biomass to buffer was determined 1:10 which extracted the highest amount of phycocyanin 300 mg/ml.

Conclusion: The optimum condition for extraction is the freeze -thaw method under -20 °C condition in the fourth repeated cycles. The optimal ratio of algal biomass and solvent was one to ten.

Keywords: Phycocyanin, ultrasonic, freeze-thaw method

P2 - 537: COMPARISON OF DIFFERENT SOLVENTS TO EXTRACT PHYCOCYANIN FROM ARTHROSPIRA PLATENSIS

Mina Mousavi[1], Dr Jamshid Mehrzad[2], Dr Hossain Mehrani[3]

1. Department of biochemistry Neyshabur Branch, Islamic Azad University, Neyshabur, Iran.
2. Department of biochemistry Neyshabur Branch, Islamic Azad University, Neyshabur, Iran.
3. Department of biochemistry Neyshabur Branch, Islamic Azad University, Neyshabur, Iran.

Background and Aim: Arthrospira platensis, commonly named as spirulina, is a cyanobacteria which is well-known as a food supplement due to a high content of essential amino

acids, fatty acids, vitamins and minerals. It also contains the blue pigment, called C-Phycocyanin(C-PC). C-PC has demonstrated some therapeutic properties (anti-cancer, anti-diabetic, heart protective). It is also a good replacement for artificial (synthetics) colors in confectionary and drinks industry. Several methods have been proposed for the extraction and purification of C-PC. Yet, less is known about the most efficient phycocyanin extraction technique. The aim of this study was to examine the effect of different solvent in phycocyanin extraction.

Methods: Spirulina biomass was suspended in different salts solutions such as (FeSO4, NaH2PO4, CH_3COONa, CaCl2, MgSO4, Nacl), Glycerol solution, acidic solusion such as (Citric acid, Boric acid) in two concentrations of 0.1M and 0.5M, buffers (GTE, Britton Robinson, Sodium Acetate), and Distilled water. They were frozen and thaw three times, and their absorbance was measured at 280, 650 and 652 nm.

Results: Purity ratio calculated by A620/A280. The results show that FeSO4 has the highest purity (4.5) while purity of other salt solutions were less than 2. The highest yield, around 6 with the purity of 1, is recorded for water, compared to MgSO4 0.5 M and NaH2PO4, Glycerol and Cacl2 0.5 M indicating a lower yield.

Conclusion: The findings show that the proper extraction method is FeSO4 0.1M, leading to the highest purity ratio, approximately 4.5 with the yield of 3.

Keywords: Phycocyanin, ultrasonic, buffers, Salt solution

Antimicrobial agents and Resistance

P3 - 1: ANTIBACTERIAL EFFECTS OF METHANOL EXTRACT OF DIFFERENT PARTS OF QUERCUS PERSICA AGAINST MRSA AND MSSA CLINICAL ISOLATES

Behnam Hajizadeh sisakht[1], Ashraf Kariminik[2]

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

Background and Aim: Anti-bacterial treatment through drugs and antibiotics, along with the rapid development of drug resistance has been associated with. Study on antibacterial activity and herbal extracts have shown that plants have provided potential sources of antimicrobial agents.

Methods: The present study describes the anti-bacterial activity of methanol extract of Querqus persica (fruit and fruit hull) from Fagaceae family on 20 methicillin resistant and 20 methicillin sensitive Staphylococcus aureus isolates. Methanol extracts were prepared by maceration method, filtered and concentrated by rotary evaporator apparatus. Different concentration of each extract were prepared in dimethyl sulfoxide: methanol (1:1 v/v) and antibiogrammed on the isolates by agar well diffusion method. Plates were incubated in 37˚C for 24 hours and zone of inhibition was measured in millimeter.

Results: According to antibiogram test, all of Staphylococcus aureus isolates were sensitive to the used extract with different MIC. 80 mg/ml concentration of Fruit methanol extract was effective on all MRSA isolates with zone of inhibition 16-20 mm. MIC value of Fruit methanol extract was 0.3mg/ml. 80 mg/ml concentration of Hull Fruit methanol extract was effective on all MRSA isolates with zone of inhibition 14-18 mm. MIC value of hull fruit methanol extract was 0.3mg/ml.

Conclusion: According to the obtained results, we expect to be able to use the extracts against Staphylococcus aureus resistant to meticillin in controling the infections or as preservatives in food sciences and in the next step separating of effective substances were suggested.

Keywords: Staphylococcus aureus, Antibacterial, Methicillin, Resistant

P4 - 2: OCCURRENCE OF BLA GENES ENCODING CARBAPENEM-RESISTANT ACINETOBACTER BAUMANNII FROM INTENSIVE CARE UNIT

Zahra Moulana[1], Mehran Shokri[2], Zohreh Eslamdost[3]

1. Babol Uni of Med Sci
2. Infectious Diseases and Tropical Medicine Research Center, Babol University of Medical Sciences, Babol, Iran
3. Department of Microbiology, Yahyanejad Hospital, Babol University of Medical Sciences, Babol, Iran

Background and Aim: The spread of carbapenem-resistant Acinetobacter baumannii is a global concern. Metallo-beta-lactamase (MBL) enzymes cause extensive drug resistance among Gram-negative bacteria. The aim of this study was to investigate the prevalence of metallo β-lactamase (MBL) genes (bla VIM , and blaIMP) among isolated multidrug-resistant A. baumannii.

Methods:A total of 50 non repetitive carbapenem-resistant A. baumannii were collected from different clinical specimens.Antibiotic susceptibility was done by disk diffusion method. MICs were determined by E test method. The resistant strains were detected for the production of carbapenemases by Modified Hodge Test (MHT) followed by EDTA-disk synergy test was performed for metallo-β-lactamases (MBL) phenotypic detection. Detection of bla VIM , and blaIMP was performed by PCR followed by sequencing.

Results: All isolates had a multidrug resistant profile, but remainded susceptible to colistin. Among these isolates, Carbapenemase production was confirmed by Modified Hodge test for 42 (84%) isolates. Phenotypic method showed productions of MBL in 15(30%) isolates. Searching for MBLs genes in all the isolates showed that 13 (26%) were positive for blaVIM and all of them were negative for blaIMP.

Conclusion: Our study concludes that high prevalence of carbapenem resistant Acinetobacter species with MBL production is oneof the main concerns in our country and this situation which needs strict infection control measures.

Keywords: Acinetobacter baumannii, Carbapenem Resistance,Metallo-beta- Lactamases,Modified Hodge Test.

P5 - 4: META-ANALYSIS STUDY FOR ANTIBIOTIC RESISTANCE OF CITROBACTER FREUNDII CLINICAL ISOLATES

Abozar Kerami[1], Abouzar Kerami[2], Arman Rostamzad[3], Mehdi omidi[4]

1. University of Ilam, , Basic Science Factuly, Department of Microbiology , University of Ilam , Ilam, Iran
2. University of Ilam, , Basic Science Factuly, Department of Microbiology , University of Ilam , Ilam, Iran
3. University of Ilam, , Basic Science Factuly,Department of Mathematics ,University of Ilam , Ilam, Iran

Background and Aim: Citrobacter freundii causes opportunistic infections in hospitalized patients, especially in intensive care units (ICUs). The prevalence of antibiotic resistant Citrobacter freundii is increasing in world, and this may cause significant clinical problems.

Methods:this study aimed to evaluate the rate of antibiotic resistance of Citrobacter freundii using meta-analysis. Eight qualified antibiotic were analyzed by using random effects model Meta-analysis method and with the software STATA Ver.12.0.

Results: The highest and lowest resistances were found against piperacillin and imipenem, respectively. This study showed that Citrobacter freundii strains shave resistance to a wide range of antimicrobial agents.

Conclusion: According to the importance of these bacteria in nosocomial infections particularly in intensive care units, it is necessary to apply appropriate strategies to control the spread of C.freundii

Keywords: Citrobacter freundii; Antibiotic resistance; Nosocomial Pathogen

P6 - 7: EVALUATION OF THE PRODUCTION RATE OF EXTENDED-SPECTRUM BETA-LACTAMASE ENZYMES BY GRAM-NEGATIVE BACTERIA IN DIFFERENT CLINICAL SAMPLES ISOLATED FROM PATIENTS

Samaneh Rouhi[1], Somayeh Ghavami[2], Fariba Bedroodiani[3], Saeed Salavati[4], Maria Abbasi[5], Saba Asadollahi [6]

1. Student Research Committee, Kurdistan University of Medical Sciences, Sanandaj, Iran. Cellular &Molecular Research Center, Kurdistan University of Medical, Sanandaj, Iran.
2. Student Research Committee, Kurdistan University of Medical Sciences, Sanandaj, Iran.
3. Toohid Hospital, Kurdistan University of Medical Sciences, Sanandaj, Iran.
4. Cellular &Molecular Research Center, Kurdistan University of Medical, Sanandaj, Iran.
5. Toohid Hospital, Kurdistan University of Medical Sciences, Sanandaj, Iran.
6. Student Research Committee, Department of Microbiology, School of Medicine, Kermanshah University of Medical Sciences, Kermanshah, Iran

Background and Aim: Treatment of infections depends on the sensitivity of these bacteria to antibiotic drugs. Therefore, the aim of this study was to detect the production rate of ESBL enzymes by bacteria from clinical samples isolated from patients.

Methods: This descriptive- cross-sectional study was conducted during a one-month period in March, 2017. The study population included all clinical samples isolated from Toohid Medical Center, Sanandaj, Kurdistan province, Iran.. Combined disk method using 30µg of ceftoxime and cefotaxime30µg/clavulanic acid 10 µg was used to detect strains producing ESBL enzymes in different bacteria. According to the CLSI, if the growth halo around the cefotaxime/ clavulanic acid was ≥5 mm apart than cefotaxime alone, the strain is considered to be an enzyme producer. Data were analyzed by SPSS16 and frequency and ANOVA method ($p<0.05$).

Results: Thirty seven clinical specimens, including bacteria producing ESBL enzymes, were observed. Of these, 31 (83.78%) were urinary culture. The bacteria producing the enzyme isolated from urine culture included 5 Klebsiella genus (16.12%) and 26 (83.87%) of Escherichia coli strains. Of 4 cases of lung secretion, 3 (75%) Klebsiella genus and 1 (25%) Acinetobacter genus was isolate. Of the two collected ulcers specimens, all 2 (100%) samples, including Klebsiella genus and producing ESBL. Also 6/37 (16.21%) samples were isolated from patients with nosocomial infections. There was no significant relationship between the production of this enzyme and the type of sample ($p> 0.05$).

Conclusion: The prevalence ESBL-producing bacteria in patients with were observed. Appropriate methods to prevent of this problem should be considered.

Keywords: Extended-spectrum beta-lactamase, gram-negative bacteria, clinical samples, patients

P7 - 8: DETECTION OF MECA GENE AMONG METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS ISOLATED FROM BLOOD INFECTION

Ali Javadi[1], Razieh Mohamadzadeh[2]

1. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran.
2. Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran.

Background and Aim:methicillin resistant staphylococcus aureus is one of the main agents rising significantly in both hospital and community acquired infections. The aim of this study was to analyze the prevalence of the MRSA among Bloodstream infection in Qom hospitals and determinative the antibiotic resistance of the isolates.

Methods: During three years (2013-2015) S.aureus was isolated from bloodstream infected patients at Qom Hospitals and their antibiotic susceptibility pattern to different antibiotics were determined. Finally, using PCR, the methicillin resistant isolates were tested for the presence of mecA gene.

Results: In this study, a total of 500 blood samples, 140 (28%) isolates were S.aureus, 48 (34.28%) were found resistant to cefoxitin disk, according to CLSI and mecA gene was detected in 48 strains (34.28%). Our study results showed that the agar screen technique like PCR is a reliable in determining of MRSA strains.

Conclusion: In this study, we found high prevalence of MRSA and the mecA is widespread in S. aureus strains isolated at Qom hospital.

Keywords: Bloodstreem infection, S.aureus, MRSA , mecA

P8 - 21: EVALUATION OF DRUG RESISTANCE PATTERN OF CANDIDA ALBICANS ISOLATED FROM DIFFERENT CLINICAL SPECIMENS IN QOM, 1396-1395

Farzaneh zarineghbal[1], Mohamad dakhili[2], Ali javadi[3]

1. Department of Microbiology, Islamic Azad University, Qom, Iran
2. Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran.
3. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran.

Background and Aim: Candida albicans is a single-celled yeast with sprout, or pseudohife or actual mycelium. This organism exists in the oral, vaginal, and digestive system mucosa of human as commensal. This yeast is an opportunistic pathogen which can cause development of diseases in different individuals, especially in individuals with immunodeficiency. Treatments expose to several problems including multi-drug resistance and virulence factors such as conjugation factors. The aim of this study was to evaluate the prevalence of Candida albicans in isolated clinical samples and the antifungal susceptibility pattern of separated isolates.

Methods: Separation and identification of Candida albicans was conducted from 400 suspected cases. Disc diffusion tests were performed to isolate the nystatin and fluconazole isolates according to CLSI standards.

Results:90 samples (22.5%) were positive in terms of Candida albicans. In this study, 56 samples (62.2%) were fluconazole-resistant and 34 cases (37.8%) were fluconazole-susceptible. In this study, 4 samples (4.4%) were nystatin resistant and 86 samples (95.6%) were nystatin susceptible

Conclusion: Candida infection is a serious and major problem in today societies, both in people with immune deficiencies and people with immune competence, hence nowadays Candida albicans is considered as one of the important pathogens and having information on its prevalence and drug resistance is important

Keywords: Candida albicans ,clinical specimens ,nystatin,fluconazole

P9 - 31: EVALUATION OF ANTIBACTERIAL EFFECTS OF NEUTRAL ELECTROLYZED WATER ON MULTI-DRUG RESISTANT PSEUDOMONAS AERUGINOSA STRAINS ISOLATED FROM PATIENTS IN GOLESTAN PROVINCE

Shamim Mahmoudjanloo[1], Leila Fozouni[2]

1. Department of Biology, Gorgan Branch, Islamic Azad University, Gorgan, Iran
2. Department of Biology, Gorgan Branch, Islamic Azad University, Gorgan, Iran

Background and Aim: Pseudomonas aeruginosa is an opportunistic bacterium and is one of the main causes of infection in burn patients.This study aims to determine the antibacterial effects of Neutral Electrolyzed Water(NEW) on the growth of multi-drug resistant strains of Pseudomonas aeruginosa.

Methods: This descriptive study was carried out on 90 patients that hospitalized in Golestan province Hospitals .Diagnosis tests were used to separate Pseudomonas aeruginosa, and disk diffusion agar method with the Kirby-Bauer standard was applied to determine the pattern of drug-resistance To prepare the Neutral Electrolysis water,sterilized deionized water was mixed with Nacl, hypochlorous acid and sodium hypochlorite and then passed through anode and cathode electrodes after PH=7 confirmation. To determine the NEW antimicrobial properties, sterilized applicators were separately infused with bacterial suspensions , each immersed in a sterile tube filled with NEW at a temperatures of 25 ° C and 37° C.

Results: In this study, 34.5% strains were diagnosed as Pseudomonas aeruginosa, out of which 87.09% showed resistance to Ceftazidime, 80.65% to Tobramycin & Cefepime, 77.41% to Gentamicin , 70.98% to Piperacillin and 70.96% to Norfloxacin. Antimicrobial properties of NEW revealed that 86% of resistant isolates and 100% of Sensetive isolates to antibiotics did not grow near NEW. In this study no considerable difference was seen between different temperatures($P<0.05$).

Conclusion: The results of this study showed that the spread of P.aeruginosa resistant to agents is very high in hospitals, and Neutral Electrolyzed Water proved anti-bacterial effects. Therefore it can be considered for prevention and cure of Burn Wound Infection in the future.

Keywords: Pseudomonas aeruginosa, Drug resistance, Neutral Electrolyzed Water

P10 - 49: PANTON- VALENTIN LEUKOCIDIN AND MECA IN METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS (MRSA) ISOLATES FROM HOSPITALIZED PATIENTS IN RASHT, IRAN

Houra Pourghafar[1], Nour Amirmozafari[2], Masoumeh Anvari[3]

1. Department of Microbiology, Shiraz Branch, Islamic Azad University, Shiraz, Iran
2. Department of Microbiology, Faculty of Medicine, Iran University of Medical Science and Health Services, Tehran, Iran
3. Department of Microbiology, Rasht Branch, Islamic Azad University, Rasht, Iran

Background and Aim: Panton-Valentine Leukocidin (PVL) producing strains of Staphylococcus aureus have a high virulence and are after accompanied with skin abscesses and acute necrosis. mecA is integrated into the orfx gene cassette in the S. aureus chromosome. The aim of this study was to investigate the prevalence of pvl gene and its relationship with mecA in isolated from hospitalized patients in Rasht, northern Iran.

Methods: During a six-month period, a total of 93 clinical isolates of staphylococcus were obtained. Initial tests were performed by use of Disk Diffusion method. Resistance to Methicillin was determined by Oxacillin disk and the prevalence of was conducted by PCR on chromosomal DNA. The pvl positive isolates were further analyzed for the presence of mecA genes by use of specific primers in PCR.

Results: Totally, 18 isolates (19.56%) were positive for pvl gene, and among them 15 isolates (83.33%) were MRSA, 3 (16.66) were MSSA and 8 (44.44%) were positive for mecA gene. 9 were obtained from wound specimens, 3 from urine 3 from body fluid, 2 from blood, and 1 from splinter spent.

Conclusion: That the majority of pvl positive isolates were MRSA and almost half of them had mecA gene, it can be postulated that there is a significant relationship between these two traits.

Keywords:MRSA, Panton Valentine Leucocidin (PVL), Methicillin, mecA.

P11 - 52: IDENTIFICATION OF KPC BETA-LACTAMASE GENE IN KLEBSIELLA PNEUMONIA ISOLATES ISOLATED FROM PULMONARY SECRETIONS

Samira Mohammadi[1], Ali Javadi[2]

1. Department of Microbiology, Islamic Azad University, Qom, Iran
2. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran.

Background and Aim: Klebsiella pneumoniae is an important human pathogen which has been considered due to the development of resistant infections in hospitals. The Multiple drug resistance, especially in urinary tract infections, has led to development of several problems. The aim of this study was to determine the prevalence of KPC β-lactamase in Klebsiella pneumonia isolates isolated from patients with pulmonary infections in Qom.

Methods: This cross-sectional study was performed on 200 pulmonary samples obtained from hospitalized patients and outpatients during a one-year period. Diagnosis was done using biochemical methods. Antibiotic susceptibility was evaluated by disc diffusion method based on CLSI2013 criteria. PCR was used for identification and amplification of blaKPC genes in Klebsiella pneumoniae isolates.

Results: Among 200 cultured pulmonary samples, 30 samples of Klebsiella pneumoniae were isolated. Isolates were resistant to more than three classes of antibiotics. The results of antibiotic resistance analysis of isolates showed that the highest resistance was obtained against trimethoprim with a resistance of 47.98%, cefalotin with 59.53% and nalidixic acid with 79.43%; however, the highest sensitivity was obtained against amikacin with 90.95% and meropenem with 37.83% and imipenemt with 62.81% respectively. The results of PCR showed that among 30 Klebsiella pneumonia, 10 isolates (33.33%) contained blaKPC gene.

Conclusion: The blaKPC enzyme is one of the most common β-lactamase enzymes. Optimization of the use of anti-microbial agents in order to control the infection and also in order to prevent increase in the population of two or three antibiotics resistant bacteria is strongly important.

Keywords:KPC beta-lactamase gene,Klebsiella pneumonia,pulmonary secretions

P12 - 53: INVESTIGATION OF THE PRESENCE OF EXOTOXIN S IN PSEUDOMONAS AERUGINOSA WITH BROAD-SPECTRUM BETA-LACTAMASE

Samira Mohammadi[1], Alireza Shahvarooghi[2], Ali Javadi[3]

1. Department of Microbiology, Islamic Azad University, Qom, Iran
2. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran.

Background and Aim: Pseudomonas aeruginosa is one of the important pathogens in hospitals. T3SS is a determining factor in the pathogenesis of Pseudomonas aeruginosa and is directly associated to the human infections. The aim of this study was to investigate the association between antibiotic resistance and the ability of bacteria to produce exo-enzyme S.

Methods: In this study, 100 clinical isolates including 50 ESBL + isolates were studied. In order to demonstrate the presence of ESBL enzymes, a disk diffusion method was used on the Muller Agar media. Ceftazidime / Ceftazidime clavulanic acid and cefotaxime / cefotaxime clavulanic acid were used for this purpose. In the following, the presence of exoS genes was investigated using PCR method.

Results: The obtained results showed the presence of exo-enzyme S in most clinical isolates with more antibiotic resistance pattern. The presence of exoS enzyme was obtained as 62.8%. Clinical isolates with ESBLs showed higher capability for production of Exoenzyme S.

Conclusion: Establishment of secretion System type 3 among clinical isolates of Pseudomonas aeruginosa is an important factor in the development of human diseases. The results of our study indicate the activity of T3S among the majority of clinical isolates. However, further studies are required to determine the relationship between the production of each exogenous species and the type of infection, and as a result, demonstrating the role of T3S in the infection of of Pseudomonas aeruginosa is necessary.

Keywords: Exotoxin S, Pseudomonas aeruginosa ,ESBLs

P13 - 58: EVALUATION OF ANTIBIOTIC RESISTANCE PATTERN AND EFFICACY OF MODIFIED HODGE TEST FOR DETECTION OF CARBAPENEM-RESISTANT KLEBSIELLA PNEUMONIAE STRAINS ISOLATED FROM CLINICAL SAMPLES.

Leila Gheitani[1], hossein fazeli[2]

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

Background and Aim: Klebsiella pneumoniae is a gram negative opportunistic pathogen that causes different infections, but in recent years the emergence of resistance to carbapenem antibiotic among these isolates causes failure in the treatment of these infections. The aim of this study was to evaluate the prevalence of carbapenemase producing Klebsiella pneumoniae strains among different wards and various clinical specimens in Isfahan.

Methods: In this cross sectional study, 100 different clinical samples were collected from different wards of teaching hospitals in Isfahan. K. pneumonia isolates were identified by different standard biochemical tests. Antimicrobial susceptibility tests were performed as standard disk-diffusion based on the instructions of Clinical Laboratory Standards Institute (CLSI). For detection of KPC-producing strains, isolates were investigated by The Modified Hodge Test based on CLSI instruction.

Results: The population study was included 62% females and 38% males (p=0.01). The highest and the lowest rate of resistance were observed for piperacillin (84%) and ertapenem (50%) respectively. The Modified Hodge Test was positive for 68 (68%) isolates that the highest rate of resistance was observed for piperacillin (91/2%) and cefotaxime (83/8%)

Conclusion: This study demonstrates the high prevalence of carbapenemase producing Klebsiella pneumoniae isolates ,Which shows an urgent need to review and modify the pattern of antibiotic consumption. In addition, In the later studies genotypic methods for all carbapenemase genes should be performed to determine the cause of the resistance

Keywords: Klebsiella pneumoniae, Carbapenemase, Modified Hodge Test

P14 - 59: PREVALENCE OF CARBAPENEMASE AND BLAKPC GENE IN KLEBSIELLA PNEUMONIAE STRAINS ISOLATED FROM ISFAHAN HOSPITALS, IRAN

Leila Gheitani[1], hossein fazeli[2]

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

Background and Aim: Klebsiella pneumoniae is a Gram-negative opportunistic pathogen. The carbapenems are effective therapeutic choice for the treatment of Klebsiella pneumonia infections. Carbapenemases are a group of enzymes capable of hydrolyzing carbapenems. This study was to introduce phenotypic and genotypic methods to identify the carbapenemase-producing isolates of Klebsiella pneumoniae.

Methods:this study was to introduce phenotypic and genotypic methods to identify the carbapenemase-producing isolates of Klebsiella pneumoniae. The Modified Hodge Test (MHT) was performed to determine the susceptibility of isolates to antibiotics. The final products of PCR were electrophoresed on agarose gel.

Results: The highest rate of resistance were observed for piperacillin (84%) and the lowest for ertapenem (50%). The majority of MHT positive isolates was from urine (64.7%), while abdominal and cerebrospinal fluids (0%) were the lowest. In addition, the ICU wards with 47 (69.1%) and the emergency units with 4 (5.9%) samples, had the most and the least frequent cases, respectively. MHT was positive in 68 K. pneumoniae isolates, but none of them were positive for blaKPC gene

Conclusion: The blaKPC gene has low prevalence in the Isfahan City, Iran.

Keywords: Klebsiella pneumonia ,Carbapenemase, PCR, Prevalence

P15 - 62: EMERGENCE OF VANCOMYCIN-RESISTANT COAGULASE-NEGATIVE STAPHYLOCOCCI IN AN EDUCATIONAL AND THERAPEUTIC HOSPITAL OF SARI, IRAN

Zahra Norouzibazgir[1], Hamidreza goli[2]

1. (Corresponding author (MSc Student of Microbiology, Faculty of Medicine, Mazandaran University of Medical Sciences, Student Research Committee
2. Assistant Professor of Microbiology, Faculty of Medicine, Mazandaran University of Medical

Background and Aim: Coagulase-negative staphylococci are one of the most important opportunistic pathogens in hospitals due to increased use of medical devices. The development of the antibiotic resistance by these bacteria, especially vancomycin resistance, has become a critical problem in hospitals as well as failure in treatment. The aim of this study was to determine the prevalence of Vancomycin-resistant clinical isolates of coagulase-negative staphylococci in Bouali Sina Hospital of Sari.

Methods: The clinical specimens were collected from patients during 9 months. Using routine microbiological methods, we identified the bacteria. The antibiotic resistance pattern of the isolates was detected by the disk agar diffraction method.

Results: Out of 13322 clinical samples, 615 (4.6%) coagulase-negative strains were isolated from 155 (25.2%) males and 460 (74.8%) females. In this regard, 543 (88.2%) isolates were identified as Staphylococcus epidermidis, and 72 (11.8%) others were Staphylococcus saprophyticus. Among these, 463 (85.2%) and 53 (73.6%) urine cultures were positive for S. epidermidis and S. saprophyticus, respectively. Among the S. saprophyticus isolates, 53 (73.6%) and 11 (15.3%) of them were resistant to co-trimoxazole and gentamicin, while 242 (44.6%) and 22 (4.1%) S. epidermidis isolates were resistant to Co-trimoxazole and Vancomycin, respectively. Meanwhile, 15 (20.8%) S. saprophyticus clinical isolates were resistant to vancomycin.

Conclusion: The increasing levels of resistance to vancomycin compared to previous studies in Iran represents an important health warning in this region of the country. Therefore, it is necessary to determine an appropriate strategy for antibiotic stewardship to treat infections caused by these organisms.

Keywords: Staphylococci, Coagulase-negative, Vancomycin, Resistance

P16 - 63: PREVALENCE OF CITROBACTER FRUNDI BACTERIUM AND ANTIBIOTIC SUSCEPTIBILITY PATTERNS IN ZARREH HOSPITALIZED BURNED PATIENTS SARI, IRAN, 2017.

Zahra Norouzibazgir[1], Bahman mirzaei[2]

1. (Corresponding author (MSc Student of Microbiology, Faculty of Medicine, Mazandaran University of Medical Sciences, Student Research Committee
2. Assistant Professor of Microbiology, Faculty of Medicine, Mazandaran University of Medical

Background and Aim: Citrobacter frundi is an important causative agent of nosocomial infections. Mentioned bacterium owing to the antibiotic resistant patterns has been considered as a main concern in hospitalized patients. The prevalence of C. frundi strains in burned patients and antibiotic susceptibility patterns are the main goals in this survey.

Methods: Following the isolation and precise identification of C. frundi species taking advantage of traditional procedure such as oxidase, catalase, motility and others antibiotic susceptibility patters was performed according to the CLSI guide lines by disc diffusion procedure.

Results: Out of 3248 Clinical samples 109 (3.35%) C. frundi isolates were identified. Frequency of isolated bacterium from clinical samples were as follows: the wound (72.50%), urine (19.3%), sputum (5.5%), blood (2.8%), and trachea (0%). Susceptibility patterns indicated that, about 10.1% of isolates were susceptible against SXT and 95% of them were resistant to the mentioned antibiotic. Susceptibility and resistance patterns against amikacin virtually were equal (47.7%). Resistant pattern to the cephalexin (93.5%), SXT (87.15), Amikacin (48.62%) were determined to.

Conclusion: The findings of this study revealed that amikacin and imipenem are more effective for treatment of the C. frundi in burn patients. So, the fast and accurate evaluation of antibiotic resistance for appropriate antibiotic therapy of patients is imperative.

Keywords: Citrobacter frundi, burned patiens, Antibiotic Resistance, Bacteria

P17 - 73: INVESTIGATION OF RESISTANCE RATE TO AMINOGLYCOSIDES, BETALACTAM, FLUOROQUINOLONES AND TETRACYCLINES IN ENTEROBACTERIACEAE ISOLATES FROM TABRIZ

Elham Sheykhsaran[1], Reza Ghotaslou[2]

1. Department of Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran
2. Department of Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran

Background and Aim: Background: One of the most common Gram-negative bacteria isolated from microbiology laboratories is Enterobacteriaceae. Enterobacteriaceae have an important role in nosocomial infections, pneumoniae, and local infections after surgery and septicemia. Common treatments for Enterobacteriaceae infections are aminoglycosides, beta-lactams, fluoroquinolones and tetracyclines. This study investigated antibiotic resistance patterns in Enterobacteriaceae isolates from Hospitals of Tabriz, Iran.

Methods: Material and Methods: A total of 250 Enterobacteriaceae isolates were gathered from clinical specimens. The organisms were identified by the microscopic feature and the differential tests. The disk diffusion susceptibility testing was performed according to the Clinical and Laboratory Standards Institute (CLSI) guidelines with 20 antibiotics.

Results: Results: According to the disk diffusion agar, the highest resistance rat was observed to ampicillin (97%), cotrimoxazole (72.6%), cefazolin (69.6%), nalidixic acid (66.4%), tetracycline (58.8), ciprofloxacin (50%), aztreonam (44.8%), doxycycline (43.6%), cefepime (39.3%), gentamicin (37.2%), ceftazidime (33.2%), amoxicillin/clavulanate (29.2%), nitrofurantoin (25.6%), minocycline (24%), piperacillin/tazobactam (14.4%), amikacin (8.9%), meropenem (4%), imipenem (3.6%), fosfomycin (1.6%) and tigecycline (0.4%).

Conclusion: Discussion: According to the results of the antibiotics susceptibility patterns, indicate that the high frequency of resistance was found to some β-lactams, sulfamethoxazole, tetracycline, quinolone and aminoglycoside agents. This finding is similar to other studies from Iran. Amikacin, carbapenems, fosfomycin and tigecycline were most effective antimicrobial agents in this area.

Keywords: Enterobacteriaceae, resistance, aminoglycoside, betalactam, fluoroquinolone, tetracycline

P18 - 74: RESISTANCE RATE TO TETRACYCLINE AND RELEVANT RESISTANCE GENES, TETA, TETB, TETC AND TETD IN E.COLI ISOLATES FROM AZERBAIJAN

Elham Sheykhsaran[1], Reza Ghotaslou[2]

1. Department of Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran
2. Department of Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran

Background and Aim: Background: Escherichia coli isolates are commonly found in the gastrointestinal tract of animals and humans, and also be implicated in infectious diseases. Resistance to various antibiotic classes is widespread in E.coli isolated from animals and humans and may compromise treatment efficacy in tetracyclines.

Methods: Materials and methods: The disc diffusion agar (DDA) was used for evaluate of tetracycline susceptibility patterns. To detect four tetracycline resistance genes (tetA, tetB, tetC, tetD,), the PCR was performed in tetracycline resistant isolates.

Results: Results: In the present study, a total of 180 non-duplicated E.coli isolates were obtained from internal, pediatrics and the burn wards. Tetracycline resistance rate in target isolates were 117(65%). The Susceptible rate in E. coli isolates were as follow: 63 (35%). The rate of tet genes was found to be tetA (24.78%), tetB (31.62%), tetC (1.70%), and tetD (4.27%).

Conclusion: There is an increasing rate of tetracycline resistance among E. coli isolates in Azerbaijan. The tet genes family especially tetA and tetB were prevalent among tetracycline resistant isolates. Resistance to antibiotics has become a serious problem for the medical community and has an increased effect on patients, doctors and even the community. Studies at clinical centers largely show that antibiotics are taking longer to be effective and cause the extended hospitalization of the patients, contribute to the increase in mortality rates and are a heavy financial burden.

Keywords:E. coli, Tetracycline, tet genes

P19 - 82: DETECTION OF CLASS 1 INTEGRONS AMONG GRAM NEGATIVE BACILLI ISOLATED FROM SPUTUM CULTURES OF PATIENTS WITH RESPIRATORY SYMPTOMS REFERING TO TEACHING HOSPITALS IN AHVAZ, IRAN

Mahtab Khoshkholgh Sima[1], Mojtaba Moosavian[2], Maryam Haddadzadeh Shoushtari[3], Mohammad amin Fazeli Naserabad[4]

1. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.
2. Infectious and Tropical Diseases Research Center, Health Research Institute, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.
3. Department of Pulmonology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.
4. Razi Teaching Hospital, Clinical Research Development Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran.

Background and Aim: Diffusion of antibiotic resistance genes by horizontal gene transfer has led to the fast emergence of multidrug resistance (MDR) among bacteria. Multiple classes of integrons are effective genetic elements which play a significant role in acquisition and nosocomial dissemination of resistance factors in different Gram-negative bacteria, Pseudomonas aeruginosa (P.aeruginosa) and Acinetobacter baumannii (A. baumannii) strains.

Methods:A total of 110 sputum samples that were collected from hospitalized patients with respiratory symptoms were examined in this study. Identification of the isolates were performed by standard biochemical tests. Susceptibility test of them to seven antibiotic disks was carried out by Kirby-bauer disk diffusion method according to CLSI guidelines and finally the class 1 integron genes were detected by PCR.

Results: Maximum resistance rate for gram negative isolates was observed for Ceftazidime, Co-trimoxazole and Cefotaxime with 89% , 87% and 82% respectively. 4 P. aeruginosa (10%) , 7 A. baumannii (17%) and 2 Enterobacteriaceae (5%) were resistant to Imipenem. Out of 6 P.aeruginosa and 9 A. baumannii isolates, 2 isolates (33.3%) and 3 isolates (33.3%) were positive for class 1 Integron gene, respectively. While all Enterobacteriaceae isolates (100%) were negative for class 1 Integron gene. Class1 integrons were detected among of MDR isolates.

Conclusion: The results of this study showed that for prevention of spreading these MDR isolates, monitoring of drug resistant isolates with investigating presence of class 1 integron and antibacterial stewardship program is necessary.

Keywords: Class 1 integron, multidrug resistance, Pseudomonas aeruginosa, Acinetobacter baumannii, Enterobacteriaceae.

P20 - 84: MOLECULAR ANALYSIS OF GENES OF ESBL)SHV.TEM.CTX) IN SHIGELLA SONNEI ISOLATED FROM CLINICAL SAMPLES BY PCR

Shadi Mosadegh[1], Moradli Gh *[2]

1. Microbiology Dept., Saveh Branch, Islamic Azad University, Saveh, I.R. Iran.
2. Microbiology Dept., Saveh Branch, Islamic Azad University, Saveh, I.R. Iran.

Background and Aim: Shigella is one of the most common causes of dysentery and sometimes mortality specially in children and immunocopromised patients and the occurrence of drug resistance, makes it difficult the choice of appropriate antibiotics to treat shigellosis. The aim of this study was to define the prevalence of blaCTX-M, blaTEM and blaSHV in Shigella Sonnei isolated from patients with diarrhea by Multiplex-PCR.

Methods: In this cross-sectional study, a total of 60 Shigella Sonnei isolates of private laboratories and hospitals in Northern Tehran different ages from diarrhea samples were collected and cultured in specific environments and with biochemical and serological confirmation. To identify resistan strains t to beta test was conducted phenotypic combine disk. The presence of blaCTX-M, blaTEM and blaSHV genes was evaluated by specific primers and Multiplex-PCR.

Results: The highest frequency resistance to the antibiotics penicillin and erythromycin was 96.6% and 95%, respectively, and prevalence maximum sensitivity has been reported to ciprofloxacin and imipenem with 70%. In the Combine disk method, 29 strains (48.3%) were found positive to beta-lactamase. Among 60 isolates, 39 samples (65%) had the blaTEM gene, 28 samples (46.6%) had the blaCTX-M gene and 1 sample (1.66%) had the blaSHV gene.

Conclusion:: Given the high prevalence of beta-lactam antibiotics resistance genes in strains of Shigella Sonnei , careful medical care and proper use of antibiotics appropriate is essential and timely to prevent the spread of resistant strains is necessary.

Keywords:ESBL, Shigella Sonnei, Multiplex-PCR

P21 - 85: IDENTIFICATION OF BLACTX-M, BLASHV, AND BLATEM GENES IN PSEUDOMONAS AERUGINOSA STRAINS ISOLATED FROM HUMAN AND ANIMAL SAMPLES USING MULTIPLEX-PCR METHOD

Farzane Farzali[1], Kioumars Amini[2]

1. Microbiology Dept., Saveh Branch, Islamic Azad University, Saveh, I.R. Iran.
2. Microbiology Dept., Saveh Branch, Islamic Azad University, Saveh, I.R. Iran.

Background and Aim: Pseudomonas aeruginosa is one of the most important causes of opportunistic infections. The infection caused by P. aeruginosa is commonly severe and life-threatening and hard to treat due to limited susceptibility to antibiotics and development of resistance during treatment. The aim of the present study was to identify blaCTX-M, blaSHV, and blaTEM genes in P. aeruginosa strains isolated from human and animal samples using Multiplex-PCR method.

Methods: In this descriptive cross-sectional study, a total of 120 isolates of P. aeruginosa were obtained from of human samples and animal raw milk. Antibiotic susceptibility test was determined by gel diffusion method and according to CLSI guidelines. Cellular DNA was extracted by CinnaPure-DNA (Cell culture, Tissues, Gram-negative Bacteria and CSF) and Multiplex-PCR was performed for identification of blaCTX-M, blaSHV, and blaTEM genes.

Results: In this study, the highest resistance in human and animal samples, was seen to amoxicillin and amikacin (100%) and the lowest resistance was to ciprofloxacin with frequency of 90% in human samples and 93.4% in animal samples. Based on the CDT results, 37(60.8%) isolates showed ESBLs phenotype, and based on the M-PCR results, 26 (21.6%) and 41 (34.2%) strains had blaCTX-M and blaTEM genes, respectively.

Conclusion: The results of this study indicated that P. aeruginosa strains have high levels of resistance. Also, the frequency of these genes is high among human and animal isolates, therefore controlling these bacteria in humans and animals is of particular importance.

Keywords: Pseudomonas aeruginosa; Beta-lactamase; Antibiotic susceptibility; Drug hypersensitivity.

P22 - 86: INVESTIGATION OF PREVALENCE OF TEM GENE AMONG ESCHERICHIA COLI STRAINS ISOLATED FROM ARAK HOSPITALS

Afsoon Shariat[1], Mahboobeh Abdoli[2], Razyeh Helali Pargali[3]

1. Assistant Professor, Department of Microbiology, Faculty of Basic Sciences, Islamic Azad University, Kazerun Branch, Kazerun, Iran
2. PhD Student, Department of Microbiology, Faculty of Basic Sciences, Islamic Azad University, Kazerun Branch
3. PhD Student, Department of Microbiology, Faculty of Basic Sciences, Islamic Azad University, Kazerun Branch

Background and Aim: In recent years, extended spectrum β-lactamases (ESBLs) producing Escherichia coli (E.coli) have emerged as a major problem worldwide. Most of the β-lactamases are members of TEM family. The main objective of this study was to investigate the prevalence of blaTEM β-lactamase gene among E. coli isolates in Arak, Iran.

Methods: This cross-sectional study was done among a total of 100 E.coli strains isolated from clinical samples in Arak hospitals. Antibiotic susceptibility pattern of all isolates was determined by disk diffusion method . The ESBLs producing strains were confirmed by combined disk-test at the presence of Cefotaxim and clavulanic acid. The presence of TEM gene in ESBL was assessed by PCR method.

Results: The results of combined disk-test show that the prevalence of ESBL producing E. coli was 26%. Among the ESBL producing E. coli, 22% were positive for TEM gene. The highest sensitive rate was observed against tazocin (88%) and aztreonam (87%) but they were resistance to cefuroxime (53%).

Conclusion:TEM gene is the most common gene among ESBL producing E.coli strains isolated from Arak hospitals. Continuous surveillance is essential to monitor the ESBLs producing E.coli in hospitals. Resistance to β-lactam antibiotics is a major challenge for the management of ESBL infections.

Keywords: Escherichia coli, Extended spectrum beta-lactamase (ESBL), TEM gene, Arak hospitals

P23 - 91: STUDY THE EFFICACY OF ANTIMICROBIAL ACTIVITIES OF EIGHT CLINICALLY APPLIED DISINFECTANTS AGAINST CLINICAL ISOLATED OF ENTEROCOCCI AND PSEUDOMONAS AERUGINOSA

Maryam Hassan[1], Farideh Dinmohamadi[2], Morteza Zareniya[3]

1. Zanjan Pharmaceutical Biotechnology Research Center, Zanjan University of Medical Sciences, Zanjan, Iran
2. Zanjan Pharmaceutical Biotechnology Research Center, Zanjan University of Medical Sciences, Zanjan, Iran
3. Zanjan Pharmaceutical Biotechnology Research Center, Zanjan University of Medical Sciences, Zanjan, Iran

Background and Aim: Hospital-acquired infections are among the most significant reasons of human mortality world-wide which can be controlled by efficient application of suitable disinfectant for hospital setting. The main goal of the present study was to determine the efficacy of eight routinely used hospital disinfectants against clinical isolates.

Methods: In our descriptive study, in the first step the antibiogram assay of 99 clinical isolates enterococci and Pseudomonas aeruginosa were determined. Then, minimum inhibitory concentration and minimum bactericidal concentration of isolates against Povidone Iodine 10%, Ethanol 70%, Savlon 3.2%, Deconex51Gastro, Procept Floor, Septo med, Surfanious and Gigasept AF were evaluated. Furthermore, the efficacy of disinfectants was reevaluated in presence of 5% (w/v) Bovine Serum Albumin.

Results: The results showed that Septo med and Surfanious are the most and less potent disinfectants against clinical isolates, respectively. It is also resulted that Povidone Iodine is the most effective choice among the conventional disinfectants in this study. Clearly, addition of 5% organic substances reduced the efficacy of selected disinfectants significantly.

Conclusion: Novel quaternary ammonium compounds are the most applicable choice for disinfection of hospital surfaces and instruments in this study.

Keywords:hospital disinfectants, enterococci, Pseudomonas aeruginosa, clinical isolates, MBC, antibiogram

P24 - 98: COMPARISON OF VIRULENCE GENES, BIOFILM FORMATION, AND ANTIBIOTIC RESISTANCE PATTERN IN E. FAECALIS AND E. FAECIUM ISOLATED FROM CLINICAL AND COMMENSAL HUMAN SAMPLES IN ISFAHAN, IRAN

Farkhondeh Poursina[1], Faezeh sadat Ghaziasgar[2], Tahmineh Narimani[3]

1. Isfahan Uni of Med Sci
2. MSc student of medical microbiology, School of Medicine, Isfahan University of Medical Science, Isfahan, Iran
3. Isfahan University of Med Sci

Background and Aim: The aim of this study was to determine and compare of antibiotic resistance profile, biofilm formation and frequency of agg and ace genes in Enterococcus species isolated from patients and healthy individual.

Methods:A total of 90 non-duplicate Enterococcus isolates were collected from patients and healthy individuals. Antibiotic susceptibility pattern was determined by disk diffusion and E-test method. Determination of virulence genes was performed by the PCR amplification. The capacity of biofilm formation was also evaluated by microplate approach.

Results:E. faecalis was the predominant species in the clinical isolates (80%). The prevalence of agg and ace genes were 37.8% and 73.3% in clinical and 8.9% and 11.1% in healthy human samples, respectively ($P < 0.05$). The rate of MDR strains were 73.3% and 11.1% in clinical and commensal isolates, respectively ($P < 0.001$). The ability of biofilm formation was notably high in clinical in comparison of commensal isolates ($P < 0.05$) (100% vs 75.6%). The frequency of ace and agg genes and biofilm formation were significantly higher in clinical than healthy isolates ($P < 0.05$).

Conclusion: Distribution of healthy individual's enterococci can lead to spread of virulence genes and resistance between clinical strains.

Keywords:antibiotic resistance; biofilm formation; Enterococcus faecalis; Enterococcus faecium; virulence gene

P25 - 106: IN SILICO IDENTIFICATION AND COMPARATIVE GENOMICS OF CANDIDATE GENES INVOLVED IN BIOSYNTHESIS NATURAL PRODUCTS IN CYANOBACTERIA STRAINS OF IRAN

Bahareh Nowruzi[1], Fatemeh Zahedi[2]

1. Department of Biology, School of Basic Science, Science and Research Branch, Islamic Azad University, Tehran, Iran. ORCID: 0000-0001-6656-777X
2. Department of Microbiology, Faculty of Advanced Sciences & Technology, Pharmaceutical Sciences Branch, Islamic Azad University ,Tehran - Iran (IAUPS)

Background and Aim: Cyanobacteria have the ability to produce a wide variety of natural bioactive compounds. Horizontal gene transfer is thought to play a role in the sporadic distribution of bioactive compounds producers among cyanobacteria. The most prevalent cyanobacterial natural products are produced in combinatorial pathways like mixed PKS/NRPS systems. Nonribosomal peptide synthetases (NRPSs) and polyketide synthase (PKSs), synthesize a diverse array of bioactive small peptides, many of which are used in medicine. Methylprolines are non proteinogenic amino acids produced by cyanobacteria.

Methods: To investigation the relationship between natural product genes and the role of horizontal gene transfer in the evolutionary history, we amplified and sequenced the NRPS, PKS and Methylprolines biosynthetic genes from from 25 cyanobacteria strains isolated from different Climatic/Geographic Regions and Habitats. The analyses were done using a combination of the genome mining softwares, AntiSMASH, and NaPDoS. Moreover, adenylation domain substrate specificity predictions for NRPS enzymes, the signature sequences and the name of the compounds, were made using NRPSpreditor2. In addition; we detected Methylprolines biosynthetic gene from 8 strains included in this study.

Results: Our results suggest that Methylprolines biosynthetic genes have a complex evolutionary history in cyanobacteria, which has been punctuated by a series of ancient horizontal gene transfer events and probably the ability of lateral gene transfer to produce the natural bioactive compound has been lost during evolutionary history in these strains.

Conclusion: The data presented here highlight the need for future studies to define the linkages between horizontal gene transfers in maintenance of bioactive compounds genes.

Keywords: Prediction of substrate, Adenylation domains, NRPSs genes

P26 - 113: INVESTIGATION OF ANTIBIOTIC SUSCEPTIBILITY PATTERN OF STAPHYLOCOCCUS AUREUS STRAINS ISOLATED FROM PATIENTS REFERRING TO SOME TREATMENT CENTERS OF QOM CITY, IRAN

Fatemeh Sadat Razavinia[1], Sara Mousae[2], Roohollah Fateh[3], Ebrahim Eshaghi[4], Mohammad Khalifeh-Gholi[5]

1. Medical Student, Research Commite, Qom University of Medical Sciences, Qom, Iran
2. Department of Biology, Nour Danesh Institute of Higher Education, Meymeh, Isfahan, Iran.
3. Cellular and Molecular Research Center, Qom University of Medical Sciences, Qom, Iran
4. Department of Biology, Nour Danesh Institute of Higher Education, Meymeh, Isfahan, Iran.
5. Cellular and Molecular Research Center, Qom University of Medical Sciences, Qom, Iran

Background and Aim: Resistance to various antibiotics, such as beta-lactams, aminoglycosides, and macrolides is one of the major problems in treatment and prevention of infections caused by Staphylococcus aureus. Therefore, accurate determination of antibiotic susceptibility pattern of organisms isolated from patients can be beneficial in treatment and prevention of dangerous infections. The objective of this study was to isolate S. aureus bacterium and to determine the antibiotic susceptibility pattern of the isolated strains in patients referred to some treatment centers of Qom city.

Methods: In this descriptive cross-sectional study, 340 clinical samples, were collected from September 2016 to July 2017. After isolation and primary identification of S. aureus isolates (using standard bacteriology methods), the isolated strains were confirmed by PCR technique and amplification of femA gene as a molecular diagnostic marker of S. aureus. Finally, antibiotic susceptibility pattern of the strains, was determined by disk diffusion method according to CLSI guideline.

Results: Out of 340 clinical samples, 86 S. aureus strains were isolated and identified based on phenotypic characteristics. The femA gene was observed only in 45 strains (52.32%) based on molecular analysis. The results of the antibiotic susceptibility test showed that the highest resistance was to penicillin (86.04%) and the lowest resistance was to chloramphenicol (0%).

Conclusion: The results of this study indicated that femA gene cannot by itself identify all the S. aureus strains. Also, with regard to the results of antibiogram test, it seems that antibiotic susceptibility test is necessary for S. aureus strains isolated from patients.

Keywords: Staphylococcus aureus; Microbial sensitivity test; femA gene

P27 - 117: ANTIFUNGAL SUSCEPTIBILITY OF OPPORTUNISTIC MEMBERS OF THE ORDER MUCORALES

Somayeh Dolatabadi[1], Seyyed Abolfazl Hosseini[2], Mohammad Javad Najafzadeh[3]

1. Faculty of Engineering, Sabzevar University of New Technologies, Sabzevar, Iran
2. Department of Biology, Hakim Sabzevari University, Sabzevar, Iran
3. Department of Parasitology and Mycology, Ghaem Hospital, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Background and Aim: Mucoralean fungi are among emerging oppourtunictic fungi with high level of mortality in susceptible patients, specially when left untreated. Number of mucormycosis cases have been rapidly increasing in recent decades. Correct identification of the etiological agents and proper choice of antifungals will lead to better management of this infection and will reduce the morbidities.

Methods: The in vitro susceptibilities of 45 molecularly identified strains of Mucorales to eight antifungals (amphotericin B, terbinafine, itraconazole, posaconazole, voriconazole, caspofungin, micafungin, and 5-fluorocytosine) were tested. These strains belong to the following species: Cunninghamella (n= 8), Rhizopus (n=12), Mucor (n=7), Syncephalastrum (n= 8), Lichtheimia (n=10). Strains were formerly identified based on the nuclear ribosomal large subunit (ITS).

Results: The susceptibility profile was variable among different species and different antifungals. Amphotericin B was the most active drug for most species. Posaconazole was the second most effective antifungal agent but showed reduced activity in Mucor and Cunninghamella strains, while voriconazole lacked in vitro activity for most strains. Cunninghamella also comprised strains resistant to all azoles but was fully susceptible to terbinafine. In contrast, the Lichtheimia and Syncephalastrum species completely lacked strains with reduced susceptibility for these antifungals. Mucor species were more resistant to azoles than Rhizopus species. Complete or vast resistance was observed for 5-fluorocytosine, caspofungin, and micafungin.

Conclusion: Accurate molecular identification of etiologic agents is compulsory to predict therapy outcome. For species of critical genera such as Mucor and Rhizopus, exhibiting high intraspecific variation, susceptibility testing before the onset of therapy is recommended.

Keywords: Antifungal susceptibility, Amphotricin B, mucormycosis

P28 - 119: DETECTION OF THE POLYKETIDE SYNTHASE (PKSS) GENES WITH ANTIMICROBIAL ACTIVITY IN SOIL CYANOBACTERIA OF THE LAVASAN

Roghaye Sadat Hosseini[1], Bahareh Nowruzi[2], Abbas Akhavan Sepahi[3]

1. 1Department of Biology, School of Basic Science, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. Department of Biology, School of Basic Science, Science and Research Branch, Islamic Azad University, Tehran, Iran.
3. Department of Microbiology, Islamic Azad University, Tehran North Branch, Tehran, Iran

Background and Aim: Cyanobacteria produce a tremendous variety of secondary bioactive metabolites. Many of these compounds have biological activity.

Methods: In the current study, we focused on the detection of polyketide synthase (PKSs) genes in seven soil cyanobacteria strains of the Lavasan. Total genomic DNA was extracted from exponential phase cultures. The sequences of the 16s rRNA region were determined. Moreover amplification of polyketide synthase was achieved. Results showed amplification of the appropriate ~700 bp for peptide synthetase. Also, analyses of antibiogram bioassay were screened. In vitro antibacterial activities of organic extracts of studied strains were evaluated against Gram-positive bacteria (Staphylococcus aureus) and Gram-negative bacteria (Escherichia coli). Dried extracts and supernatants were dissolved in methanol and antimicrobial activity was determined by the disc method.

Results: The extract of Nostoc sp. Ft11 showed more potent activity against Staphylococcus aureus and no inhibitory effect was found against Escherichia coli.

Conclusion: According to these results, it is concluded that the antibiogram bioassay and molecular detection of polyketide synthase (PKSs) genes in the soil cyanobacterial strains of Iran may be useful techniques for the assessment of natural product -producing species.

Keywords: Polyketide synthase (PKSs), Soil cyanobacteria, Antimicrobial activity

P29 - 121: DETERMINATION OF ANTIBIOTIC RESISTANCE AND FREQUENCY EXTENDED-SPECTRUM BETA LACTAMASES IN ACINETOBACTER BAUMANNII STRAINS ISOLATED FROM PATIENTS HOSPITALIZED IN BURNS WARD IN TEHRAN

Farid Tarafdar[1], Behboud Jafari[2]

1. Msc Student of Microbiology, Department of Microbiology, Ahar branch, Islamic Azad University, Ahar, Iran.
2. Assistant professor, Department of Microbiology, Ahar branch, Islamic Azad University, Ahar, Iran

Background and Aim: Acinetobacter baumannii is an opportunistic and rapidly appearing pathogen that is a major contributor to hospital infections world wide. Which causes urinary tract infections, burns and infections in hospitals due to Acinetobacter baumannii drug resistance. The aim of this study was to evaluate the prevalence of extended-spectrum beta-lactamases (ESBL) in patients hospitalized in the burn ward of the Erfan Hospital in Tehran.

Methods: In this study, 23 strains of Acinetobacter baumannii were isolated from patients in the burn ward of Erfan Hospital and identified by biochemical tests. resistance commonly used antibiotics was determined by the Kirby-Bauer method. To study ESBL production, a combination and double discs was performed.

Results: The antibiotic resistance rates used in this study were: Cefotaxime and Ceftriaxone (98%), Ceftazidime (96%), Meropenem and Imipenem (94%), and Piperacillin+ Tazobactam (90%). And the abundance of ESBL production (4.34%) is identified.

Conclusion: In this study Only (4.34%) of isolates have been produced ESBL. Therefore, in these bacteria other mechanisms than broad-spectrum beta-lactams such as secreted pumps and changes in purines cause resistance, which rapid identification plays an important role in preventing their spread.

Keywords: Acinetobacter baumannii, Antibiotic Resistance,ESBL

P30 - 122: THE STUDY MOLECULAR OF OXA-48 AND DETERMINATION OF RESISTANCE PATTERN IN CLINICAL ISOLATE OF PSEUDOMONAS AERUGINOSA IN PATIENTS HOSPITALIZED IN BURNING WARD OF ERFAN HOSPITAL, TEHRAN

Farid Tarafdar[1], Behboud Jafari[2]

1. Msc Student of Microbiology, Department of Microbiology, Ahar branch, Islamic Azad University, Ahar, Iran
2. Assistant professor, Department of Microbiology, Ahar branch, Islamic Azad University, Ahar, Iran

Background and Aim: Pseudomonas aeruginosa is a gram-negative, non-fermentative bacillus and one of the most common opportunistic human pathogen causing 10-15% of nosocomial and burn wound infections worldwide. In this study, the plenty of OXA-48 gene and antibiotic resistance of clinical specimens in isolates isolated from burn wound infection in patients hospitalized in the ward of Erfan hospital in Tehran was performed.

Methods: In this study, 20 strains of Pseudomonas aeruginosa were isolated from patients in the burn ward of Erfan Hospital and identified by biochemical tests. Antibiotic resistance pattern was determined by disk diffusion method. The genotype of OXA-48 gene was evaluated by PCR method and analyzed by SPSS23 software.

Results: The highest resistance to antibiotics Ceftriaxone and Cefotaxime (100%), Meropenem (93.75%), Cefepime (89.55%), Amikacin (85.40%) And the lowest resistance to other antibiotics was observed for ceftazidime (55%). In genotypic study, 14 strains (68%) of OXA-48 gene were identified.

Conclusion: The results show that most of the samples are resistant to the drug and OXA-48 genes were observed among the strains. Therefore, rapid measurement and accurate examination of antibiotic resistance is essential.

Keywords: Pseudomonas aeruginosa, Antibiotic Resistance,OXA-48

P31 - 144: THE FIRST REPORT OF EMERGING MOBILIZED COLISTIN RESISTANCE (MCR) GENES IN E.COLI AND KLEBSIELLA PNEUMONIAE ISOLATES FROM CLINICAL SPECIMENS AND TYPING OF THEM BY ERIC-PCR METHOD IN IRAN

Nasrin Emam[1], Mojtaba Moosavian[2]

1. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
2. Infectious and Tropical Diseases Research Center, Health Research Institue, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Background and Aim: The emergence of the plasmid-mediated mcr colistin resistance gene in the community poses a potential threat for treatment of patients, especially when hospitalized. The aims of this study were to search of presence of mcr-1 and mcr-2 genes among colistin resistant Escherichia coli and Klebsiella pneumoniae isolates from clinical specimens and fingerprint determination of the strains by ERIC-PCR.

Methods: In this study, 712 non-duplicate Enterobacteriaceae isolates from clinical specimens, were examined. All of the isolates were subcultured on suitable media and the isolated colonies were identified by standard biochemical tests. Antimicrobial susceptibility test to 7 antibiotics were performed by disk diffusion method, and MIC of isolates to colistin were determined by E-test method. These isolates were typed by ERIC-PCR method, and the presence of mcr-1 and mcr-2 genes were investigated by PCR method.

Results: Out of 470 isolates, including 351 E. coli and 119 K. pneumoniae isolates were detected. The results of antibiogram test showed that the most isolates (81.3%) were resistante to ceftazidime, however, the most susceptibility (81.5%) to colistin were seen among of isolates. The typing results by ERIC-PCR method showed 6 and 23 fingerprint patterns, respectively for colistin resistant E.coli and K. pneumoniae strains. Among of 64 (8.98%) colistin-phenotypically- resistant Enterobacteriaceae, 8 isolates (1.12%) had mcr-1 gene. Also the mcr-2 gene was not detected.

Conclusion: Spreading of entrobacterial strains harboring mcr containing plasmids could fail the colistin included therapy regimen as the last line agent against MDR entrobacterial infections.

Keywords: Enterobacteriaceae, colistin, ERIC-PCR, mcr1, mcr-2 genes

P32 - 146: CHARACTERIZATION OF EMBCAB GENE MUTATIONS ASSOCIATED WITH ETHAMBUTOL RESISTANCE IN MYCOBACTERIUM TUBERCULOSIS ISOLATES FROM IRAN

MAHTAB ABDI[1], Azar Dokht Khosravi[2], Mehrandokht Sirous [3], Nazanin Ahmadkhosravi[4]

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. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
4. Khuzestan Tuberculosis Regional Reference Laboratory, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Background and Aim: Ethambutol (EMB) is one of the first line drugs in the standard combination therapy for tuberculosis (TB). As the embCAB operon is considered to be involved in resistance to EMB, this study was aimed to analyze the mutations within embCAB operon among MTB isolates from Iran, to find out a possible association between these mutations and EMB resistance.

Methods:A total of 307 clinical isolates of MTB were screened for EMB resistance by phenotypic drug susceptibility testing. PCR amplification was performed on extracted DNA from all EMB-resistant and randomly selected EMB-susceptible isolates by using sets of primers for various gene loci of embC, embA and emb, followed by sequencing for the detection of most common alterations.

Results: In total 10 isolates showed resistance to EMB by phenotypic susceptibility testing (3.25 %). The mutation rate in 10 EMB-resistant MTB strains was 20.0% (n=2), comprises one mutation in embB (10.0%), at codon 306 Met to Val, and one in embC (10.0%), at codon 270 Thr to Ile. A non-synonymous mutation in embA gene in one of the randomly selected EMB susceptible isolates located in codon 330 Lue to Lue were also noticed. The majority of our EMB-resistant isolates (n=8/ 80%) could not be explained by the mutations within embCAB.

Conclusion: So, these mutations alone, are not sufficient for the development of full resistance to EMB in MTB isolates. Additional mechanisms of resistance other than mutations within embCAB operon should also be considered.

Keywords: Ethambutol resistance in Mycobacterium tuberculosis

P33 - 151: PHYLOGENETIC ANALYSIS AND ANTIBIOTIC PATTERN DETERMINATION OF ESCHERICHIA COLI STRAINS ISOLATED FROM THE COAST OF THE GENAVEH REGION

Roya Sardari[1], samin Alipoordolatabad[2]

1. Department of microbiology, shiraz branch, Islamic Azad University, shiraz, Iran
2. Department of microbiology, shiraz branch, Islamic Azad University, shiraz, Iran

Background and Aim: Escherichia coli belong to the group of bacteria with the name of coliform which is member of Entrobacteriacea family.Escherichia coli is as an important organism which could disseminate antibiotic resistancy in water shoreline. Accordingly, the present study tried to isolate the bacterium from Genaveh shoreline and sediments. Then phylogenetically chategorized based on Clermont technique and evluate their antibiotic and enzymatic pattern.

Methods: In the present study 60 samples (30 water and 30 sediment) were collected from water and sediments between april to agust 2016. Then they were evaluated by MPN technique and serially dilutied samples were cultivated on MacConkey and Eosin methylene blue agar. After that they were identified using Gram stain, Catalase and oxidase tests. The phylogentical analyasis of E.coli were done using primers: ChuA, yjaA, TSPE 4.C2 and enzymatic pattern were evaluated usin APizyme kit

Results: Out of 60 collected samples, 13 samples were E.coli, 9 from water and 4 from sediments. Based on antibiogram were resistancy to Ampicillin were 54% while and the sensitive pattern belong to Gentamicin (100%) and Ceftriaxone (92%). The most common phylogenic group were A, B2 and D. Although most of them belong to group D and the group have most of the virulent genes therefore, they had most of enzymes which is not common for other strains. Based on our finding human and animal commensal group with less enzymes had different enzyamatic pattern with group D

Conclusion: Overall, the best antibiotic for treatment on the same isolates is gentamicin and ceftriaxone which could be use in this geographical area

Keywords: Escherichia coli, Antibiotic pattern, Enzymatic pattern, Triplex PCR, Genaveh shoreline

P34 - 155: THE EFFECT OF THE DEHYDROZINGERONE ON THE BIOFILM FORMATION IN CANDIDA ALBICANS

Sepideh Nejatbakhsh[1], Fattah sotoodeh nezhad[2], Mahdi Razaghi-Abyaneh [3], Zahra Jahanshiri [4]

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 Mycology, Pasteur Institute of Iran, Tehran 13164, Iran
4. Department of Mycology, Pasteur Institute of Iran, Tehran 13164, Iran

Background and Aim:: Candida albicans is an important fungal pathogen of humans which is responsible for the majority of mucosal and systemic candidiasis. This study was conducted to determine the inhibitory effects of Dehydrozingerone, as a natural based material, on the biofilm formation in C. albicans.

Methods: Dehydrozingerone was solved in DMSO and two-fold serial concentrations were prepared. C. albicans standard strain ATCC102331 was cultured on SDA medium, and spore suspension was prepared at a concentration of 3×107 CFU/ml. Fungal cells were planted in a flat-bottom 96-well microtiter plates with different concentrations of DHZ in RPMI medium as triplicate, and incubated for 48 h at 35°C. After incubation time, planktonic cells were removed by discarding of upper medium and each well was washed with buffer (PBS) and fixed by methanol (99%), biofilm formation was measured using 0.4% crystal violet method. the absorbance was measured at 590 nm. The effect of DHZ on biofilm formation of C. albicans was calculated using determination of the percent transmission (%*T*), the %*T* value of each test sample was subtracted from the %*T* of the reagent blank to obtain %*T* bloc.

Results: The results indicated that the biofilm formation was inhibited dose-dependently with increasing the concentrations of dehydrozingerone. The biofilm formation was suppressed in the range of 22.5 to 50.34 % of DHZ with an IC50 equal 500 µg/ml for tested concentrations after 48 h.

Conclusion: Taken together, dehydrozingerone can be considered as a safe compound for potential use in preventing adherent and biofilm formation of C. albicans at oral candidiasis.

Keywords: Dehydrozingerone, Candida albicans, biofilm formation, inhibition

P35 - 157: STUDY OF THE ANTIMICROBIAL EFFECTS OF METHANOLIC EXTRACT OF OLIVE LEAVES ON PATHOGENIC STRAINS UNDER LABORATORY CONDITIONS

Shabnam Torabi[1], Mohammad asghari[2]

1. Graduated from the Department of Food Science and Technology, Shahreza Azad University
2. Graduated from the Department of Food Science and Technology, Higher Agricultural and Animal Husbandry Complex, Torbat Jam Branch

Background and Aim: Olive leaf is a medicinal plant containing phenolic and oleuripine compounds known as a cheap and accessible source of polyphenols. Olive leaf is a medicinal plant that has been used extensively in ancient medicine. In this study, the effect of methanolic leaves of this plant on pathogenic pathogens such as Escherichia coli, Pseudomonas aeruginosa, Bacillus cereus and Staphylococcus aureus is investigated.

Methods: In this experimental study, olea europaea was used to evaluate its antimicrobial effects. Methanolic extracts of this plant were prepared at concentrations of 50, 100, 200, 400, 400 mg / ml, and analyzed by Escherichia coli, Pseudomonas aeruginosa, Bacillus cereus and Staphylococcus aureus. The test was to determine the minimum inhibitory concentration and minimum microbial concentration.

Results: In this study, the highest effect of methanolic extracts of olive leaves on Pseudomonas aeruginosa and E. coli was observed at concentrations of 400 mg / ml. There was a significant difference between the inhibitory concentrations of these different extracts on the growth of bacteria at the level of $P \leq 0.05$. The minimum germination concentration of the extract from these bacteria was also obtained from 12.5 to 200 mg / ml.

Conclusion: In this study, methanolic extracts of ovine leaves were affected by Staphylococcus aureus, Escherichia coli, and Osmosis spp., But did not inhibit Bacillus cereus.

Keywords: Vegetable extract, olive leaf, minimum inhibitory concentration.

P36 - 160: PHENOTYPIC AND GENOTYPIC SCREENING OF ADHESIVE VIRULENCE FACTORS OF ACINTOBACTER BAUMANNII ISOLATED FROM ZANJAN HOSPITALS

Fakhri Haghi[1], Fatemeh Valadkhani[2]

1. Research Committe,Zanjan university of Medical Sciences,Zanjan,Iran
2. Research Committe,Zanjan university of Medical Sciences,Zanjan,Iran

Background and Aim: Acintobacter baumannii is an opportunistic pathogen associated with multidrug-resistant infections. Antibiotic resistance profils and biofilm formation are two important properties in the pathogenicity of Acinetobacter baumannii. The aim of this study was to measure the frequency of genes involved in biofilm production and to investigate antibiotic resistance patterns and to find a relationship between them.

Methods: In total 63 Acinetobacter baumannii were collected from teaching hospitals of zanjan, Iran during 2014-2016 All isolates were tested for antimicrobial susceptibility by Kiry-Bauer disk diffusion method. frequency of blaPER-1،bap ،bfmS ،ptk ،pgaB ،fimH ،csgA ، kpsmTII ،csuE،epsA ،ompA genes was measured by PCR method.

Results: All 63 isolates encoded csuE gene, while none of isolates had csgA and fimH genes.The results of this study revealed that a high prevalence of biofilm-forming phenotypes among A.baumannii strains obtained from different hospitals. prevalence of blaPER-1،bap ، bfmS ،ptk ،pgaB،kpsmII ،epsA,ompA was 1.6%, 42.8%, 92.1%, 95.2%, 98.4%, 57.1%, 95.2%, 80.9% respectively. Effective strategies to prevent infections due to A.baumannii that produce biofilms are therefore needed.

Conclusion: The present study showed a high prevalence of adhesive virulence factors and multidrug resistant Acintobacter baumannii

Keywords: Acinetobacter baumannii, PCR, biofilm-forming phenotypes

P37 - 167: ANTIBIOTIC SUSCEPTIBILITY PATTERN AND PREVALENCE OF MECA GENE AMONG CLINICAL ISOLATES OF STAPHYLOCOCCUS AUREUS FROM SANANDAJ, IRAN

Samira Saedi[1], Safoura Derakhshan[2], Ebrahim Qaderi [3]

1. Department of Microbiology, Faculty of Medicine, Kurdistan University of Medical Sciences, Sanandaj, Iran
2. Department of Microbiology, Faculty of Medicine, Kurdistan University of Medical Sciences, Sanandaj, Iran. E. mail: s.derakhshan@muk.ac.ir
3. Department of Statistics and Epidemiology, Faculty of Medicine, Kurdistan University of Medical Sciences, Sanandaj, Iran

Background and Aim: Staphylococcus aureus is one of the main causes of infection in the community and the hospital. This bacterium is becoming increasingly resistant to antibiotics. The resistance of S. aureus to methicillin is due to the presence of mecA gene. The aims of this study were to investigate the antibiotic susceptibility and frequency of mecA in S. aureus isolated from patients in Sanandaj, Iran.

Methods:A total of 74 isolates of S. aureus were obtained from different clinical samples of patients admitted to Besat and Tohid hospitals in Sanandaj during 2017. Identification of isolates was performed by biochemical methods. The antibiotic susceptibility test for 11 antibiotics was performed using agar disk diffusion method and E-test (for vancomycin) according to the CLSI 2017 (Clinical and Laboratory Standards Institute). After extraction of DNA from isolates the frequency of mecA gene was investigated using polymerase chain reaction.

Results: The most effective antibiotic was vancomycin. Of the 74 isolates, the sensitivity to mupirocin was 98.6%, followed by trimethoprim-sulfamethoxazole 95.9%, linzolide 91.9%, cefoxitin 83.8%, gentamicin 82.4%, tetracycline 75.7%, ciprofloxacin 68.9%, clindamycin 59.5%, erythromycin 45.9%, and penicillin 4.1%. All isolates (100%) were susceptible to vancomycin. Of the 74 isolates, 9 (12.16%) carried the mecA gene.

Conclusion: The result of our study showed the high susceptibility of isolates to vancomycin and relatively low prevalence of the mecA in our samples. Therefore, we suggest that vancomycin is a suitable drug for treatment, but care should be taken in order to avoid emergence of antibiotic resistance.

Keywords: Staphylococcus aureus, Methicillin resistance, Drug resistance

P38 - 176: EXPRESSION OF AAP AND ICAR GENES INVOLVED IN BIOFILM PRODUCTION IN CLINICAL STRAINS OF STAPHYLOCOCCUS AUREUS RESISTANT TO METHICILLIN AND GENTAMICIN

Narges Heidari[1], Mohammad reza Arabestani[2]

1. Asadabad school of medical sciences. asadabad. Iran
2. Hamedan university of medical sciences

Background and Aim: Staphylococcus aureus biofilms are involved in a multitude of serious chronic infections. Production of biofilms is a defensive-invasive process controlled and regulated by the aap and icaR genes. The expression levels of these genes play an important role in the formation of biofilm. The aim of this study was to investigate the expression of icaR and aap regulatory genes in clinical isolates of S. aureus resistant to methicillin and gentamicin

Methods: In this analytical study, among 285 samples, we detected 100 isolates of methicillin resistant and 82 isolates of gentamicin resistant S. aureus. Resistant strains were evaluated for the presence of biofilm regulatory genes. The expression levels of regulatory genes were measured by real-time PCR method. We used SPSS software 16 for statistical analysis and also REST 2008 V3 software for analysis of quantitative results.

Results: Among 100 methicillin resistant and 82 gentamicin resistant isolates of S. aureus the highest expression levels of icaR and aap genes were detected in the smears obtained from the wounds and catheters. Moreover, a different pattern of gene expression was observed in multidrug resistant strains in comparison to the strains with lower rate of resistance. Also, there was a significant relationship between the presence and activity of regulatory genes and biofilm formation in different samples ($p \leq 0 / 05$).

Conclusion: Considering the frequency of biofilm producing strains of S. aureus in the smears from the catheters and wounds and also increased gene expression, appropriate therapeutic measures should be considered for methicillin and gentamicin resistant of S. aureus.

Keywords: Drug resistance, S. aureus, Virulence factors, Methicillin, Gentamicin, Gene expression

P39 - 183: THE EFFECT OF ZN NANOPARTICLES (ZNNPS) ON CIPROFLOXACIN-RESISTANT STAPHYLOCOCCUS AUREUS ISOLATES FROM SKIN INFECTIONS IN QOM PROVINCE

Mohammad hossein Soleimani[1], Mohammad Reza Zolfaghari[2]

1. Departmentof microbiology,Qom Branch,Islamic Azad University,Qom,Iran
2. Departmentof microbiology,Qom Branch,Islamic Azad University,Qom,Iran

Background and Aim: Staphylococcus aureus is one of the most important causes of bacterial skin infection in humans and its resistance to antimicrobial drugs is important. The aim of this study is to evaluate the effect of ZnNPs on ciprofloxacin-resistant Staphylococcus aureus strains isolated from skin infections in Qom Province.

Methods: To this end, 187 Staphylococcus aureus strains from skin infection samples in Qom province were identified in genotypic and phenotypic manner using different biochemical methods. The antimicrobial effects of the compounds were measured by disc diffusion and MIC methods according to the CLSI protocol.

Results: Of 187 strains isolated by phenotypic methods, 165 strains (88.2%) were diagnosed as Staphylococcus aureus, of which 50 (30.3%) were resistant to ciprofloxacin by disc diffusion method and MIC microdilution was done on them. The highest concentration of inhibitor in 24 strains (48%) was obtained at 256 µg / ml during microdilution. Zn nanoparticles alone did not have an effect on Staphylococcus aureus growth inhibition, but in microdilution with ciprofloxacin in the presence of nanoparticles, the minimum growth inhibition concentration of strains was half that of Nano-free MIC.

Conclusion: With the use of zinc nanostructures, the dose of ciprofloxacin used in the treatment of Staphylococcus aureus can be reduced which leads to the reduction of resistance to ciprofloxacin.

Keywords: Zn nanoparticles (ZnNPs) ciprofloxacin-resistant Staphylococcus aureus skin infections

P40 - 184: INVESTIGATING THE ABILITY OF BIOFILM PRODUCTION IN MULTIDRUG-RESISTANT STAPHYLOCOCCUS AUREUS STRAINS (MDR) ISOLATED FROM SKIN INFECTIONS IN QOM PROVINCE

Mohammad hossein Soleimani[1], Razieh Mohammadzadeh[2], Ali Javadi[3]

1. Departmentof microbiology,Qom Branch,Islamic Azad University,Qom,Iran
2. Departmentof microbiology,Qom Branch,Islamic Azad University,Qom,Iran
3. Phd Student,departmentof pathobiology,School Of Public Health,Tehran University Of Medical Sciences,Tehran,Iran

Background and Aim: Biofilm formation is one of the pathogens that can cause Staphylococcus aureus bacteria to bind to different surfaces and also increase the antibiotic resistance. This study was performed to determine the ability of biofilm formation in multidrug-resistant (MDR) Staphylococcus aureus strains isolated from skin infections in Qom province.

Methods: In this study 148 patients who referred to Qom healthcare centers due to skin infections have been sampled. Using different methods of microbial diagnose, S. aureus strains were identified and isolated. Antibiotic resistance of Staphylococcus aureus isolates was investigated based on The CLSI instruction using Disk Diffusion method. The MDR strains were identified and biofilm production ability was evaluated by microplate method.

Results: Of the 148 samples taken from patients including 85 women and 63 men, 67 Staphylococcus aureus strains (45.27%) were diagnosed. After the evaluation of antibiotic resistance of the strains, the highest resistance to penicillin and Cefoxitin (71.64%) and the lowest resistance to chloramphenicol (11.94%) were observed. 21 strains (31.34%) were isolated as multidrug resistant Staphylococcus aureus strains, all 21 strains were able to produce biofilms strongly.

Conclusion: The ability to produce biofilms by bacteria can be one of the most important factors contributing to antibiotic resistance, which is a serious threat to the spread of hospital infections.

Keywords: biofilm multidrug-resistant Staphylococcus aureus skin infections

P41 - 191: EVALUATION OF ANTIBIOTIC RESISTANCE IN ESCHERICHIA COLI STRAINS ISOLATED FROM URINARY TRACT INFECTIONS IN IMAM REZA HOSPITAL, BOJNURD, IN 1396

Reza Behzadfar[1], Sara Nojoumi[2], Seyedeh Zahra Hoseini[3], Reza Ghorbani[4], Mina Chabaki[5], Saghar Safamanesh[6], Amir Azimian[7]

1. B.Sc of Microbiology, Imam Reza Hospital, North Khorasan University of Medical Sciences, Bojnurd, Iran.
2. M.Sc of Medical Virology, Imam Reza Hospital, North Khorasan University of Medical Sciences, Bojnurd, Iran.
3. B.Sc of Laboratory Sciences, Imam Reza Hospital, North Khorasan University of Medical Sciences, Bojnurd, Iran.
4. B.Sc of Laboratory Sciences, Imam Reza Hospital, North Khorasan University of Medical Sciences, Bojnurd, Iran.
5. B.Sc of Laboratory Sciences, Imam Reza Hospital, North Khorasan University of Medical Sciences, Bojnurd, Iran.
6. M.Sc of Medical Virology, Imam Reza Hospital, North Khorasan University of Medical Sciences, Bojnurd, Iran.
7. ph.D of Medical Bacteriology, Faculty of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.

Background and Aim:E. coli is a member of the Enterobacteriaceae family, which is part of the normal flora of the gastrointestinal tract of humans. This bacterium is a most common cause of urinary tract infections. Given the importance of urinary tract infection and may spread to the bloodstream and other parts of the body correct and efficient treatment is very important. The aim of this study was to determine antibiotic resistance in Escherichia coli strains isolated from urinary tract infections Imam Reza Hospital, Bojnurd, in 1396.

Methods: After isolation and confirmation of strains of E. coli in Urine samples with conventional approaches, investigation of antibiotic resistance performed by disk diffusion method in accordance with CLSI standards using amikacin, ciprofloxacin, imipenem, ampicillin, ofloxacin, trimethoprim-sulfamethoxazole, gentamicin, nitrofurantoin, ceftriaxone, cefotaxime, Nalidixic acid, cefazolin and amoxicillin disks.

Results: In the 1396 a total of 1754 urine culture 193 (11%) were positive. Among these 154 cases (79/8%) were E. coli. Of these isolates 52.8% were resistant to amikacin, 22.3% to ciprofloxacin, 0% to imipenem, 48.2% to ampicillin, 88.1% to ofloxacin, 51.8% to co-trimoxazole, 23.8% to gentamicin, 29% to nitrofurantoin, 3.6% to Nalidixic acid, 77.7% to cefazolin and 88.1% were resistant to amoxicillin.

Conclusion: According to results, relatively high rates of antibiotic resistance are seen compared to previous reports. Given the importance of E. coli in urinary tract infections, need to revise and correct diagnosis and appropriate treatment in order to reduce the spread of antibiotic resistance of urinary tract infections can be felt.

Keywords: Escherichia coli, antimicrobial resistance, urinary tract infection

P42 - 198: ISOLATING LYTIC COLIPHAGES FROM SEWAGE

Salehe Sabouri[1], Sahar Amirpour-Rostami[2], Maryam Kianpour[3]

1. Herbal & Traditional Medicines Research Center, Kerman University of Medical Sciences, Kerman, Iran
2. Pharmaceutics Research Center, Institute of Neuropharmacology, Kerman University of Medical Sciences, Kerman, Iran
3. Student Research Committee, Student of Pharmacy, Faculty of Pharmacy, Kerman University of Medical Sciences, Kerman, Iran

Background and Aim:E.coli is a normal flora of human body, but some strains are pathogenic. Nowadays, as antibiotic resistance is a problem in medicine, scientists are searching for alternatives to combat this challenge. One option are bacteriophages- viruses that infect bacteria. In this study, we searched sewage samples to find lytic coliphages that lyse E. coli strains isolated from patients.

Methods: Sewage samples from different places of Iran were collected. The samples were enriched in mid- log cultured host. After overnight incubation, drop test was carried out to check the presence of phages. Positive samples were purified to determine the host range of each isolated phage. Transmission electron micrographs were also prepared to identify phage families.

Results: Two phages were isolated. Both could efficiently lyse E. coli strains even E. coli O157. TEM graphs showed that both phages belong to Myoviridae family.

Conclusion: Bacteriophages are abundant and easy to isolate. Therefore, they can be considered as alternatives to antibiotics.

Keywords:bacteriophage, E. coli, Myoviridae

P43 - 199: IN VITRO ANTIMICROBIAL ACTIVITY OF CINNAMON, GARLIC, AND GINGER EXTRACTS ON METALLO-B-LACTAMASE-PRODUCING PSEUDOMONAS AERUGINOSA: A POTENTIAL THERAPEUTIC APPROACH

Neda Yousefi[1], Gita Eslami[2], Ali Hashemi[3], Mehrzad Sadredinamin[4], Samira Tarashi[5], Mahdane Roshani[6], Elahe Taki[7], Sajjad Yazdansetad[8]

1. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
2. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
3. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
4. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
5. Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran.
6. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
7. Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran.
8. Department of Microbiology, School of Medicine, Golestan University of Medical Sciences, Gorgan, Iran.

Background and Aim: Metallo-β-lactamase (MBL)-producing Pseudomonas aeruginosa is a leading cause of nosocomial infections, especially in burn patients worldwide. The antimicrobial properties of Cinnamomum verum, Allium sativum, and Zingiber officinale known as cinnamon, garlic, and ginger, respectively have not yet been reported in clinical isolates of P. aeruginosa producing metallo-β-lactamase. The present study was aimed to detect MBL genes and evaluate the inhibitory effect of cinnamon, garlic and ginger extracts on MBL-producing P. aeruginosa.

Methods: Antibiotic resistance pattern of MBL-producing P. aeruginosa isolates was evaluated by Kirby-Bauer disk diffusion method. MBL-producing isolates were phenotypically tested by combined disk test (CDT). The prevalence of blaVIM-1 and blaIMP-1 genes encoding metallo-β-lactamase were detected by PCR. Minimum inhibitory concentration (MIC) of the acetonic, methanolic, and chloroformic extracts of cinnamon, garlic, and ginger on MBL-producing isolates was evaluated by the broth microdilution method.

Results:81 out of 95 (85.2%) imipenem resistant P. aeruginosa isolates were MBL-producing strains. 13 out of 81 (16.04%) and 18 out of 81 (22.22%) MBL-producing P. aeruginosa were positive for blaIMP-1 and blaVIM-1 genes, respectively. The inhibitory concentrations of the acetonic, methanolic, and chloroformic extracts of cinnamon, garlic, and ginger ranged from ≥1.50 mg/ml to ≥12.50 mg/ml.
Conclusion: We find that the methanolic extract of cinnamon and garlic as well as the acetonic extract of ginger has significant antibacterial activity against the MBL-producing P. aeruginosa. This medicinal plants can be considered as a source of forgotten antimicrobial agents to avoid treatment failure and mortality.

Keywords: Burns, Pseudomonas aeruginosa, Cinnamon, Garlic, Ginger

P44 - 233: EVALUATION ANTIMICROBIAL SUSCEPTIBILITY PATTERNS AND PRESENCE OF ESBLS AMONG CLINICAL ISOLATES OF P. AERUGINOSA COMPARED TO THE ENVIRONMENTAL AND COCKROACH ISOLATES

omid zarei[1], faezeh kosari[2], ali mohammadi bardbari[3], pezhman karami[4], hassan mahmoudi[5], mosoud moghaddam shakib[6], abas moradi[7], mohammad yousef alikhani[8]

1. 1Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran.
2. 1Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran.
3. University of Medical Sciences, Shahrekord, Iran
4. 1Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran.
5. 1Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran.
6. 1Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran.
7. 3Department of Social Medicine Group, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran.
8. 3Department of Social Medicine Group, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran.

Background and Aim: The incidence of extended-spectrum β-lactamases (ESBLs) in Pseudomonas aeruginosa being increasingly reported globally. Knowledge of the prevalence of ESBLs enzymes among clinical isolates compared to the environmental and cockroach isolates is limited. Therefore, the aim of this study was to evaluate the antimicrobial susceptibility and the presence of ESBLs among clinical P. aeruginosa isolates compared to the environmental and cockroach isolates

Methods:A total of 34 clinical, 19 environmental, and 7 cockroaches isolates of the P. aeruginosa were collected from three hospitals in Hamadan, west of Iran, and identified via API 20NE. The antimicrobial patterns were tested by disk diffusion method as recommended by CLSI. ESBLs encoding genes included blaCTX-M, blaTEM, and blaSHV were amplified by PCR method.
Results: Susceptibility pattern of P. aeruginosa isolates showed that, clinical isolates were highly resistant to imipenem 18 (52.9%) and ciprofloxacin 15 (44.1%). In the environmental isolates, the highest resistance rate was seen against imipenem 10 (52.6%) followed by ciprofloxacin 8 (42.1%). However, all cockroaches' isolates were susceptible to all of studied antibiotics. The difference in resistance rates between the clinical, environmental and cockroach isolates were statistically significant (P>0.05). The prevalence of blaCTX-M, blaTEM, and blaSHV among P. aeruginosa were 48.3%, 36.7% and 38.3%, respectively.
Conclusion: Our data indicated a high prevalence of ESBLs among clinical and environmental P. aeruginosa isolates carrying blaTEM, blaCTX-M, and blaSHV genes. The presence of ESBL-producing bacteria within the healthcare setting in should be considered a public health concern, as it causes limitations to the antimicrobial agents for optimal treatment of patients.

Keywords:P. aeruginosa, ESBLs genes, environmental, cockroach

P45 - 237: INVESTIGATION OF BETA-LACTAM ANTIBIOTIC RESISTANT E.COLI ISOLATED FROM URINARY TRACT INFECTIONS (UTI) PATIENTS REGARDING SHV, CTX-M AND IMP GENES

Anna Abdolshahi[1], Aliakbar Shabani [2], Zahra Aminian [3], Tahereh Zinati [4], Mehrdad Khaledi[5], vajiheh Zarrinpour [6]

1. Food Safety Research Center (salt), Semnan University of Medical Sciences, Semnan, Iran
2. Department & Center for Biotechnology Research, Semnan University of Medical Sciences, Semnan, Iran
3. Damghan Velayat Hospital, Semnan University of Medical Sciences, Semnan, Iran
4. Student Research Committee, Semnan University of Medical Sciences, Semnan, Iran
5. Damghan Velayat Hospital, Semnan University of Medical Sciences, Semnan, Iran
6. Department of biology, Damghan branch, Islamic Azad University, Damghan, Iran

Background and Aim: The resistance of E.coli to beta-lactam antibiotics is related to the acquisition of plasmids that encode broad-spectrum beta-lactamases. Extended-spectrum β-lactamases (ESBLs) have particular importance in antimicrobial therapy

Methods: In this study the ferquency and role of SHV, CTX-M and IMP genes in resistance to Ceftriaxone, Imipenem and Piperacillin antibiotics in E.coli isolated from urinary tract infections (UTI) were determined. In total 270, non-duplicate E.coli producing ESBL were collected from the hospitilized patients of two genders in all ages with UTI at hospital of Damghan, Iran. The samples were isolated using screening test and double disc phenotypic test. All isolates were screened for the detection of SHV, CTX-M and IMP genes using PCR.

Results: Among them 44.4% were positive for ESBLs which include 30% CTX-M gene, 27.5% SHV and 0% IMP gene. Results showed that the responses of male and Females patients to examind antibiotic was different. The distribution of underlying diseases also was different in UTI patients

Conclusion: However, ESBLs producing strains of bacteria such as E.coli should be considered as a major threat for consumption of broad-spectrum cephalosporins. Therfore, overused antibiotic should be avoided to prevent resistance to them.

Keywords:antibiotic resistant, E.coli, urinary tract infections (UTI), CTX-M, SHV

P46 - 240: ANTIMICROBIAL EFFECT OF ATRAGIN HERBAL CREAM ON DIFFERENT MICROBIAL ISOLATES

Narges Golab[1], Mohammad Mehdi Kamkar[2], Pejvak Khaki[3], Soheila Moradi Bidhendi[4], Mehdi Gharakhani[5], Farahnaz Ghasemian[6]

1. Department of Microbiology, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
2. Atragin company and International laboratories of Dr Kamkar
3. Department of Microbiology, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
4. Department of Microbiology, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
5. Department of Microbiology, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
6. Atragin company , International laboratories of Dr Kamkar

Background and Aim: The emerging problem in treatment of infectious diseases are the rapidly increasing drug resistance to currently recommended antibiotics. Atragin cream is a miracle herbal medicine complex for treatment of chronic wounds like Bedsore, Diabetic Foot Ulcer, surgical wounds. This cream include a mixture of natural product complexes from more than nine different components. The aim of the study was to examine the antimicrobial effects of Atragin herbal cream on different microbial isolates.

Methods: The bacterial isolates were used for this study include Staphylococcus aureus (RTCC1885), Staphylococcus epidermidis(RTCC1892), Streptococcus pyogenes (RTCC1911), Bucillus subtilis (RTCC1053), Bucillus cereus (RTCC1046), Bucillus anthracis (RTCC 1036), Pseudomonas aeruginosa (RTCC1477), Acinetobacter baumanii (RTCC1015), Escherichia coli (RTCC2325).The susceptibility of isolates to the Atragin herbal cream was evaluated using disk diffusion, cylinder, well diffusion, MIC and MBC methods.
Results: The results showed that Staph. aureus, B. subtilis, B.cereus,B. anthracis, P. aeruginosa , A. baumanii were susceptible to the Atragin herbal cream and Staph.epidermidis, E.coli and Strep.pyogenes were resistant. The results of MIC of the Atragin cream was: Staph. aureus (3 mg/ml) , B. subtilis (3 mg/ml), B.cereus (7.5 mg/ml), B. anthracis(12.5mg/ml), A. baumanii (12.5 mg/ml), P. aeruginosa (25 mg/ml).
Conclusion: The results of this study demonstrate that the most susceptible isolates were Staph. aureus, B. subtilis, B.cereus. Atragin herbal cream has a broad in vitro spectrum of antimicrobial activity against some bacterial pathogens and may be particularly useful for treatment of infections by multidrug-resistant organisms.

Keywords: Atragin herbal cream, Antimicrobial effect, bacterial isolates

P47 - 251: STUDY AND MOLECULAR CHARACHTRIZATION OF KLEBSIELLA PNEUMONIAE RESISTANT TO ANTIBIOTIC FROM PATIENTS REFERRING TO HOSPITALS IN TEHRAN BASED ON PER, SHV AND VEB GENES

ZAHRA Kohanrooz bijarpas[1], Dr.Saeed Zaker Bostanabad[2], Dr.Farzaneh Tafvizi[3]

1. Department of Biology, Islamic Azad University- Parand Branch, Tehran, Iran.
2. Microbiology Department, Islamic Azad University-Parand Branch, Tehran, Iran.
3. Department of Biology, Islamic Azad University-Parand Branch, Tehran, Iran.

Background and Aim:: Extended-spectrum beta-lactamaseS of SHV,PER and VEB type is considered as an Important mechanism resistant to beta-lactamases in gram- negative pathogen and is widely increasing. Klebsiella pneumonia species are able to produce extended-spectrum beta- lactamase (ESBLs).

Methods: In this analytical- descriptive study antibacterial susceptibility patterns of 176 Klebsiella pneumonia has been tested to Cefepime, Ampicillin, Gentamicin, Cefalotine, Ceftazidime, Ciprofloxacin, Imipenem, Cefotaxime , Nitrofurantoin using disk diffusion method. The presence of SHV,PER and VEB genes were assessed by using PCR Method

Results: Confirmatory phenotypic test showed 56/81% of the isolates were ESBL positive. The prevalence of SHV,PER and VEB genes in isolated Klebsiella pneumonia was 34%,%13 and %17 respectively. In this study, the highest resistance was observed for ampicillin antibiotics (%89) and the least resistance to antibiotic imipenem (%7).

Conclusion: High frequency of SHV,PER and VEB genes in ESBL produsing isolates indicates that this enzyms plays an important role in resistance to beta lactam containing anti biotics. Therefore, proper infection control tools and appropriate therapeutic approaches in different parts of the hospitals are necessary to prevent their release

Keywords: Klebsiella pneumonia ,ESBL , bla SHV,PER , VEB,PCR

P48 - 252: ANTIBACTERIAL EFFECT OF GERANIUM OIL ON E. COLI, BACILLUS, STAPHYLOCOCCUS AUREUS, AND PSEUDOMONAS AERUGINOSA

Saeedeh Ghiasvand[1], ali shalilian[2]

1. assistant professor, Department of Biology,faculty of Science Malayer University
2. Department of Biology,faculty of Science Malayer University

Background and Aim: Today, overtaking different antibiotics transformed organisms into resistant phase, which few antibiotics can effect on them. Geranium oil contains citronellal (31.7%), citronellal format (12.8%), and geraniol (9.8%) as major components. Geraniol plays effective role in antibacterial effect of geranium oil. The aim of present study was to evaluate the effect of geranium oil on bacteria and a new component for antibiotics.In this study the effect of Geranium oil was evaluated on E. coli, Bacillus, Pseudomonas aeruginosa and Staphylococcus aureus.

Methods: For antibacterial effect evaluation, bacteria were cultured in nutrient broth media overnight and then cultured in nutrient agar media and effect of Geranium oil evaluated by well diffusion method and the inhibition region diameter were measured

Results: The inhibition diameter for E. coli was 12mm, the inhibition diameter for Bacillus was 25mm, the inhibition diameter for Staphylococcus aureus was 15mm and inhibition diameter for Pseudomonas aeruginosa was 0 mm.

Conclusion: Based on these results, Geranium oil can be used as new component for antibiotics to have better effects on bacteria and therefore can have good effect on resistance of bacteria and can be used in recombinant drugs instead of new chemical and harmful new components.

Keywords: Geranium, Resistant bacteria, recombinant drugs, herbal essences.

P49 - 256: EFFECTS OF METHANOLIC EXTRACT OF CALCEOLARIA HERBEOHYBRIDA ON MICROORGANISMS

Nasim Nasiri[1], Vida Tafakori[2]

1. : Department of Cell & Molecular Biology, Faculty of Biological Sciences, Kharazmi University, Tehran, Iran.
2. : Department of Cell & Molecular Biology, Faculty of Biological Sciences, Kharazmi University, Tehran, Iran.

Background and Aim: From the past to the present, plants have been used in the treatment of diseases. One of these diseases is infectious diseases. For this purpose, plant extracts are used. Different solvents have been used for the preparation of plant extraction. In this research study on antimicrobial effects of ornamental plant namely Calceolaria herbeohybrida.

Methods: The plant material used in this study was the flower of Calceolaria herbeohybrida. The flower, stem, and leaf of the plant were harvested and identified at Kharazmi University, Farabi Herbarium. 10 gram of fresh flowers were dried, grained and macerated in 80% methanol, overnight. The macerates were then concentrated with solvent evaporation and then 1 ml of sterile distilled water was added to solve it. The Antimicrobial activity of this concentrated extract, performed with well-diffusion agar method on E.coli ،P.aeroginosa, MRSA, B.subtilis and, C.albicans.

Results: According to other research paper, strains showing an inhibition zone more than 1 mm were considered as sensitive strains. So all of the used strains in this research were resistant to methanol extraction of Calceolaria herbeohybrida.

Conclusion: There was no effective constitute in methanolic extract of Calceolaria herbeohybrida as the antimicrobial agent against used strains. So this plant cannot use for treatment of infectious disease.

Keywords: Calceolaria herbeohybrida, diffusion, methanol, extraction

P50 - 270: ANTIBIOTIC RESISTANCE AND FREQUENCY OF CLASS 1 AND 2 INTEGRONS AMONG PSEUDOMONAS AERUGINOSA

Mehrdad Halaji[1], Saba Jalalifar[2], Samereh Nouri[3], Mehrdad Zalipoor[4], Jamshid Faghri [5]

1. Students Research Committee, 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, Clinical Laboratory of ALZAHRA Medical Center, 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

Background and Aim: The role of integrons in the transfer of antibiotic resistance is one of the important issue, therefore, this study is aimed to investigate antibiotic resistance pattern and prevalence of class 1 and 2 integrons in P.aeruginosa isolated of nosocomial infection

Methods:P.aeruginosa isolates were collected during the April 2016 to August 2016 at a teaching hospital affiliated to Isfahan University of Medical Sciences, Isfahan, Iran. Antibiotic susceptibility pattern was assessed using disk diffusion method. PCR was carried out to detect the tox-A, class 1 and 2 integrons gene using the specific primers.

Results:A total of 72 confirmed P. aeruginosa isolates that half of them from ICU and most of the isolates were isolated from trachea samples. Antibacterial susceptibility pattern showed that ceftazidime revealed the most resistance (76.4%) and colistin was the most effective antibiotic (100%) and molecular analysis of class I and II integrons showed 55.5% and 29.1% of isolates were positive, respectively and The proportions of MDR isolates were significantly higher among integron-positive isolates with 43.3% compared to negative isolates with 22.9%.

Conclusion: Our results showed relevance among class 1 and 2 integrons and MDR P. aeruginosa isolates. According to the importance of integrons in acquisition and dissemination of antibiotics resistance genes among these pathogens, so, the performance of antibiotic surveillance programs is recommended for control the spreading of antibiotics resistance genes.

Keywords: Pseudomonas aeruginosa; Antibiotic Resistance; Integrons

P51 - 288: FREQUENCY OF SEPSIS IN THE NEONATES AND DETERMINATION OF ANTIBIOTIC RESISTANCE OF ISOLATES IN ISFAHAN

Vajihe Karbasizadh[1], Vajihe Karbasizade[2], Taiebeh Shakiba[3]

1. 1Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
2. 1Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran

Background and Aim: Sepsis is one of the serious infection in neonates. Prompt diagnosis and treatment play an important role in reducing neonatal mortality rate . The aim of this study was to determine the origin of this infection and antibacterial resistance pattern of the isolates.

Methods: In this study 108 cases of Umbilical cord blood culture ،153 peripheral blood culture were performed using BACTEC system. Bacterial isolates were identified by phenotypic and molecular methods. Antibiotic resistance patterns were determined using disk diffusion and Epsilometery methods . The PCR technique was used to determine the frequency of beta – lactamase genes.

Results: Out of the 21 neonates with sepsis 6 were early – onset and 15 were late onset . Escherichia coli ،Staphylococcus epidermidis and Klebsiella pneumoniae were the most common isolates from peripheral blood culture. Escherichia coli and Stenotrophomonas maltophilia were isolated from two neonatal cord blood. Most resistance was to cefixime, ceftriaxone ،cefotaxime in Gram positive isolates and to ampicillin in Gram negative bacteria. The frequency of bla – OXA48 gene and bla- CTXM15 gene was 25 % and 50 %respectively.

Conclusion: High prevalence of late – onset sepsis supports the role of the environment as a source of the neonatal sepsis . High drug resistance in the isolates reveals the importance of monitoring and accuracy in the use of antibiotics and improving infection control measures in the neonatal ward .

Keywords: Neonatal sepsis ،Antibiotic resistance ،Umbilical cord blood

P52 - 296: ANTIBIOFILM POTENTIAL OF CURCUMIN AGAINST AEROMONAS HYDROPHILA FISH ISOLATES

Hadi Tanhay[1], Hojjatolah Zamani[2], S. Shirin Shahangian[3]

1. Department of Biology, Faculty of Science, University of Guilan, Rasht, Iran
2. Department of Biology, Faculty of Science, University of Guilan, Rasht, Iran
3. Department of Biology, Faculty of Science, University of Guilan, Rasht, Iran

Background and Aim: Aeromonas hydrophila is a Gram-negative bacterium that can cause a variety of infections in fish and humans. Curcumin is a natural component of Curcuma longa rhizome. Several studies have reported the broad spectrum biological activities of curcumin such as anti-inflammatory, immunomodulatory, antioxidant, anticancer and antimicrobial effects. Biofilm formation is regarded as the main determinant factor in establishment of infection and bacterial pathogenicity. Antibiofilm potential of Curcumin has rarely been investigated. Thus, in this study antibiofilm activity of Curcumin was investigated.

Methods: Briefly, cultures of A. hydrophila fish isolates with the approximate cell populations of 1.5×108 CFU/mL were incubated for 48 h at 28 ℃ in Mueller-Hinton broth containing different concentration of Curcumin (32-512µg/mL) in 96 well microtiter plates. Cultures were removed, biofilm was washed three times with distilled water and stained using 150 µl of 0.3% (w/v) crystal violet for 15 min at room temperature. Crystal violet was dissolved using 30% (v/v) glacial acetic acid for 20 min and the absorbance was measured at 550 nm.

Results: Curcumin inhibited biofilm formation of A. hydrophila in a range of 31-75% compared to the control. In addition, the Biofilm inhibitory concentration (BIC) value of Curcumin was determined 64µg/mL.

Conclusion: Curcumin efficiently inhibited biofilm formation of A. hydrophila and thus, could be regarded as an efficient antibiofilm agent which could be used for preventive and therapeutic approaches.

Keywords: Curcumin, biofilm. Aeromonas, infection.

P53 - 306: SIX-YEAR EVALUATION OF THE ANTIMICROBIAL SUSCEPTIBILITY PATTERNS OF GRAM-POSITIVE BACTERIA CAUSING BLOODSTREAM INFECTIONS IN IRAN.

Babak Pourakbari[1], Shima Mahmoudi[2], Mina Moradzadeh[3], Masumeh Mahzari[4], Mohammad Taghi Haghi Ashtiani[5], Setareh Mamishi[6]

1. Pediatric Infectious Disease Research Center, Tehran University of Medical Sciences, Tehran, Iran.
2. Pediatric Infectious Disease Research Center, Tehran University of Medical Sciences, Tehran, Iran.
3. Pediatric Infectious Disease Research Center, Tehran University of Medical Sciences, Tehran, Iran.
4. Department of Infectious Diseases, Pediatrics Center of Excellence, Children's Medical Center, Tehran University of Medical Sciences, Tehran, Iran.
5. Department of Pathology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran.
6. Department of Infectious Diseases, Pediatrics Center of Excellence, Children's Medical Center, Tehran University of Medical Sciences, Tehran, Iran.

Background and Aim: Bloodstream infections (BSI) are considered as a serious cause of morbidity and mortality in children. The aim of this study was to report the common Gram-positive bacteria (GPB) responsible for bloodstream infections in children and determine their antimicrobial resistance patterns in Children Medical Center (CMC) Hospital, Tehran, Iran.

Methods: This retrospective study was conducted within a six-year period (March 2011 to September 2016) for pediatric patients with BSI. Standard bacteriological methods were performed for identification of the bacteria. Antimicrobial susceptibility tests were evaluated by using the disk diffusion method according to the CLSI recommendations.

Results: Among 68233 blood cultures, 2349 isolates were obtained which 59% of them (N=1393) were GPB and 41% (n=956) were Gram-negative. The most common GPB isolates were Coagulase negative Staphylococcus (CoNS) (N= 609, 44%), followed by Staphylococcus aureus (N=319, 23%), Enterococcus spp. (N=139, 10%), Streptococcus pneumonia (N= 106, 8%), Streptococci viridans (N= 180, 13%) Micrococcus spp. (N=24, 1.7%) and Streptococcus group B (N= 16, 1%). The rate of methicillin resistance in S. aureus and CoNS was 47% (N=116/246) and 91% (N=557/609), respectively. Isolates of S. pneumoniae showed high-level of resistance to trimethoprim/sulfamethoxazole (N=28/33, 85%) and erythromycin (N=59/91, 65%). S. viridans isolates and Micrococcus spp. were highly sensitive to linezolid (100%). All of the tested isolates of Streptococcus group B were sensitive to all the antibiotics used in this study. Among Enterococcus spp., 52% (N=69/133) of the m were resistant to vancomycin.

Conclusion: Our results emphasize the importance of a valuable guide in identifying resistance trends and selecting appropriate antibiotic.

Keywords: Bloodstream infection; Iran; antimicrobial resistance; children; gram-positive bacteria

P54 - 308: ANTIBACTERIAL ACTIVITY OF NIGELLA SATIVA EXTRACT AGAINST TWO PATHOGENIC BACTERIA

Mohammad Mehdi Attarpour Yazdi[1]

1. Department of Microbiology, Faculty of Medicine, Shahed University, Tehran, Iran

Background and Aim: Background: Medical herbs with anti microbial activity have always been important in traditional medicine and might be useful in antibacterial activity against the many pathogenic bacteria cause serious infections. The aim of this study was to determine the antibacterial activity of methanolic extract from Nigella sativa against 2 pathogenic bacteria in vitro.

Methods: Methods: At first the seed of Nigella sativa extracts were prepared by the methanolic wetting extraction method in five different concentrations (400, 200, 100, 50, 25µg) and then its antibacterial activity against 2 standard strain bacteria (Escherichia coli or E.coli and Pseudomonas aeruginosa) was tested for the determination of MIC (minimum inhibitory concentration) and inhibitory zone diameter (ZOI) using disk diffusion method and agar serial dilution assays. Also the antibacterial activity of 11 antibiotics such as chloramphenicol, trimethoprim, streptomycin, gentamicin, erythromycin, doxycycline, nalidixic acid, ampicilline and est. was tested by the disk diffusion method.

Results: Results: Statistical methods were using to analyze the data. The results demonstrated that the Nigella sativa methanolic extracts been effective against the 2 standard strain bacteria. (E.coli and Pseudomonas aeruginosa) .The methanolic extract of Nigella sativa was highly effective with 400 µg concentration. The methanolic Nigella sativa extract exhibited greater antibacterial activity than all of the selective antibiotics,

Conclusion: Conclusion: This study demonstrates that methanolic extracts from the combination of the Nigella sativa constituents have excellent antibacterial activity against the 2 standard strain pathogenic bacteria. Further investigations will be necessary.

Keywords: Keywords: pathogenic bacteria, Antibacterial activity, Nigella sativa

P55 - 314: ANTIBIOTIC RESISTANCE PATTERN OF METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS (MRSA) STRAINS ISOLATED OF CLINICAL SPECIMENS IN AHVAZ, IRAN

Simin Ariyarad[1]

1. Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Ahvaz, Iran

Background and Aim: Staphylococcus aureus (S. aureus) is an important pathogen causing hospital-associated infections. Because of emerging resistance to many antimicrobial drugs, treatment of this bacterium is difficult. Methicillin-resistant S. aureus (MRSA) have emerged as a clinically relevant human pathogen. The aim of this study was to determine the frequency and pattern of antibiotic resistance among MSRA strains isolated from patient in Ahvaz hospitals.

Methods: In this descriptive study, Staphylococcus aureus isolates has been collected from hospitals of Ahvaz city. Biochemical and phenotypic tests were performed to identify MRSA strains. Determination of antibiotic resistance pattern of MRSA strains was done using disk diffusion method against nine antibiotics based on CLSI protocol. Antibiotic disks were included erythromycin, clindamycin, penicillin, methicillin, cefoxitin, ceftazidime, ciprofeloxacin, gentamycin and imipenem. To determine the resistance and sensitive to methicillin cefoxitin disk (30 µg) was used.

Results: In this descriptive study, 155 samples were collected from patients during 9 month. Antibiotic resistance pattern was reported as follow: penicillin (97%), methicillin (94%), ceftazidime (93.5%), cefoxitin (77.5%), erythromycin (72%), clindamycin (62%), ciprofeloxacin (60%), gentamycin (54%) and imipenem (55%). Sixty five (42%) of the bacterial samples were resistant to all antibiotics

Conclusion: The high frequency of antibiotic resistance among these strains indicates the improper administration of antibiotics in a non-bacterial infections, incomplete course of treatment and easy access to antibiotics. These reasons can help the development of multi-resistance isolates.

Keywords: Staphylococcus aureus, Methicillin, MRSA, Antibiotic resistance

P56 - 315: OCCURRENCE OF THE METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS (MRSA) AMONG RESPIRATORY TRACT SAMPLES IN PATIENTS ADMITTED IN IMAM REZA HOSPITAL, BOJNURD, IRAN IN 1396

Zahra AliAbadi[1], Mahsa Mirzaei[2], Saghar Safamanesh[3], Mahsa Khosrojerdi[4], Amir Azimian[5]

1. B.Sc of Laboratory Sciences, Food and Drug Laboratory, North Khorasan University of Medical Sciences, Bojnurd, Iran.
2. B.Sc of Laboratory Sciences, Bentolhoda Hospital, North Khorasan University of Medical Sciences, Bojnurd, Iran.
3. M.Sc of Medical Virology, Faculty of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
4. M.D, Specialist in Pediatrics, Department of Pediatrics, Faculty of Medicine, Semnan University of Medical Sciences and Health Services, Semnan, Iran.
5. Department of Pathobiology and Laboratory Sciences, faculty of medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.

Background and Aim:: Staphylococcus aureus is one of the major pathogens. Methicillin-Resistant Staphylococcus aureus (MRSA) is responsible for an increasing number of serious nosocomial and community acquired infections including superficial lesions and wound infections, osteomyelitis, endocarditis, pneumonia, bacteremia, Toxic shock syndrome and food poisoning. The purpose of this study was to define the prevalence of MRSA strains among S. aureus strains isolated from Respiratory tract samples of patients of selected Tehran hospitals with conventional and molecular methods.

Methods:A total 55 isolates from Respiratory tract samples were evaluated by disk diffusion and MIC agar dilution tests according to the guidelines of the Clinical Laboratory Standards Institute (CLSI) and PCR assay for mecA gene.

Results: Prevalence of MRSA strains were %50 with disk diffusion method, %51.74 with MIC method and %50.9 using PCR method for detection of mecA gene. Also the drug resistance for other antibiotics of isolates was to Rifampin (%26.66), Penicillin (%100), Vancomycin (%0), Co-trimoxazole (%47.27), Gentamycin (%58.18), Tetracycline (%67.27), Erythromycin (%65.45), Ciprofloxacin (%50.9), Amikacin (%49.09) and Doxycycline (%34.54).

Conclusion:our results show relatively good correlation between phenotypic and genotypic methods for antibiotic susceptibility tests. These differences were not statistically significant (P>0.05). It's necessary to stablish a solution for control and suitable treatment of the MRSA isolates and prevention of hazardous epidemy.

Keywords: Staphylococcus aureus, Methicillin, Resistance, mecA

P57 - 318: FIRST PREVALENCE OF METALLO BETA-LACTAMASES PRODUCING ENTEROBACTERIACEA IN IRANIAN CANCER PATIENTS

Donya Zare[1], Hossein Fazeli[2]

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

Background and Aim: Hospital-associated infections (HAIs) are among the most common life-threatening complications of hospitalized patients, especially the immunocompromised patients. Regarding the significant role of Enterobacteriaceae in nosocomial infections and also the increasing trends of carbapenem-resistant strains, the present study aimed to evaluate the antibiotic resistance pattern and the occurrence of metallo-beta-lactamases (MBLs) in Enterobacteriaceae strains from Iranian cancer patients.

Methods: This hospital-based cross-sectional study was conducted in teaching hospitals of two cities in the central parts of Iran during the 6 months period from December 2015 to May 2016. The Enterobacteriaceae isolates were obtained from different clinical specimens and were identified using standard microbiological methods. Antimicrobial susceptibility pattern for the bacterial isolates was determined using the disk diffusion method. The presence of antibiotic resistance genes was determined by PCR method.

Results: The distribution of Enterobacteriaceae isolates were 74 (71.8%) E. coli, 23 (22.3%) Klebsiella spp., 3 (2.9%) Proteus spp., 2 (1.9%) Salmonella spp., and 1 (1%) Shigella spp. The results of antibiotic susceptibility revealed that all of the isolates were multiple-drug resistant (MDR) and 60% of them were (excluded Salmonella and Shigella) carbapenem-resistant. Of all the carbapenem-resistant isolates, 31.7% were MBL-positive. Meanwhile, fosfomycin and minocycline were the most effective antibiotics against MBL-positive bacteria. Moreover, none of the investigated carbapenemases genes were found in MBL-positive isolates.

Conclusion: This study highlights the importance of MBLs producing Enterobacteriaceae in causing nosocomial infections in cancer patients. However, carbapenem resistance was not associated with the presence of MBL genes such as IMP, VIM, and SPM.

Keywords: Enterobacteriaceae, Metallo-beta-lactamases, Carbapenemases, Antibiotic resistance, Cancer patients

P58 - 321: GENETIC ANALYSIS OF STAPHYLOCOCCUS AUREUS STRAINS ISOLATED FROM PATIENTS ADMITTED TOM EMAM REZA HOSPITAL IN BOJNURD

Amir Azimian[1], Seyed Ahmad Hashemi [2], Majid Ghafouri [3], Saghar Safamanesh [4], Sara Nojoomi[5], Khosrojerdi Mahsa [6], 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 its 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

P59 - 323: EVALUATION OF SOME HEAVY METALS AND ANTIBIOTICS RESISTANCE IN SOME OF PROBIOTIC BACTERIA

Leila Goudarzi[1], Rouha Kasra Kermanshahi[2], Gholamreza Jahed Khaniki[3], Sara Gharavi[4]

1. PhD student in Microbiology, Department of Microbiology, Faculty of Science, Alzahra University, Tehran, Iran
2. Full Professor, Ph.D. in Microbiology, Department of Microbiology, Faculty of Science, Alzahra University, Tehran, Iran
3. Professor, Ph.D. in food hygiene, Department of food hygiene, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
4. Associate Professor, Ph.D. in Genetics, Department of Biotechnology Faculty of Science, Alzahra University, Tehran, Iran

Background and Aim: The emerging development of the industry has caused a serious problem for human health. One of the most important issues, is food contamination with heavy metals. The entry of heavy metals into the food chain at critical concentrations will have adverse metabolic and physiological effects on living organisms. This study was conducted to determine the resistance profile of probiotic bacteria to heavy metals (lead and cadmium) and different antibiotics.

Methods: In this study, six standard Lactobacillus species were investigated. The susceptibility of bacterial species to lead and cadmium as heavy metals, and different antibiotics such as erythromycin, vancomycin, tetracycline, chloramphenicol, streptomycin, kanamycin and gentamicin by Broth Microdilution Method in a 96-well micro-titer plate for determining Minimum Inhibitory Concentration (MIC) were assayed. Combination of different antimicrobial agents as FIC index (Fractional Inhibitory Concentration) were also calculated consequently.

Results: The results showed that the growth of all studied bacteria were inhibited for vancomycin at higher concentration and for erythromycin at the lowest concentration. Also the growth of all strains for lead as a heavy metal was inhibited at higher concentrations than cadmium. Combination of vancomycin and cadmium in Lactobacillus acidophilus ATCC 4356 and Lactobacillus plantarum ATCC 8014, and streptomycin and cadmium in Lactobacillus rhamnosus ATCC 7469 resulted in synergistic effects.

Conclusion: All studied bacteria had different antibiotic and heavy metal resistance patterns. Because of that these bacteria are continually challenging with different antimicrobials agents, throughout their lives, the persistence of this exposure could convert the probiotic bacteria as a resistance reservoir related to food for antibiotics and heavy metals.

Keywords: Heavy metal resistance, Antibiotic resistance, Minimum Inhibitory Concentration, Fractional Inhibitory Concentration, Synergistic effects

P60 - 324: EVALUATING THE SIMULTANEOUS IMPACT OF NANOPARTICLES WITH NETTLE EXTRACT AGAINST KLEBSIELLA THROUGH A CHECKERBOARD METHOD

Mahsa Dadgar[1], Sara Minaeian[2], Somayeh Samimi[3], Meisam Sadeghpour Karimi[4]

1. Department of Biology, East Tehran Branch, Islamic Azad University, Tehran, Iran.
2. Antimicrobial Resistance Research Center, Institute of Immunology and Infectious Diseases, Rasoul-e-Akram Hospital, Iran University of Medical Sciences, Tehran, Iran
3. Ebnemasouyeh pharmaceutical company
4. Center of Excellence in Electrochemistry, University of Tehran, Tehran, Iran.

Background and Aim: Klebsiella pneumonia is seen numerously in people hospitalized at the hospitals as well as people with weak immunity, so antibiotic resistance is a serious threat in this bacteria. Silver nanoparticles and many herbal extracts influence a wide range of bacteria due to the large antibacterial effect. The purpose of this study is to investigate the simultaneous effect of silver nanoparticles with nettle extract against Klebsiella bacteria through a checkerboard method.

Methods:350 samples were collected from patients hospitalized in all wards of Rasool-e-Akram hospital. 112 Klebsiella strains were isolated using biochemical tests. Among them, resistant isolates were separated. The effects of silver nanoparticles, nettle extract, the combination of nettle extract and silver nanoparticles on the isolated bacteria were investigated using MIC and checkerboard methods.

Results: The results showed that MIC for nettle extract is 0/7mg/ml against both isolates and is 0/78mg/ml for silver nanoparticles against ATCC isolate and is 3/125 mg/ml against MDR isolate. Simultaneous application of silver nanoparticles and nettle extract has a synergistic effect against the resistant isolate and an incremental effect against the standard isolate.

Conclusion: Due to the increasing number of hospital infections and because bacteria are resistant against existing antibiotics, it is important to find a substitute for antibiotics with new materials having antibiotic characteristic, in near future. Because their production is cost effective and they have a good effect on resistant bacteria, they can be used in antibiotic treatments and their antibacterial effect can be exploited.

Keywords: silver nanoparticles, Klebsiella, nettle extract, synergism

P61 - 325: PREVALENCE OF SALMONELLA SEROGROUPS IN CHICKEN MEAT OF ARDABIL, NORTHWEST OF IRAN

Aidin Azizpour[1], Ciamak Ghazaei [2], Zahra Amirajam [3], Rahem Khoshbakht[4]

1. Assistant Professor, University of Mohaghegh Ardabili, Ardabil, Iran
2. Assistant Professor of Microbiology, University of Mohaghegh Ardabili, Ardabil, Iran
3. Assistant Professor of Cardiology, Ardabil University of Medical Sciences, Ardabil, Iran
4. Assistant Professor, Amol University of Special Modern Technologies, Amol, Iran

Background and Aim: Salmonellosis is one of the most common digestive diseases in the world. Salmonellosis is caused by varieties of salmonella serotypes and there are concerns about the contamination of poultry and its products by this microorganism.The purpose of this study was to investigate the prevalence of Salmonella serogroups in chicken meat of Ardabil, northwest of Iran.

Methods: One-hundred chicken meats were collected from chicken carcass retailers between January and March 2018. Salmonella spp were isolated from suspected positive cultures.Then, they were identified and confirmed by means of biochemical and serological tests.

Results: Salmonella was isolated from 6 samples (6%). Serogrouping results revealed that 66.7 % of samples belong to serogroup C and 16.6% of them were serogroup D and 16.6% serogroup B.

Conclusion: The results of this study show that the dominant serogroup was C .This finding is important for public health. Applying a health strategy for reduction of contamination level is necessary.

Keywords: Salmonella, Chicken Meat, Serogroups, Ardabil

P62 - 329: BIODEGRADATION OF TETRACYCLINE BY BASIDIOMYCETE FUNGUS PLEUROTUS OSTREATUS

Ayda Maadani mallak[1], Amir Lakzian[2], Elham Khodaverdi[3], Gholamhossein Haghnia[4]

1. Ferdowsi University of Mashhad, FUM Campus, Department of Soil Science
2. Ferdowsi University of Mashhad, FUM Campus, Department of Soil Science
3. Mashhad university of medical sciences, MUMS, Department of pharmaceutics
4. Ferdowsi University of Mashhad, FUM Campus, Department of Soil Science

Background and Aim: Nowadays, widespread use of pharmaceuticals in modern medicine has been raised as an environmental hot topic which is called them as emerging contaminants. Among diverse group of pharmaceuticals, antibiotics as over the counter therapeutic drugs, has aroused much public health attention. The most important following threat is easily spread of antibiotic-resistant bacteria through different routes as not completely metabolized drugs via excretion to the wastewater. To avoid the entry of these compounds into the land and human food chain, finding a suitable method which is capable of antibiotic degradation before entering to the environment can be afforded.

Methods: In this way, a study was conducted to investigate the biodegradability of tetracycline by Pleurotus ostreatus fungi in potato dextrose broth. The experimental factors consisted of inoculated and noninoculated treatments with P. ostreatus), three concentrations of tetracycline (0, 50 and 100 µgml-1) and three times (4, 7, 10 days).Tetracycline removal from the medium was detected by LC-MS/MS analysis. Fungal laccase and peroxidase activity as involved degrading agents were also monitored during the experiment.

Results: Results showed P. ostreatus was capable of suppressing 50 µgml-1 tetracycline within earlier than 4 days to undetectable concentrations. Almost Complete removal of tetracycline at 100 µgml-1 was occurred within the first 4 days of incubation. Whereas in noninoculated treatments just negligible removal of 9% tetracycline at 100 µgml-1 up to the end of the experiment was detected. Steady increase in enzymatic activity was simultaneously occurred during the experiment.

Conclusion: All evidences coincide with significant degradation capability of P. ostreatus.

Keywords: Biodegradation, Tetracycline, P. ostreatus, Laccase, peroxidase

P63 - 339: A COMPARISON STUDY OF PYRAN AND PYRAN NANOPARTICLES INHIBITORY EFFECT ON AMPC BETA-LACTAMASE PRODUCING KLEBSIELLA ISOLATES

Sara Doodi [1], Azam Haddadi[2], Zohreh Moemani [3]

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: The prevalence of extended spectrum beta-lactamses (ESBLs)-producing strain and their resistance to beta-lactam antibiotics has had a daily increase.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 105 clinical Klebsiella isolates. Antimicrobial susceptibility was performed using Kirby-Bauer disk diffusion method against cefepime, ceftazidime, ceftriaxon and cefotaxime. These isolates were also tested for ESBLs production by phenotypic confirmatory test (PCT). MIC of pyran and pyran nanoparticles were determined using sterile 2ml 96-well plates. The tested dilutions ranged from 2500 to 9.76 µg/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:ESBLs screening of strains by phenotypic combined disc test showed that out of 105 samples 13% (14) were ESBLs positive. ESBLs-producing isolates were tested for MIC valus. Pyran and pyran nanoparticles showed antibacterial activity with MIC values of 312.5 and 154.25 µg/mL respectively. Furthermore MBC pyran and pyran nanoparticles were 1250 and 312.5 µg/mL respectively.

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: Klebsiella, ESBLs, nanoparticles

P64 - 343: ANTIBACTERIAL ACTIVITY OF CINNAMOMUM ZEYLANICUM ETHANOLIC EXTRACT AGAINST ESCHERICHIA COLI ISOLATED FROM URINARY TRACT INFECTIONS

Mohammad Mehdi Attarpour Yazdi[1]

1. Department of Microbiology, Faculty of Medicine, Shahed University, Tehran, Iran

Background and Aim: Background: Escherichia coli (E.coli) are 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 ethanolic extract of Cinnamomum zeylanicum against E.coli isolated from UTI in vitro.

Methods: Methods: This research is a descriptive analytic study. First, samples of ethanolic extract of Cinnamomum zeylanicum were prepare by maceration method. Then its antibacterial activity against 75 isolates of E.coli from 100 samples of UTI was evaluated by well diffusion and then agar serial dilution method. Also, the MIC (Minimum Inhibitory Concentration) and MBC (Minimum Bactericidal Concentration) of extract was determined. Also the antibacterial activity of 11 antibiotics such as chloramphenicol, trimethoprim, streptomycin, gentamicin, erythromycin, doxycycline, nalidixic acid, and est. was tested by the disk diffusion method.

Results: Results: The diagrams, T- test were used to compare the results. The results demonstrated that the ethanolic extracts of Cinnamomum zeylanicum show an average inhibitory zone diameter of 17mm. The ethanolic extract shows best result having ZOI greater than that of the selective antibiotics. There was no significant difference between the effects of the plant ethanolic extract and the antibiotics on E.coli (P>0.05).

Conclusion: Conclusion: This study demonstrates that an ethanolic extract of Cinnamomum zeylanicum have antibacterial activity against E.coli isolated from UTI and its effect is similar selective antibiotic. Further investigations will be necessary.

Keywords: Key words: UTI, Escherichia coli, Cinnamomum zeylanicum, Antibacterial Activity

P65 - 347: THE STUDY OF EFFECTIVE BACTERIAL FACTORS IN FORMING THE POST BURN INFECTION IN BURN SECTION OF NEKUEI – HEDAYATI HOSPITAL OF QOM

Mohammad Khodadad Motlagh[1]

1. qom university, qom

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

P66 - 350: SEROTYPING AND ANTIBIOTIC RESISTANCE PATTERNS OF ISOLATED SALMONELLA FROM ANIMAL FEED IN ARDABIL, NORTHWEST OF IRAN

Ciamak Ghazaei[1], Aidin Azizpour[2], Zahra Amirajam [3], Saeed Seifi[4]

1. Assistant Professor of Microbiology, University of Mohaghegh Ardabili, Ardabil, Iran
2. Assistant Professor of Poultry Diseases, University of Mohaghegh Ardabili, Ardabil, Iran
3. Assistant Professor of Cardiology, Ardabil University of Medical Sciences, Ardabil, Iran
4. Assistant Professor of Poultry Diseases, Amol University of Special Modern Technologies, Amol, Amol, Iran

Background and Aim: Salmonellosis is one of the most important zoonotic diseases. Antimicrobial therapy is an important tool in reducing Salmonella infections, but the indiscriminate use of antibiotics in poultry farms can lead to the emergence of resistance and inefficacy of antimicrobials. The purpose of this study was to investigate the prevalence of Salmonella serogroups in animal feed of Ardabil, northwest of Iran

Methods: Fifty animal feed were collected from different farms between January and March 2018. Salmonella spp were identified. After microbial culture and isolation, serotyping with commercial antiserum was performed. The Antibiotic resistance rate of isolates was determined by Kirby Bauer disc diffusion method

Results:8 % animal feed samples were positive to Salmonella spp. The Salmonella isolates belonged to serogroups D (50 %), C (25 %) and Unknown (25 %). Isolates D and C were resistant to tetracycline. The highest resistance was to cloramfenicol (66.6%), ampicillin (66.6%), Sulfadiazin + trimethoprim (66.6%), amikacin (66.6%) and cotrimoxazole (66.6%). The lowest levels of resistance were for doxycycline (33.3%), florfenicol (33.3%) and ciprofloxacin (33.3%). All isolates were sensitive to enrofloxacin.

Conclusion: The high prevalence of resistant salmonellae among animal feed indicates that the administration of antimicrobial drugs has to be made with more caution.

Keywords: Animal feed, Salmonella, Antibiotics resistance, Ardabil

P67 - 356: MOLECULAR STUDY OF PMRA, PMRB AND MCR-1 GENES IN PSEUDOMONAS AERUGINOSA ISOLATES AMONG BURN PATIENTS IN SHAHID MOTAHARI HOSPITAL, TEHRAN, IRAN

Ghazaleh Talebi[1], Ali Hashemi[2], Mojdeh Hakemi Vala[3]

1. Dept. of Microbiology, Faculty of Basic Sciences, Tehran Science and Research Branch, Islamic Azad University, Tehran, Iran
2. Dept. of Microbiology, Medical school, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. Dept. of Microbiology, Medical school, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim:P. aeruginosa is a major cause of hospital acquired infection, especially in patients admitted in burn care unit. Colistin is the last chance in multi drug resistant (MDR) isolates. In this experiment, molecular study of PmrAB (as a two component regulatory system), presumptive mutation and frequency of mcr-1 which are relayted to Colistin resistance were detected.

Methods:80 P. aeruginosa isolates from burn wounds, in Shahid Motahari Hospital during Feb-Jun 2017 were collected. According to CLSI guideline 2017, antibiotic susceptibility test was performed by using disk diffusion method. Detection of pmrA, pmrB and mcr-1 genes was administrated by PCR. Also, sequencing was applied to finding the mutations in pmrA and pmrB genes.

Results: Among 80 isolates of P. aeruginosa the highest resistance were against: Gentamycin, Piperacillin and Ceftazidime 95.1%, Imipenem 93.5%, Ciprofloxacin, Aztreonam, Piperacillin-Tazobactam 88.7%, Cefepime 85.5% and 83.8% were resistant to Amikacin. Also, all of the isolates were susceptible to Colistin. PCR results showed that 100% of the isolates had pmrA and pmrB . All were negative for mcr-1. One of the isolates show different mutations in pmrA gene (Cys 429 to Ala, Gly 457 to Cys, Gly 460 to Cys, Gly 475 to Cys, Gly 477 to Cys, Ala 518 to Gly). In pmrB the mutations were as follows: (Ala 1000 to Gly, Gly 1098 to Ala, Ala 1230 to Gly and Cys 1341 to Gly).

Conclusion: To confirm the phenotypic results, doing molecular tests are recommended which may help physicians to prescribe the best and most appropriate antibiotic.

Keywords: Colistin, Pseudomonas areruginosa, burn, antibiotic resistance

P68 - 360: ANTIFUNGAL EFFECT OF ALLIUM CEPA ETHANOLIC EXTRACT AGAINST TRICHOPYTON RUBRUM

Zeynab Mosazadeh[1], Masoomeh Shams- Ghahfarokhi[2], Mehdi Razzaghi – Abyaneh[3]

1. Department of Mycology, Tarbiat Modares University, Iran
2. Department of Mycology, Tarbiat Modares University, Iran
3. Department of Mycology Pasteur Institute, Iran

Background and Aim: Dermatophytosis is one of the most common superficial fungal infections worldwide. Trichophyton rubrum is one of the most common of dermatophytes that caused variety of clinical forms. Due to the recurrence of recurrent infections due to the resistance of the organism to the drug and the side effects of prolonged use of anti-inflammatory drugs, including long-term therapeutic strategies the aim of this study was to investigate the effect of ethanolic extract of Alium cepa (AEC) on T.rubrum growth.

Methods: The inhibitory effect of (ACE) extract against T. rubrum was assessed by broth microdilution (CLSI, M-38) methods in comparing with terbinafine.

Results: The results showed that the minimum inhibitory concentration (MIC) of ACE and terbinafin for fungi growth was 1.46 and 1µg/ml and MIC 50 for these compounds was 0.73and 0.5 µg/m l, respectively.

Conclusion: The results of this study showed that ACE is an effective factor that inhibit Thrichophyton rubrum growth and can be considered as a target for antifungal design methodology.

Keywords: Allium cepa, Trichophyton rubrum, MIC, Antifungal effect

P69 - 365: THE PREVALENCE OF GYRA GENE MUTATIONS IN FLUOROQUINOLONES-RESISTANT PSEUDOMONAS AERUGINOSA ISOLATES IN GUILAN PROVINCE

Pouria Sheikhi[1], Saeed Veysi[2], Somayeh Hosseini khomeirani[3], Gholamreza safari[4], Afshin Taravati[5]

1. Department of Microbiology, Rasht Branch, Islamic Azad University, Rasht, Iran
2. Young Researchers and Elite Club, Rasht Branch, Islamic Azad University, Rasht, Iran
3. Department of Microbiology, Faculty of Advanced Sciences & Technology, Pharmaceutical Sciences Branch, Islamic Azad University,Tehran, Iran (IAUPS)
4. Department of Biology, Rasht Branch, Islamic Azad University, Rasht, Iran
5. Department of Veterinary Science, Rasht Branch, Islamic Azad University, Rasht, Iran

Background and Aim: Pseudomonas aeruginosa is one of the most common causes of opportunistic infections. There are several mechanisms for resistance to antibiotics in this bacterium. Fluoroquinolones are the only accessible antibiotics for effective oral treatment of infections caused by this organism. Among fluoroquinolones, ciprofloxacin is widely used in the treatment of P. aeruginosa infections. The aim of this study was to evaluate the prevalence of gyrA mutations in fluoroquinolones-resistant P. aeruginosa isolates in Guilan Province.

Methods: In this study, a total of 68 clinical isolates of P. aeruginosa were collected. All isolates were identified by standard biochemical tests. The antibiotics susceptibility was determined by disk diffusion method and MIC; Then, PCR-sequencing was carried out to identification mutation involved in fluoroquinolones resistance.

Results: From 68 clinical isolates of P. aeruginosa, 12 isolates were fluoroquinolone resistance. Ciprofloxacin resistant isolates showed MIC between 32 to 1024 µg/ml. PCR-sequencing showed all 12 fluoroquinolone resistance isolates had at least one or more mutation in gyrA gene.

Conclusion: The results of this study showed that the rate of resistance to ciprofloxacin is significantly increasing, which may be due to various mutations in the gyrA gene. Early detection and infection-control are the best antimicrobial strategies for this organism.

Keywords: Pseudomonas aeruginosa, Ciprofloxacin, gyrA, mutation

P70 - 374: EVALUATION OF ANTIMICROBIAL AND HEALING PROPERTIES OF BDELLIUM,DRACOCEPHALUM AND DIANTHUS EXTRACTS ON PSEUDOMONAS AERUGINOSA,STAPHYLOCOCCUS AUREUS,ESCHERCHOA COLI AND ENTREROCOCCUS FEACALIS INFECTIONS IN THE IN_VITRO AND MICE MODEL

Fateme Zayer[1], Reza shapori[2], Khatereh sayadi[3]

1. Tel:09147589174 E-mail:F.zayerr@gmail.com
2. Tel:09123255364 E-mail:rezashapouri@yahoo.com
3. Tel:09125417064 E-mail:kh.sayyadj@gmail.com

Background and Aim:P.a,S. a,E.c and E.fare the most important common hospital infactions that have high antibiotic resistance.Aim of this study is avalution of antimicrobial effects of Bdellium,Bracocephalum and Dianthus acetonic and ethanolic extracts in the invitro and animal model

Methods: Extracts of plants were prepared,then MIC and MBC of extracts on bacteria were determind by broth macrodilution method. In animal model,burning infection was induced by P.a and S.a separately,then Eucerin and Euerin with plant extracts were used as ointment for treatment (1g for 3 day)in female mice .Then number of colonies of bacteria counted on muller_hinton agar

Results: Ethanolic and acetonic extracts of Dianthus had strong effect on P.a and S.a (MBC=4/ 562 mg/ml) and 11/396 MBC of ethanolic ectact of Dracocephalum was 15/292 mg/ml four P.a and ethanolic extract for Bdellium was 68/167 mg/ml for E.f .Dianthus had strong effect on P.a and S.a with MBC =4/562 mg/ml for ethanolic extract and shown same MBC=11/396 mg/ml for all of bacteria on acetonic extracts.Dracocephalum had strong effect on P.a with MBC=15/292 mg/ml and E.f with MBC =39/333 mg/ml for ethanolic and acetonic extracts ,repectively.Bdellium had strong effect on E.f with MBC=68/167 mg/ml and 42/083 mg/ml for ethanolic and acetonic extracts, repectively .Results of animal model shown thw prepered ointment from these plants extracts were usefull fortreatment of infection in mice burning model

Conclusion: The results of this study were shown that extracts of Bdellium,Dracoce phalum and Dianthus have effective antimicrobial and healing properties that may be used in clinic

Keywords:P.a,S.a,E.c, E.f,medicinal plants

P71 - 375: ANTIBIOTIC RESISTANCE AMONG ESCHERICHIA COLI, PSEUDOMONAS AERUGINOSA AND ACINETOBACTER BAUMANNII ISOLATES OBTAINED FROM SHIRAZ NAMAZI HOSPITAL ICU WARDS

Reza Khashei[1], Zahra Navabi[2], Samaneh Mohebi[3], Naser Samadi[4]

1. Department of Bacteriology and Virology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran
2. Department of Bacteriology and Virology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran
3. Department of Bacteriology and Virology, School of Medicine, 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: The monitoring of the causative agents of nosocomial infections (Nis), particularly in the Intensive Care Unit (ICU) ward to detect any change in pattern of infection and their resistance profile are crucial. The aim of this study was to investigate the antibiotic resistance pattern among Gram-negative rods isolated from inpatients in ICU different wards in Shiraz, Iran.

Methods: In this cross-sectional study from Jaunary to June 2017, 91 different clinical samples were collected from Nemazi teaching hospital ICU wards. After confirmation of all the isolates by the conventional microbiologic methods, antimicrobial susceptibility pattern of them against 11 antibiotics using the disk diffusion test were investigated. Extended-spectrum β-lactamase (ESBL) production was also examined.

Results: The isolated bacteria were Acinetobacter baumannii (n=72, 79.1%), Pseudomonas aeruginosa (n=14, 15.4%), and Escherichia coli (n=5, 5.5%). The majority of bacteria were isolated from the respiratory infections. The highest and the lowest resistance rates were observed against ampicillin (100% and 95.8%) among P. aeruginosa and A. baumannii and imipenem and amikacin (0%) among P. aeruginosa and E. coli isolates, respectively. The frequency of multidrug-resistant (MDR) and ESBL-producing isolates was found 84.6% and 19.8%, respectively. Of the MDR isolates, 23.4% were ESBL producers. A significant difference was determined between ESBL production and MDR isolates.

Conclusion: Regarding the high rate of antimicrobial resistace among clinical isolates in our region, the antibiotic susceptibility results may be a useful guide for empirical therapy used by physicians.

Keywords: Nosocomial infections, ICU, Antimicrobial resistace, Iran

P72 - 386: FREQUENCY OF ISOLATION AND ANTIMICROBIAL RESISTANCE PATTERN OF GRAM-POSITIVE BACTERIA ISOLATED FROM PATIENTS REFERRED TO PRIVATE DIAGNOSTIC MEDICAL LABORATORIES IN FARS, SOUTHWEST IRAN

Fatemeh Moradi[1], Sepide Namdari[2], Ali Farhadi[3]

1. B.Sc Department of Medical Laboratory Sciences, School of Paramedical Sciences, Shiraz University of Medical Sciences, Shiraz, Iran
2. M.S Diagnostic Laboratory Sciences and Technology Research Center, School of Paramedical Sciences, Shiraz University of Medical Sciences, Shiraz, Iran.
3. PHD Diagnostic Laboratory Sciences and Technology Research Center, School of Paramedical Sciences, Shiraz University of Medical Sciences, Shiraz, Iran.

Background and Aim: Private laboratories play an important role as specialized units in diagnosis of many diseases including bacterial infections. Although, the prevalence and antimicrobial resistance of Gram-positive bacteria isolated from nosocomial origins are frequently reported in many studies but there is no data available regarding the prevalence and antimicrobial resistance of Gram-positive bacteria isolated from patients referred to private diagnostic medical laboratories in Fars, Southwest of Iran.

Methods: In a cross-sectional study during a one year period from February 2015, microbiological data of all biological samples of patients referred to five different private diagnostic medical laboratories in Shiraz in favor of gram-positive bacteria were analyzed retrospectively. In all included laboratories, protocols of identification of Gram-positive bacteria and antimicrobial susceptibility testing by Kirby–Bauer disc diffusion method were checked to assure that reported data are within the standard values.

Results: The most common isolated Gram-positive bacteria from 74 urine, 40 wound, 6 sputum, 5 discharge and 4 throat positive culture samples were Enterococcus spp. (67%), Staphylococcus aureus (40%), S. aureus (100%), S. aureus (75%) and S. aureus (80%), respectively. All Enterococcus spp. isolates were resistant to nalidixic-acid and trimethoprim-sulfamethoxazole and 96% of them were resistant to Cephalexin, Amikacin, Ciprofloxacin and Norfloxacin. Furthermore, 50% of all identified S. aureus isolates were resistant to Erythromycin as well.

Conclusion: These results inform the physicians which antibiotics are not to be prescribed to the patients; however, due to high sensitivity rate of Enterococcus spp. and S. aureus to Vancomycin, it can be remained as the first line treatment of related infections.

Keywords: Gram- positive bacteria; Antimicrobial resistance; private diagnostic medical laboratories

P73 - 389: ANTIBIOTIC SENSITIVITY PATTERN IN PATIENTS WITH URINARY TRACT INFECTIONS

Zohreh Khazaee[1], Mr Jaber Imanifard[2], Mr Javad Dehghani[3]

1. Dr Neshat's clinical Laboratory, Shiraz, Iran
2. Dr Neshat's clinical Laboratory, Shiraz, Iran
3. Dr Neshat's clinical Laboratory, Shiraz, Iran

Background and Aim: Urinary tract infections are one of the most infectious diseases which happen in different ages. If they are not cured appropriately, this can lead to serious consequences. Evaluation of antimicrobial resistance pattern is essential to improving treatments and also for considering increase of drug resistance.

Methods: In this study, a total of 930 samples which recognized as Enterobacteriaceae, were analyzed during 2014 to 2017 at Neshat's clinical laboratory.

Results: In this descriptive study, the frequency of enteric bacteria was E.coli (72%), Klebsiella (11%), Proteus (4.94%), Entrobacter (2.79%), Serratia (2.47%) and Pseudomonas (0.64%) respectively. Among all these bacteria, the most susceptibility belonged to the ciprofloxacin, while E.coli, had the most sensitivity to FM (Nitrofurantoin) antibiotic. The results show that, SXT (trimethoprim-sulphamethoxazole) and CN (cephalexin) are the most resistant antibiotics

Conclusion: An annual survey of E. coli shows that this bacteria is becoming resistant to CP antibiotic. To overcome, drug resistance levels of common intestinal bacteria are developing. To conclude, it has been found that the most effective antibiotic in urinary tract infections is ciprofloxacin.

Keywords: Urinary tract infections, Antibiotic, Suceptibility,resistance

P74 - 391: ANTIBIOTIC RESISTANCE PATTERN IN E.COLI ISOLATES IN PATIENTS WITH URINARY TRACT INFECTION IN IMAM REZA HOSPITAL IN MASHHAD

Maryam Hafiz[1], Gholamreza Hashemi Tabar [2], masoud hafiz[3]

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: Background: Escherichia coli E. coli(is the most common causative agent of urinary tract infection (UTI). The UTI caused by antibiotic-resistant isolates are increasing. The type of selected antibiotics for the experimental treatment of UTI is currently under discussion. By now, 20 to 50 percent of the strains of E. coli have been resistant to first-line antibiotics, even in developed countries. The aim of this study was to determine the pattern of antibiotic resistance in E.coli isolates from patients with urinary tract infection in Mashhad.

Methods: Methods: In this study, 60 strains of E. coli isolated from urine specimens were studied in Imam Reza Hospital in 1395 and 1396. After biochemical tests, antibiogram test were performed using Kirby-Bauer method.

Results: Results: Of the 60 isolates of E. coli, 55% of women and 45% of men had urinary tract infections. Based on the results, the lowest resistance to Amikacin was 3.3%, Nitrofurantoin 10%, Imipenem and Meropenem 11.6%, Gentamicin 20%, and the highest resistance was to Ampicillin 86.6%. Resistance in the cephalosporin family was Cefotaxime 71.7%, Cefazolin 61.7%, ceftriaxone 60%, Cefixime 55.6%, Cefepime 46.7%, and Ceftazidime 45%, respectively. Among the quinolones, Ciprofloxacin was 58.3% and Nalidixic acid was 48.3% resistant.

Conclusion: Conclusion: In the treatment of urinary tract infections, antibiotic therapy is experimental and accurate information on the susceptibility of bacteria in the area can be useful for achieving the best treatment.

Keywords: Keyword: Escherichia Coli, Urinary Tract Infection, Drug resistance.

P75 - 398: EVALUATION OF ANTIBACTERIAL EFFECT OF LAVENDER,LAVENDULA ANGUSTIFOLIA,AND MELISSA , MELISSA OFFICIALIS,EXTRACTS ON HUMAN PATHOGENS

NASIM GHORBANI[1], parichehr hanachi[2], hojat sadeghi[3]

1. senior student,department of biotechnology,falzahra biology,alzahra university,lran,tehran,ghorbani 20n@ gmail.com
2. faculty of biotechnology,alzahra university,tehran,lran,hanachi wrc@yahoo.com
3. faculty of pharmacology,esfahan medical university,lran,hojat sadeghi sadeghi@pharm_mui.ac.ir

Background and Aim: Introduction : Staphylococcus aureus and E.coli are important pathogens in humans. The aim of this study is to investigate the antibacterial effects of Lavender extract and Melissa on gram-negative/positive bacteria of E. coli and Staphylococcus aureus.

Methods: Leopheliz plant powder was prepared with three solvents, water, ethanol 80%and methanol80%. To prepare the appropriate concentration of bacteria to determine MIC, we used the MacroFerland half-solution method containing 1.5 * 108CFU / ML for evaluation. The antibacterial activity of these extracts was performed using measuring inhibition zone diameter. Minimum Bactericidal Concentration (MBC) was assessed using disk diffusion method and MIC (Minimum Inhibitory Concentration) with dilution method. The mcg10 gentamicin disk was used as a positive control in this study

Results: The results showed that MBC methanolic extract of Melissa and Lavender with concentration 60 mg / ml were effective on both Staphylococcus aureus and E-coli and MIC with a concentration less than 60 mg / ml extract of lavender methanol and ethanol and ethanol of Melissa had a weak effect on both bacteria and Staphylococcus aureus; respectively, and in the first dilution of microb have not grown.

Conclusion: The results showed that the extract of these two plants has mild inhibitory effects on microbial degradation

Keywords:MBC.MIC;Lavender;Melissa; E.coli;staphylococcus aureus

P76 - 399: DETECTION OF METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS (MRSA) IN CLINICAL SAMPLE OF PATIENTS WITH EXTERNAL OCULAR INFECTION

Ashkan Faridi [1], Amir Tavakoli Kareshk [2], Mehdi Fatahi-Bafghi [3], Amir Hossein Rezaei [4], Seyedeh Zeinab Seyyed-Yousefi[5], Noshin Shakeri [6], Davood Kalantar-Neyestanaki5[7], Mohammad Reza Kandehkar Ghahraman[8]

1. Student Research Committee, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran.
2. Student Research Committee, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran.
3. Department of Microbiology, Faculty of Medicine, Shahid Sadoughi University of Medical Sciences Yazd Iran.
4. Student Research Committee, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran.
5. Department of pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran.
6. Shahid Labafi Nejad Hospital, Tehran, Iran.
7. Department of Microbiology and Virology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran.
8. Student Research Committee, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran.

Background and Aim: Staphylococcus aureus is the main gram-positive bacteria isolated from patients with ocular infections. Herein, we describe the pattern of antibiotic resistance, presence of resistance genes including ermA, ermB, ermC, msrA, mecA genes and pvl cytotoxin gene in S. aureus isolates were collected from patients with external ocular infection.

Methods: In this study, 8 S. aureus isolates were collected from 81 patients that suffered from eye damages. Antibacterial susceptibility of isolates was determined using the Kirby-Bauer disk diffusion method. Resistance genes including ermA, ermB, ermC, msrA, mecA and pvl virulence gene were detected by PCR method. Staphylococcal cassette chromosome mec (SCCmec) in MRSA isolates were detected by multiplex-PCR method.

Results: Three isolates were resistance to cefoxitin that considered as MRSA. The mecA gene identified in MRSA isolates. SCCmec type IV and pvl gene were detected in one of MRSA isolates that recovered from a diabetic patient.

Conclusion: The emergence of S. aureus isolates belonged to SCCmec type IV; pvl gene among patients with ocular infection is very serious, so genetic characteristics of MRSA isolates for empirical therapy and infection control is very important.

Keywords: Eye infection, MRSA, PVL

P77 - 403: NITAZOXANIDE AND DOXYCYCLINE SENSITIVITY AMONG METRONIDAZOLE RESISTANT HELICOBACTER PYLORI ISOLATES FROM PATIENTS WITH GASTRITIS

Ali Baradaran[1], Masoud Alebouyeh[2], Ali Baradaran-Moghaddam[3]

1. Gastroenterology, Research Center for Gastroenterology and Liver Diseases, Firoozgar Hospital, Iran University of Medical Sciences, Tehran, Iran
2. Microbiology Department, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran

Background and Aim: Antibiotic therapy should be done based on resistance characteristics of Helicobacter pylori strains to commonly prescribed antibiotics in areas with higher resistance rates.This study examined antibacterial activity of nitazoxanide and doxycycline against clinical H. pylori isolates showing different metronidazole resistance levels.

Methods:A total of 122 patients, who underwent endoscopy were enrolled in this study from 3 hospitals of Tehran, during November2014 to July 2015. Helicobacter pylori isolates were obtained from gastric biopsies of the patients after culture in specific culture medium and characterization by both biochemical and molecular methods. Antimicrobial using the agar dilution method and minimum inhibitory concentrations of nitazoxanide and doxycycline were determined susceptibility to metronidazole was detected for metronidazole resistant strains.

Results: From a total of 122 gastric biopsy specimens, 55 H. pylori strains were recovered (45%). Thirty-three of these strains (60.0%) were resistance to metronidazole. MIC50 and MIC90 values for metronidazole were 32 and 64_g/mL, respectively. MIC50 and MIC90 values for doxycycline and nitazoxanide were measured as 4 and_8 _g/mL, and 8 and_32 _g/mL, respectively

Conclusion: Dominance of high level metronidazole resistance H. pylori strains among the studied patients questioned its usefulness for first-line therapy in Iran. Nitazoxanide and doxycycline showed superior activity against H. pylori strains in comparison to metronidazole, which should be considered for alternative therapies.

Keywords: Antibiotic Resistance,Helicobacter Pylori,Minimum Inhibitory Concentration

P78 - 405: COMPARISON OF GREEN AND BLACK TEA EXTRACT ON THE DOMINANT PATHOGENS OF ENTERIC

Fatemeh Bazmani[1], Hadi Hosseini[2], Roghayeh Gholizadeh doran mahale[3], Iman hormozi[4]

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. Faculty Member of Dpartment of Laboratory Sciences, Faculty of Medicine, Islamic Azad University, Zahedan, Iran
4. Expert of Microbiology Laboratory, Faculty of Medical Sciences, Islamic Azad University, Zahedan, Iran

Background and Aim: Green tea leaf (Camellia sinensis) contains polyphenolic compounds with antibacterial effects, thus studying its inhibitory effect on gastrointestinal pathogenic bacteria is very important. In this study, the inhibitory effects of aqueous extract of green and black tea leaves on Pseudomonas aeruginosa and Escherichia coli were compared.

Methods:: In this study, the aqueous extract of the samples was taken by soxhlet, then diluted by 10% by means of a blank disc and disc diffusion agar method with equal dilutions of tea extract, Muller Hinton Agar culture medium and the same Parameters for 18 hours in the vicinity of the bacteria were incubated.

Results: Black tea extract on E. coli bacteria with a growth avoidance hole with diameter of 25 mm and the same extract were determined on Pseudomonas aeruginosa with a hole diameter of 22 mm. Also, the effect of green tea extract on E. coli a diameter of 18 mm was applied to Pseudomonas aeruginosa with a diameter of 15 mm.

Conclusion: Black tea extract has a more effective inhibitory effect on compare green tea extract, Which can reduce the risk of intestinal infections, and can also be used to condense this extract and use black tea polyphenols as an anti diarrhea syrup, In the pharmaceutical industry.

Keywords: Camellia sinensis, Disc diffusion agar, Inhibitory effect, Pseudomonas aeruginosa, E. coli

P79 - 409: DETECTION OF SGI1 AND ITS VARIANTS IN SALMONELLA SEROVARS ISOLATED FROM DIFFERENT HUMAN AND ANIMAL SOURCES

Arefeh Ghoddusi[1], Bahar Nayeri Fasaei[2], Taghi Zahraei Salehi[3]

1. Department of microbiology, Faculty of Veterinary medicine, University of Tehran
2. Department of microbiology, Faculty of Veterinary medicine, University of Tehran
3. Department of microbiology, Faculty of Veterinary medicine, University of Tehran

Background and Aim: The Salmonella genomic island 1 (SGI1) is a 42.4-kb mobilizable integrated element that contains several antibiotic resistance genes. The resistance genes are all located within the boundaries of a complex class 1 integron, which belongs to the In4 family. Variants of SGI1, containing different sets of resistance genes, have been found. SGI1, identified as a public health concern, is a horizontally transmissible genomic island. Lack of information exists on the presence of SGI1 variants among Salmonella isolates in Iran. This study was conducted to identify the MDR and SGI1 carrying Salmonella strains isolated from various sources

Methods:A total of 242 Salmonella strains isolated from human, chicken, and cattle belonging to 11 serovars were studied. The strains were tested for their antimicrobial susceptibility and the prevalence of multidrug-resistance patterns. The isolates were investigated for the presence of SGI1 and its variants by PCR.

Results:132 Salmonella isolates (54%) were resistant to at least one antibiotic, and more than 40% of the isolates were multidrug-resistant. Based on PCR, we distinguished 8 variants of Salmonella genomic island 1 including SGI1, SGI1-J, SGI1-F, SGI1-I, SGI1-O, SGI1-C, SGI1-B and SGI1-D in 102 human and animals isolates.

Conclusion: This study showed the high prevalence of SGI1 and the variants (as the mechanism of multidrug resistance) in Salmonella serovars isolated from different animal and human sources. The high prevalence of this multidrug-resistance among Salmonella strains highlights the need for regulation of the use of antimicrobials in animals and humans, and to reduce the opportunity for organisms to develop resistance.

Keywords:SGI1; Salmonella; Multidrug-resistance; Animals; Humans

P80 - 423: EVALUATION AND ENUMERATION OF ANTIBACTERIAL EFFECTS OF XYLITOL AGAINST PNEUMOCOCCAL GROWTH BY MTT ASSAY

Ali Asgari[1], Ramezan Ali Ataee[2], Ali mehrabi Tavana[3]

1. 1- Department of Microbiology. Faculty of medicine, Baqiyatallah University of Medical Sciences, Tehran, IR Iran. Sky.asgari@gmail.com
2. 1- Department of Microbiology. Faculty of medicine, Baqiyatallah University of Medical Sciences, Tehran, IR Iran.
3. 2- Health Management Research Center, Baqiyatallah University of Medical Sciences ,Tehran, IR Iran.

Background and Aim: Xylitol as a five-carbon sugar alcohol has been widely used as a sweetener, mainly in chewing gums. Because of its antibacterial activity against acute otitis media in children qualitatively was reported. In this regards, quantitatively of antibacterial activity procedures may be crucial for Streptococcus pneumonia infections control. This study aimed was quantitative evaluate the antibacterial effect of xylitol on growth and survival of Streptococcus pneumoniae by MTT assay.

Methods: Streptococcus pneumoniae ATCC strain 49619 were exposed to 2.5, 5 and 7.5% of xylitol with or without fructose in a period of 24 hours. During of incubation (Every three hours once) ,200 µl of each media was transferred to 96-well plate .Next 20 µl of MTT solution was added to each well and were incubated at 37°C in a 5%CO2 atmosphere. after 4 hours' supernatant was removed and 50 µl DMSO was added to Dissolved blue colored formazan crystals. The plate was again incubated for 30 minute and OD rate was measured with ELISA reader in the wavelength of 570 nm.

Results: Statistical analysis results has indicated a significant growth difference in the various test media which contain concentrations of 2.5, 5 and 7.5% of xylitol without fructose. (P value < 0.0001)

Conclusion:the results revealed that the reductive effect of xylitol on growth and survival of Streptococcus pneumoniae. This finding supports previous results where exposure to xylitol changed the ultrastructure of the pneumococcal capsule and could explain further the high clinical efficacy of xylitol in preventing otitis media.

Keywords: Streptococcus pneumoniae, xylitol, MTT assay

P81 - 425: THE ANTIBACTERIAL ACTIVITY OF ETHANOL EXTRACT OF KHORASANI PROPOLIS ISOLATED FROM BINALOUD MOUNTAINS

Fatemeh Shahab navai[1], Fatemeh Shahab-navaei [2], Ahmad Asoodeh [3]

1. -
2. Department of Chemistry, 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: Propolis is a complex resinous mixture collected by bees from plant saps and mixed with beeswax and pollen. It is known that propolis possesses antimicrobial, antioxidative and anticancer activities. Therefore, propolis has attracted much attention in recent years as a potential substance used in medicine. The aim of this study was to determine the antibacterial properties of EEP (Ethanol Extract Propolis), collected from Khorasan, against Escherichia coli, Staphylococcus aureus, Bacillus subtilis and Pseudomonas aeruginosa.

Methods: Pulverized raw propolis (2g) placed inside a paper timber was submitted to 8h Soxhlet extraction at a maximum temperature of 70°C, using 250 mL of ethanol (98%). The resulting extracts were evaporated in a rotary evaporator with thermostatic bath (70°C) to obtain the dry extract. The MIC (Minimum Inhibitory Concentration) of EEP (dissolved in 4%v/v DMSO) was evaluated by broth microdilution method in a range of 0.5-4 mg/ml. The MBC (Minimum Bactericidal Concentration) was determined by the lowest concentration that kills 99.9% of the initial bacterial population.

Results: The MIC values of EEP against E. coli, S. aureus and B. subtilis were calculated to be 2,2 and 4 mg/ml, respectively. The MBC values of EEP were the same as MIC. No significant antibacterial properties were determined against P. aeruginosa. Results exhibited that, EEP had better inhibitory effect on Gram positive bacteria than Gram negative bacteria.

Conclusion:EEP showed good antimicrobial activity against tested pathogens. It appears that propolis could be considered as an antimicrobial agent in several materials such as wound band, toothpaste and etc.

Keywords:propolis, ethanol extract, antibacterial activity, MIC

P82 - 429: PREVALENCE AND ANTIBIOTIC RESISTANCE PATTERN OF GRAM POSITIVE UROPATHOGENIC BACTERIA ISOLATED FROM URINE SAMPLES IN BANDAR TORKAMAN, IRAN

Mohammad Bartimar[1], Ania Ahani Azari [2]

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

Background and Aim: Urinary tract infection (UTI) is one of the most common bacterial infections in humans, so updated epidemiological data on antibiotic resistance pattern of agents will be a big help for physicians to prescribe the choice antibiotic. The aim of this study was to determine antibiotic resistance pattern of Gram positive uropathogenic isolated from urine samples referred to clinical laboratories of Bandar Torkaman, Iran.

Methods: In this study from April to June 2017, midstream urine samples were collected from patients who had clinical manifestation of UTI. In positive samples uropathogenic bacteria were identified by biochemical tests and their antibiotic resistance pattern were determined by disk diffusion method against different antibiotics.

Results: Out of 1754 urine samples, 89 samples were positive for urinary infection. The most commonly isolated were as follows: Staphylococcus epidermidis (30), Staphylococcus saprophyticus (6), Micococcus sp. (3), Group B Streptococcus (28), Non-hemolytic Streptococcus (10), Alpha-hemolytic Streptococcus (5) and Group D Streptococcus (7). Among the isolates, the highest resistance rates were observed for Ampicilin and Cotrimoxazole. All the isolates were sensitive to Vancomycin.

Conclusion: The result of this study revealed that Staphylococcus epidermidis and Group B Streptococcus were the most common isolated bacteria from the urine samples. Moreover, according to more than half of the isolates were resistant to antibiotics commonly used in clinical practices, performing an accurate Antibiogram test before prescribing antibiotics is recommended and is an inevitable necessity.

Keywords: Antibiotic, Gram positive, Prevalence, Resistance, Uropathogen

P83 - 430: ANTIBIOTIC RESISTANCE PATTERN AND FREQUENCY OF EXTENDED SPECTRUM B-LACTAMASES (ESBLS) IN GRAM NEGATIVE UROPATHOGENIC BACTERIA ISOLATED FROM URINE SAMPLES IN BANDAR TORKAMAN, IRAN

Ania Ahani Azari[1], Mohammad Bartimar[2], Aydin Khajeh[3]

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

Background and Aim: Antibiotic resistance is rising in Gram negative bacteria causing urinary tract infections (UTI). The aim of this study was to assess antibiotic resistance pattern and frequency of extended spectrum β-lactamases (ESBLs) in Gram negative uropathogenic bacteria isolated from urine samples referred to clinical laboratories of Bandar Torkaman, Iran.

Methods: In this study from March to May 2017, midstream urine samples were collected from patients who had clinical manifestation of UTI. In positive samples uropathogenic bacteria were identified by biochemical tests and their antibiotic resistance pattern was determined by disk diffusion method. Then, phenotypic confirmatory test was performed for detection of ESBLs producers

Results: Out of 1388 urine samples, 96 samples were positive for urinary infection. The most commonly isolated were as follows: Escherichia coli (85), Klebsiella pneumonia (5), Enterobacter cloace (4) and pseudomonas aerouginosa (2). The highest resistance rates among the majority of the isolates were observed for ampicilin and nalidixic acid. The lowest resistance of E. coli isolates was observed to Norfloxacin. Out of 35 cefotaxime resistant isolates, 29 isolates were positive for ESBLs.

Conclusion: In this study, the most prevalent cause of UTI was E. coli (88.5%). The frequency of ESBLs in E. coli isolates was similar to the results of other studies in this field but it was very high in K. pneumonia. The results of this study demonstrated increasing trend of resistance in extended-Spectrum cephalosporins. Therefore before prescribing antibiotics by physicians performing an accurate Antibiogram test seems rational and is an inevitable necessity.

Keywords: Antibiotic, ESBLs, Gram Negative, Frequency, Uropathogen

P84 - 431: EVALUATING THE EFFECT OF HEAT-KILLED PATHOGENS ON ANTIMICROBIAL COMPOUNDS PRODUCTION IN STREPTOMYCES SP.AC117

Hanieh Shakeri Moghaddam[1], Bahar Shahnavaz[2], Ali Makhdoumi[3]

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: Many secondary metabolites are not expressed under conventional laboratory condition because growth conditions differ from natural environment.The co-cultivation of bacteria has recently been described as a promising strategy to induce the production of novel metabolites through possible gene activation.In this study the production enhancement of antimicrobial compounds in Streptomyces sp.AC117 was examined through co-cultivation with heat-killed Staphylococcus aureus and Bacillus subtilis.

Methods: An overnight culture of S.aureus and B.subtilis was centrifuged and the cell numbers were adjusted to 1×108 cells/ml. The bacterial pathogen suspensions were placed in boiling water for 30 min. The heat-killed S.aureus (5% v/v) and B. subtilis (2.5% v/v) was introduced to the flask at the same time as inoculation with Streptomyces sp.AC117. Every 48 hours the extracts from pure and co-culture were evaluated with agar well diffusion method against Staphylococcus aureus, Bacillus subtilis, Escherichia coli and Pseudomonas aeruginosa.

Results: The inhibition zone diameter for elicited culture with S.aureus in the first 48 hours was increased 3 mm against S.aureus, 4 mm against E.coli and 2 mm against P.aeruginosa compared to the pure extracts. The increase in inhibition zone diameter for B.subtilis elicited culture was only seen against S.aureus (4 mm).

Conclusion: Since microorganisms live in a complex environment, elicitation may mimic the inter-species interactions in nature resulting in metabolic production. In general, the mechanisms of inter-species interactions such as elicitation, signaling, and quorum sensing are not completely understood at molecular level.

Keywords: Streptomyces, co-culture, secondary metabolites, antimicrobial compounds

P85 - 432: ELICITING THE ANTIMICROBIAL COMPOUNDS PRODUCTION IN STREPTOMYCES SP.AC117 BY DIFFERENT INOCULATION AMOUNT OF HEAT-KILLED PSEUDOMONAS AERUGINOSA

Hanieh Shakeri Moghaddam[1], Bahar Shahnavaz[2], Ali Makhdoumi[3]

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: There is an immediate need to discover and develop new antibiotics because of the steady rise of conventional antibiotic resistant bacteria which is an imminent threat to public health. Genomic sequence data have revealed the presence of silent biosynthetic gene clusters in the genomes of actinomycetes that encode for secondary metabolites, which are not detected under standard fermentation conditions. Co-cultivation-based elicitation can therefore lead to the production of compounds that are not produced in monoculture. This research is focused on the effect of Pseudomonas aeruginosa inoculum amount on antimicrobial compounds production in Streptomyces sp.AC117.

Methods:P.aeruginosa was cultured in liquid medium for 24 hours. Then, the cell numbers was adjusted to 1×107 cells mL−1. This inoculum was added at 0.25%, 0.5%, 1% and 1.5% (v/v) to the flask at the same time of Streptomyces inoculation. Every 48 hours the extracts from pure and co-culture were evaluated with agar well diffusion method against Staphylococcus aureus, Bacillus subtilis, Escherichia coli and Pseudomonas aeruginosa.

Results: The best increase in inhibition zone diameter was at 1%(v/v).The diameter in elicited extracts compared to pure one was increased for 5mm against S.aureus and 2mm against B. subtilis.

Conclusion: Co-culture could be a valuable method for activating silent genes or the ones that are not normally expressed. Moreover, some factors such as the amount of inoculation could play a major role in activation. Although, detailed mechanisms of the interaction are rarely understood.

Keywords: Streptomyces, Co-cultivation, antimicrobial compounds, inoculation amount

P86 - 444: FIRST REPORT OF SOME CLASS 1 INTEGRON-ASSOCIATED GENE CASSETTE ARRAYS AMONG ESCHERICHIA COLI AND KLEBSIELLA PNEUMONIAE ISOLATED FROM PATIENTS WITH URINARY TRACT INFECTION IN SOUTHWEST OF IRAN

Fariba Jahanbin[1], Seyed Sajjad Khoramrooz[2], Masoud Marashifard[3], Seyed Ali Asghar Malek Hosseini[4], Asghar Sharifi[5]

1. Department of Basic Sciences, Islamic Azad University, Yasooj Branch,Yasooj, Iran
2. Cellular and Molecular Research Center, Yasuj University of Medical Sciences, Yasuj, Iran
3. School of veterinary Medicine, Shiraz University, Shiraz, Iran
4. Student Research Committee, Yasuj University of Medical Sciences, Yasuj, Iran
5. Cellular and Molecular Research Center, Yasuj University of Medical Sciences, Yasuj, Iran

Background and Aim: In the current study,we aimed to determine the antibiotic resistance pattern, prevalence of classes 1-3 integrons and distribution of gene cassettes in Escherichia coli and Klebsiella pneumoniae isolated from patients with urinary tract infection (UTI)in southwest of Iran.

Methods: Antibiotic susceptibility pattern of 340 clinical isolates of E. coli and K. pneumoniae were determined by Disk Agar Diffusion method. Polymerase chain reaction (PCR) was used for detection of class1, 2 and 3 Integrons. To analyze the gene cassettes, variable regions of class 1 integron were amplified by PCR and subjected to sequencing.

Results:: Highest rates of resistance were observed to amoxicillin/clavulanic acid (38.8%) and cephalotin (32.1%) in K. pneumoniae and to amoxicillin/clavulanic acid (73.6%), trimethoprim-sulfamethoxazole (63.9%) and tetracycline (63.2%) in E. coli isolates. While Class 1 and class 2 integrons were identified in 62.5% and9% of E. coli isolates, only 12.2% of K. pneumoniae isolates were found to harbor the intI1 gene. Totally 10 and 7 different gene cassette arrays were found in theintI1 gene of E. coli and K. pneumoniae respectively. The dfrA17-aadA5 and aadA1 were the most prominent gene cassette arrays among E. coli and K. pneumoniae isolates respectively.

Conclusion: Integrons played a more important role in the development of antibiotic resistance in E. coli compared to K. pneumoniae in our urinary isolates. For the first time we identified dfrA5-catB3-aacA4 andaadA1-blaOXA-30genecassette arrays in E. coli and also aadB-cat-blaOXA-10-aadAgene cassette array in K. pneumoniae isolates from Iran.

Keywords: Escherichia coli; Klebsiella pneumoniae; Integron; Antibiotic resistance; Gene cassettes

P87 - 445: ANTIMICROBIAL ACTIVITY OF MENTHA PULEGIUM ESSENTIAL OIL

Marzieh Bahramian[1], Mansour Amin [2]

1. Department of Microbiology, school of medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, IR Iran
2. Department of Microbiology, school of medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, IR Iran

Background and Aim: The antimicrobial activity of plant oils and extracts has been recognized for many years; With regard to rapid emerging antibiotic resistance in bacteria, the importance of developing new, reliable, cost-efficient, and non-toxic herbal antimicrobial agents is undeniable.In this research, the essential oil from leaves of Pennyroyal (Mentha pulegium) plant was evaluated against some bacteria and fungi.

Methods: The essential oil was obtained by water-distillation using clevenger-type system. The minimum inhibitory concentration (MIC) of essential oil was determined by modified E-test.

Results: The results indicated that Mentha pulegium essential oil, had high inhibitory activity against Gram positive (Bacillus Cereus(MIC=31mcg/ml) and Staphylococcus aureus(MIC=62mcg/ml)), and Gram negative (Escherichia coli(MIC=15mcg/ml), Klebsiella and shigella(MIC=31mcg/ml)) bacteria. The Candida albicans also showed a considerable sensitivity to this essential oil.

Conclusion: Based on these results, it can be suggested that essential oil of M. pulegium with high effective antibacterial activity can be used as a new source for producing antibiotics against bacterial and fungal pathogens.

Keywords: Mentha Pulegium_agents, antimicrobial

P88 - 450: ANTIMICROBIAL EFFECTS OF ETHANOL EXTRACTS OF PLANTS MEDICAGO SATIVA AND ECHINOPHORA PLATYLOBA D.C ON ENTEROCOCCUS FAECALIS BACTERIA IN VITRO

Mansoor Khaledi[1], Majid Asadi-Samani[2], Fatemeh Khaledi[3]

1. M.Sc. of Microbiology, Department of Microbiology and Immunology, sharekord University of Medical Sciences, sharekord, Iran
2. Young Researchers and Elite Club, Shahrekord Branch, Islamic Azad University, Shahrekord, Iran
3. Students Research Committee, Shahrekord University of Medical Sciences, Shahrekord, Iran

Background and Aim: Since drug resistance has become a global health problem, new methods to fight these resistant bacteria are needed. One of the ways to cope with these resistance is through the use of herbs and their derivatives. This study was designed to determine the antimicrobial efficacy of the hydroalcoholic extracts of Medicago sativa and Echinophora platyloba D.C against Enterococcus faecalis bacteria in vitro.

Methods:hydro alcoholic extract of two medicinal plants collected from The scope of Chaharmahal va Bakhtiari; the hydroalcoholic extracts of the plants were prepared by maceration then The MIC values and MBC of the Medicago sativa and Echinophora platyloba D.C extract against E.fecalis ATCC 29212 were determined by a micro broth dilution method based on instructions CLSI

Results: The MIC value for the hydro alcoholic extract of Medicago sativa was 512 µg/mL for E.fecalis and The MIC value for the hydro alcoholic extract of Echinophora platyloba D.C was 32 µg/mL also The MBC value of the ethanol extract of Medicago sativa was 1024 µg/ml for E.fecalis and The MBC value of the ethanol extract of Echinophora platyloba D.C was 128 µg /ml

Conclusion: The findings of the study showed that the most antibacterial effect on E.fecalis is related to Echinophora platyloba D.C And the lowest microbial activity against this bacterium is Medicago sativa. the necessity of further research on this plant in order to extract its effective compounds and its effects on a variety of pathogens is suggested.

Keywords: Antimicrobial effects, Medicago sativa, Echinophora platyloba D.C , Enterococcus faecalis

P89 - 466: SYNTHESIS AND EVALUATION OF ANTIBACTERIAL ACTIVITY OF 2,5-DISUBSTITUTED 1,3,4-OXADIAZOLES DERIVATIVES CONTAINING HALOGEN

Mahnaz Karimi[1], Elahe Tajbakhsh[2], Ali Souldozi[3], Ali Souldozi[4]

1. Faculty of Basic Science, Shahrekord Branch, Islamic Azad University, Iran
2. Faculty of Basic Science, Shahrekord Branch, Islamic Azad University, Iran
3. Faculty of Basic Science, Shahrekord Branch, Islamic Azad University, Iran
4. Faculty of Science, Urmia Branch, Islamic Azad University, Iran

Background and Aim: Oxadiazoles are the heterocyclic compounds containing one oxygen and two nitrogen atoms in a five membered ring possessing a diversity of useful biological effects. Oxadiazole is considered to be resultant from furan by replacement of two methane (–CH=) groups by two pyridine type nitrogen atoms (–N=). Several methods have been reported in the literature for the synthesis of 1,3,4-oxadiazoles. The aim of this study was to evaluate the antibacterial properties of oxadiazole synthesized derivatives and compare it with common antibacterial drugs on bacterial pathogens.

Methods: In this study in a singleprocess reaction of N- isocyanimino triphenyiphosphorane, carboxylic acid derivatives and 2-pyridinecarbalhyde in acetonitrile solvent, new derivatives of Oxadiazole were attained. The structures of synthesis compounds were surveyed and established by the use of IR, H-NMR and C-NMR spectrometer. The synthesized compounds were tested for their antimicrobial activity against Entrococcus faecalis PTCC 1788 and Proteus vulgaris PTCC 1861 by disc diffusion method and Minimal Inhibitory Concentration (MIC) and determination of Minimal Bactericidal Concentration (MBC).

Results: The results that show all the synthesized compounds had antibacterial activity against gram positive bacteria, but they did not have that much influence on gram negative bacteria.

Conclusion: This is important that the synthesis of Oxadiazole compounds has antibacterial nature which is a single-process reaction and it was accomplished with high efficiency and in a very short time.

Keywords: Antibacterial, Oxadiazole, Enterococci, Proteus

P90 - 467: EVALUATION OF EFFECTS OF ESSENTIAL OIL OF THREE SPECIES THYMUS ON E.COLI , PESUDOMONAS AERUGINOSA, STAPHYLOCOCCUS AUREUS AND CANDIDA ALBICANS AND COMPARE EFFECT OF ANTIMICROBIAL AGENT

Emad Vahidi manesh[1]

1. azad qom univercity, qom

Background and Aim: Thymus used as a medicinally plant from 16 century. Important effective material in the thymus is compounds phenoly of thymol and carvacrol. Essential oil of thymus is a yellow or purple liquid with pleasant smell and hot taste.

Methods: For compare thymus antimicrobial agents with antibiotics, after to prepare essential oil of thymus with use of way of disk diffusion for bacterial and fungal, compare result of strains antibiogram. We put on disks of antibiogram on culture media and it incubatied in 24 hours at 37°c. Then We report Inhibitory Zone to mm.

Results: Results of this study showed that Inhibitory Zone in essential oil Thymus transcaspicus for E.coli, Pesudomonas aeruginosa, staphylococcus aureus and candida albicans in order to 17, 24, 10, and 26 mm. Ampicillin antibiotic for E.coli, Pesudomonas aeruginosa and staphylococcus aureus in order to 18, 29 and 0 mm. Gentamicin antibiotic for E.coli, Pesudomonas aeruginosa and staphylococcus aureus in order to 21, 18 and 16 mm.

Conclusion: This essential oils had good antibacterial effect on E.coli, staphylococcus aureus and candida albicans, but this essential oils not much effect on the Pesudomonas aeruginosa.

Keywords: Thymus, Antibacterial activity

P91 - 472: INVESTIGATION OF THE CHARACTERISTICS AND EFFICIENCY OF LYTIC PHAGE MDRACINETOBACTERBAUMANNII SEPARATED FROM THE ICU

Behnam Sisakhtpour[1], Sharareh Moghim[2], seyedeh saeedeh ebrahimi[3], Vajihe Karbasizadeh[4], Arezoo mirzaei[5]

1. M.Sc student of medical bacteriology at Isfahan University of medical science
2. Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
3. M.Sc student of medical bacteriology at Isfahan University of medical science
4. Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
5. Ph.D. student of medical bacteriology at Isfahan University of medical science

Background and Aim: Introduction: Acinetobacterbaumannii is resistant to most commonly used antibiotics due to inherent mechanisms.Therefore, today it is considered as one of the most important bacteria in hospital infections, especially in ICU (intensive care unit). The increasing rate of multi-drug-resistant (MDR) bacteria has led to a renewed focus on alternative therapies, especially phage therapies.Bacteriophages are viruses that specifically use bacteria as their host. Aim: The purpose of this study is isolation, characterization and evaluation of the efficacy of Acinetobacterbaumannii (MDR)phage, so theyare good choice to substitutewith antibiotic treatment as an effective disinfectant or disinfecting the hospital.

Methods: In a cross-sectional study in 1395, 84 samples of Acinetobacterbaumannii isolated from patients admitted to the intensive care unit. At first, the samples were identified by biochemical method and then amplified with blaOXA-51 gene. Then,antibiotic resistance patterndeterminedwith a diffuse method according to the CLSI instruction and finally separation of phage from water sources occurred.

Results:the result of antibiotic resistance showed, 82% Amikacin, 97% Cefepime, 96% Ceftazidim, 99% Ciprofloxacin and 86% resistance to Rifampin.In the sewage water sample, the phage was isolated and Effective on Acinetobacterbaumanniiby creating plaque.

Conclusion: Due to the resistance of Acinetobacterbaumannii to the majority of antibiotics,Phage Therapy could be the right candidate for Consideringsubstitute antibiotics to treat infections of this bacterium.

Keywords: Acinetobacterbaumannii, Bacteriophage, Phage Therapy, Antibiotic Resistance

P92 - 473: ANTIMICROBIAL EFFECTS OF PHENOXY ETHANOL AND CAPROLYL GLYCOL (VERSTATIL PC) AS PRESERVATIVES IN COSMETIC PRODUCTS

Mojtaba Sade[1], , Samira Sepehri[2]

1. Department of Microbiology, Islamic Azad University, Tehran Medical Branch, Iran.
2. Microbiology expert of Pars Azmaye Teb Co.

Background and Aim: The probability of transmission of contamination and its risks in the cosmetics industry is considered as one of the important health problems for the consumers of these products and, on the other hand, due to the widespread use and non-standardization of some of the raw materials And the presence of some of the compounds in these products as a food source for microorganisms can provide the context and conditions f or the infection to consumers.

Methods:: In this study, the bacterial and fungal contamination of cosmetic products produced by Pars Azma Medical was evaluated by evaluating the power of maintenance of Verstatil pc. In this study, the minimum inhibitory concentration of verstatil pc was investigated against five microorganisms of Candida albicans (PTCC), Escherichia coli (ATCC: 25922), Pseudomonas aeruginosa (ATCC: 27853), Aspergillus niger (PTCC), Staphylococcus aureus (ATCC: 25923) It turned out.

Results: The results of microbial tests showed that the verstatil pc bacteriuria and fungal power for the above microorganisms was Log level ≥ Log 7.

Conclusion: Due to the repeated use of cosmetics, measures should be taken to prevent the growth of bacteria and pathogenic fungi in these products. According to the results of this study, it is recommended that the substance The preservative (V.PC) is used to prevent the growth of microbial and fungal contaminating agents in the cosmetics industry.

Keywords:: Logarithmic Reduction, Verstatil pc, PTCC, ATCC, Concentration inhibition, Preservatives

P93 - 485: ASSESSMENT OF COLISTIN SENSITIVITY IN CLINICAL GRAM-NEGATIVE BACTERIA IN THE NORTHWEST OF IRAN

Zahra Aghapour[1], Pourya Gholizadeh[2], Hossein Samadi Kafil[3]

1. Drug applied research center, Tabriz University of Medical Sciences,Tabriz, I.R. Iran
2. Student Research Committee, Tabriz University of Medical Sciences, Tabriz, I.R. Iran.
3. Drug applied research center, Tabriz University of Medical Sciences, Tabriz, I.R. Iran

Background and Aim: Colistin is a last line antibiotic for treating severe infections caused by multidrug-resistant Gram-negative bacteria. Unfortunately, the increased use of this agent has led to the emergence of colistin-resistant bacteria. The aim of this study was to determine colistin resistance in clinical Gram-negative isolates.

Methods: Nine-hundred clinical isolates were collected from hospitalized patients in Imam-Reza and Pediatric, teaching and treatment hospitals, Tabriz, Iran, during the period from 2014 to 2016. The Gram-negative bacteria belong to Enterobacteriaceae such as Escherichia coli, Klebsiella spp., Acinetobacter baumannii, Enterobacter agglomerans and Pseudomonas aeruginosa were selected. Antibiotic susceptibility of the isolates was determined by disk diffusion and agar dilution methods.

Results: Of the 900 clinical isolates, 30 (3.33%) were identified as a colistin resistance and 26.6% of them were highly resistant. Colistin resistant of E.coli were 43.3%, Klebsiella spp.13.3%, A. baumannii, E. agglomeranse, and P. aeruginosa were 13.3%, 10%, 13.3%, respectively.

Conclusion: The frequency of resistance to colistin was low in the Northwest of Iran. In the battle against rapidly emerging bacterial resistance we can no longer rely entirely on the discovery of new antibiotics; we must also pursue rational approaches to the use of older antibiotics such as colistin.

Keywords: Colistin-resistant, Gram negative bacteria, Agar dilution, Disk diffusion

P94 - 493: PRODUCTION OF COML RECOMBINANT AND ITS FUNCTIONAL ROLE IN ANTIBIOTIC RESISTANCE

Elahe Abiri[1], D.Iraj Rasooli[2], D.Shakiba Darvish Alipour Astaneh[3]

1. Department of Biology, Shahed University
2. Department of Biology, Shahed University
3. Department of Biotechnology, Semnan University

Background and Aim: Resistance to antimicrobial drugs in the treatment of infectious diseases causes problems. The absorbent protein of the DNA, ComL, is one of the proteins involved in the transformation of resistance plasmid. This protein is located on the outer membrane of Acinetobacter baumannii. In this study the immunogenicity of ComL protein and its role in absorbing antibiotic-resistant plasmids was investigated.

Methods: Coml gene in A. baumannii ATCC19606 genome was amplified, cloned in pET28a vector and the recombinant construct was transformed into E.coli BL21 (DE3). The recombinant protein was purified by Ni-NTA chromatography column and injected into BALB/C mice for immunization.

Results: The Kanamycin sensitive and to ampicillin resistant A. baumannii ATCC19606 was exposed to immune serum of mice for 1 hour showed resistance to Kanamycin In vitro, and reduction of about 60% in CFUs. A. baumannii were prepared as described above and injected to non-immunized mice at lower than LD50. The number of Kanamycin -resistant bacteria colonized in the spleen was 30% lower than that of control in the Kanamycin-ampicillin medium. The number of bacteria colonized in the spleen of the immune mice was been observed to be 3 fold lower than the control.

Conclusion: Antibodies against the 22KD ComL could prevent A. baumannii resistance to antibiotic, is an option for infection treatment.

Keywords: ComL protein; A. baumannii; Antibiotic –resistance; Recombinant Protein

P95 - 496: THE DANGER OF INCREASE MBLS PRODUCTER IN HOSPITAL SAMPLES

Seyede Fateme Daymad[1], Davood Esmaeeli[2], seyed Reza Hashemi miyan abad[3]

1. Micribiology, Faculty of Medicine, Baqiyatqllqh University of Medical Sciences, tehran, Iran
2. Micribiology, Faculty of Medicine, Baqiyatqllqh University of Medical Sciences, tehran, Iran
3. Micribiology, Faculty of Medicine, Baqiyatqllqh University of Medical Sciences, tehran, Iran

Background and Aim: According to a report from the World Health Organization Acinetobacter baumannii and Pseudomonas aeruginosa are one of the most important pathogens causing disease in humans ,which also are one of the most important causes of nosocomiale in hospitalized patients. The purpose of this study was determine the VIM-1 gene in Acinetobacter baumannii and Pseudomonas aeruginosa isolated from clinical samples of Baqiyatallah Hospital

Methods: In this study , 150 samples of Acinetobacter baumannii and Pseudomonas aeruginosa were collected from different clinical specimens of Baqiyatallah Hospital during years 2016-2017 . First , collected isolates were confirmed by biochemical methods and then were detected by disc diffusion method according to CLSI 2017 for several antibiotics. Combined disc methods were used to determine the phenotypes of MBLs producing isolates and at the end , study presence of the VIM-1 gene by PCR methods.

Results: The most antibiotic resistance in Acinetobacter baumannii and Pseudomonas aeruginosa was related to cefotaxime(100%) and ciprofloxacin (94.93%), respectively. Also ,using the combined disc method show that 78.83% and 87.64% of Acinetobacter baumannii and Pseudomonas aeruginosa isolates are the producer of MBLs. Molecular studies also shows that the prevalence of VIM gene in these Acinetobacter baumannii and Pseudomonas aeruginosa isolates was 64.38% and 100% , respectively.

Conclusion: This study demonstrates increase antibiotic resistance in both Acinetobacter baumani and Pseudomonas aeruginisa isolate . Control of the use types of antibiotics and the replacement of a more suitable treatment than antibiotic for treatment of infection are best solve to prevent the harms caused of increase resistance antibiotic.

Keywords:MBL.Pseudomonas aeruginosa.Acinetobacter baumannii

P96 - 502: DETECTION OF PLASMID MEDIATED QUINOLONE RESISTANCE GENES AMONG KLEBSIELLA PNEUMONIAE ISOLATES COLLECTED FROM URINARY TRACT INFECTIONS

Shaghayegh Shahkolahi[1], Mohammad Reza Asadi Karam[2], Saeid Bouzari[3], Mehri Habibi[4]

1. Department of Microbiology, Faculty of Basic Sciences, 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
4. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran. E. mail: m_habibi1362@yahoo.com

Background and Aim: Urinary tract infections (UTIs), including cystitis and pyelonephritis, are among the most common infectious diseases in human. Klebsiella pneumoniae is an opportunistic microorganism cause of UTI. Multi drug resistance K. pneumoniae isolates have been reported and the rate of them is increasing worldwide. The aim of this study was assessment the rate of resistance to quinolone antibiotics and frequency of quinolone resistance genes qnrA, qnrB and qnrS in K. pneumoniae isolates obtained from UTI patients.

Methods: In this study, 100 K. pneumoniae isolates were collected from UTI patients from different hospitals in Tehran, Iran and were confirmed by convectional biochemical tests. Antimicrobial susceptibility testing for quinolone antibiotics ciprofloxacin and norfloxacin was determined by disk diffusion method. Then, the presence of qnrA, qnrB and qnrS genes among the isolates was investigated using PCR with specific primers.

Results: Out of 100 isolates of K. pneumoniae, resistance rates to ciprofloxacin and norfloxacin antibiotics were 31% and 32%, respectively. The qnrB and qnrS genes were found in 22 (71%) and 16 (51.6%) of the 31 resistant isolates to both ciprofloxacin and norfloxacin. In this study, qnrA gene was not found among the isolates tested.

Conclusion: With respect to the significant rate of resistance to quinolone antibiotics and the high frequency of qnr genes in K. pneumoniae isolates, quinolones agents should be used with caution.

Keywords: Urinary tract infection, K. pneumoniae, Antimicrobial resistance, Quinolone

P97 - 506: ASSESSMENT OF CHEMICAL COMPOSITION AND ANTI-DERMATOPHYTE ACTIVITY OF TREE MEDICINAL PLANT ESSENTIAL OILS.

Rezvan Heidary tabar[1], Mohaddese Mahboubi[2], Elaheh Mahdizadeh[3]

1. Department of microbiology, Research center of Barij, Kashan, Iran
2. Department of microbiology, Research center of Barij, Kashan, Iran
3. Department of microbiology, Research center of Barij, Kashan, Iran

Background and Aim: Superficial fungal infections caused by dermatophytes occur in approximately 10 – 20% of the global population. Because of limited effectiveness of chemical antifungal agents, more investigations to identify new compounds with fungistatic or fungicides activities are needed. Thus, this study aimed determines chemical compositions and anti-dermatophyte activities of Laurus nobilis, Citrus medica and Pistacia atlantica Desf. Subsp. Kordica essential oils which used in folklore medicine to control microbial infections.

Methods: The chemical composition of essential oils from studied plants were isolated by hydro-distilation method and investigated by GC and GC–MS analysis. Antifungal effects of essential oils against Trichophyton mentagrophytes, T. rubrum, T. schoenleinii, Microsporum canis and M. gypseum were evaluated by micro broth dilution assay and mycelium inhibition technique.

Results: High contents of 1,8-cineol (38.8%), terpinyl acetate (21.0%), in Laurusnobilis, linalool (19.6%), cis linalool oxide (11.8%) in Citrus medica and α-pinene (19.8%), trans verbenol (17.1%) in Pistacia atlantica Desf. Subsp. Kordica were detected by GC-MS. All tree tested oils showed strong antifungal activity with MIC and MFC values in the range of (0.005±0.0 - 0.5±0.0) and (0.005±0.0-1.3±0.57) µl/ml, respectively. However, moderate mycelium inhibitory effect was observed (3.17%-21.44%) in examined (150 ppm) concentration.

Conclusion: According to the results, it may be concluded that these essential oils possess compounds with antifungal activity against dermatophytes especially in micro-broth dilution assay. Therefore, further investigations should be performed to fully evaluate on the pharmacological properties of these oils for skin infections treatments.

Keywords: Essential oil,Chemical composition, Anti-dermatophyte.

P98 - 515: ANTIFUNGAL EFFECT OF EUGENOL EXTRACT AGAINST ASPERGILLUS FUMIGATUS

Parvin Aghakhani[1], Masoumeh shams Ghhfarokhi[2], Mehdi Razzaghi Abyaneh[3]

1. Department of Mycology, Tarbiat Modares University, Iran
2. Department of Mycology, Tarbiat Modares University, Iran
3. Department of Mycology Pasteur Institute, Iran Introduction

Background and Aim: Aspergillus fumigatus is an opportunistic pathogen in all parts of the world, which causes different clinical forms, including invasive Aspergillosis, in immunocompromised patients. In recent years, increased levels of resistance to antifungal drugs have been observed, so other treatments that are more effective and safer than new treatments are being studied, including the use of herbal extracts.

Methods: The inhibitory effect of: Eugenol extract against was as Aspergillus fumigatus sessed by micro broth dilution (CLSI, M-38) methods in comparing with fluconazole.

Results: The results showed that the minimum inhibitory concentration (MIC) of: Eugenol and fluconazolen for fungi growth was 62.5 And128µg/ml and MIC 50 for these compounds was 31.25 and 64 µg/m l, respectively

Conclusion: The results of this study showed that: Eugenol is an effective factor that inhibit Aspergillus fumigatus growth and can be considered as a target for antifungal design methodology.

Keywords: Keywords: Eugenol, Aspergillus fumigatus MIC, Antifungal effect.

P99 - 533: AN INVESTIGATION OF ANTIBACTERIAL ACTIVITY OF ZNO NANOPARTICLE ON STAPHYLOCOCCUS AUREUS AND E.COLI

Fatemaeh Akbarzadeh[1], mohammad mehdi motaghi[2], yasser fattahian[3]

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

Background and Aim: In recent years, in order to prevent excessive use of antibiotics, disinfectant agents have gained particular significance. There are several reports on the antimicrobial effect of ZnO on Gram-positive and Gram-negative bacteria and fungi. this study was conducted to evaluate the antibacterial effects of zinc oxide nanoparticles in vitro.

Methods: In this study, minimum bactericidal concentration (MBC) and minimum inhibitory concentration (MIC) of this substance were determined using standard liquid dilution and disk diffusion methods for Gram-positive strain (S. aureus) and Gram-negative strain (E. coli) have calculated according to. Data analysis was performed using oneway ANOVA and Duncan tests at the level of p<0/05.

Results: According to the results of this study, MBC values of ZnO nanoparticle for S. aureus and E. coli bacteria were calculated to be 0.095 and 0.8µg/ml, respectively, and MIC values for S. aureus and E. coli were calculated 0.09, 0.095µg/ml, respectively.

Conclusion: Our study indicates that zinc oxide nanoparticles could potentially be an antibacterial reagent to treat diseases caused by S. aureus and E.coli.

Keywords: Zinc oxide, nanoparticle, Staphylococcus aureus, Escherichia coli, antibacterial activity

P100 - 541: ANTIBACTERIAL ACTIVITY OF JUNIPERUS POLYCARPUS AND GERANIUM ROBERTIANUM LEAF EXTRACTS AGAINST PATHOGENIC STAPHYLOCCOCAL STRAINS

Abolfazl Shirmohamadi[1], Abolfazl Shirmohamadi sosfad[2], Mohammad Reza Sharifmoghadam[3], Masumeh Bahreini[4], Bahman Khameneh[5]

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
4. Department of Pharmaceutical Control, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran

Background and Aim: Staphylococcus epidermidis, the main pathogen in implant-related infections, is common bacteria of human skin that form biofilms on the surface of surgical implants. Staphylococcus aureus is a gram positive, commensal bacterium that colonize the human skin, nasopharynx and gastrointestinal tract which causes a variety of localized and invasive infections such as bacteremia, osteomyelitis, arthritis and prosthetic joint infections. Juniperus genus has 6 species in Iran and is used in traditional medicine for wound healing, diabetes, tuberculosis, pneumonia and gastric ulcer. Geranium genus is used as an antidiarrheal, anti-inflammatory and antidiabetic. The aim of this study was to investigate the possible antibacterial properties of leaf extract of these plants.

Methods:methanolic extracts of freeze-dried plant leafs were prepared by Perculation method. Then Serial dilution of herbal extracts from 0.19 to 100mg/ml in distilled water and 5% DMSO were prepared and the Minimum Inhibition Concentrations (MICs) were performed according to the CLSI standard protocols in 96-well microplates. The plates were titrated with TTC (Triphenyl tetrazolium chloride)-dye after 24hours of incubation to determine the MIC value.

Results:the outcomes revealed that the MICs of both extracts had the same results for S. aureus and S. epidemidis that was 1.57mg/ml and 12.5mg/ml respectively. The Minimum Bactericidal Concentration (MBC) of Geranium extract for S. aureus and S. epidemidis was obtained 12.5mg/ml and 3.12mg/ml respectively, and for the Juniperus extract was obtained 25mg/ml for both bacteria.

Conclusion:according to this study, both leaf extracts demonstrated high bacteriostatic and bactericide properties which could be great candidates for staphylococcal infections treatment.

Keywords: Antibacterial, Plant extract, Geranium robertianum, Juniperus polycarpus, Staphylococcus epidermidis, Staphylococcus aureus.

P101 - 542: ANTIBACTERIAL PROPERTIES OF THE LEAF AND ROOT EXTRACTS OF EREMOSTACHYS BIOSSERIANA AGAINST STAPHYLOCOCCUS EPIDERMIDIS AND STAPHYLOCOCCUS AUREUS BACTERIA

Abolfazl Shirmohamadi[1], Abolfazl Shirmohamadi sosfad[2], Mohammad Reza Sharifmoghadam [3], Masumeh Bahreini[4], Bahman Khamene[5]

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
4. Department of Pharmaceutical Control, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran

Background and Aim: The most important pathogens in nosocomial infections are Staphylococcus aureus and Staphylococcus epidermidis that are associated with catheters and medical implants. Secretion of toxins and exogenous enzymes by S. aureus causes bacteremia and skin abscesses. S. epidermidis is involved in infections of prosthetic joints, intracardiac devices and artificial heart valves. Eremostachys genus is a member of Lamiaceae family and has 5 endemic species in Iran. The aim of this study was to investigate the possible antibacterial properties of Eremostachys extracts against these bacteria.

Methods:methanolic extracts of freeze-dried plant leaf and root were prepared by Perculation method. Then Serial dilution of herbal extracts from 0.19 to 100mg/ml in distilled water and 5%DMSO were prepared, the Minimum Inhibition Concentrations (MICs) and Minimum Bactericidal Concentrations (MBCs) were performed according to the CLSI standard protocols in 96-well microplates. The plates were titrated with TTC (Triphenyl tetrazolium chloride)-dye after 24-hours of incubation to determine the MIC value.

Results:the outcomes revealed that the MICs of leaf extract for S. aureus and S. epidemidis was 25mg/ml and the MICs of root extract were 50mg/ml and 0.7mg/ml for both bacteria. The MBCs of root extract for S. aureus and S. epidemidis were 25mg/ml and 100mg/ml respectively while there was no bactericidal evidence for leaf extract.

Conclusion: According to the study, Eremostachys root extract, in addition to the therapeutic use of traditional medicine such as cardiovascular disease, anti-inflammatory, antitumor and anti-viral, has the ability to inhibit pathogenic bacterial growth that is a good option for the treatment of Staphylococcal disease.

Keywords: Antimicrobial, Plant extract, Eremostachys biosseriana, Staphylococcus epidermidis, Staphylococcus aureus, MIC

P102 - 554: EGG YOLK IMMUNOGLOBULIN AGAINST PSEUDOMONAS AERUGINOSA OPRF, PREVENTION AND TREATMENT OF INFECTIONS

Fatemeh Noroozi[1], Seyed. Latif Mousavi Gargari[2]

1. Master Student, Department of Cell Biology, Faculty of Basic Sciences, Shahed University, Tehran, Iran
2. Professor, Department of Cell Biology, Faculty of Basic Sciences, Shahed University, Tehran, Iran

Background and Aim: Nosocomial infection is a main problem for patients after hospitalization. Pseudomonas aeruginosa is an opportunistic bacteria which can cause these hospital acquired infections. To prevent development of novel resistant strains, antibiotic therapy should be replaced with other methods. Based on existing condition, antibody utilization can be an appropriate approach. In comparison to other antibodies, egg yolk immunoglobulin (IgY) is a reasonable choice as it has many advantages like easy production and extraction procedure.

Methods: In this study hens were immunized intramuscularly with OprF recombinant protein which is highly conserved among various P.aeruginosa strains. IgY was extracted from egg yolks in two stages. First, egg yolks diluted 7 times (by volume) with water, pH adjusted to 5.0 with 0.5 M HCl, and the mixture was frozen at -20 °C. The frozen mixture was transferred to a funnel with conventional filter paper and allowed to melt freely at room temperature. In the second isolation stage, IgY precipitated with 8.8% w/v NaCl, pH was adjusted with 0.5 M HCl to 4.0. Mixtures were stirred for 2 hours at room temperature and then centrifuged at 3,380 g for 20 min at 4 °C. Supernatants were discarded and the pellets dissolved in PBS. The antibody titers were measured by ELISA technique.

Results:ELISA results showed that antibody titers significantly increased in comparison to control samples and the produced immunoglobulin had the ability of detection and attachment to the OprF.

Conclusion: The obtained immunoglobulin could be an effective choice for passive immunotherapy against P.aeruginosa infections.

Keywords: Pseudomonas aeruginosa,OprF, IgY

P103 - 562: LINEZOLID, QUINUPRISTIN/DALFOPRISTIN AND DAPTOMYCIN RESISTANCE IN VANCOMYCIN RESISTANT ENTEROCOCCI IN TEHRAN HOSPITALS

Jaber Ghorbani[1], Fereshteh Jabalameli[2]

1. Department of Microbiology, School of medicine, Tehran university of medical science, Tehran, Iran
2. Department of Microbiology, School of medicine, Tehran university of medical science, Tehran, Iran

Background and Aim: This study aimed to determine the prevalence of linezolid, quinopristin/dalfopristin and daptomycin resistance among vancomycin resistant enterococci (VRE) isolated from various clinical specimens in selected Tehran hospitals.

Methods: Between March 2015 and August 2017, 240 enterococci were isolated from different types of clinical specimens (urine (189), blood (32), abdominal fluid (10), CSF (5), wound (3) and others (11)). One hundred and seventy-four were enterococcus faecium (72.5%), 52 (21.7%) enterococcus faecalis and 14 were other species. E. faecium and E. faecalis isolates were tested for vancomycin resistance. The vancomycin resistant isolates were tested for linezolid, quinopristin/dalfopristin and daptomycin resistance by disk diffusion and micro-dilution methods.

Results: Eighty (33.3%) of the isolates were resistant to vancomycin. All vancomycin resistant enterococci (VRE) were susceptible to both linezolid and daptomycin. Sixteen (9.1%) of vancomycin resistant enterococcus faecium (VREF) were resistant to quinopristin/dalfopristin (QD). Vat E gene which is the most common gene in QD enterococcal resistant strains was not detected. All E. faecalis isolates were resistant to QD, as expected.

Conclusion: Although in this study, resistance to linezolid and daptomycin was not observed, but it must be administered with caution given that linezolid is used as the main treatment for VRE strains in our country, as a result of possible over-treatment, bacterial resistance is expected and the resistance to linezolid have been reported in neighboring countries. Thus clinicians may have to deal with linezolid resistant-VRE in the near future.

Keywords:linezolid, VRE, enterococci

P104 - 566: EVALUATION OF ANTIBACTERIAL ACTIVITY OF MATHANOL,ETHYL ACETATE AND HEXANE EXTRACTS OF CRUCIATA TAURIACA

Behnaz Asadi[1], Shiva Khalil_Moghaddam[2], Atousa Aliahmadi[3]

1. Department of Biology, Yadegar-e-Imam Khomeini (RAH) Shahre Rey Branch, Islamic Azad University, Tehran, Iran
2. Department of Biology, Yadegar-e-Imam Khomeini (RAH) Shahre Rey Branch, Islamic Azad University, Tehran, Iran
3. Medicinal Plants and Drug Research Institute, Shahid Beheshti University

Background and Aim: Medicinal plants are considered new resources for producing agents that could act as alternatives to antibiotics. The aim of this study was to evaluate the antibacterial activity of Cruciata Tauriaca extracts against two Gram-posetive bacterial species.

Methods: This plant have been collected in spring. Methanol and n-hexan was used for extraction of plant polar and nonpolar materials. Then minimum inhibitory concentration (MIC) of the plant materials were determined against Bacillus cereus and Staphylococcus aureus by broth micro-dilution method. Mueller hinton broth was used for preparation of serial diluted samples which were checked against 0.5-1 × 106 CFU (Colony forming unit) of bacteria. Incubation was done for 20 hrs at 37oC. MICs were recorded as the lowest concentrations which could inhibit visible growth of bacterium. Chloramphenicol was used as standard antibiotic.

Results: Methanolic extract of Cruciata Tauriaca could show the best result (MICs 0.467 mg/ml for Bacillus cereus) and Staphylococcus aureus was inhibited in higher concentration of methanolic extract. (3.74 mg/ml).

Conclusion: According to the result of this study, methanolic and hexane extracts can exhibit antibacterial effects.

Keywords: Antibacterial activity, MIC, Cruciata Tauriaca

P105 - 573: BACTERIAL BIOFILM IN VENTILATOR-ASSOCIATED PNEUMONIA

Elnaz Shahrukhi[1], Alka hasani[2]

1. MSc Fellow, Tuberculosis and Lung Diseases Research Center and Department of Medical Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran
2. . Associate Professor, Tuberculosis and Lung Diseases Research Center and Department of Medical Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran

Background and Aim: Introduction Development of Ventilator-associated pneumoniae (VAP) presents an intricate chemistry comprising of intubation and invading bacteria which often are tied up with biofilm production Aims To assess the phenotypic and genetic basis of biofilm formation by isolated from Acinetobacter baumannii and klebsiella pneumoniae mechanically ventilated and VAP developed patients.

Methods: Materials and Methods Endotracheal aspirate obtained from 40 mechanically ventilated patients were collected for culture at least in four episodes including, 48 hours, 72 hours, 7 days and 10 days after being ventilated. . Isolates were identified using standard phenotypic methods and the antibiotic susceptibility of them was determined by agar diffusion method. The ability of isolates to form biofilms was evaluated quantitatively using micro titer plate method and finally, the presence of biofilm genes was investigated by molecular method.

Results: The prevalence of VAP was 15%. A.baumannii (n=68) K. pneumoniae (n=32). 60.2% A.baumannii produced either moderate or strong biofilm, whereas 67.7% K.pneumoniae, isolates revealed either moderate or strong biofilm on micro titer plate. In the present investigation, 57.4% of A.baumannii showed the presence of bap gene producing product of 400bp. Gene type3 product of 817bp was present in all K. pneumoniae isolates while, mrkA product of 328bp and fimK product of 597bp genes were shown in 65.6% and 81.2% isolates respectively by multiplex PCR.

Conclusion: Drug resistance phenotypes require specific national and regional therapeutic studies focusing on antimicrobial stewardship programs. Presence of biofilm requires routine surveillance of VAP, to track endemic VAPs.

Keywords: Ventilator-associated pneumonia- , Biofilm

P106 - 580: PREVALENCE OF TEM, CTX-M AND SHV GENES IN KLEBSIELLA PNEUMONIAE ISOLATED FROM PATIENTS WITH VENTILATOR-ASSOCIATED PNEUMONIA

Kamal Ahmadi[1], Gholamreza Yousefi-Fatmesari[2], Mohsen Azizi[3], Alireza Janbakhsh[4], Ali Karbasfrushan[5], Mohammad Hossein Zamanian[6]

1. Ph.D. Student of Medical Bacteriology, Department of Microbiology, Pasteur Institute of Iran, Tehran, Iran
2. Assistant Professor, Department of Pediatrics, School of Medicine, Kermanshah University of Medical Sciences, Kermanshah, Iran
3. MSc, Department of Microbiology, School of Medicine, Kermanshah University of Medical Sciences, Kermanshah,Iran
4. Associate Professor, Department of Infectious Disease, Kermanshah University of Medical Sciences,Kermanshah, Iran
5. Department of Anesthesiology, Critical Care and Pain Management, Imam Reza Hospital, Kermanshah University of Medical Sciences, Kermanshah, Iran
6. Assistant Professor, Department of Infectious Disease, Kermanshah University of Medical Sciences,Kermanshah, Iran

Background and Aim: Ventilator-associated pneumonia (VAP) is one of the most common infections in intensive care unite with high mortality rate. The aim of this study was to determine the prevalence of TEM, CTX-M and SHV genes in Klebsiella pneumoniae isolated from Ventilator-associated pneumonia in Kermanshah.

Methods: The study was carried out on Bronchoalveolar lavage (BAL) samples from hospitalized patients in intensive care unit. After samples collection, 57 Klebsiella pneumoniae isolates were confirmed by bacteriology and biochemistry tests. Then antibiotic sensitivity test was done by disk diffusion method and ESBL enzymes existence was phenotypically determined by combined disk method. The frequency of ESBL genes was determined by their specific primer and PCR method.

Results: The highest antibiotic resistance in Klebsiella pneumoniae was to Ceftriaxone and cotrimoxazole (78.9%), whereas the lowest antibiotic resistance was to Colistin (3.5%) and Imipenem (33.3%). Genotypically the frequency of SHV, TEM and CTX-M genes was 18(31.6%),13 (22.8%) and 7(12.3%) Respectively.

Conclusion: According to the high resistance of Klebsiella pneumoniae isolated from patient's samples with Ventilator-associated pneumonia to third generation Cephalosporin and the prevalence of ESBL producing strain in these patients, identification of broad-spectrum beta-lactamase producing strain and selecting proper antibiotic seem to be necessary.

Keywords: Ventilator-associated pneumonia, Bacterial resistance pattern, Intensive Care Unit

P107 - 585: THE CORRELATION BETWEEN BIOFILMS FORMATION CAPABILITIES WITH THEIR RELATED GENES AND ANTIBIOTIC RESISTANCE PATTERNS IN CLINICAL AND ENVIRONMENTAL ISOLATES OF PSEUDOMONAS AERUGINOSA

Pezhman Karami[1]

1. Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran

Background and Aim: Pseudomonas aeruginosa is an important nosocomial pathogen which its infection is life-threatening because of their antimicrobial resistance. The integron genes and biofilm formation of P. aeruginosa have a significant role in antibiotic resistance. This study aimed at evaluating the correlation between biofilms formation capabilities of clinical and environmental P. aeruginosa isolates with their related genes.

Methods: This cross-sectional study during 2017 was performed on 58 clinical and 20 environmental isolates of P. aeruginosa with collecting the 547 samples (439 of clinical and 108 of environmental samples). The isolates were identified by phenotypic and genotypic tests. Kirby-Bauer agar disk diffusion method was used for susceptibility testing. The prevalence of class I, II and III Integrons and rhlA and lasB genes was determined by PCR. Determining of biofilm formation was performed using a microtiter plate method. The Stata software was used for statistical analysis.

Results: In total, the most prevalent of resistance was observed against Ticarcillin/Clavulanic Acid (55%). Generally, 44 (56.4%) of strains were producers of strong biofilm in both environmental and clinical isolates. The prevalence of strong biofilms producers in clinical isolates was more than environmental isolates. Also, a significant correlation was observed between IntI, IntII and rhlA genes with biofilm formation capability of isolates (P=0.02).

Conclusion: Regarding more than fifty percent of both environmental and clinical isolates were producers of strong biofilms and because the source of clinical isolates may be from the environment, the necessary hygiene measurements should be performed for prevent of transferring the environmental isolates to hospitalized patients.

Keywords: Biofilm, integron, rhlA, lasB, Pseudomonas aeruginosa

P108 - 587: APPLICATION OF MULTIPLEX-PCR IN THE DETECTION OF OXA PLASMID GENES IN CLINICAL ISOLATES OF KLEBSIELLA PNEUMONIAE

Reza Yari[1], Maryam Saki[2], Mohsen Mirzaei[3]

1. Assistant Professor of Cell Biology, Department of Biology, Faculty of Sciences, Borujerd Branch, Iran.
2. M.Sc in Cell Biology, Department of Biology, Faculty of Sciences, Borujerd Branch, Islamic Azad University, Borujerd, Iran.
3. Assistant Professor of Bacteriology, Department of Laboratory Sciences, Medical Faculty, Borujerd Branch, Iran.

Background and Aim:A large proportion of clinical samples are infected by Klebsiella. Nowadays, the extensive use of braodspectrum β-lactams has increased resistance to β-lactams worldwide. Nowadays, the extensive use of braodspectrum β-lactams has increased resistance to β-lactams worldwide. The goal of this research was to investigate the effectiveness of multiplex-PCR technique in simultaneous detection of pathogenic genes in Klebsiella pneumoniae.

Methods:96 isolates were collected from Imam Khomeini and Chamran Hospital in Boroujerd. Disc diffusion sensitivity test was performed according to CLSI standard. To identify the oxa genes, multiple PCR tests were used.

Results:10 isolates had oxa-1 gene with the highest resistance to ceftriaxone and the highest sensitivity to meropenem. Two isolates of were reported to had the oxa-9 gene with the highest resistance to ceftriaxone and the highest sensitivity to meroponem. 1 isolstes had both of the oxa-1 and oxa-9 genes with was resistant to amoxicillin-clavulanate and susceptible to meropenem, ertapenem, aztreonam and ceftriaxone. oxa-2 and oxa-48 genes were not detected in any of the samples. The highest susceptibility to maropenem and orthranem was and and the highest resistance was reported for amoxicillin-clavulanate and ceftriaxone. Of the 96 isolates of Klebsiella, 68 were susceptible to antibiotics and 11 isolates had oxa family genes.

Conclusion: The isolates with oxa family genes, mostly in the emergency department, were isolated from the urinary tract from women and have the highest resistance to ceftriaxone and the highest sensitivity of to meropenem. the meropenem, ertapenem and aztreonam are more effective in treatment.

Keywords: Klebsiella pneumoniae, oxa genes, Multiplex-PCR, Borujerd

P109 - 588: DETERMINATION OF ANTIBIOTIC RESISTANCE PATTERN AND THE PREVALENCE OF BETA-LACTAMASE GENE BLATEM, SHV AND DHA IN PSEUDOMONAS AERUGINOSA CLINICAL SAMPLES

Reza Yari[1], Mohammad Torkashvand[2], Mohammad Reza Mehrabi[3]

1. Assistant Professor of Cell Biology, Department of Biology, Faculty of Sciences, Borujerd Branch, Iran.
2. MSc. Student, Department of Biology, Faculty of sciences, Borujerd Branch, Islamic Azad University, Borujerd, Iran.
3. Department of Laboratory Sciences, Medical Faculty, Borujerd Branch, Islamic Azad University, Borujerd, Iran.

Background and Aim: The presence of ESBL genes play an important role in resistance to beta-lactam antibiotics producing strains of these enzymes play . Gram-negative bacteria including Pseudomonas aeruginosa resistance to various antibiotics , beta-lactams and carbapenems especially increasingly been reported . This study aimed to investigate the prevalence of beta-lactamase genes in Pseudomonas aeruginosa isolates was performed by PCR method.

Methods:103 strains of Pseudomonas aeruginosa isolated from clinical samples of urine, sputum, burn wounds and devices dialysis pediatric hospitals in the cities of Qom and Tehran, with the Gram stain, a test of biochemical differentiation and PCR District 16s rRNA detection were identified. Resistance to Ceftazidime/clavulanic acid and cefotaxime/ clavulanic acid 10 other common antibiotics was determined by disk diffusion method. Genomic DNA was extracted by method kit was performed and the beta-lactamase gene amplification with primers Amplicon available and were designed and genes were analyzed by PCR.

Results: Of the total 103 isolates of Pseudomonas aeruginosa, 50 isolates with broad-spectrum beta-lactamase phenotype were observed. 46 isolates (47/38%) were carriers of TEM-1 beta-lactamase gene. 35 isolates had SHV gene and none of the isolates was observed in DHA gene.

Conclusion: Pseudomonas aeruginosa beta-lactamase largely resistant to other common antibiotics and to select a suitable drug for destroying their antibiotic susceptibility testing should be done.

Keywords: Pseudomonas aeruginosa, ESBL, blaTEM, blaSHV, blaDHA.

P110 - 593: FREQUENCY OF MULTI-DRUG RESISTANCE IN ENTEROBACTER ISOLATED FROM PATIENTS WITH URINARY TRACT INFECTION IN GORGAN

Hanieh Bagheri[1], Dr Ezzat Allah Ghaemi[2]

1. Golestan university of medical science
2. Golestan university of medical science

Background and Aim: Several species within the genus enterobacter have been recognised as important causative agents of hospital acquired infections. The aim of this study is consideration of Frequency of Multi-Drug Resistance In Enterobacter Isolated From Patients With Urinary Tract Infection In Gorgan.

Methods: In this study 29 Enterobacter isolated from Urinary tract, confirmed with biochemical test. Then antibiogram with Kirby-Bauer method based on CLSI standards were done with different antibiotics. Then, results were studied and analysed in the program was SPSS18.

Results: In this study, considered 18 antibiotics from 10 classes. The most resistance belonged to Clindamycin*(100%), Cephalosporins (65.5%) and then Nitrofurantoin (57.1%). The most sensitivity belonged to Carbapenems(100%) and then Aminoglycosides(79%). MDR also considered too, in this research, 27.6% resistance to 1-2 classes of antibiotics together.38% patients had resistance to >7 classes of antibiotics. 75% were women. 55.4% were hospitalized. In inpatients the most resistance after clindamycin, belonged to Cephalosporins (81.2%), then Sulfonamides(68.8%), %). The most sensitivity belonged to Carbapenems(100%) and then Piperacillin/tazobactam,(75%). In inpatients, prevalence of MDRs belonged to more than >7 classes of antibiotics.(56.2%) In 4-6 classes of antibitics was not seen any resistance.

Conclusion: High antibiotic resistance was observed in Enterobacters specially in inpatients. Resistance to >7 classes of antibiotics in this bacteria was seen more than others

Keywords: Multi-Drug Resistance(MDR), Enterobacter, Urinary Tract Infection(UTI), Gorgan

P111 - 600: PROPOSING A POTENTIAL SMART DIGITAL NETWORK FOR TREATMENT WITH PROBABLE ANTIBIOTICS

fateme elahi[1], sajede rajabi[2], Dr. Majid Zare Bidaki[3]

1. Student Research Committee, Medical tudent, Birjand University of Medial Sciences
2. Student Research Committee, Medical tudent, Birjand University of Medial Sciences
3. Infectious Disease Research Center, Associate Professor, Department of Medical Microbiology, Faculty of Paramedical Sciences, Birjand University of Medical Sciences, Birjand, Iran

Background and Aim: Emerging high and variable rate of antibiotic resistance and the lack of clinical laboratories in many remote areas making it impossible to exactly determine antibiotic sensitivity of bacterial pathogens and this encounter antibiotic administration with a number of dilemmas. The aim of this project is to build a decision support system for antibiotic treatment of inpatients with moderate to severe infections. The use of this system should lead to high percentages of appropriate antibiotic treatment, reducing complications, mortality and hospital stay.

Methods: This project is based on a causal probabilistic digital network and uses a cost–benefit model for antibiotic treatment in inpatients with common bacterial infections. The system works based on an artificial intelligence algorithm and use clinical and laboratory data available within hours of admitting the patient to the hospital. The system will be tested in a randomized controlled trial in different parts of our country and show to improve the percentage of appropriate antibiotic therapy.

Results: Search in medical databanks revealed some recent similar studies. One project, known as TREAT was conducted in Denmark, Germany and Italy aiming to produce and test a system to improve antibiotic therapy beyond current clinical practice. The initial results were acceptable. Here, we will discuss the advantages of using this probabilistic model

Conclusion: Recent studies have shown that using a smart digital network for antibiotic treatment can improve the speed of appropriate empirical antibiotics treatment and reduces therapeutic costs. We suggest to produce and apply a similar but national digital networking system in Iran.

Keywords: Prediction, antibiotic treatment, decision support system

P112 - 606: ANTIMICROBIAL PROPERTIES OF CLOVE EXTRACT (SYZYGIUM AROMATICUM)

Hamideh Asayeshtalab[1], Amir Arasteh[2]

1. MSc student of microbiology, Department of biology, Rasht Branch, Islamic Azad University, Rasht, Iran
2. Assistant Professor, Department of biology, Rasht Branch, Islamic Azad University, Rasht, Iran

Background and Aim: The clove, known as Syzygium aromaticum, and the English name Clove, is a plant whose leaves are always green and permanent, and a tree with a size of 8 to 12 meters from the native Mirtaceae family of Malacca Island in eastern Indonesia.

Methods: The aim of this study was to investigate the antimicrobial activity of hydroalcoholic extract of clove plant. First, the cloves were powdered and 96% hydroalcoholic extract of clove was prepared with ethanol. The antimicrobial effects of the extract on E. coli and S. aureus were evaluated using antibiogram method and MIC and MBC values of hydroalcoholic extract of clove were determined.

Results: The diameter of the non-growth halo of hydroalcoholic extract of clove in the well method on E.coli and S. aureus bacteria was 21 mm and 40 mm, respectively. The results of MIC and MBC in E.coli and S.aureus bacteria were 0.625 mg / ml and 1.25 mg, respectively.

Conclusion: These results, introduce the clove extract as an antimicrobial formulation and a suitable alternative to chemical compounds.

Keywords: Antimicrobial, Clove, Escherichia coli, Staphylococcus aureus

P113 - 608: METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS (MRSA) AND STAPHYLOCOCCAL CASSETTE CHROMOSOME MEC GENOTYPES (SCCMEC) IN FASA, FARS

Abbas Abdollahi[1], Sohrab Najafipoor[2]

1. Department of Microbiology, Fasa University of Medical Sciences
2. Department of Microbiology, Fasa University of Medical Sciences

Background and Aim: Staphylococcus aureus is one of the most important pathogenic bacteria causing community and hospital acquired infections. Treatment of this pathogen is complicated because of resistance to many antimicrobial drugs. Methicillin-resistant S. aureus (MRSA) is considered as a cause of clinically infectious disease in public health. The aim of this study is determination of the antibiotic resistance pattern in MSRA strains (based on SCCmec genotyping) isolated from patient in hospitals of Fasa.

Methods: Staphylococcus aureus is one of the most important pathogenic bacteria causing community and hospital acquired infections. Treatment of this pathogen is complicated because of resistance to many antimicrobial drugs. Methicillin-resistant S. aureus (MRSA) is considered as a cause of clinically infectious disease in public health. The aim of this study is determination of the antibiotic resistance pattern in MSRA strains (based on SCCmec genotyping) isolated from patient in hospitals of Fasa.

Results: Among 164 isolated S. aureus, 78 samples were MRSA. Sensivity pattern of Antibiotic were reported as: chloramphenicol (19.2%), gentamicin (74.4%), kanamycin (85.9%), erythromycin (89.7%), tetracycline (92.3%), ciprofloxacin (92.3%), tri-methoprime (92.3%), methicillin (100%) and cefoxitin (100%); there were any resistance to vancomycin. Most and less common genotypes of SCCmec were related to II and IV types, respectively.

Conclusion: Easy access and improper administration of antibiotics and also incomplete course of treatment in infectious disease can led to development of multi-resistance isolates such as MRSA.

Keywords:SCCmec, S. aureus, MRSA, resistance

P114 - 610: EVALUATION OF ANTIBIOTIC RESISTANCE OF ACINETOBACTER BAUMANNII STRAINS ISOLATED FROM CLINICAL SAMPLES OBTAINED IN ZAHEDAN HOSPITALS

Elnaz Arzhang[1], Farokh Rokhbakhsh-zamin[2]

1. Department of Microbiology,Kerman Branch,Islamic Azad University,Kerman,iran

Background and Aim: Acinetobacter baumannii is a major cause of nosocomial infections. It has the ability to develop resistance to antibiotics quite easily. The present study aimed to evaluate the patterns of antibiotic resistance of different clinical isolates of A.baumannii.

Methods: Acinetobacter baumannii strains were isolated from sixty clinical samples obtained from 3 hospitals of Zahedan during January to May 2018. They were identified by staining and biochemical methods as discussed by bouvet and grimont. Antibiotic resistance pattern of all isolates were checked by disc diffusion test, Kirby Bauer disc diffusion method. Pure bacterial culture suspended in buffer, standardized to turbidity and swabbed uniformly on Muller Hinton agar. Antibiotic discs were then placed on agar plate. Inhibition zones were compared with standard table of CLSI.

Results: Ampicillin , Gentamicin, Tetracycline , Ceftazidim, , Amikacine , Meropenem , Colistin and Streptomycin were used in this experiment and majority (99%) of Acinetobacter baumannii strains were resistant to meropenem and mostly they were sensitive to colistin and some isolates were recognized as Multi drug resistant (MDR) A.baumannii.

Conclusion: During last decades, resistance of A.baumannii to different antibiotics was elevated, according to our experiment and similar researches; it was shown each isolate stayed susceptible to one or more tested and common antibiotics. But, according to possibly transformation of resistant genes to the other strains, reconsideration in antibiotic consumption patterns should be highlighted in better ways.

Keywords: Acinetobacter baumannii, Antibiotic resistance, Disc diffusion test, Colistin

P115 - 611: ANTIMICROBIAL EFFECTS OF THE HYDRO-ALCOHOLIC EXTRACT OF FALCARIA VULGARIS

Azadeh Foroughi[1], Mehrdad Pooyanmehr[2], Saber Rahimi[3]

1. Pathobiology and Basic Sciences department, Veterinary School, Razi University, Kermanshah, Iran
2. Pathobiology and Basic Sciences department, Veterinary School, Razi University, Kermanshah, Iran
3. Pathobiology and Basic Sciences department, Veterinary School, Razi University, Kermanshah, Iran

Background and Aim: Nowadays, secondary metabolites of medicinal plants are investigated well and assigned antibacterial properties of most of the plant extracts. One of the most common ways to keep foodstuff from spoilage is using of preservatives. Moreover the prevention of microbial contamination in food, these materials help to increase in shelf-life of fruits, vegetables and processed food. On the other hand, anomalous applying of chemical drugs has resulted in microbial resistence development. Plants and their derivatives have potentials to be used instead of chemicals while their side effects are less.

Methods: Hydro-alcoholic extract of Falcaria vulgaris was used. The extracts were prepared in different dilutions (240, 120, 60, 30, 15, 7.5 and 3.75 mg/ml) and applied on Escherichia coli and Staphylococcusaureus by Macro-broth dilution and Disk-diffusion methods. Tetracycline and distilled water were used as positive and negative control, respectively. Minimum inhibitory concentration (MIC) and Minimum bactericidal concentration (MBC) were determined.

Results: The extract prevented from E. coli growth in 240 mg/ml. So, MIC is reported equivalent to 240 mg/ml for this bacterium. Although, 240 mg/ml is reported as MBC. About S. aureus, Falcariavulgaris in 240 and 120 mg/ml dilutions could prevent from its growth. Thus, 120 mg/ml is considered as MIC and 240 mg/ml is calculated as MBC. In Disk diffusion method, no inhibition zone was observed in any of the bacteria.

Conclusion: The results achieved in this study showed that Falcaria vulgaris extract has growth inhibitory impact on both E.coli and S. aureus and S. aureus is known as more sensitive than E. coli.

Keywords: Falcaria vulgaris, E.coli, S. aureus, MIC, MBC

P116 - 613: EVALUATION OF ANTIBACTERIAL ACTIVITY OF HYDRO-ALCOHOLIC EXTRACT IN HERBAL PLANT SPECIES, NATIVE OF FASA, FARS

Abbas Abdollahi[1], Reza Ganjali[2], Mohammad Ghaedi[3], Hanieh Moghtader[4], Mahdie Omidi[5], Shabnam Esfandiari[6], Hengameh Tavoosi[7], Amin Dakhili Ardestani[8], Sohrab Najafipoor[9], Ghazaleh Ghaznavi[10]

1. Laboratory of Herbal Plants and Department of Microbiology, Faculty of Medicine, Fasa University of Medical Sciences
2. Laboratory of Herbal Plants and Department of Microbiology, Faculty of Medicine, Fasa University of Medical Sciences
3. Laboratory of Herbal Plants and Department of Microbiology, Faculty of Medicine, Fasa University of Medical Sciences
4. Laboratory of Herbal Plants and Department of Microbiology, Faculty of Medicine, Fasa University of Medical Sciences
5. Laboratory of Herbal Plants and Department of Microbiology, Faculty of Medicine, Fasa University of Medical Sciences
6. Laboratory of Herbal Plants and Department of Microbiology, Faculty of Medicine, Fasa University of Medical Sciences
7. Laboratory of Herbal Plants and Department of Microbiology, Faculty of Medicine, Fasa University of Medical Sciences
8. Laboratory of Herbal Plants and Department of Microbiology, Faculty of Medicine, Fasa University of Medical Sciences
9. Laboratory of Herbal Plants and Department of Microbiology, Faculty of Medicine, Fasa University of Medical Sciences
10. Laboratory of Herbal Plants and Department of Microbiology, Faculty of Medicine, Fasa University of Medical Sciences

Background and Aim: The excessive use of antibiotics has led to increase in drug resistance in most pathogens. Research shows that medicinal plants and their natural derivatives can have similar effects to synthetic drugs; the aim of this study was evaluate the antibacterial activity of hydro-alcoholic extract of ten native herbs of Fasa, Fars province.

Methods: In this study, antibacterial effects of hydro-alcoholic extract (Punica granatum, Salvia officinalis, Zataria multiflora, Artemisia adamsii, Malva sylvestris, Peganum harmala, Heracleum persicum, Chamaemelum nobile, Trachyspermum, Achillea millefoliom) evaluared by well-established and disk diffusion methods. Experiments were carried out on S. aureus (PTCC 1431) and E. coli (PTCC 1399), three times. Disks containing 20, 30, 40 and 50 µl of plant extract according to standard antibiotic concentrations as well as wells created with a diameter of 6 mm with similar concentrations (Muller Hinton Agar); inhibition zone diameter of bacterial growth was measured accurately after 24 hrs.

Results: Compared with standard antibiotic disks, the antibacterial effects against S. aureus indicate the highest inhibition zone in Punica granatum with 22 mm diameter (well method) and 20 mm in Peganum harmala (disk method); antibacterial effects against E. coli, in both methods related to Peganum harmala with 15 to 12 mm diameter, respectively. The lowest effect related to Salvia officinalis, Heracleum persicum and Achillea millefoliom.

Conclusion: Considering the results in comparison with standard antibiotic disks, further research on the mechanism of the effect of these plants, extraction and purification of effective substances and determination of focal doses are undergoing.

Keywords:herbal plants, Hydro-alcoholic extract, Antibacterial, Drug resistance, Antibiotic

P117 - 614: ANTIBIOTIC RESISTANCE PATTERN AND FREQUENCY OF ESBL PRODUCING ENTEROBACTERIACEAE ISOLATED FROM LETTUCE AND SPINACH IN GORGAN

Neda Kouroshzadeh[1], Ania Ahani Azari[2], Anegol Kheradmand[3], Ahmad danesh[4]

1. Gorgan Branch, Islamic Azad University, Gorgan, Iran
2. Department of Microbiology, Gorgan Branch, Islamic Azade University, Gorgan, Iran
3. Gorgan Branch, Islamic Azad University, Gorgan, Iran
4. Department of Health and Social Medicine, School of Medicine, Golestan University of Medical Sciences

Background and Aim: In recent years, there have been many epidemic outbreaks caused by consumption of contaminated vegetables. In most cases, Enterobacteriaceae were responsible for these epidemics. The purpose of this study was to investigate antibiotic resistance pattern and frequency of strains producing broad-spectrum beta-lactamase (ESBL) isolated from lettuce and spinach produced in Gorgan, Iran.

Methods: After culturing the isolates on MacConkey medium, colonies with specific morphological characteristics were selected. After preparation of pure culture, strains resistant to cefotaxime were identified and strains belonging to the Enterobacteriaceae family were isolated. The isolates were then studied for broad-spectrum beta-lactamases (ESBL) and their antibiotic resistance patterns were determined.

Results: The results of this study showed that ESBL Enterobacteriaceae is present in vegetables such as lettuce and spinach. It was also found that all isolated ESBL Enterobacteriaceae from spinach samples were resistant to Cotrimoxazole, Nalidixic Acid, Tetracycline, Chloramphenicol, and Amoxicillin, and sensitive to Imipenem. Isolated ESBL Enterobacteriaceae from lettuce samples was sensitive to Amikacin and Imipenem. Multiple antibiotic resistance was observed in all isolates

Conclusion: It can be concluded that use of animal fertilizers increases the risk of antibiotic-resistant bacteria in vegetables and ultimately in human and animals.

Keywords: Enterobacteriaceae, broad-spectrum beta-lactamases, vegetables, antibiotic resistance

P118 - 616: QUINOLONE SUSCEPTIBILITY AND PHYLOGENETIC ANALYSIS OF ESCHERICHIA COLI STRAINS ISOLATED FROM HUMAN AND CALVES

Mojdeh Barzan[1], Mehrnaz Rad[2]

1. PhD of bacteriology of Shahid Chamran University of Ahvaz
2. Department of Pathobiology, School of Veterinary Medicine, Ferdowsi University of Mashhad

Background and Aim: It has been suggested that widespread use of antibiotics is a driving force for the emergence of resistant bacterial strains, and epidemiologic evidence supports the view that there is a link between resistant human pathogen and farm animals. Recent findings indicate that phenotypic characterizations including resistant to quinolones are associated with genotypic characterization such as phylogenetic groups and virulence factors.

Methods:A total of 80 Escherichia coli isolates from human with urinary tract infection and healthy calves (40 isolates from each samples) were used. Triplex PCR was used to determine the phylogenetic groups of isolates. Antimicrobial susceptibility testing was performed by disc diffusion method.

Results: Phylogroup A isolates from calves were significantly more resistant to nalidixic acid than human isolates (P= 0.034). Also, Phylogroup B2 strains from human were significantly more resistant to ciprofloxacin than calves isolates (P= 0.028). There were no ciprofloxacin resistant E. coli from calves belonged to phylogroup B1.

Conclusion: The presence of cross resistance among fluoroquinolones used in veterinary and human medicine is a source of debate on the use of these antibiotics for the treatment of infections in animals. Calves can be a source for nalidixic acid resistant phylogroup B2 isolates. It may represent an emerging problem in public health, perhaps due to transfer of such strains from calves to humans

Keywords: Quinolone susceptibility, phylogenetic analysis, Escherichia coli strains

P119 - 623: TRENDS OF ANTIMICROBIAL RESISTANCE AMONG UROPATHOGENIC ESCHERICHIA COLI ISOLATES IN RUDBAR, NORTH OF IRAN

Susan Khanjani[1], Hadi Sedigh Ebrahim-saraei[2], Ali Mojtahedi[3]

1. 1Microbiology Department, Faculty of Medicine, Guilan University of Medical Sciences, Rasht- Iran.
2. 2Microbiology Department, Faculty of Medicine, Fars University of Medical Sciences, Shiraz- Iran.
3. Microbiology Department, Faculty of Medicine, Guilan University Campus, 7th Km of Rasht-Tehran Highway, Rasht- Iran.

Background and Aim: Escherichia coli (E. coli) is a clinically important pathogen, which frequently isolated from various infections, including urinary tract infections (UTIs), neonatal meningitis, blood stream infections (BSIs), gastroenteritis. Based on recent finding of global antibiotic resistance, E. coli is considered as an important cause of nosocomial and community-acquired infections and is one of the most common Extended-Spectrum Beta-Lactamases (ESBLs) producers. Antimicrobial resistance pattern evaluation among E. coli isolates is a necessary. The aims of this study were to determine the frequency and antimicrobial resistance pattern of E. coli isolates isolated from UTIs.

Methods: This retrospective study done within 12 months from March 2017 to February 2018 in a Rudbar central Hospital, North of Iran. E. coli isolates were obtained from urine specimens and identified using standard microbiological procedures. Antimicrobial susceptibility patterns were determined using disk diffusion method in accordance with CLSI recommendation.

Results: Of totally 792 urine cultures, 75 (9.5%) cultures showed noteworthy E. coli growth. Overall, the most of E. coli strains (80%) isolated from female specimens. The results of antibiotic susceptibility showed that the effective antibiotic for tested E. coli isolates was ciprofloxacin with 63.4% sensitivity rate, followed by nitrofurantoin (58.6%), ceftriaxone (58%) and co-trimoxazole (56%). Moreover, the lowest antibiotic susceptibility rate was seen toward cefazolin (42%).

Conclusion: The results showed that fluoroquinolones was the most effective antibiotic against E. coli infections in our region. Additionally, nitrofurantoin and ceftriaxone as effective substitution of fluoroquinolones are recommended for UTIs treatment.

Keywords: Escherichia coli, Urinary tract infections, Antibiotic susceptibility

P120 - 628: DETERMINATION OF ANTIBIOTIC RESISTANCE PATTERN IN ENTROBACTERIACEAE ISOLATED FROM HOSPITAL WASTEWATER IN KARAJ

Sina Foruzmand[1], Azam Haddadi[2], Mahmoud Shavandi[3]

1. Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran.
2. Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran.
3. Microbiology and Biotechnology Research Group, Research Institute of Petroleum Industry, Tehran, Iran.

Background and Aim: Over the past decades, awareness of the environmental load of resistant organisms has grown tremendously. The presented paper focuses on determination of antibiotic resistance pattern in Entrobacteriaceae strains isolated from hospital's wastewater in Karaj.

Methods:A total of 100 Entrobacteriaceae strains isolated from hospital's wastewater in Alborz province during the summer of 2018. Bacterial strains were identified by standard microbiological and biochemical tests. The antimicrobial susceptibility test was determined according to Kirby Baur assay.

Results: Of 100 Entrobacteriaceae isolates, 27 were E.coli followed by entrobacter 27, cirobacter frundi 24, proteus vulgaris 5, Klebsiella oxitoca 7, Klebsiella pneumoniae 3, citrobacter koseri 2, Shigella sonei 2,Psudomonas aeroginosa , Serratia marcescens and Klebsiella ozaenae 1, respectively in decreasing order. Resistance to amoxicillin was observed in 66% of isolates. Resistance to other antibiotics were as follows: nalidixic acid 40%, tetracycline 36%, ciprofloxacin and cefotaxim 13%,ceftazidim 10%, ceftriaxone 7% and cefepim 2%.

Conclusion: This study reflects an increasing prevalence of antibiotics resistant strains circulating in the wastewater. Dissemination of these resistance genes is of particular concern.

Keywords:wastewater, Entrobacteriaceae, antibiotic resistance

P121 - 629: ESBL PREVALENCE IN ENTROBACTERIACEAE ISOLATED FROM HOSPITAL'S WASTEWATER IN KARAJ.

Maryam Afshari[1], Azam Haddadi[2], Mahmoud Shavandi[3]

1. Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran.
2. Islamic Azad Uni, Karaj
3. Microbiology and Biotechnology Research Group, Research Institute of Petroleum Industry, Tehran, Iran.

Background and Aim: Hospitals are hotspots for antimicrobial-resistant bacteria (ARB) and will be ejected from hospitals via wastewater systems. In this study, we present AmpC and ESBL prevalence in Entrobacteriaceae strains isolated from hospitals wastewater in Karaj.

Methods:A total of 100 Entrobacteriaceae strains isolated from hospital's wastewater in Alborz province during the summer of 2018. Bacterial strains were identified by standard microbiological and biochemical tests. The antimicrobial susceptibility test was determined according to Kirby Baur assay. ESBLs producers were screened by phenotypic confirmatory test (PCT).

Results: Among the organisms cultured, Escherichia coli (74%) was the most common organism followed by Klebsiella oxytoka (7%). Antibiotic resistance pattern were observed as follows: cefotaxim 13%, ceftriaxone 19%, ceftazidim 15% and cefepim 7%. The ratio of isolates was detected as ESBLs and AmpC producers were 17% and 23%, respectively.

Conclusion: Antimicrobial resistance should now be seen as an 'environmental pollutant', and new wastewater treatment processes must be assessed for their capability in eliminating ARB, especially from hospital effluents.

Keywords: ESBL, Entrobacteriaceae, wast

P122 - 635: DIFFERENT VIRULENCE CAPABILITY AND PATHOGENIC STRATEGY AMONG CLINICAL ISOLATES OF MULTI-DRUG RESISTANT ACINETOBACTER BAUMANNII

Armaghan Soltani Shirazi[1], Farzad Badmasti[2], Omid Azizi[3], Morvarid Shafiei[4], Mohammad Mehdi Aslani[5], Hamid Solgi[6]

1. 1Department of Bacteriology, Microbiology Research Center, Pasteur Institute of Iran, Tehran, Iran
2. 1Department of Bacteriology, Microbiology Research Center, Pasteur Institute of Iran, Tehran, Iran
3. Department of Laboratory Sciences, Torbat Heydariyeh University of Medical Sciences, Torbat Heydariyeh, Iran
4. 1Department of Bacteriology, Microbiology Research Center, Pasteur Institute of Iran, Tehran, Iran
5. 1Department of Bacteriology, Microbiology Research Center, Pasteur Institute of Iran, Tehran, Iran
6. 1Department of Bacteriology, Microbiology Research Center, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Acinetobacter baumannii causes a variety of nosocomial infections. Serum resistance and antimicrobial resistance are two major capabilities of A. baumannii to establish its infections in patients.

Methods: Fifty clinical isolates of multi-drug resistant (MDR) A. baumannii were analyzed for clonal relatedness, serum resistance and in vivo assays.Also, some virulence genes, sequence variation of ompA and its expression were studied.

Results: The MLST results showed that there were three sequence types among MDR isolates including ST2 (64%, 32/50), ST513 (30%, 15/50) and ST1 (6%, 3/50). Whereas, all isolates recovered from host interior fluids had high serum resistance. The results of PCR assays and in silico analysis represented that the patterns of virulence genes and ompA variations among MDR isolates were clonally dependent. The in vivo analysis showed that the selected strains differently proliferated in spleen of C57/BL6 mice. Strains causing bacteremia in mice induced higher and significant level of IL-6 in serum compared to isolates without bacteremia capability. qRT-PCR analysis showed that bacteremia producing strains significantly overexpress ompA matched to the level of IL-6 in bloodstream of mice and its expression is clonally independent. Interestingly, AB-38 and AB-40 strains efficiently released in bloodstream, while they had low Log10 CFU/g scores during spleen colonization (4.69 and 4.1, respectively).

Conclusion: Our data showed that the patterns of virulence genes strongly related to MLST sequence types. Whereas the virulence traits of clinical isolates were clonally independent.

Keywords: Acinetobacter buamanii, serum resistance, In vivo

P123 - 646: COMPARISON OF DISK DIFFUSION AND E-TEST METHODS TO DETERMINE ANTIMICROBIAL ACTIVITY OF CEFTAZIDIME AND CIPROFLOXACIN ON CLINICAL ISOLATES OF ACINETOBACTER BAUMANNII

Mojtaba Mirshekari Soleimani[1], Hossein Hosseini Naveh[2], Mostafa Rezaeifar[3], Mahdi Rezaeifar[4]

1. Department of Biology, Faculty of Sciences, Shahid Bahonar University of Kerman, Kerman, Iran
2. Department of Microbiology and Virology, School of Medicine, Kerman University of Medical Sciences, Kerman, Iran.
3. Student Research Committee, Tehran University of Medical Sciences, Tehran, Iran
4. Pharmaceutics Research Center, Kerman University of Medical Sciences, Kerman, Iran

Background and Aim: This study was aimed to find a specific method to test the clinical isolates of Acintobacter baumannii in terms of antimicrobial susceptibility and resistance to two drugs of Ceftazidime and Ciprofloxacin using E-test and Disk Diffusion methods.

Methods: Totally 100 samples were collected from hospitalized patients at the general hospitals of Kerman Province, Southeastern, Iran between November 2013 to April 2014. They were identified by standard microbiological methods. Susceptibility by Disk diffusion and MIC by E-test were performed according to the Clinical and Laboratory Standards Institute breakpoints.

Results: In the disk diffusion method for ciprofloxacin antibiotic, the Acinetobacter specimens were reported to be 85% resistant, 4% intermediate, and only 11% susceptible. Also, for Ceftazidime antibiotic, the specimens were reported as 75% resistant, 15% intermediate, and only 10% susceptible. In the E-test method for ciprofloxacin antibiotic, the Acinetobacter specimens were reported to be 95% resistant, 0% intermediate, and 5% susceptible. Also, for Ceftazidime, the specimens were reported to be 93% resistant, 4% intermediate, and 3% susceptible. After performing the statistical Chi square test at confidence level of 95%, the P value for these two antibiotics was obtained ($p<0.199$) in both methods.

Conclusion: The findings of present study revealed the high resistance of this bacterium in Kerman Province and feeling the necessity of thinking of some strategies and solutions for reducing that microbial resistance as well as paying more attention to the selective treatments, antibiotic treatment course duration, and other instances that should be taken into account in any antibiotic diet.

Keywords: Acintobacter; antibiotic; resistance; disk diffusion; E-test

P124 - 653: MODIFIED CONGO RED AGAR METHOD TO DETECT BIOFILM PRODUCTION BY ENTEROCOCCUS FAECIUM

Saber Soltani[1], Mohammad Reza Pourmand[2]

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

Background and Aim: Enterococcus faecium in Hospitalized patients can cause urinary tract infection related to the use of catheter due to biofilm production. There are various phenotypic methods to detect biofilm formation. One method is based on culture in brain heart infusion agar (BHIA) including Congo red and sucrose. The aim of the present study was to determine the biofilm formation ability of vancomycin-resistant E. faecium isolates using Modified Congo red agar(MCRA).

Methods:A total of 29 isolates of E. faecium were collected from hospitalized patients at Ahvaz educational hospitals. Biochemical and molecular techniques were used to identify vancomycin- resistant E. faecium strains. We have confirmed MCRA capacity to detect biofilm production in 29 E. faecium strains, including 100% vanA gene–positive strains.

Results: All 29 isolates were resistant to vancomycin and 75.7% of them were also biofilm producers. The rate of isolates with Very black, Black, Almost black and Red biofilm formation were 27.5%, 31%, 17.2% and 24.3%, respectively.

Conclusion: As shown in the results, there is an association between vancomycin resistance E. faecium isolates and biofilm formation The MCRA method is fast, reproducible, and presents advantage to determine differences colonies in biofilm production between E. faecium strains. Also the MCRA method is a confident tool and can help to determine the real contribution of E. faecium in the biofilm formation process.

Keywords: Congo red agar, Biofilms, Vancomycin-resistant Enterococcus faecium

P125 - 655: FALSE COMBINED DISCS TEST FOR DETECTION OF EXTENDED-SPECTRUM B-LACTAMASE (ESBL) IN ACINETOBACTER ISOLATES

Nasim Shams[1], Mojtaba Moosavian [2], Mehrandokht Sirous[3]

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: The combination disc test (CDT) was used for phenotypic detection of ESBL production. The CDT methods compare the zones of cephalosporin discs to those of the same cephalosporin plus clavulanate. β-Lactamases Responsible for Resistance to Expanded-Spectrum Cephalosporins in Acinetobacter baumannii isolates. Enzymes with marginal ESBL activity, those expressed weakly, and those produced alongside other enzymes are the hardest to detect.

Methods:A total of 100 Acinetobacter baumannii isolates identified from patients at hospitals in Ahvaz, Iran, were studied. The CDT method was used for detection of ESBL production. The isolates were examined for the inhibition zone of ceftazidime (CAZ) 30 µg + clavulanic (CA) 10 µg adjacent to disk containing ceftazidime (CAZ) alone and cefotaxime (CTX) 30 µg + clavulanic (CA) 10 µg adjacent to disk containing cefotaxime alone on Muller Hinton agar. ESBL test was considered positive if the inhibition zone diameter in presence of clavulanic acid was ≥ 5 mm larger than that in the lack of it.

Results: Among 100 Acinetobacter baumannii isolates, combined disc test showed that only one isolate (1%) has been considered as ESBL producing isolate.

Conclusion: The results of this study showed that the majority of Acinetobacter baumannii isolates were resistant to the antibiotics ceftazidime and cefotaxime alone or in combination with clavulanic acid. So the CDT method outlined here will never be as precise as the best molecular analysis, but will detect most producers.

Keywords: Acinetobacter baumannii, Combination disc test, ESBL

P126 - 657: COMPARISON OF METHODS FOR THE DETECTION OF BIOFILM FORMATION BY ENTEROCOCCUS FAECIUM ISOLATED FROM HOSPITALIZED PATIENTS

Saber Soltani[1], Mohammad Reza Pourmand[2]

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

Background and Aim: Enterococcus faecium is nosocomial pathogen that can form biofilms, which being increasingly associated with urinary tract infections, endocarditis, catheter-related infections, surgical wound infections, and central nervous system infections. The objective of this study was to comparison two techniques for the detection of biofilm formation in E. faecium strains.

Methods:A total 29 vancomycin-resistant Enterococcus faecium were collected from hospitalized patients in a hospital in Ahvaz. Biochemical and molecular techniques were used to identify VREfm strains. The ability of biofilm formation was determined by Tissue Culture Plate (TCP) and Congo Red Agar (CRA) methods.

Results: The results revealed that 75.7% of the isolates tested produced biofilm on the CRA, 82.7% of the isolates produced biofilm in vitro by TCP. In TCP method, 13.7% of the isolates formed strong and 17.2% formed weak biofilm. According to the CRA method 27.5% of the isolates formed strong biofilm, 17.2% had a weak biofilm.

Conclusion: According to the results the difference in biofilm formation in each method can be affect by various factors such as concentration of nutrients, laboratory techniques and solutions used.

Keywords: Tissue culture plate, Congo red agar, Biofilms, Vancomycin-resistant Enterococcus faecium

P127 - 673: IDENTIFICATION OF A NEW SMALL MOLECULE FROM TAXUS BACCATA PLANT AS A POTENTIAL INHIBITOR OF VIRB8 OF BRUCELLA BACTERIA BY HIGH-THROUGHPUT VIRTUAL SCREENING ON TRADITIONAL CHINESE MEDICINE DATABASE

Seyede Solmaz Moosavi[1], Milad Lagzian[2], Malihe Mohammadi[3]

1. Dept. of Biology, Faculty of Science, University of Sistan and Baluchestan
2. Dept. of Biology, Faculty of Science, University of Sistan and Baluchestan
3. Dept. of Biology, Faculty of Science, University of Sistan and Baluchestan

Background and Aim: The type IV secretion system (T4SS) is one the most important virulence factor of Brucella. VirB8 is a central assembly factor for all type IV secretion systems. Thus, it can be a potential target for novel antimicrobial drugs.

Methods: In this study, a database with more than 57,000 active compounds originating from medicinal plants of China was used for high-throughput virtual screening against VirB8. Ligand preparation was done by Discovery Studio 2017 to optimize valance, charges and tautomeric form created for each ligand which finally made the library with more than 229656 records. Afterward, receptor preparation was conducted on CLC Drug Discovery 4.0 to prepare the structure of 4AKZ. Active Site Mapping was used based on the previous reports to identify key catalytic residues. Docking was accomplished in a pipeline with an increasing level of precision including HTVS (output: 5731), SP (output: 54) and finally XP (output: 6) by Screen Ligands module in CLC Drug Discovery 4.0. To select the final candidate, the output of the XP step was re-evaluated using more sophisticated MM-GBSA scoring.

Results: The compound 6439 that originated from Taxus baccata plant, was the best selection as ultimate hit for VirB8 inhibition. This molecule can strongly interact with key residues, Q144 and K182, of VirB8 via hydrogen bonding and ionic interactions.

Conclusion: For the final evaluation, a Molecular Dynamics simulation will be conducted on this ligand and if a satisfactory result obtains, the ligand will be synthesized and in-vitro experiments will perform.

Keywords: Brucella, High-Throughput Virtual Screening, VirB8, Inhibitor

P128 - 680: MOLECULAR ASSESSMENT OF INTEGRONS IN ISOLATES OF ESCHERICHIA COLI OBTAINED FROM CHILDREN WITH URINARY TRACT INFECTIONS IN KERMANSHAH

Nahid Madadigoli[1], Ramin Abiri[2], Amirhooshang Alvandi[3], Jale Moradi[4], Mohsen Azizi[5], Kamal Ahmadi[6]

1. Ph.D. Student of Medical Bacteriology, Department of Microbiology, Pasteur Institute of Iran, Tehran, Iran
2. Associate Professor, Department of Microbiology, Kermanshah University of Medical Sciences, Kermanshah, Iran
3. Associate Professor, Department of Microbiology, Kermanshah University of Medical Sciences, Kermanshah, Iran
4. Assistant Professor, Department of Microbiology, Kermanshah University of Medical Sciences, Kermanshah, Iran
5. Research Assistant, MSc in Medical Microbiology, Kermanshah University of Medical Sciences, Kermanshah, Iran
6. Ph.D. Student of Medical Bacteriology, Department of Microbiology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: The most common manner to spread of antibiotic resistance and appearance of species with multidrug resistance, transmission of resistance genes to antibiotics through integrons. The aim of this study was to determine the prevalence of class I and 2 integrons and its association with drug resistance patterns in isolates of Escherichia coli obtained from children with urinary tract infections in Kermanshah.

Methods: The cross-sectional study were collected 89 isolates of Escherichia coli. After determination of isolates by specific biochemical methods, their antibiotic susceptibility was performed by using disk diffusion. The frequency of class I and 2 integrons were determined by using specific primers and PCR methods.

Results: Among of 89 isolates 53(59.3%) isolates were multidrug resistance. The highest antibiotic resistance was to Ampicillin (85.4%) and Cotrimoxazole (68.5%) and the most antibiotic sensitivity was to Imipenem (12.4%) and Nitrofurantoin (16.8%). The frequency of class I and 2 integrons were 71.9% and 3.5%, respectively. There was a significant association between the integrons frequency and resistance to tetracycline and gentamicin ($P<0.05$).

Conclusion: This study showed that the high frequency of multidrug resistance isolates, the prevalence of class I and 2 integrons was high in Escherichia coli isolates. As a result, the identification of the integrons frequency and their relationship to drug resistance patterns is important in bacterial isolates.

Keywords: Integrons , Drug Resistance , Escherichia coli

P129 - 683: COMPARISON OF ANTIMICROBIAL RESISTANCE PATTERN OF ENTEROCOCCUS FAECALIS NORMAL FLORA AND ENVIRONMENTAL ISOLATES

Saba Asgharzade[1], Hamidreza Goli[2]

1. Department of Medical Microbiology and Virology, Faculty of medicine, Mazandaran University of Medical Sciences, Sari, Iran.
2. Department of Medical Microbiology and Virology, Faculty of medicine, Mazandaran University of Medical Sciences, Sari, Iran.

Background and Aim: Enterococci are bacteria reside in soil, water, surfaces and intestinal lumen of human and animals. These organisms have been known as one the main reasons of opportunistic infections in hospitals.

Methods: The main purpose of this study is to compare the antibiotic resistance pattern of the enterococci isolated from 100 stool samples of healthy personnel of hospitals and 45 samples collected from hospital environmental surfaces. Samples were transferred to laboratory and the stool samples were dissolved in PBS buffer. Then they were cultured in ME agar medium. Enterococci species were separated after purification with biochemical tests.Then the antimicrobial susceptibility testing were performed by disk agar diffusion method against 14 antibiotics.

Results: The results showed that 42%, 81%, 6% and 20% of the E. faecalis strains isolated from the stool specimens were resistant to tetracycline, erythromycin, Vancomycin, and high levels of gentamicin, respectively. These features were 60%, 66%, 10%, and 30% for the strains isolated from hospital surfaces, respectively.

Conclusion: These results confirms that the normal flora and environmental enterococci may be the source of antibiotic resistance genes, as a problem. There are some concerns about the normal flora enterococci and elements of environment, because these organisms can transfer the antibiotic resistance genes to other bacteria by horizontal transmission path

Keywords: Antimicrobial Resistance, Enterococcus faecalis, normal Flora, Environmental Isolates

P130 - 687: ANTIMICROBIAL EFFECT OF ROSEMARY EXTRACT

Faezeh Fallah[1], amir arasteh[2]

1. author

Background and Aim: Rosemary is a herbaceous, stable plant that has a wooden stem to a height of half to one meter. Its green leafs are permanent and very fragrant, also they are slim and long and sharp. This plant is native to the Mediterranean but it is cultivated in different parts of the world. Historical reports on Rosemary therapeutic use as a herbal medicine are available. From centuries ago, Rosemary was one of the oldest known medicinal plants that has been used to strengthen memory and brain activity.

Methods: Antimicrobial effect of Rosemary extract on E .Coli and Staph bacteria with disc diffusion method and minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) with the tubular method was tested.

Results:inhibition zone of E .Coli and Staph are, the well diffusion 20mm and disc diffusion 14mm, the well diffusion 31mm and disc diffusion 20mm respectively .and the results of MBC and MIC are 0.625 mg/ml and 1.25 mg/ml for E .Coli and 0.625 mg/ml and 1.25mg/ml for Staph respectively.

Conclusion: Today, because of the medicine resistance that is one of the world's greatest concern, Rosemary can be used for medical purposes.

Keywords: Antimicrobial - Rosemary - E .Coli and Staph

P131 - 689: THE FREQUENCY OF RESISTANCE TO ANTIFUNGAL DRUGS IN CANDIDA ALBICANS ISOLATES ISOLATED FROM CASES OF VAGINITIS IN TABRIZ ALZAHRA HOSPITAL

Leila Mohammadi[1], Mehdi Ghiami rad[2], Mehrdad Asadi[3]

1. Department Of Microbiology-Tabriz Rab Rashid Higher Education Institute
2. Department Of Microbiology- Faculty Of Science- Islamic Azad University Ahar Brench – Ahar- Iran
3. Department Of Microbiology- Faculty Of Medical - Islamic Azad University Tabriz Brebch – Tabriz - Iran

Background and Aim: Gardenerlla vaginalis, Tricomonas vaginalis and Candida species especially Candida albicans consider as major causes of vaginitis.There are three classes of antifungal drug used for treatment of candidiasis: Azoles, Polyenes and Echinocandin. : Azoles, Polyenes , and Echinocandin. The occurrence of resisdence to antifungal drug is a major problem in treatment of vaginits. Therefore study was aimed to determine the prevalence of resistance to antifungal drugs, especially fluconazole in Candida albicans strains isolated from hospital Alzahra Tabriz.

Methods: Isolates identification was done by direct microscopic exam(wet mount) cultivated in sabouraud dextrose agar medium. Diffreatiation betwen candida species was done by chrom Agar medium and Germ tube test and chlamidia conidi performed.

Results:104 of 140 sampels were identified as candida albicans.Antibiotic resistance to fluconazol detected in 24 isolates.Antibiotic resisrance to amphotericin B identified 6 isolates.1 sampele finded resistance to nystatin.Resistance to ketoconazol diagnosed in 72 isolates and 72 sampel detected resistance to itraconasol.

Conclusion: Due to incresed antibiotic resistance in candida albicans strain,Antibogram befor started the treatment in neccessery.

Keywords: Candida albicans, Resistance to antifungal draugs, Vaginitis

P132 - 691: THE PREVALENCE OF PANTON VALENTINE LEUKOCIDIN POSITIVE IN S. AUREUS ISOLATED FROM SKIN AND SOFT TISSUE INFECTION

Zeinab Faghee[1], Ahmad Khorshidi[2], Rezvan Moniri[3], Tahereh Soori [4]

1. 1. Antimicrobial resistance research Centre, Institute of Immunology and infection diseases, Iran University of medical sciences. 2. Department of Microbiology and Immunology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran
2. Department of Microbiology and Immunology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran
3. Professor of Medical Microbiology, Department of Microbiology and Immunology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran; Anatomical Sciences Research Center, Kashan University of Medical Sciences, Kashan, Iran
4. Infectious Diseases Specialist, Razi Hospital, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: Panton Valentine Leukocidin (PVL) has been linked with invasive Staphylococcus aureus skin and soft tissue infections. Aim: To determine the prevalence of Panton-Valentine leukocidin gene and antibiotic susceptibility pattern of S. aureus isolated from skin and soft tissue infection (SSTI).

Methods:A cross-sectional study was conducted in 400 patients with skin and soft tissue infection in Razi skin Hospital, Tehran, Iran. Sterilized swab was used to collect samples of skin infections. Staphylococcus aureus isolates were identified using standard biochemical tests. The susceptibility of isolates to different antibiotics was determined by disk diffusion method according the guidelines of the Clinical and Laboratory Standards Institute (CLSI). PCR was used to investigate the presence of mecA and pvl gene.

Results:A total Of the 400 isolates were collected from patients referred to Razi skin Hospital in Tehran, Iran. 205 out of 400 isolates (51.3%) were S. aureus, 96(46.8%) isolates were methicillin-resistant staphylococcus aureus (MRSA). 136 out of 205 patients with S. aureus infection (66.3 %) had bullous pemphigoid and pemphigus skin disease. 94.6% of the isolates were penicillin resistant, all of the isolates showed sensitivity to vancomycin, linezolid and 98% of the isolates were susceptible to daptomycin. 116(56.6%) of isolates were MDR (Multi Drug Resistance).

Conclusion:in this study, more than half of the skin and soft tissue infections caused by MDR S.aureus. The presence of pvl in MRSA isolates was high.

Keywords:S.aureus, MRSA, SSTI, pvl

P133 - 692: PHENOTYPIC AND GENOTYPIC DETECTION OF EXTENDED-SPECTRUM B-LACTAMASE (ESBL)-PRODUCING ESCHERICHIA COLI IN PATIENTS WITH COMMUNITY-ACQUIRED URINARY TRACT INFECTIONS

Zahra Naziri[1], Abdollah Derakhshandeh[2], Mohammad Motamedifar[3], Meisam Poormaleknia[4], Bahare Behzadnia[5], Jamil Ataei[6], Negar Azimzade[7]

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. Department of Bacteriology and Virology, Shiraz University of Medical Science, Shiraz, Iran
4. Department of Pathobiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
5. Department of Pathobiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
6. Department of Pathobiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
7. Department of Pathobiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran

Background and Aim: Extended-Spectrum β-lactamases (ESBLs) are enzymes which cause resistance to most cephalosporins, penicillins and monobactams. There were various groups of ESBLs, including CTX-M, SHV and TEM enzyme types. β-lactam antibiotics are widely used for treatment of urinary tract infections (UTIs). The presences of ESBL-producing E. coli in UTIs can lead to treatment failure with the listed classes of antibiotics. Therefore phenotypic or genotypic detection of these isolates is important.

Methods: Seventy eight E. coli isolates were obtained from 78 urine samples of patients with community-acquired UTIs. The isolates were studied for ESBLs production by combination disk diffusion method using cefotaxime (30µg), ceftazidime (30µg), ceftriaxone (30µg) and cefotaxime-clavulanic acid (30/10µg) disks. Presence of blaTEM, blaSHV, blaCTX_M genes were determined by PCR.

Results: Prevalence of resistance to ceftazidime, ceftriaxone and cefotaxime were 42.3%, 53.8% and 55.12%, respectively. Since the ≥5 mm increase in the zone of inhibition diameter for cefotaxime-clavulanic acid compared to zone for cefotaxime alone indicates ESBL activity, the prevalence of ESBL-producing E. coli was 41%. Among the 32 ESBLs- producing E. coli, 29(90.6%) harbored CTX-M, 19(59.3%) harbored SHV, 4(12.5%) harbored TEM, 1(3.1%) harbored both TEM and CTX-M, 17(53.1%) harbored both SHV and CTX-M, and 2(6.25%) harbored all the three types of ESBLs.

Conclusion: The worldwide increase in prevalence and spread of ESBL- producing E. coli can limit therapeutic options for UTIs and addition of healthcare costs. Therefore, the proper usage of extended-spectrum cephalosporins, regular surveillance of antibiotic resistance of clinical isolates and detection of ESBL-producers by accurate laboratory testing methods are crucial.

Keywords:E. coli, Community-acquired UTIs, ESBLs, PCR

P134 - 696: MULTIPLEX PCR OF QNRB, AAC(6'),16SRRNA METHYL TRANSFERASE GENES AMONG MDR PSEUDOMONAS AERUGINOSA ISOLATES FROM BURN WOUND INFECTIONS OF MOTAHARI HOSPITAL, TEHRAN, IRAN

Atiyeh Shaban Ghahrood[1], Mojdeh Hakemi Vala[2], Ali Hashemi[3]

1. Pharmacy student, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, Iran.
2. Associate Professor, Microbiology Department, Medical school, Shahid Beheshti University of Medical Sciences, Tehran, Iran m.hakemi@sbmu.ac.ir
3. Assistant Professor, Microbiology Department, Medical school, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: Pseudomonas aeruginosa, is a gram negative and opportunistic pathogen in immune-compromised patients such as burn wound infections. Due to increasing of antibiotic resistance, this study investigated the prevalence of qnrB , aac(6') and rmtA genes in multi-drug resistance (MDR)P. aeruginosa isolates from burn wound infections.

Methods:92 isolates of P. aeruginosa from patients with burn wound infections of Motahhari hospital in Tehran during 2017-2018 based on standard tests were collected. According to CLSI protocol, antibiotic susceptibility test (AST) was performed by using the disk diffusion method. Then, the PCR and Multiplex PCR was used to evaluate of qnrB , aac(6') and rmtA genes. P. aeruginosa ATCC 27853, qnrB+,aac(6') + and rmtA+ strains were used, simultaneously.

Results: Among 92 isolates of P. aeruginosa, 75 (81.88%) were resistant to Amikacin, 79(85.56%) to Cefepime, 80 (87.4%) to Meropenem, 63 (69%) to Ceftazidime, 81 (88.32%) to Ciprofloxacin, 66 (71.74%) to Aztreonam, , 78 (84.64%) to Gentamicin, and 0(0%) to Colistin. By PCR results 0(0%) ,8(9.2%) and 38(41.4%) of the isolates had QnrB, aac(6') and rmtA genes.By multiplex PCR result 2 (1.84%) concurrent presence of aac(6') and rmtA genes.

Conclusion: The results of this study showed the high rate of antibiotic resistance. Among the most of antibiotics that were tested, Colistin is the best choice for treatment. The frequency of rmtA gene is higher than QnrB, aac(6') in P. aeruginosa by PCR. To reduce the rate of resistance it is necessary to control bacterial dissemination.

Keywords: Pseudomonas aeruginosa, Drug resistance, QnrB, aac(6') and rmtA

P135 - 702: PREVALENCE OF SUL1 IN CLINICAL ISOLATES OF PESUDOMONAS AERUGINOSA

Sahar Alishanni[1], seyed reza hosseini doust[2], saiid akbarzadeh[3]

1. Islamic Azad University Pharmaceutical Sciences Branch, faculty of advance sience and technology,tehran,iran
2. Islamic Azad University Pharmaceutical Sciences Branch,faculty of advance sience and technology,department of microbiology,teharn.iran.
3. Islamic Azad University Pharmaceutical Sciences Branch,faculty of advance sience and technology,department of biotechnology,tehran ,iran.

Background and Aim: Pseudomonas aeruginosa is one of the important opportunistic pathogen associated whit nosocomial infections.show high level of antibiotic resistance. Therefore, finding an appropriate treatment is challenging for infection caused by pseudomonas aeroginosa. The aim of this study was to determine the frequency of sulfonamide resistance gene (sul1) and antimicrobial resistance profile of P.aeruginosa isolates.

Methods:70 clinical isolates were collected from various clinical specimens in Tehran hospital. all isolates were identified by biochemical tests .Antimicrobial susceptibility profile were determined against 12 antibiotics and using the standard kirby -bauer disk diffusion method according to Clinical and Laboratory Standard Institute (CLSI) guideline. Moreover, macro broth dilution method used in order to determining of minimum inhibitory concentration (MIC) for Impenem,Gentamycin,Cefepime,Ciprofloxacin. PCR assay was performed for detection Sul1 gene using specific primer.

Results:among 70 evaluated strain of P.aeruginosa isolate, (55.71%) were multi drug resistant .based on Kirby-baure method, co-trimoxazole with (98.3%) and Meropenem (1.6%) resistance showed the highest and lowest resistance against isolate.among the antibiotics studied to determine mic ,the most resistance was observed to Imipenem (54.8%).the Sul1 gene were detected in (35.71%) of isolates.

Conclusion: The result of study indicated that had high range of resistance to different antibiotics among strain of P.aeroginosa isolated from different clinical sample ,so fast and accurate measurement and evaluation of antibiotic resistance for appropriate antibiotic therapy is imperative

Keywords: Pseudomonas aeruginosa, antimicrobial resistance ,sul1

P136 - 706: IDENTIFICATION AND ANTIBIOGRAM ANALYSIS OF VARIOUS BACTERIAL ISOLATES FROM URINE IN ROUTINE DIAGNOSTIC LOBORATORIES OF KERMAN, IRAN

Mohammad Dehvari[1], Shiler Delpasand[2], Mostafa Moshrefi nezhad[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: Drug resistance is a burning issue for bacterial isolates and inappropriate use of antibiotics is one of the important factors of increasing of resistance. The aim of this study were determination and comparison of antibiotic susceptibility pattern among isolates from urine.

Methods: Totally 104 samples were collected from urinary tract infections. The bacterial isolates were identified by gram's staining. Conventional biochemical tests were used for detection of bacteria. Antimicrobial susceptibility tests were performed using the Kirby-bauer disc diffusion method.

Results: The results revealed that escherichia coli (48%) was the most common bacterial isolate followed by staphylococcus spp. (22%), klebsiella spp. (18%) and proteus spp. (12%). Antibiogram results shown that the most resistant antibiotic to e.coli was (ampicillin 78%), staphylococcus spp. (penicillin 83%), klebsiella spp. (amoxicillin 100%) and proteus spp. (sulphamethoxazole 67%). Also the most effective antibiotic to e.coli was (fosfomycin 96%), staphylococcus spp. (fosfomycin 65%), klebsiella spp. (gentamicin 84%) and proteus spp. (gentamicin 67%).

Conclusion: Level of resistance in referred isolates were very high. It is very important to reduce frequent misuse, inadequate dosage and easy availability of antimicrobials to avoid antibiotic resistance.

Keywords:antibiogram, antibiotic resistance, urinary infections, biochemical methods

P137 - 708: FREQUENCY OF FIM GENE IN ESCHERICHIA COLI ISOLATES FROM URINARY TRACT INFECTIONS OF IMAM KHOMAINI HOSPITAL IN TEHRAN

Sepide Ghasemshahi[1], Maryam Bikhof Torbati1[2], Mojdeh Hakemi-Vala[3]

1. 1. Department of Biology, College of science, Yadegar-e-Imam Khomeini(RAH) Shahr-e-Rey Branch, Islamic Azad University, Tehran, Iran
2. 1. Department of Biology, College of science, Yadegar-e-Imam Khomeini(RAH) Shahr-e-Rey Branch, Islamic Azad University, Tehran, Iran
3. 2. Department of microbiology, Medical school, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: The most common etiologic factor of urinary tract infections (UTIs) is Escherichia coli (E.coli), accounting for 80% of these cases. The ability of the Uropathogenic Escherichia coli (UPEC) strains to cause the marked urinary tract infection depends on adhesion and binding of these strains to the urethral duct tissue cells made by fimbriate and non-fimbriate adhesions. Accordingly, in the present study one of the most well-known fimbrial adhesion in Escherichia coli type 1 fimbria expressed by fim gene was investigated

Methods: Urine samples were collected from patients referred or admitted to Imam Khomeini Hospital in Tehran in 2016 and 90 isolates of Escherichia coli were detected according to standard bacteriological tests. Then, the frequency of fim gene was evaluated by PCR method. E.coli ATCC25922 was used simultaneously.

Results: All isolates with positive motility, negative urea, IMViC ++ - -, TSI A / A gas +, were confirmed as Escherichia coli. 70 of the 90 isolates (77.8%) of Escherichia coli had fim gene by PCR method.

Conclusion: According to the results, fim gene can be considered as one of the most common invasive factors of UPEC, which causes the adhesion of bacteria to the urethral duct tissue. And so the bacteria are not washed off by the flow of urine. In 22.2% of the investigated isolates of Escherichia coli, the fim gene was not detected, in which the infection could be due to other invasive factors.

Keywords: Escherichia coli, adhesion, fimbria

P138 - 714: THE OCCURRENCE OF CTX-M-15 EXTENDED-SPECTRUM B-LACTAMASE AMONG CLINICAL ISOLATES OF KLEBSIELLA PNEUMONIAE IN KHORRAMABAD, IRAN

Gholamreza Goudarzi[1], Pegah Shakib[2]

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

Background and Aim: During the recent decade, CTX-M enzymes, mainly CTX-M-15 extended-spectrum β-lactamase (ESBL), have strikingly developed through the world. The objective of this study was to investigate the frequency of CTX-M-type β-lactamases and blaCTX-M-15 among Klebsiella pneumoniae isolated from hospitals in Khorramabad city.

Methods: In this cross-sectional study, 60 isolates of K. pneumoniae were collected from selected teaching hospitals in Khorramabad, Iran. ESBL producing isolates were identified using phenotypic double-disk synergy test. The presence of CTX-M-types, as well as CTX-M-15 gene were investigated by PCR method

Results: While the highest resistance rates of isolates were found for nalidixic acid (65%) and trimethoprim/sulfamethoxazole (60%) antibiotics, the least resistance was to imipenem (15%). Moreover, 31(51.7%) isolates were resistant to at least three classes of antibiotics and designated as multidrug resistance (MDR). Fifty-two (86.7%) of 60 isolates, were ESBL positive. Thirty-five (58.3%) isolates harbored CTX-M-type β-lactamases, and also 29 (48.3%) isolates carried blaCTX-M-15.

Conclusion: For the first time, our results prove the alarming dissemination of CTX-M-type β-lactamases, particularly CTX-M-15 in west of Iran. To better control of MDR K. pneumonia expansion, awareness and education of healthcare professionals as well as general population to true and limited using of antibiotics are urgently suggested.

Keywords: Extended-Spectrum β-lactamase, Klebsiella pneumoniae, CTX-M-15

P139 - 721: EVALUATING THE IN VITRO INHIBITORY EFFECT OF NANOEIZED PARTICLES OF PYRANS ON ESBLS PRODUCING ESCHERICHIA COLI STRAINS ISOLATED FROM CLINICAL SPECIMENS IN KARAJ CITY

Parasto Saadai[1], Parasto Saadati[2], Leila Jabalameli[3], Akram Sadat Tabatabaee Bafroee[4]

1. -
2. M.Sc. Student of Microbiology, Department of Microbiology, Faculty of Sciences, Karaj Branch, Islamic Azad University, Karaj, Iran
3. Department of Microbiology, Faculty of Sciences, Karaj Branch, Islamic Azad University, Karaj, Iran
4. Department of Biology, Faculty of Basic Sciences, East Tehran Brach (Ghiamdasht), Islamic Azad University, Tehran, Iran

Background and Aim: The increase of ESBLs producing Escherichia coli among patients with urinary tract infection is a significant concern. Drug resistance of these bacteria is very important especially in nosocomial infections. Because of acquiring plasmids encoding broad beta-lactamases, Escherichia coli has become resistant to beta-lactam antibiotics. Increasing in antibiotic resistance rushed researchers to the use of nanoparticles for creating modern remedies.

Methods: This descriptive-observational study performed on 60 samples of Escherichia coli collected from Karaj city. Isolates were identified by biochemical standard tests. Antimicrobial susceptibility performed by four antibiotics, including Cefepime, Ceftazidime, Ceftriaxone and Cefotaxime. ESBLs producing isolates were screened by phenotypic confirmation test. Minimum inhibitory concentration (MIC) of pyran nanoparticles was determined by using sterile 96 microwell plates microbroth dilution method. The dilution range tested by using dimethyl sulfoxide, as solvent, was between 2.44-1250 mg/ml.

Results: In total, 14 out of 60 Escherichia coli isolates have been observed as ESBLs producers. Antibiotic resistance level among isolates was as follows: FEB 23.33%, CAZ 16.66%, CRO 30% and CTX 31.66%. ESBL producing isolates were tested for MIC values. Bacterial growth wasn't observed at 833.33 mg/ml of concentration which was considered as MIC. Furthermore MIC was equal to MBC.

Conclusion: As a result, due to the ever-increasing number of antibiotic-resistant strains use of nanoparticles can help antimicrobials design and it can be a new hope for modern therapies design against bacterial threats and dilemmas.

Keywords:ESBL genetic Escherichia coli, Drug resistance, Nano-particles

P140 - 722: COMPARISON OF THE PREVALENCE OF METALLO-B-LACTAMASE RESISTANCE OF PSEUDOMONAS AERUGINOSA BETWEEN 1396 AND 1397 BY DOUBLE DISK SYNERGY TEST AND COMBINE DISK METHODS IN MASHHAD'S HOSPITALS

Kowsar Assad allah pour[1], Gholamreza Hashemi tabar[2], Mehrnaz Rad[3]

1. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad iran
2. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad iran
3. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad iran

Background and Aim: In recent years, Pseudomonas aeruginosa infection has been one of the most commonly reported nosocomial infections, especially in patients with poor deficiency. These days treatment of this infection is a serious problem due to the spread of antibiotic resistance. The aim of this study is to compare the development of metallo-β-lactamase resistance of this bacteria with phenotypic potential in the period 1396 to 1397.

Methods:80 samples of Pseudomonas aeruginosa have been collected from hospitals in Mashhad during the last two years, which 40 samples are related to1396 and the rest to1397. Then we investigated the resistance of metallo-β-lactamase of the samples by phenotypic methods Double disk synergy (DDST) and Combine disk.

Results: Of the 80 collected samples (60.5%) belonged to men and (39.5%) belonged to women. The samples had been obtained by: urine (45%), wound (23.75%), respira¬tory tract (21.25%), Secretion (5%), blood culture (3.75%) and eyes (1.75%). Meanwhile, (20%) of samples from 1396 demonstrated metallo-β-lactamase resistance by DDST method and (40%) by Combine disk. And in 1397 (45%) by DDST and (55%) Combine Disk were Positive.

Conclusion: Most of the samples were isolated from the urine and the level of resistance of metallo-β-lactamase in 1397 have increased compared to 1396: DDST (25%) and Combine disk (15%). Considering the increasing of antibiotic resistance, identifying the type of resistance and selecting the appropriate drug can be a major step in the treatment and control of infections caused by this bacteria.

Keywords: Pseudomonas aeruginosa, Metallo-β-lactamase resistance, Combine disk, Double disk synergy test

P141 - 723: FREQUENCY OF INTESTINAL CARRIAGE OF HIGH-LEVEL STREPTOMYCIN RESISTANT ENTEROCOCCAL ISOLATES IN HEALTHY CHILDREN ATTENDING SCHOOLS IN ARDABIL, 2017

Elham Jannati[1], Mohsen Arzanlou [2], Nour Amirmozafari [3]

1. department of biology,Science and research Branch ,Islamic Azad University,Tehran ,Iran.
2. Department of Microbiology and Parasitology, School of Medicine, Ardabil University of Medical Sciences, Ardabil, Iran
3. Department of Microbiology,Faculty of medicine,Iran University of Medical Science and Heaith Services,Tehran,Iran.

Background and Aim: Enterococci are common intestinal microflora. Their ability to acquire high-level resistance to antimicrobial agents enterococci have emerged as nosocomial pathogens worldwide. Treatment of severe enterococcal infections typically include combination of a beta-lactam agent and an aminoglycoside antibiotic.

Methods: Totally 305 fecal specimens were collected from healthy children during last year. Enterococcus spp identified to the genus level using biochemical tests. The species (E. faecalis and E. faecium) were identified by screening the ddlE gene using PCR technique. High level streptomycin (HLSR) resistance was determined using BHI agar-screen method according to CLSI. The genes encoding aminoglycoside modifying enzymes ant(6') and ant(3') in the genome of HLSR isolates were detected using multiplex PCR method.

Results: Enterococcal isolates were isolated from stool specimens in all 305 subjects. E faecium was found as commonest 77%(235) species followed by E. faecalis as 18%(56) and other enterococci 38%(118). Totally 23%(71)enterococcal isolates were found to be HLSR. Out of those 56%(40) isolates were E. faecium7%(5) were E. faecalis and other enterococci were 36%(26) in numbers.Thirty five (23%) out of 71 HLSR isolates were ant(6') positive. Overall, 7%(2), 56%(19) and 36%(14) of E. faecalis, E. faecium, other enterococcal spp. contained ant(6') respectively. The ant(3') gene was not detected in this study.

Conclusion: Colonization of HLSR enterococci is found to be high in the study population. Colonized antibiotic resistant enterococci could be act as a source for nosocomial infection. The data of the antibiotic resistant bacteria could be implemented in infection control measures.

Keywords: Enterococci, carriage, High level streptomycin resistance, healthy children

P142 - 733: PHYTOCHEMICAL STUDY AND ANTIBACTERIAL ACTIVITY OF GLYCYRRHIZA GLABRA L. AND ITS COMBINATION WITH GENTAMICIN AGAINST KLEBSIELLA PNEUMONIAE, IN VITRO

Vahid Reisi Vanani[1], Vahid Reisi-Vanani[2], Zahra lorigooini[3], Sajad Maghareh-Dehkordi[4], Abolfazl Gholipour[5]

1. -
2. Student Research Committee, Shahrekord University of Medical Sciences, Shahrekord, Iran.
3. Medical Plants Research Center, Basic Health Sciences Institute, Shahrekord University of Medical Sciences, Shahrekord, Iran.
4. Pharmacy Students' Research Committee, School of Pharmacy, Isfahan University of Medical sciences, Isfahan, Iran.
5. Department of Microbiology and Immunology, Shahrekord University of Medical Sciences, Shahrekord, Iran.

Background and Aim: Klebsiella pneumoniae is one of those bacteria that its multidrug resistance has increased its mortality. One solution is finding natural bioactives that have synergistic interactions with antibiotics. The root of Glycyrrhiza glabra L. (RG) is one of those sources with many therapeutic properties, as result, we aimed to evaluate antibacterial effect of its combination with Gentamicin.

Methods: In this experimental study, total phenolic content (TPC) and total flavonoids content (TFC) of hydroalcoholic extract of RG were determined by Folin-Ciocalteu and Aluminum chloride colorimetric method. Minimal inhibitory concentration (MIC) of Gentamicin and RG extract on the standard strain of K. pneumoniae were determined by resazurin-microdilution assay and finally, for detecting an interaction between them we used Checkerboard assay, each test was repeated for three times.

Results:TPC and TFC of this extract were measured 57.19 mg equivalent Gallic acid/g dried extract and 40.1 mg equivalent Rutin/g dried extract respectively. MICs for gentamicin (4 µg/ml) and RG (131 mg/ml) were reported by detecting the last wells with the lowest concentration of agents that had no color change from blue to pink. Mean Fractional Inhibitory Concentration (FIC) Index for their combination was 5 which showed great antagonistic effect between RG extract and gentamicin.

Conclusion: Results indicated that RG is a good source for phenolic and flavonoid components and although this crude extract contains some antibacterial components, there are some with notable antagonistic interaction with Gentamicin which is wildly used against this bacteria, as result, this drug interaction should be considered in patients infected by this bacteria.

Keywords: Drug Combination, Glycyrrhiza, Gentamicin, Drug Antagonism, Klebsiella pneumoniae

P143 - 739: STUDY THE PREVALENCE OF RESISTANCE GENE, QACE TO QUATERNARY AMMONIUM COMPOUNDS IN THE ISOLATED ACINETOBACTER BAUMANNII OF HOSPITAL OF QAZVIN (2015-2016)

Samaneh Keshavarz hedayati[1], Amir peymani[2], Narges habibollah pourzereshki[3]

1. Department of Microbiology, Zanjan Branch, Isiamic azad university, Zanjan, Iran
2. Medical Microbiology Research Center, Qazvin University of Medical Sciences, Qazvin, Iran
3. Medical Microbiology Research Center, Qazvin University of Medical Sciences, Qazvin, Iran

Background and Aim: Acinetobacter baumannii is one of the important agent of hospital infections. In recent years, there are several report about frequency of resistant acinetobacter against quaternary ammonium compounds (QACs) in the clinical unit of hospitals in the world. It has used different antiseptics and disinfectants for preventing hospital infections in clinical centers and hospitals. QACs like benzalkonium has widely used as wound and skin antiseptic and hospital disinfectant. The mechanism of resistance to disinfectants was happened by resistance genes type qacE that was isolated from gram negative bacteria. As the importance of preventing hospital infection due to acinetobacter, the aim of this study, was to determine prevalence of resistance gene, qacE to disinfectant in the clinical isolated acinetobacter baumannii

Methods: Totally, 141 isolated acinetobacter baumannii were studied from specimens of hospital of Qazvin Province from Sep 2015 for year. The isolated were characterized as acinetobacter baumannii via standard methods. Then, all isolated were studied using polymerase chain reaction (PCR) and sequencing for qacE resistance gene

Results: Isolated acinetobacter of trachea, urine, and blood were 82(58%), 23(16%), 14(9%) respectively from all specimens. Also, 24 (17%) isolated have qacE gene and the most frequency of isolated acinetobacter baumannii that contain qacE gene were in ICU 14(58%). The result of this study showed the significant resistance to disinfectants in the evaluated hospitals

Conclusion: Thus, more attention to acinetobacter baumannii as an important agent in the hospital infection and applying disinfectant is necessary

Keywords: Acinetobacter baumannii, Quaternary ammonium compounds, qacE gene

P144 - 743: COPPER OXIDE AND TITANIUM DIOXIDE NANOPARTICLES IMPACT ON GROWTH OF ENTEROBACTER AEROGENES IN LIQUID MEDIUMS

Shervin Shabani[1], Hamed Charkhian[2], Ehsan Soleimannezhadbari[3], Ali Ghahremany[4]

1. Department of Microbiology, Urmia branch, Islamic Azad University, Urmia, Iran.
2. Department of Biotechnology, Urmia branch, Islamic Azad University, Urmia, Iran.
3. Young Researchers Club, Urmia Branch, Islamic Azad University, Urmia, Iran.
4. Microbiology Lab ,Urmia Branch, General Bureau of Standards West Azerbayjan, Urmia, Iran.

Background and Aim: High incidence of infectious diseases and the growing resistance of bacteria to traditional antibiotics has led to widespread investigation of alternative antibacterial compounds such as nanoparticles. The current study was conducted in vitro to investigate Impaction of CuO and TiO2 nanoparticles on Enterobacter aerogenes growth in liquid medium.

Methods: Enterobacter aerogenes bacterium ATCC:13048 was purchased from microbiological reservoir of the Pasteur Institute of Iran. CuO nanoparticles with a size of 40 nm and 10 to 25 nm TiO2 provided from US Research Nanomaterials. To do this test following incubation of bacteria and different concentrations of nanoparticles, optical density of cultures were monitored for five hours-every half hour. At 30, 60 and 120 minutes after incubation, colony forming unites of culture was determined.

Results: In the liquid test; Copper oxide nanoparticles significantly decreased the CFU of Enterobacter aerogenes in comparison to Titanium dioxide nanoparticles, while the measurement of optical density (OD) of bacteria and nanoparticle incubations were slightly different. We assumed that, TiO2 optical properties interfere with OD monitoring assay and did not allow reading real values during time of incubation.

Conclusion: Bactericidal property of CuO nanoparticles was remarkably higher than TiO2 nanoparticles in the same condition. The concentration of nanoparticles has a direct impact on bactericidal ability. Possibly by more research and investigation, CuO nanoparticles can be consider as adjunctive therapy in combination with other antibacterial compounds.

Keywords: Enterobacter aerogenes, Copper oxide, Titanium dioxide, Nanoparticles, Antibacterial compounds

P145 - 748: STUDY OF ANTIADHISION/ANTIBIOFILM EFFECTS OF RHAMNOLIPID-TYPE BIOSURFACTANT AGAINST CLINICAL ISOLATES OF PSEUDOMONAS AERUGINOSA AND ACINETOBACTER BAUMANNII

Ahya Abdi-Ali[1], Minoo Monzavi[2], Kambiz Akbari Noghabi[3]

1. Department of Microbiology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
2. Department of Microbiology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
3. Department of Molecular Genetics, National Institute of Genetic Engineering and Biotechnology (NIGEB), P.O. Box 14155-6343, Tehran, Iran

Background and Aim:P. aeruginosa and A. baumannii are major causes of nosocomial infections due to their highly antibiotic resistance and biofilm formation. In this study, the anti-adhesion and anti-biofilm effects of rhamnolipid against planktonic and biofilm-producing clinical isolates of the P. aeruginosa and A. baumannii were investigated.

Methods:26 clinical isolates of P. aeruginosa and A. baumannii were collected from respiratory secretions and burn wounds. The production and purification of rhamnolipid biosurfactant was carried out as described earlier (Hajfarajollah et al. 2015). Rhamnolipid-type biosurfactant was assessed for 1) its ability to inhibit planktonic growth and 2) as an approach to decrease adhesion and disruption of pre-formed P. aeruginosa and A. baumannii biofilms.

Results: The MIC of rhamnolipid against planktonic growth of selected isolates of P. aeruginosa and A. baumannii was 1.4 ×107 - 5.9×107 µg/ml and 0.7 ×107 -1.4 ×107 µg/ml, respectively. The effect of the rhamnolipid on the adhesion of P. aeruginosa and A. baumannii cells to polystyrene microtitre-plates was studied. Accordingly, the effectiveness of biosurfactant on different isolates was shown a decrease in cell adhesion varying from 46 to 93%. Biofilms of clinical isolates of P. aeruginosa and A. baumannii were disrupted efficiently by rhamnolipid concentrations between 5.9×107 - 23.6×107 µg /ml and 2.9×107 - 5.9×107 µg /ml, respectively.

Conclusion: Our results suggest the possible use of rhamnolipid-type biosurfactant as efficient anti-adhesive and biofilm-disrupting agent in controlling planktonic and biofilm-producing P. aeruginosa and A. baumannii. Further evaluation is required to validate anti-adhesive and anti-biofilm activities observed, at cellular and molecular levels.

Keywords: Pseudomonas aeruginosa; Acinetobacter baumannii; Biosurfactant; rhamnolipid;

P146 - 754: ANTIBIOTIC SUSCEPTIBILITY AND FREQUENCY OF RESISTANCE GENES PENA AND AMPC AMONG L.MONOCYTOGENES ISOLATES WITH CLINICAL, FOOD AND LIVESTOCK ORIGINS

Ali Mohamadi[1], lida lotfollahi[2], ali mohammadi[3], saber yousefi[4]

1. Urmia University of Medical Sciences, faculty of medicine, department of microbiology
2. Urmia, Urmia University of Medical Sciences, faculty of medicine, department of microbiology
3. Urmia University of Medical Sciences, faculty of medicine, department of microbiology

Background and Aim: Since 1988 that Poyart & Salmeron were reported the first resistant Listeria monocytogenes (L.monocytogenes) strain, increasing rates of resistance is reporting continuously all over the world. The aim of this study was the evaluation of resistance patterns in L.monocytogenes isolated from food, human, and livestock samples.

Methods: In this research, 51 L.monocytogenes strains isolated from various specimens since 2009 to 2016 evaluated for antibiotic sensitivity pattern and minimum inhibitory concentration (MIC) of isolates to the following antibiotics (penicillin G, ampicillin, cotrimoxazole, Gentamicin and tetracycline) was investigated using Agar Dilution Method . After DNA extraction from the isolates, PCR was done for evaluation of genetic basis of resistance to penicillinG and ampicillin.

Results: According to MIC evaluation, 13 isolates of L.monocytogenes (25%) were resistant to ampicillin, 21 (40.38%) to penicillinG and 11 (21.15%) to Gentamicin . Resistance rate to tetracycline was 25%. The listeria isolates appeared susceptible to cotrimoxazole. PCR for amplification of resistance genes in β-lactam resistant isolates showed that 11(21.5%) and 5(9.61%) of strains contain penA and ampC genes respectively.

Conclusion: In this study, relatively high level resistance to the first choice therapeutic drugs in treatment of listeriosis (penicillin and ampicillin) is important for clinicians. It is northworthy that cotrimoxazole as an alternative agent to penicillin (in allergic persons) has still good effect and all of L.monocytogenes are sensitive to it , however clinical isolates had higher levels of c resistance in comparison to the food and livestock ones.

Keywords:L.monocytogenes , MIC, penA, ampC

P147 - 755: THE COMPARISON OF ZOUSH OINTMENT WITH SILVER SULFADIAZINE OINTMENT IN BURN WOUND INFECTION

Maryam Meskini[1], Davood Esmaeili[2]

1. Department of Microbiology and Applied Microbiology Research Center, Systems Biology and Poisonings Institute, Baqiyatallah University of Medical Sciences, Tehran, Iran
2. Department of Microbiology and Applied Microbiology Research Center, Systems Biology and Poisonings Institute, Baqiyatallah University of Medical Sciences, Tehran, Iran

Background and Aim: Increasing the resistance of Pseudomonas aeruginosa to antibiotics brings about infection control in patients with burns. Burn is considered to be one of the worst medical conditions that, in addition to causing damage to all physical and mental dimensions, is able to infect at all ages.(1)

Methods:ZOUSH ointment was formulated with natural ingredients. In 80 mice, burn was induced by Ian Allen Holder. Two treatments per day and 20 days with silver sulfadiazine and ZOUSH ointment were performed in two separate groups.

Results: In the treatment group with silver sulfadiazine ointment, the average number of Pseudomonas aeruginosa isolated at exit 2 was significantly higher than Exit 1. At the interval between exit 1 and 2, two of the mice die of this group, which could be due to a sudden increase in the average number of bacteria and, consequently, the inability of the body and the silver sulfadiazine ointment used to control the infection, which eventually resulted in death. Also, the mean number of Pseudomonas aeruginosa isolated in the treatment of silver sulfadiazine ointment group from the 10th day was reduced, but the effect of bactericidal was significantly higher in the ZOUSH ointment group, so that the average number of Pseudomonas aeruginosa isolated after 15 days Treatment with silver sulfadiazine ointment group is even more than the average number of Pseudomonas aeruginosa isolated after 5 days of treatment with ZOUSH ointment group.

Conclusion: These results indicate that bactericidal has a ZOUSH ointment with an effect more than triple, the silver sulfadiazine ointment.

Keywords:ZOUSH ointment, Silver sulfadiazine, wound infection

P148 - 759: EVALUATION OF SEVERAL PHENOTYPIC METHODS FOR DETECTION OF KPC AND MBL PRODUCTION IN PSEUDOMONAS AERUGINOSA ISOLATES

Masoumeh Beig[1], Mohammad Reza Arabestani[2]

1. MSc student of Microbiology,Students Research Committee,Hamadan University of Medical Sciences,Hamadan,Iran.
2. Assistant Professor, Department of Microbiology, Hamadan University of Medical Sciences, Hamadan, Iran

Background and Aim: Carbapenems are one of the first-choice antibiotics for the treatment of Pseudomonas aeruginosa infections. Therefore, early and correct identification of carbapenemase-producing isolates for management of antimicrobial therapy is very important.

Methods: A total 97 of Pseudomonas aeruginosa isolates from different clinical samples were collected during the September 2017 to February 2018. Antibiotic susceptibility tests were conducted by Kirby-Bauer disc diffusion according to the clinical and laboratory standards institute (CLSI) guidelines. Determination the minimum inhibitory concentration was done by E-test. To identify metallo-betalactamase enzymes, combined disk tests (CDT) carbapenem inactivation method (CIM) and Modified Hodge test (MHT) were used.

Results: From 97 P. aeruginosa isolates, 47 (48/4 %) were carbapenem resistant. Among these, 27 (57/44%) were identified as MBL-producing P.aeruginosa isolates using DDST, 14 (29/78%) CIM positive and 25 (53/19%) KPC were positive.

Conclusion: Our results showed that combined disk tests (CDT), carbapenem inactivation method (CIM) and Modified Hodge test are very sensitive and useful tools which can be performed in the routine laboratory test for identification of carbapenemase producing in P. aeruginosa isolates.

Keywords:KPC, MBL, Pseudomonas aeruginosa

P149 - 760: THE COMPARISON OF ZOUSH OINTMENT WITH AKBAR 1 OINTMENT IN BURN WOUND INFECTION

Maryam Meskini[1], Davood Esmaeili[2]

1. Department of Microbiology and Applied Microbiology Research Center, Systems Biology and Poisonings Institute, Baqiyatallah University of Medical Sciences, Tehran, Iran
2. Department of Microbiology and Applied Microbiology Research Center, Systems Biology and Poisonings Institute, Baqiyatallah University of Medical Sciences, Tehran, Iran

Background and Aim: Pseudomonas aeruginosa is a gram negative and pathogen bacilli that causes high mortality in immunocompromised patients. It is also the third leading cause of nosocomial infections, and is the second most common pathogens in burn wounds.(1) So we decided to formulated natural ointment can inhibit Pseudomonas aeruginosa's infection in burn patient.

Methods:ZOUSH ointment was formulated with natural ingredients. In 80 mice, burn was induced by Ian Allen Holder. Two treatments per day and 20 days with Akbar 1 and ZOUSH ointment were performed in two separate groups.

Results: In the treatment group with Akbar 1 ointment, the average number of isolated Pseudomonas aeruginosa is declining, but this decrease was much lower than the ZOUSH ointment treatment. The mean number of Pseudomonas aeruginosa isolated in treatment with Akbar 1 ointment after 20 days of treatment is approximately equal to 10 days of treatment with ZOUSH ointment. In the ZOUSH ointment group, during the treatment, the mean number of isolated Pseudomonas aeruginosa was not only reduced, but the mean number of Pseudomonas aeruginosa isolated after 20 days of treatment was zero. However, this result was not achieved in the treatment groups of Akbar 1 ointment. These results also indicate the beneficial effect of bactericidal ZOUSH ointment compared to Akbar 1 ointment.

Conclusion: Our results indicate that bactericidal has a ZOUSH ointment with an effect more than double, the Akbar 1 ointment.

Keywords:ZOUSH ointment, Akbar 1, wound infection

P150 - 763: RELATIVE FREQUENCY BIOFILM FORMAITON STRAIN AMONG MULTI DRUG RESISTANCE PSEUDOMONAS AERUGINOSA, ISOLATED FROM PATIANT WITH BURN WOUND OF RASHT BURNE CENTER (VALAYET HOSPITA)

Farhad Afrasiabi[1]

1. Department of microbiology Medicine Faculty, Rasht , IR Iran

Background and Aim: Pseudomonas aeruginosa (pseudomonas aeruginosa) is one of the most important opportunistic pathogens in infections in patients hospitalized in different parts of hospitals, especially the burn. Various pathogenic factors, including secretion toxins on the one hand, and the increasing resistance of these bacteria to antibiotics, on the other hand, increase the importance of studying on strains isolated from patients. The purpose of this study was to simultaneously investigate the antibiotic resistance pattern and the presence of psla gene and biofilm production from pathogenicity indices in Pseudomonas aeruginosa. This study was performed on pseudomonads isolated from burn wounds of hospitalized patients at burn center of burn injury in Rasht province

Methods: In this study 100 samples of Pseudomonas aeruginosa were isolated from hospitalized patients in Velayat Hospital of Rasht. Antibiotic resistance to 8 antibiotics (Gentamicin, Amikacin, Tobramycin, Ceftazidime, Piperacillin, Carbencililin, Ciprofloxacin and Imipenem) was assessed after confirmation of isolates and purification. Also, The production of biofilms and the presence of the psla gene were examined.

Results:he antibiotic resistance levels were as follows: Carbenicilin (81%), Tobramycin (60%), Gentamicin (54%), Piperacillin (50%), Ciprofloxacin (49%), Stifaridium (25%), Amikacin (24%), (22%). Multidrug resistant isolates (MDR) (35%) and resistance to aminoglycosides (16%) were more biofilm generators than the antibiotics tested. (P = 0.001).

Conclusion: The results of this study showed that AmiPenum was the most effective antibiotic and 100 (71%) strains produced biofilms, and 29 (29%) did not produce biofilms, and in 37 strains of production The psla gene was biofilm

Keywords: Pseudomonas aeruginosa ،PCR ،antibiotic resistance ،biofilm،psla gene

P151 - 766: ANTIBACTERIAL EFFECTS OF COPPER DIOXIDE AND TITANIUM DIOXIDE NANOPARTICLES ON ENTEROBACTER AEROGENES BACTERIA IN SOLID MEDIUMS

Hamed Charkhian[1], Ehsan Soleimannezhadbari[2], Ali Ghahremany[3], Shervin Shabani[4]

1. Department of Biotechnology, Urmia branch, Islamic Azad University, Urmia, Iran.
2. Young Researchers Club, Urmia Branch, Islamic Azad University, Urmia, Iran.
3. Microbiology Lab ,Urmia branch, General Bureau of Standards West Azerbayjan, Urmia, Iran.
4. Department of Microbiology, Urmia branch, Islamic Azad University, Urmia, Iran.

Background and Aim: High incidence of infectious diseases and the growing resistance of bacteria against traditional antibiotics has led to widespread investigation of alternative antibacterial compounds such as nanoparticles. The current study was conducted in vitro to investigate impact on growth of CuO and TiO2 nanoparticles on Enterobacter aerogenes bacteria in solid mediums.

Methods: In solid media, well diffusion and disk diffusion methods (In five concentrations 10, 50, 100, 250 and 500 ppm) and cylinder diffusion method were used 50, 250, 500, 1250, 2500 ppm concentrations of nanoparticles. In this test, for better measurement of zone of inhibition, Triphenyl tetrazolium chloride (TTC) were used. Plates incubated at 37 °C for 24 h. Inhibition zones measured by caliper subtly and reported.

Results: In well diffusion, disk diffusion and cylinder diffusion tests, the diameter of inhibition zone of Copper oxide nanoparticles was larger than the Titanium oxide inhibition zone. Copper oxide nanoparticles could form a non-growth zone at all concentrations other than the initial concentration. But titanium dioxide nanoparticles could not form any inhibition zone.

Conclusion: Bactericidal property of CuO nanoparticles was remarkably higher than TiO2 nanoparticles in the same condition. The concentration of nanoparticles has a direct impact on bactericidal ability. Possibly by more research and investigation, CuO nanoparticles can be consider as adjunctive therapy in combination with other antibacterial compounds.

Keywords: Enterobacter aerogenes, Copper oxide, Titanium dioxide, Nanoparticles, Antibacterial compounds

P152 - 767: INVESTIGATION OF THE ANTIBACTERIAL EFFECT OF HUMAN BIOLOGICAL PRODUCTS, PLATELET CONCENTRATE & AMNIOTIC MEMBRANE, AGAINST BETA-LACTAMASE PRODUCER ISOLATES OF PSEUDOMONAS AERUGINOSA AND STAPHYLOCOCCUS AUREUS

Shahrzad Soumeh saraei sabet[1], teena dadgar[2], hadi bazzazi[3]

1. life science department, islamic azad university of gorgan, gorgan, iran
2. life science department, islamic azad university of gorgan, gorgan, iran
3. life science department, islamic azad university of gorgan, gorgan, iran

Background and Aim: World health organization has published its first ever list of antibiotic-resistant "priority pathogens" – a catalog of 12 families of bacteria that pose the greatest threat to human health. In this list, Pseudomonas aeruginosa and Staphylococcus aureus placed in priority one and priority two respectively. The aim of this study was the investigation of the antibacterial effect of amniotic membrane and PRP on beta-lactamase producing Pseudomonas aeruginosa and Staphylococcus aureus to find a natural source of antibacterial agents against drug-resistance pathogens.

Methods:PRP was ordered from Iranian blood transfusion organization, and the amniotic membranes were collected aseptically from Gorgan city's hospitals from pregnant mothers at parturition day. Beta-lactamase producer Pseudomonas aeruginosa and Staphylococcus aureus isolates identification were performed with microbiological methods, iodometric test, and CLSIA protocol. Then isolates were cultured on MHA medium, and bactericidal effects of amniotic membrane and PRP were assessed using well diffusion and disk diffusion method respectively.

Results: Results showed that among all of the isolates, six isolates of Pseudomonas aeruginosa and six isolates of Staphylococcus aureus were beta-lactamase producer. PRP has an antibacterial effect on all of six MRSA isolates while does not affect any of six Pseudomonas aeruginosa isolates. Also, results inferred that amniotic membrane has an antibacterial effect on all of the both MRSA and Pseudomonas aeruginosa isolates

Conclusion: Amniotic membrane and PRP showed strong antibacterial potential against highly dangerous multi-drug resistance pathogens. Therefore human source natural products must be considered as a new source of antibacterial for drug discovery to address concerns about multi-drug resistance pathogens.

Keywords: Pseudomonas aeruginosa, Staphylococcus aureus, Multi dug-resistance, Amniotic membrane, platelet concentrate

P153 - 768: HERBAL EXTRACTS ANTIBACTERIAL EFFECT ON STAPHYLOCOCCUS AUREUS – ELECTROCHEMICAL VS DISK DIFFUSION AGAR METHODS

Sarvenaz Esmaeilee[1], Mohammad Dehsaraei[2]

1. Department of Microbiology, Faculty of Basic Sciences, Islamic Azad University, Lahijan Branch, Lahijan, Iran; sarvi_e520@yahoo.com
2. Electroanalytical Chemistry Laboratory, Faculty of Science, University of Guilan, Rasht, Iran

Background and Aim: Detection of pathogen microorganisms, such as Staphylococcus aureus, which can be harmful for public health is so important. This study tried to design a simple and sensitive biosensor based on multi-walled carbon nanotubes.

Methods:S. aureus PTCC1112 was sub-cultured in tryptic soy agar medium and incubated at 37 °C . 20 µL of 0.001 g of MWCNTs suspension in 1mL ethanol were spiked on the polished surface of glassy carbon electrode and dried at room temperature. Three different concentrations of S. aureus suspension in PBS were prepared in accordance with 0.5, 1 and 2 McFarland concentrations. Current increased by increasing the concentration of S. aureus suspension. The effect of modifier on microorganism detection, scan rate (νopt=0.05 V s–1) and linear dynamic range (3.7 × 106–3.0 × 108 cfu mL–1) were studied by electrochemical methods. The antibacterial effect of three herbal essential oils, tea, bergamot and lemon, were compared by electrochemical and biological methods

Results: The results of the study based on disk diffusion agar method and symmetrically by cyclic voltammetry revealed that this biosensor can be used for comparing the effectiveness tea essential oil, bergamot essential oil and lemon essential oil to inhibit the growth of bacteria. By adding the essential oils into the S. aureus growth media, the related currents were vanished or largely decreased.

Conclusion: It demonstrates the anti-bacterial effect of these herbal essential oils and the ability of MWCNTs/GCE to detect the presence or absence of S. aureus in a few minutes.

Keywords: Staphylococcus aureus; antibacterial effect; modified electrode; herbal essential oils

P154 - 769: ANTIMICROBIAL ACTIVITY OF LACTIC ACID BACTERIA ISOLATED FROM TRADITIONAL DAIRY PRODUCTS OF VARZEGHAN

Manigheh Hajizadeh Varzeghan[1], Gholamreza Zarrini[2], Farzad Sheikhzadeh Hesari[3], Mohammad Hossein Modarressi[4]

1. Department of Biology Science and Research Branch, Islamic Azad University,Tehran,Iran
2. Department of Animal biology, Faculty of Natural Science, University of Tabriz
3. Department of Animal biology, Faculty of Natural Science, University of Tabriz
4. Professor in Human Genetics Medical Genetics & Molecular Medicine Departments,Tehran University of Medical Sciences, Tehran, Iran.

Background and Aim: Many pathogens, which have become resistant to antibiotics therapy, have turned into an increasing public health problem worldwide. Lactic acid bacteria, which are considered as one of the most important probiotics, can be a resource of achieving new antimicrobial compounds. With expansion of microbial resistance against antibiotics, obtaining novel antimicrobial compounds from LAB can be a very vital benefit for the human health. In this study, antimicrobial activity of metabolites of produced by Lactic acid bacteria was examined

Methods: Sixty isolated of lactic acid bacteria purified from traditional dairy samples. These isolates were identified by physiological, biochemical and molecular methods. Antimicrobial activity of the isolates evaluated with well-diffusion and microdilution methods.

Results: The results showed antimicrobial activity for supernatants of three Lactobacillus strains isolated from traditional dairy products against Escherichia coli, Klebsiella pneumoniae, and Candida kefyr in Agar-well-diffusion method. Antimicrobial potency of the strains was confirmed by their low MIC values. These strains didn't show any activity against gram positive test strains.

Conclusion: The antimicrobial activity of the lactic acid bacteria isolated from traditional dairy products was most effective against gram negative bacteria specially Klebsiella pneumoniae.

Keywords: Antimicrobial activity, Lactic acid bacteria, Traditional dairy products.

P155 - 777: PREVALENCE OF QNR GENES IN EXTENDED-SPECTRUM B-LACTAMASE PRODUCING KLEBSIELLA PNEUMONIAE ISOLATED FROM CLINICAL URINE SPECIMENS IN UNIVERSITY TEACHING HOSPITALS, IRAN

Amin Dehghan banadkouki[1], Amin Dehghan-banadkouki[2], Gilda Eslami[3], Hengameh Zandi[4], Ali Dehghan-Banadkouki[5]

1. -
2. Department of Pathobiology, Faculty of Public Health, Tehran University of Medical Sciences, Tehran, Iran
3. Research Center for Food Hygiene and Safety, Shahid Sadoughi University of Medical Sciences, Yazd, Iran
4. Research Center for Food Hygiene and Safety, Shahid Sadoughi University of Medical Sciences, Yazd, Iran
5. Laboratory of Imam Khomeini Hospital, Karaj, Iran

Background and Aim: Extended-spectrum β-lactamase (ESBL) producing gram negative bacteria are resistant to penicillins, narrow and extendedspectrum cephalosporins, and aztreonam; also they are frequently resistant to trimethoprim-sulfamethoxazole, aminoglycosides, and quinolones. This study aimed to investigate the prevalence of plasmid-mediated quinolone resistance (PMQR) determinants qnrA, qnrB and qnrS in ESBL producing Klebsiella pneumoniae isolates.

Methods: In this descriptive-sectional study, 130 Klebsiella pneumoniae isolates were collected from urine specimens and identified by convectional biochemical tests from December 2013 to August 2014,. Antimicrobial susceptibility testing was performed by disk diffusion method (Kirby-Bauer). The presence of ESBLs was confirmed by combination disk tests. E.test method was used for determination of ceftazidime and ciprofloxacin minimum inhibitory concentration (MIC). qnr genes were investigated by multiplex polymerase chain reaction and after sequencing, indexed in Genbank database.

Results: Out of 130 isolates, 46 (35.4%) isolates were identified as ESBL producers, considering all, the highest rate of resistance belonged to amoxicillin, cefotaxime and ceftriaxone (each one 100%) and the lowest rate of resistance was for meropenem and ertapenem (each one 4.3%). 45 (97.8%) isolates were resistant to ceftazidime (MIC ≥ 16) and 24 (52.2%) isolates were resistant to ciprofloxacin (MIC≥4). qnrB and qnrS genes were detected in 21 (45.7%) and 7 (15.2%) isolates, respectively. 7 (15.2%) isolates were positive for both qnrB and qnrS genes. qnrA was not detected.

Conclusion: With respect to the high prevalence of qnr genes in ESBL producing Klebsiella pneumoniae isolates, quinolones and beta-lactam agents should be used with caution.

Keywords:ESBL, Klebsiella pneumoniae, PCR, qnr genes, Quinolone

P156 - 783: PRODIGIOSIN AGAINST SALMONELLA THYPHIMURIUM

Sorayesh Hajian[1], Sorayesh Hajian , Department Of Biology , Sanandaj Branch,Islamic Azad University,Sanandaj,Iran.[2], Bahareh Rahimian Zarif, Department Of Biology , Sanandaj Branch,Islamic Azad University,Sanandaj,Ira[3]

1. -
2. Sorayesh Hajian , Department Of Biology , Sanandaj Branch,Islamic Azad University,Sanandaj,Iran.
3. Bahareh Rahimian Zarif , Department Of Biology , Sanandaj Branch,Islamic Azad University,Sanandaj,Ira

Background and Aim:ubject: Prodigiosin is an natural red pigment produced by Serratia marcescens. Prodigiosin has antimicrobial, antimalarial and antitumor properties. Special attention has been paid to effects of silver nanoparticles and it's the antimicrobial impact due to development of microbial resistance. The aim of this study was comparison of antibacterial effect of prodigiosin, nanosilver and common antibiotic against Salmonella typhimurium.

Methods: The standard strains Serratia marcescens PTCC 1111 and Salmonella typhimurium PTCC 1609 were used. Pigment produced by Serratia marcescens was extracted by the acidic methanol. Finally, antimicrobial properties of nanosilver and pigment was investigated by disc diffusion, and microdilution.

Results: The inhibition zone of ciprofloxacin, piperacillin, cefpime, ampicemin, gentamicin and azithromycin was 33.0 ± 2.64, 30.66 ± 1.51, 30.33 ± 2.51, 28 ± 2, 19.66 ± 2.51 and 19.66 ± 0.57 mm, respectively. The mean diameter of the inhibition zone of nano silver and prodigiosin was 17.33 ± 0.57 mm and 15.66 ± 0.57 mm, respectively. The MIC and MBC of the nano silver are 6.25 and 12.5 µg/ml. This size is approximately close to the amount of MIC and MBC of some antibiotics such as azithromycin and piperacillin. But prodigiosin has MIC and MBC of 25000 and 50000 µg/ml, respectively.

Conclusion: Prodigiosin produced by the Serratia marcescens, has promising bacteriostatic and bactericidal effects and suggests further studies on its use in antibiotic treatment. In this study, nano silver had an appropriate antibacterial activity against Salmonella typhimurium. So, after examining of the antimicrobial properties of nano silver and prodigiosin in In Vivo, they can be used to treat infection with this bacterium.

Keywords: Prodigiosin, Nano silver, Salmonella typhimurium, Serratia marcescens, Antimicrobial

P157 - 795: RELATION OF TOXA AND TOXS GENES AND ANTIMICROBIAL RESISTANCE IN PSEUDOMONAS AERUGINOSA

Niloufar Mohseni[1]

1. Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran.

Background and Aim: Pseudomonas aeruginosa is one of the most important nosocomial pathogens that causes opportunistic infections in human. It can tolerate a wide variety of antibiotics by different resistance mechanisms Such as efflux pupms. P. aeruginosa also possesses several virulence factors such as exotoxin A (toxA) and exoenzyme S (toxS). The study aim to show the relation between presence of toxA and toxS genes and antimicrobial resistance in this bacteria.

Methods: At first, species identify using biochemical tests, and their antibiogram pattern obtain according to CLSI standards. Antimicrobial susceptibility testing will be done by disk diffusion method and Then The presence of toxA and tox s genes will investigate using PCR (Real-time PCR or multiplex pcr)

Results:results show that there is a relationship between antimicrobial resistance and presence of virulence factors, such as exotoxin and exoanzime, most of resistant isolates have these exotoxin genes . this relationship can be an important warning to treatment centers in terms of control of disease caused by pseudomonas aeroginosa.

Conclusion:P. aeruginosa as one of the most common cause of nosocomial infections exhibits remarkable ability to acquire resistance to antimicrobial agents and MDR P. aeruginosa nosocomial infections are increasingly recognized worldwide .toxA and toxS both genes are almost contribute to pathogenicity and antimicrobial resistance in isolates of P. aeruginosa and studies show that there is relationship between presence of these genes and antimicrobial ability.

Keywords: Pseudomonas aeruginosa , toxA and toxS ,Antimicrobial Resistance

P158 - 804: INHIBITORY POTENCY OF HUMAN ANTIMICROBIAL PEPTIDE DCD-1L ON THE BIOFILM FORMATION OF ACINETOBACTER BAUMANNII

Zahra Farshadzadeh[1], Behrouz Taheri[2], Abbas Bahador[3]

1. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
2. Department of Medical Laboratory Sciences, School of Paramedicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran,
3. Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: The high ability to develop biofilm as a critical factor in chronic infections along with high rate of drug-resistant Acinetobacter baumannii highlights the need to identify novel antibiotics. The aim of this study was to assess in vitro and in vivo anti-biofilm activities of dermcidin-1L (DCD-1L) against clinical A. baumannii strains.

Methods: In vitro antibacterial, anti-adhesive, and anti-biofilm activities of DCD-1L to clinical and standard (ATCC 19606) A. baumannii strains were investigated. Furthermore, effect of DCD-1L treatment on expression of several biofilm-associated genes including abaI, ompA, bfmRS, csuE, pgaAB, and wspR was evaluated using RT-qPCR. In addition to in vitro study, the catheter infection model was used to assess anti-biofilm activity of DCD-1L against standard A. baumannii strain.

Results: Minimum inhibitory concentration (MIC) of DCD-1L was 16 µg/ml. DCD-1L also inhibited biofilm formation at sub-inhibitory concentration (1/4MIC), whereas the high value of MBEC (1024 µg/ml) indicates disability of DCD-1L to eradicate existing biofilm. Using RT-qPCR, we were able to demonstrate that DCD-1L affected biofilm formation by decreasing the attachment of bacterial cells and influencing quorum sensing system, leading to the down-regulation of genes involved in biofilm development. Furthermore, in mouse catheter infection model following treatment with DCD-1L at 1/2 MIC and 1 MIC, the biofilm was significantly reduced as compared to the untreated control.

Conclusion: In the present study a new, previously unreported function for the human anionic antimicrobial peptide DCD-1L was described, suggesting that DCD-1L could play a critical role in human innate immune system through its anti-adhesive, and anti-biofilm activities.

Keywords: Acinetobacter baumannii, Antimicrobial peptide, Dermcidin-1L

P159 - 805: A STUDY OF PREVALENCE OF SHIGELLA SPECIES AND ESBL PRODUCING ISOLATES IN ARDABIL, IRAN

Sahar Sabour[1], taher azimi[2], Hadi Peeri Dogaheh[3]

1. School of Medicine. Ardebil University of medical science. Ardebil.IR Iran
2. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
3. School of Medicine. Ardebil University of medical science. Ardebil.IR Iran

Background and Aim: Shigellosis is the main cause of gastrointestinal disease and is a public health concern worldwide. Nearly forty serotypes are clustered into 4 species includes: Shigella flexneri (S.flexneri), S. sonnei, S. boydii and S. dysenteriae that can cause insignificant to severe dysentery. The aim of this study was to determine the prevalence of S. sonnei and extended-spectrum beta-lactamases (ESBLs) isolates in Ardabil province.

Methods: In this study, 1280 fecal samples were collected from patients and biochemical and molecular test (invc and wbyz genes for Shigella spp and shigella sonnei detection, respectively) were used to determine bacterial strains. In addition, Phenotyping of ESBL-producing Shigella isolates was performed using cefotaxime combined with ceftazidime in the presence or absence of clavulanic acid, as recommended by CLSI.

Results: In total, biochemical tests revealed that 113 fecal samples were positive for shigella spp. Moreover, result of molecular tests revealed that 36 and 21 fecal samples were positive for shigella spp and Shigella sonnei, respectively. In the other hand, ESBLs were produced by 8 of the 36 (22.2 %) Shigella isolates

Conclusion: The results suggested that there was a high prevalence of the shigella spp and shigella sonnei among patients with gastrointestinal disease, therefore, appropriate programs should be considered in order to control and treat the patients

Keywords: Shigella sonnei,Bacterial unfection, Gastrointestinal disease,PCR

P160 - 809: EVALUATION OF ANTIBACTERIAL ACTIVITY OF MATHANOL AND HEXANE EXTRACTS OF CRUCIATA TAURIACA

Behnaz Asadi[1], Shiva Khalil_Moghaddam[2], Atousa Aliahmadi[3]

1. Department of Biology, Yadegar-e-Imam Khomeini (RAH) Shahre Rey Branch, Islamic Azad University, Tehran, Iran
2. Department of Biology, Yadegar-e-Imam Khomeini (RAH) Shahre Rey Branch, Islamic Azad University, Tehran, Iran
3. Medicinal Plants and Drug Research Institute, Shahid Beheshti University, Tehran, Iran

Background and Aim: In response to the propagation of bacteria resistant to many antibiotics also called multi-drug resistant bacteria, the discovery of new resources for producing agents that could act as alternatives to antibiotics is primordial. The aim of this study was to evaluate the antibacterial activity of Cruciata Tauriaca extracts against two Gram-posetive bacterial species..

Methods: This plant have been collected in spring. Methanol and n-hexan was used for extraction of plant polar and nonpolar materials. Then minimum inhibitory concentration (MIC) of the plant materials were determined against Bacillus cereus PTCC 1015 and Staphylococcus aureus ATCC 25923 by broth micro-dilution method. Mueller hinton broth was used for preparation of serial diluted samples which were checked against 0.5-1 × 106 CFU (Colony forming unit) of bacteria. Incubation was done for 20 hrs at 37°C. MICs were recorded as the lowest concentrations which could inhibit visible growth of bacterium. Chloramphenicol was used as standard antibiotic.

Results: Methanolic extract of Cruciata Tauriaca could show the best result (MICs 0.467 mg/ml for Bacillus cereus) and Staphylococcus aureus was inhibited in higher concentration of methanolic extract. (3.74 mg/ml) and hexane extract could show the best result for Staphylococcus aureus(MICs 0.116 mg/ml).

Conclusion: According to the result of this study, methanolic and hexane extracts can exhibit antibacterial effects.

Keywords: Antibacterial activity, Cruciata Tauriaca

P161 - 825: ISOLATION AND ANTIMICROBIAL SUSCEPTIBILITY OF METHICILLIN-RESISTANT STAPHYLOCOCCUS PSEUDINTERMEDIUS (MRSP) IN PETS, VETERINARIANS, AND THE ENVIRONMENT

Arash Najafifar[1], Ali Nemati[2], Mahdi Askari Badouei[3], Ehsan Khaksar[4]

1. 1 Department of Pathobiology, Faculty of Veterinary Medicine, Gamsar Branch, Islamic Azad University, Semnan, 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
4. Department of Pathobiology, Faculty of Veterinary Medicine, Gamsar Branch, Islamic Azad University, Semnan, Iran

Background and Aim: The genus Staphylococcus consists of a variety of opportunistic pathogens that causes a wide range of infections in humans and animals. Staphylococcus pseudintermedius is an important opportunistic pathogen that can cause infections of the skin and other tissues in animals. The aim of this study was to investigate the prevalence of methicillin-resistant Staphylococcus pseudintermedius (MRSP) in pets and veterinary personnel.

Methods: The samples were collected from companion animals (n=157), veterinary clinic environment (n=22), and veterinarians and veterinary healthcare personnel (n=98). Samples were immediately streaked onto manitol salt agar and sheep blood agar. These isolates were subjected to biochemical tests and then DNA was extracted and screened for mecA gene by PCR (n=277). All mecA+ isolates were subjected to molecular identification and finally the antibiotic susceptibility of MRSP were determined by disc-diffusion method.

Results: Of 277 isolates tested, 82 isolates possessed the mecA gene; of which 20 were MRSP including 13 isolates from dogs (65%) and 7 from cats (35%). Antimicrobial susceptibility showed the highest resistance rate against tetracycline (90%), ceftriaxone (85%), erythromycin (80%), lincomycin (75%), and gentamicin (65%); all isolates were resistant to betalactams.

Conclusion: Despite the fact that MRSP was not isolated from humans, the high carriage rate of this emerging pathogen in animals is of particular concern because infection due to MRSP is hard to treat and also can be transmitted to humans.

Keywords: Staphylococcus pseudintermedious; Antimicrobial resistance; mecA gene; Humans; Animals

P162 - 826: THE ROLE OF ADEABC, ADEFGH AND ADEIJK EFFLUX PUMPS IN REDUCED SUSCEPTIBILITY TO TIGECYCLINE IN ACINETOBACTER BAUMANNII ISOLATED FROM BURN PATIENTS

Behrouz Taheri[1], Zahra Farshadzadeh[2], Abbas Bahador[3]

1. Department of Medical Laboratory Sciences, School of Paramedicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran,
2. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
3. Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: The wide use of tigecycline in the treatment of severe infections caused by multidrug-resistant (MDR) Acinetobacter baumannii has led to emergence of tigecycline resistant strains in recent years. In this study the relationship between tigecycline resistance and the expression of efflux pumps was investigated.

Methods: Clinical A. baumannii isolates were collected from hospitalized burn patients. The minimum inhibitory concentration (MIC) of tigecycline was determined by the broth microdilution method. Expression levels of efflux pump genes (adeB, adeG, and adeJ) were assessed by quantitative real-time reverse transcription polymerase chain reaction (RT-qPCR). The correlations between tigecycline MICs and gene expression levels were evaluated. In addition, to confirm observational findings an insertional inactivation using a suicide plasmid construct was performed.

Results: Overall, 221 A. baumannii strains isolated from burn wound were investigated among which 29% were tigecycline resistant. Overexpression of AdeABC efflux system was observed in clinical tigecycline resistant isolates. A linear relationship between the tigecycline MIC and the adeB expression level, but not the adeG and adeJ, was found. There were significant linear trends in the overexpression of adeB as the tigecycline MIC increased in A. baumannii isolates. Besides, inactivation of the adeB gene in one tigecycline-susceptible isolate decreased tigecycline MIC from 16 to 1 µg/ml.

Conclusion: Tigecycline resistance in A. baumannii was strongly associated with the overexpression of AdeABC efflux systems. More studies are needed to elucidate whether there are other regulators that affect the expression of adeB in A. baumannii

Keywords: Acinetobacter baumannii, Efflux pump, Tigecycline

P163 - 828: BIOSYNTHESIS OF ZINC OXIDE NANOPARTICLES USING EUCALYPTUS MELLIDORA LEAF EXTRACT AND EVALUATION OF ITS ANTIMICROBIAL EFFECTS

Behnam Rafiee[1], Sepideh Ghani [2], Farhad Ghani [3], Davoud sadeghi [4]

1. PhD student of Bacteriology ,Department of Pathobiology, Faculty of Veterinary Medicine, Shahrekord University, Iran
2. PhD student of Medical Biotechnology , Shahid Beheshti University of Medical Science, Tehran,iran
3. General Practitioner , Arak University of Medical Science
4. PhD OF Nano biotechnology .Biology Research Center, Faculty of Science & Basic Sciences, Imam Hossein University of Technology, Tehran, I.R..Iran

Background and Aim: The biological approaches to synthesis of nanoparticles are better than chemical and physical procedures because of low energy and time expenditure.This method do not require toxic solvents material for environment.Green synthesis of nanoparticles is an eco-friendly method and uses natural solvent.The purpose of this study is to biosynthesis of zinc oxide nanoparticles and to evaluate its antibacterial activity

Methods: In this experimental study,the extract of Eucalyptus melliodora was combined at a ratio of 1: 1 with 0.1 M zinc sulfate and kept at room temperature for 15 minutes.Synthesis of ZnO NPs was confirmed by spectrophotometer (UV-Vis) methods and DLS, Zeta potential ,PDI,SEM and X-ray diffraction.Then antibacterial properties of nanoparticles were evaluated by disk diffusion method and dilution tube MIC (Minimum inhibitory concentration) on standard strains of Staphylococcus aureus PTCC 1431,Bacillus cereus 1015 PTCC and Escherichia coli PTCC 1399,Pseudomonas aeruginosa PTCC 1571 and was compared with the antimicrobial effects of Eucalyptus extract and zinc sulfate.

Results: The absorption peak of ZnO NPs was observed at of 350 nm.The SEM showed ZnO nanoparticles was spherical shape of size ranging from 30 to 50 nm ,and a zeta potential of -19.6 mV was recorded,indicating a very good stability of nanoparticles. MIC was measured for Bacillus cereus,Staphylococcus aureus,Pseudomonas aeruginosa and Escherichia coli 0.0078, 0.0019, 0.0019, 0.0019, mg / ml,respectively.

Conclusion:results showed biological nanoparticles of ZnO and extract of Eucalyptus as well as zinc sulfate have antimicrobial properties against pathogenic bacteria,but the most antimicrobial effects were observed by ZnO NPs.

Keywords: Eucalyptus melliodora, Anti-Bacterial Activity, ZnO Nanoparticles.

P164 - 829: PHENOTYPIC AND GENETIC BASIS OF BIOFILM FORMATION BY ESCHERICHIA COLI AND PSEUDOMONAS AERUGINOSA IN MECHANICALLY VENTILATED AND VAP DEVELOPED PATIENTS

Elnaz Shahrukhi[1], Alka hasani[2], Khalil ansarin[3], Haleh mikaiili[4], Akbar sharifi[5], Saeed mosavi[6], Akbar hasani[7], Mohammad aghazadeh[8]

1. Tabriz University of Medical Sciences, Tabriz, Iran
2. Tabriz University of Medical Sciences, Tabriz, Iran
3. Tabriz University of Medical Sciences, Tabriz, Iran
4. Tabriz University of Medical Sciences, Tabriz, Iran
5. Tabriz University of Medical Sciences, Tabriz, Iran
6. Tabriz University of Medical Sciences, Tabriz, Iran
7. Tabriz University of Medical Sciences, Tabriz, Iran
8. Tabriz University of Medical Sciences, Tabriz, Iran

Background and Aim:VAP is the second most common nosocomial infection in the intensive care unit (ICU). We aimed to study the phenotypic and genetic basis of biofilm formation by Escherichia coli and Pseudomonas aeruginosa isolated from mechanically ventilated and VAP developed patients.

Methods: The study was conducted from May 2015 to March 2016, in a respiratory ICU of a University Teaching hospital. Endotracheal from 40 patients were collected for culture at least in four episodes including, 48 hours, 72 hours, 7 days and 10 days after being ventilated. The bacterial culture was performed quantitatively and colonies more than 105 CFU/ml were considered pathogens. The ability of isolates to form biofilms was evaluated quantitatively using micro titer plate method and finally, the presence of biofilm genes was investigated by PCR method.

Results: The prevalence of VAP was 15%. Among 148 bacterial isolates obtained from ventilator patients included Pseudomonas aeruginosa (n=18) Escherichia coli (n=12). Escherichia coli)100%) and Pseudomonas aeruginosa (83.4 %) were able to form biofilms on micro titer plate method. Frequency of pslA and algC genes in Pseudomonas aeruginosa isolates was 50%, 11.1%, respectively and papC, pgaA, ang43, csgA, genes in Escherichia coli isolates were observed in 33.3%, 100%, 66.7%, 25% of isolates respectively.

Conclusion: Biofilm genes in organisms contributed to biofilm formation. This feature triggers strong multi-drug resistance and their dissemination in the hospital environment.

Keywords: Ventilator-induced pneumonia; Biofilm;

P165 - 831: EXPERIMENTAL EVALUATION THE EFFECT OF IRON SALT ON THE INHIBITION OF STREPTOCOCCUS MUTANS

Mohammad Motamedifar[1], Yalda Malekzadegan[2], Elham Rastegar[3], Sahar Sorourian [4]

1. Department of Bacteriology and Virology, School of Medicine, Shiraz University of Medical Sciences Shiraz, Iran
2. Department of Bacteriology and Virology, School of Medicine, Shiraz University of Medical Sciences Shiraz, Iran
3. Department of Bacteriology and Virology, School of Medicine, Shiraz University of Medical Sciences Shiraz, Iran
4. Student Research Committee, Shiraz University of Medical Sciences Shiraz, Iran

Background and Aim: Dental caries is a common infectious process that occurs by Streptococcus mutans. Considering the high frequency of dental caries and iron starvation in Iran, the study aimed to investigate the inhibitory effect of iron salts including iron sulfate and iron acetate against Streptococcus mutans in vitro.

Methods: In this study, aqueous solutions of iron sulfate and iron acetate were prepared. Antibacterial effects of different concentrations of iron sulfate and iron acetate on Streptococcus mutans was evaluated using disk diffusion and broth micro-dilution methods. The minimum inhibitory concentration (MIC) and minimum bacteriocidal concentration (MBC) if these salts for Streptococcus mutans were determined. Then, the results were compared with the results of inhibitory effects of penicillin and chlorhexidine as controls.

Results:MIC and MBC of iron sulfate solution was higher than those for penicillin and chlorhexidine ($p<0.001$) while, there was not statistically significant differences between the MIC and MBC of sulfate acetate solution, penicillin and chlorhexidine. In concentrations of 25 and 50 µg/mL inhibitory zone of iron sulfate in disk diffusion method was more than that for iron acetate solution.

Conclusion: Iron sulfate and iron acetate solutions had antibacterial activity against Streptococcus mutans in the culture medium, so these salts was effective in reducing the range of MIC and MBC

Keywords: Streptococcus mutans, Iron sulfate, Iron acetate

P166 - 833: INVESTIGATION OF FREQUENCY AND ANTIMICROBIAL RESISTANCE PATTERN OF PSEUDOMONAS AEROGINOSA AND STAPHYLOCOCCUS SPP. ISOLATED FROM CORNEAL ULCER IN SHIRAZ

Mohammad Motamedifar[1], Yalda Malekzadegan[2], Ali Abdi[3], Ali Mirzaei[4]

1. Department of Bacteriology and Virology, School of Medicine, Shiraz University of Medical Sciences Shiraz, Iran
2. Department of Bacteriology and Virology, School of Medicine, Shiraz University of Medical Sciences Shiraz, Iran
3. Department of Bacteriology and Virology, School of Medicine, Shiraz University of Medical Sciences Shiraz, Iran
4. Student Research Committee, Shiraz University of Medical Sciences Shiraz, Iran

Background and Aim: Corneal ulcer is one of the ophthalmology emergencies that rapid diagnosis and treatment is important in preventing side effects. Two important infectious agents of corneal ulcer are Staphylococci spp. and Pseudomonas isolated from corneal ulcer to current antibiotics.

Methods: The study is performed on 60 corneal ulcer samples. After diagnosing corneal infectious ulcers and taking samples from the active site of the wound, the specimens were transferred and incubated, and faced samples which pseudomonas was isolated to 11 different antibiotics and faced isolated staphylococcus to 9 different antibiotic.

Results: From 60 samples collected, 7 pseudomonas, 3 Methicillin Sensitive Staphylococcus aureus (MSSA), 2 Methicillin Sensitive Coagulase Negative Staphylococcus aureus (MSCONS), 1 Methicillin Resistance Coagulase Negative Staphylococcus (MRCONS) and 1 Methicillin Resistance Staphylococcus aureus were isolated. Pseudomonas had the highest susceptibility to amikacin, colistin and levofloxacin, and staphylococci was 100% sensitive to amikacin and rifampin.

Conclusion: In an experimental treatment of corneal ulcer, use of an aminoglycoside along with fluoroquinolone is recommended for complete coverage of Staphylococcus and Pseudomonas.

Keywords: Corneal ulcer, Pseudomonas aeroginosa, Staphylococcus spp.

P167 - 835: PHENOTYPIC DETECTION OF ANTIBIOTIC RESISTANCE AND EXTENDED SPECTRUM B-LACTAMASE IN ECOLI STRAIN ISOLATES IN TABRIZ SINA HOSPITAL

Tahereh Eskandari[1], Mehdi Ghiamirad[2]

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: Production of β-lactamase enzymes by Gram-negative bacteria is the most common mechanism to acquire drug resistance to β-lactam antibiotics. This study was carried out to determine the frequency of occurrence and the antimicrobial susceptibility pattern of ESBL producing E. coli species from clinical isolates at Sina hospital in Tabriz.

Methods: This cross- sectional study was carried out in Tabriz sina hospital during 2017 .A total of 100 ecoli samples were selected randomly. The isolates, identification was done by biochemical method. Antibiotic resistance of isolates was detected by disk diffusion method. These multidrug-resistant strains were phenotypically screened for ESBL production by phenotypic confirmatory disc diffusion test and double disc synergy test.

Results: Among the 100 isolates, 49 were ESBL producers. All ESBL producers were highly resistant to Ampicilin (91%), cotrimoxazole (72%), and Ceftazidime (65%). However, these bacterial strains were sensitive to Ciprofloxacin (76%) and Amikacin(71%).

Conclusion: This study showed that ESBL producing organisms were not only resistant to cephalosporins but also to other group of drugs and also that multiple mechanisms play a role in drug resistance among Gram-negative bacteria.

Keywords: Extended spectrum β-lactamase, Eschersia coli, Antibiotic resistance

P168 - 839: COMPARISON OF THE ANTIFUNGAL ACTION POTENCY OF TEUCRIUM POLIUM L. AND AMPHOTRICIN B AGAINST CANDIDA PARAPSILOSIS

Elham Rezaei[1]

1. Mahboobeh madani

Background and Aim: Teucrium species have been used in traditional medicine for treatment of different diseases. The mechanism of antifungal action potency of Teucrium polium L. and amphotricin B against candida parapsilosis was investigated in this study.

Methods:plant was collected from Isfahan during the spring and the mechanism of antifungal activity of Teucrium polium was studied. Candida parapsilosis was added to ethanolic extract in tubes, then presence of sodium, potassium, glucose and amino acids in the tubes was examined by flame photometer, autoanalyzer, and HPLC.

Results: Results showed that sodium, potassium, glucose and amino acids were releasd from Candida parapsilosis.

Conclusion: According to the result, the antifungal activity of Teucrium polium is similar to Amphotricin B.

Keywords: Teucrium polium, Candida parapsilosis, flame photometer, autoanalyzer, and HPLC.

P169 - 840: GREEN SYNTHESIS OF SILVER NANOPARTICLES BY EXTRACT OF JUGLANS REGIA LEAF AND EVALUATION OF ITS ANTIBACTERIAL EFFECTS

Behnam Rafiee[1], Sepideh Ghani[2], Amin Nematolahi[3], Davoud sadeghi [4], Farhad Ghani[5], Seyed Amir Hosseini[6], Niloofar Noori [7], Nadia mahmoodi[8]

1. PhD student of Bacteriology ,Department of Pathobiology, Faculty of Veterinary Medicine, Shahrekord University, shahrkord .Iran
2. PhD student of Medical Biotechnology , Shahid Beheshti University of Medical Science, Tehran,iran
3. Associate Professor Food Hygiene and Quality Control Faculty of Veterinary Medicine. Shahrekord University, Iran.
4. Biology Research Center, Faculty of Science & Basic Sciences, Imam Hossein University of Technology, Tehran, I.R.Iran
5. General Practitioner , Arak University of Medical Science . Arak .Iran
6. Biology Research Center, Faculty of Science & Basic Sciences, Imam Hossein University of Technology, Tehran, I.R.Iran
7. Department of Biology ,Faculty of science, Arak University . Arak .Iran
8. Department of Biology ,Faculty of science, Shiraz University . shiraz .Iran

Background and Aim: The biological approaches to synthesis of nanoparticles 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. The aim of this study is to biosynthesis of silver nanoparticles and to evaluate its antibacterial activity

Methods: In this experimental study AgNPs were prepared by the reaction of 1mM silver nitrate and extracts of juglans regia lesf . Antibacterial activity of AgNPs was assessed by using disc diffusion method against Staphylococcus aureus PTCC 1431, Bacillus cereus 1015 PTCC and Escherichia coli PTCC 1399, Pseudomonas aeruginosa PTCC 1571 and Acinetobacter baumannii PTCC 1855 . The AgNPs were characterized by UV-visible (vis) spectrophotometer, particle size analyzer by dynamic light scattering (DLS) method, and SEM techniques.

Results: In this study, . Antibacterial activity was observed against all tested bacteria , so that most antibacterial effect observed on P.aeroginosa and A.baumannii and the lowest effect was observed on E. coli . The formation of silver nanoparticles was confirmed by the presence of an absorption peak at 450 nm using spectrophotometer, The SEM showed AgNPs was spherical shape of size ranging from 33 to 45 nm . and a zeta potential of -19.6 mV was recorded,indicating a very good stability of nanoparticles.

Conclusion:results showed biological nanoparticles of Ag and extract of juglans regia leaf as well as AgNO3 have antimicrobial properties against pathogenic bacteria ,but the most antimicrobial effects were observed by Ag NPs.

Keywords: Anti-Bacterial Activity , Green synthesis , Nanoparticle , Silver

P170 - 841: SILVER NANOPARTICLES ECOFRIENDLY SYNTHESIS BY SATUREJA HORTENSIS AND EVALUATION ANTIBACTERIAL PROPERTIES

Behnam Rafiee[1], Sepideh Ghani[2], Amin Nematolahi [3], Davoud sadeghi [4], Farhad Ghani[5], Seyed Amir Hosseini[6]

1. PhD student of Bacteriology ,Department of Pathobiology, Faculty of Veterinary Medicine, Shahrekord University, Iran
2. PhD student of Medical Biotechnology , Shahid Beheshti University of Medical Science,iran
3. Associate Professor Food Hygiene and Quality Control Faculty of Veterinary Medicine. Shahrekord University, Iran.
4. PhD OF Nano biotechnology .Biology Research Center, Faculty of Science & Basic Sciences, Imam Hossein University of Technology, Tehran, I.R.Iran
5. General Practitioner , Arak University of Medical Science . Arak .Iran
6. Biology Research Center, Faculty of Science & Basic Sciences, Imam Hossein University of Technology, Tehran, I.R.Iran

Background and Aim: Ecofriendly or Green synthesis of metal nanoparticles has become an important branch of nanotechnology and there is an increasing commercial demand for nanoparticles due to their wide applications.The aim of this work is to green synthesis of silver nanoparticles and to evaluate its Review of the properties of nanoparticles and antibacterial activity.

Methods: In this study AgNPs were prepared by the reaction of 1mM silver nitrate and extracts of Satureja hortensis lesf , the reaction did at room temperature and the color changed from pale yellow to dark showed the silver nanoparticles were generated . Antibacterial activity of AgNPs was assessed by using disc diffusion method against Staphylococcus aureus PTCC 1431, Bacillus cereus 1015 PTCC and Escherichia coli PTCC 1399, Pseudomonas aeruginosa PTCC 1571 and Acinetobacter baumannii PTCC 1855 . The AgNPs were characterized by UV-visible spectrophotometer,particle size analyzer by dynamic light scattering method,and scanning electron microscopy techniques.

Results: The formation of silver nanoparticles was confirmed by the presence of an absorption peak at 450 nm using spectrophotometer. The shape of particles was spherical and average size of them was about 73 nm. Antibacterial activity was observed against all tested bacteria,so that most antibacterial effect observed on P.aeroginosa and E.coli,on the other hand the lowest effect was observed on B.cereus and A.baumannii .

Conclusion:results showed biological AgNPs and extract of Satureja hortensis leaf as well as AgNO3 have antimicrobial properties against pathogenic bacteria,but the most antimicrobial effects were observed by Ag NPs.

Keywords: Antibacterial .Ecofriendly Synthesis . Nanoparticle .Satureja hortensis . silver.

P171 - 842: COMPARISON OF ANTIFUNGAL EFFECTS OF SPARTIUM JUNCEUM AND MELISSA OFFICINALIS HERBS EXTRACTS ON CANDIDA ALBICANS IN COMPARISON WITH THE ANTIBIOTICAL EFFECT

Razieh Taghavizad[1], Sanaz Gagonani[2]

1. Associate professor of the Department of Biology, Yadegar -e- Imam Khomeini (RAH) Shahre-Rey Branch, Islamic Azad University, Tehran, Iran.
2. M.Sc. Student of Microbiology, Yadegar -e- Imam Khomeini (RAH) Shahre-Rey Branch, Islamic Azad University, Tehran, Iran.

Background and Aim: Medicinal Plants extracts were used to suggest the use of low-risk drugs in treating diseases that involve sensitive and vulnerable mucosae such as vagina and mouth.

Methods: The aqueous, methanolic, and hydroalcoholic extracts were prepared by maceration and condensed by rotary. Four concentrations of 20, 30, 40 and 50 mg/ml of extracts were used. Sabouraud dextrose agar medium was used to cultivate fungus. For the effectiveness of extracts, the agar well method was used and each effect was replicated three times.

Results: Hydroalcoholic extracts of both Spartium junceum and Melissa officinalis plants had the greatest inhibitory effect on growth of Candida albicans, so that with S. junceum hydroalcoholic extract, the mean halo of lack of microbial growth was 10-12 mm, but S. junceum aqueous extract had a lower effect and the methanolic extract of S. junceum was also unaffected. With the hydroalcoholic extract of M. officinalis, the mean halo diameter of lack of microbial growth was 11.75- 14.25 mm, but the M. officinalis aqueous extract was less effective (diameter of 10.75- 13.25 mm) and the methanolic extract of M. officinalis showed the halo of lack of microbial growth of 8.75-11.25 mm. To compare, nystatin antibiotic was more effective in all cases.

Conclusion: It can be concluded that if infectious diseases of the vagina and oral thrush are in the early stages, the use of the hydroalcoholic extract of M. officinalis will be more effective for disinfection. Of course, clinical trials should be done.

Keywords:antifungal effects, Candida albicans

P172 - 843: COMPARISON OF THE ANTIFUNGAL EFFECTS OF SPARTIUM JUNCEUM AND MELISSA OFFICINALIS HERBS EXTRACTS ON SAPROLEGNIA SP. IN COMPARISON WITH ANTIBIOTICAL EFFECTS

Razieh Taghavizad[1], Sanaz Gagonani[2]

1. Associate professor of the Department of Biology, Yadegar -e- Imam Khomeini (RAH) Shahre-Rey Branch, Islamic Azad University, Tehran, Iran.
2. M.Sc. Student of Microbiology, Yadegar -e- Imam Khomeini (RAH) Shahre-Rey Branch, Islamic Azad University, Tehran, Iran.

Background and Aim: Contamination of Saprolegnia sp. fungi in edible and ornamental fish is one of the common problems of fish aquaculture ponds and aquariums and has economic losses.

Methods: The aqueous, methanolic, and hydroalcoholic extracts of Spartium junceum and Melissa officinalis were prepared by maceration and condensed by rotary. Four concentrations of 20, 30, 40 and 50 mg/ml of the extracts were used. The fungus was isolated from fins of the infected fish and cultivated in sabouraud dextrose agar medium. For the effectiveness of extracts, the agar well method was used and each effect was replicated three times.

Results: The methanolic extract of S. junceum had the most inhibitory effect on the growth of Saprolegnia sp. (mean halo of lack of microbial growth was 11.5-14 mm), and subsequently the hydroalcoholic extract was more effective but the aqueous extract of S. junceum did not produce a halo. In comparison, the M. officinalis aqueous extract with a mean halo of lack of microbial growth of 16-18 mm had the highest inhibitory effect on growth, followed by a hydroalcoholic extract with halo of lack of microbial growth of 13.5-15.5 mm, but the methanolic extract of M. officinalis did not affect Saprolegnia sp.. The nystatin antibiotic did not produce any halo of lack of microbial growth.

Conclusion: Using plant extracts instead of antibiotics and malachite green could be a good alternative. Particularly, aqueous extract of M. officinalis is recommended because it has the greatest effect and is also beneficial to the health of fish and humans.

Keywords:antifungal effects, Melissa officinalis, Saprolegnia sp.

P173 - 846: MOLECULAR AND SEROLOGICAL DETECTION OF MYCOPLASMA PNEUMONIAE AND DETERMINE OF THE CIPROFLOXACIN RESISTANCE PATTERN

Zohre Darabi[1], Mohammd Niakan[2]

1. MSc of Medical Microbiology , Department of Medical Microbiology, Shahed University , tehran, iran.
2. PhD of Medical Microbiology , Department of Medical Microbiology, Shahed University , tehran, iran.

Background and Aim:M. pneumoniae, which causes atypical pneumonia, is a well established pathogen of the respiratory tract. This Bacteria is intrinsically susceptible to fluoroquinolones. But Recently, drug-resistant forms of this bacteria have been reported. aim of this study is determine of prevalence of this bacateria by ELISA and PCR and MIC to ciprofloxacin

Methods: The clinical samples (blood and nasopharyngeal swab) were collected from 135 patients who was referred to selective hospitals in Tehran with respiratory complaints were enrolled in 2017. nasopharyngeal swab sample collections were cultured on PPLO broth and PPLO agar. After culturing and DNA extraction with phenol / chloroform, polymerase chain reaction was performed by specific P1 gene's primers. Ciprofloxacin's MIC of Mycoplasma pneumonia Isolated was determined by Micro-broth dilution method . Also measure serum IgG antibody titers were measured by ELISA Mycoplasma pneumonia.

Results: In this study, out of 135 samples 32, bacteria were isolated on PPLO agar. Using specific primers, 24 samples (17%) of Maycoplasma speciesiem- specific were positive for the presence of Mycoplasma pneumoniae. 15 Ciprofloxacin resistant isolates were evaluated. 35/5% of patients had positive antibody and 2/2% had borderline antibody and in 62/3% antibody titer was negative.

Conclusion: This study showed that PCR is a sensitive and reliable method for rapid detection of Mycoplasma pneumoniae bacteria in respiratory infectious samples. but the results of this method are different from the ELISA method. also, It seams that the Resistance to ciprofloxacin is Relative common among Mycoplasma pneumoniae.

Keywords:ciprofloxacin, Micro-broth dilution, Mycoplasma pneumoniae,

P174 - 855: ANTIMICROBIAL EFFECT OF PISTACIA ATLANTICA (BANEH) FOR CURING INFECTION OF CANDIDA ALBICANS IN MOUTH

Aminollah Yaghoubi[1], Omid javanmard-Ghoochan[2], Faeze Fakour-Kargaran[3], Ali Mokhtari[4], Bahare Ghouchannejad[5], Mahboobe Nakhai[6]

1. Department of Biology, Faculty of Science, Islamic Azad University, Mashhad,Iran
2. Department of Biology, Faculty of Science, Islamic Azad University, Mashhad,Iran
3. Department of Biology, Faculty of Science, Islamic Azad University, Mashhad,Iran
4. Department of Biology, Faculty of Science, Islamic Azad University, Mashhad,Iran
5. Department of Biology, Faculty of Science, Islamic Azad University, Mashhad,Iran
6. Department of Biology, Faculty of Science, Islamic Azad University, Mashhad,Iran

Background and Aim: Candida albicans is a fungi that coexists in the mouth, the digestive tract and the genital area, which accounts for nearly half of the normal flora of the oral area. This microorganism, in the event of a change in the natural environment of normal flora, which is mainly due to the use of antibiotics and chemotherapy, develops rapidly and progressively. By using the antimicrobial properties of plants, antibiotics can be reduced.Pistacia atlantica (that called Baneh) is a plant that has a lot of antimicrobial effects and can be a good alternative to antibiotics. Baneh is germinate in semi-arid and dry climatic regions of Iran.In this research, the local tree of the Sistan-Baluchestan region was used.

Methods: After culturing of candida, this microorganism was transferred to the culture medium Blood-agar or TSB-medium. The extract of the Baneh is divided into three parts of the extract of the skin, the subcutaneous tissue and the brain, each of them is separately prepared and then diluted with DMSO in the microtube and after 24 hours at 77 °F, they added to the Blanc-disks.

Results: Antibiogram test was performed on the MHA-medium. After placement of a blanc-disc containing a triple extract of Baneh, after 24 hour there was no aura on the MHA-medium, which indicates that all species of this plant do not have the same antimicrobial effect.

Conclusion: So we decided to investigate in further researches on another variety of Baneh.

Keywords: Candida albicans; Fungi; Antibiotic; Sistan and Baluchestan; Baneh

P175 - 856: IN VITRO ANTI-BACTERIAL AND ANTI-BIOFILM FORMATION ACTIVITIES OF FOUR MEDICINAL PLANTS OF LAMIACEAE FAMILY AGAINST KLEBSIELLA PNEUMONIAE

Fateme Yazdani[1], Parviz Owlia[2], Bahare Salman Mahini[3], Navid Saidi[4]

1. 1. Molecular Microbiology Research Center, Faculty of Medicine, Shahed University, Tehran, Iran
2. 1. Molecular Microbiology Research Center, Faculty of Medicine, Shahed University, Tehran, Iran
3. 1. Molecular Microbiology Research Center, Faculty of Medicine, Shahed University, Tehran, Iran
4. 1. Molecular Microbiology Research Center, Faculty of Medicine, Shahed University, Tehran, Iran

Background and Aim: Introduction: Klebsiella pneumoniae is among the most frequently recovered from nosocomial infections. This opportunistic pathogen has a high potential for antibiotic resistance and also it can generate a thick layer of biofilm. Antibiotic resistant strains were emerging and widely spread worldwide. Thus, it is necessary to combat drug resistant strains through the use of novel drugs. Some medicinal plants possess remarkable activity against bacterial agents. Among them, Lamiaceae family are in pharmaceutical interest. So, the aim of the study was to evaluate the in vitro antibacterial and anti-biofilm formation activities of Satureja rechingeri, S. khuzestanica, S. bachtiarica and S. mutica essential oils against K. pneumoniae.

Methods: Method: The Essential oils were obtained from Medicinal Herbs Research Center of Tehran.The tested strain was a standard strain of K. pneumoniae ATCC700603 For evaluation of the minimum inhibitory concentration (MIC) of essential oils, the microdilution method was used. Also standard method was used for evaluation of anti-biofilm activities of Sub-MIC value of essential oils.

Results: Result: According to our data, the MIC value of essential oils was 4096µg/ml. Sub-MIC value of essential oils were inhibited biofilm formation of K. pneumoniae. But S. khuzestanica had more activity and S. mutica had less activity than others.

Conclusion: Conclusion: According to our analysis S. khuzestanica had a good antibacterial and anti-biofilm formation against K. pneumoniae, but additional studies and researches is required to explore the exact mechanisms of the antibacterial action and functions of this phytocompound.

Keywords: Klebsiella pneumoniae, Lamiaceae, S. khuzestanica

P176 - 859: VIRULENCE FACTORS AND ANTIMICROBIAL RESISTANCE IN UROPATHOGENIC ESCHERICHIA COLI STRAINS ISOLATED FROM CYSTITIS AND PYELONEPHRITIS

Shiva Mirkalantari[1], Hosseinali ghazvini[2]

1. Microbiology Department, Faculty of Medicine, Iran University of Medical Science, Tehran, Iran
2. Biology Department, Islamic Azad University of Damghan branch, Damghan, Iran

Background and Aim: The aim of this study was to investigate the prevalence of virulence genes as well as patterns of antibiotic resistance and Extended-Spectrum β-Lactamase (ESBL) production in cystitis and pyelonephritis UPEC isolates.

Methods:200 UPEC isolates were collected from hospitalized patients with pyelonephritis (n=50) and cystitis (n=150) in Shafa Hospital, Iran between September 2014 and February 2015. Antimicrobial susceptibility and ESBL production was determined with confirmatory tests. Polymerase Chain Reaction (PCR) assay was performed in order to determine the prevalence of virulence genes including fimH, papC and hly in UPEC strains.

Results: Of a total 200 UPEC isolates, the highest and lowest resistance rates to antibiotics were for Cefalexine (74%) and Nitrofurantoine (9%), respectively. Of these isolates, 72 (36%) and 128 (64%) strains were ESBL-positive and ESBL-negative, respectively. Virulence genes studied in this research were found in 104 (52%) isolates. The frequency of virulence genes fimH, papC and hly were 64%, 38% and 12% respectively. The most commonly identified virulence gene in ESBL and non-ESBL producing strains was fimH 46 (23%) and 86 (43%), respectively. The hlyA gene was more prevalent among patients with pyelonephritis than cystitis.

Conclusion: The frequency of studied virulence genes was not significantly different between pyelonephritis and cystitis UPEC strains, but the prevalence rates of hlyA and papC genes were higher among UPEC strains isolated from inpatients compared to outpatients; hence, they could be considered as useful targets for prophylactic interventions.

Keywords: Urinary tract infections; Escherichia coli; Extended spectrum β-lactamase; Virulence genes; Pyelonephritis; Cystitis

P177 - 862: FREQUENCY OF BACTERIAL INFECTIONS AND ANTIBIOTIC RESISTANCE AMONG CLINICAL SPECIMENS IN SHAHID RAHIMI HOSPITAL, KHORRAMABAD

Gholamreza Goudarzi[1], Raziyeh Mosapour[2], Khatereh Anbari[3], Mohammadreza Nazer[4]

1. Department of Microbiology, Faculty of medicine, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Faculty of medicine, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Social Determinant of Health Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran
4. Department of Infectious Diseases, Faculty of medicine, Lorestan University of Medical Sciences, Khorramabad, Iran

Background and Aim: Determination of the pattern of microbial susceptibility in each hospital is needed to make clinicians successful in selecting precise treatment options. The present study was conducted to determine the relative frequency of the leading causes of bacterial infections and its antibiotic resistance profile in clinical samples of Shahid Rahimi Hospital, Khorramabad.

Methods: This retrospective cross-sectional study included all of the clinical specimens which had been sent to laboratory from different wards of Shahid Rahimi Hospital for cultivation in the second six months of 201. Antibacterial susceptibility testing was carried out by disk diffusion method according to the Clinical and Laboratory Standards Institute (CLSI) instructions. The data were collected by a questionnaire containing variables such as organism, sample type, antibiotic susceptibility and ward.

Results: Out of the 979 tested clinical samples, 322 (32.9%) were male and 657 (67.1%) were female. The mean age of the patients was 47.8 ± 4.42 years. According to the culture results, the most frequent isolates were Escherichia coli (38.4%), followed by Staphylococcus epidermidis (11.7%), Entrococcus faecalis (7.5%), Alcaligenes sp. (6.9%), and Staphylococcus aureus (8 / 4%). The most common bacterial agents isolated from urine, wound, stool, and broncho-alveolar lavage (BAL) cultures were E. coli, Staphylococcus aureus, E. coli, and Acinetobacter baumannii, respectively. The most prevalent resistance rates of the clinical samples were found for erythromycin (67.4%), ampicillin (65.2%), tetracycline (63.8%), clindamycin (63.7%), co-trimoxazole (63%), ceftriaxone (62.9%) and penicillin (62.3%).

Conclusion: Continuous surveillance of trends in resistance patterns of infectious agents in each region is necessary to provide guidelines and appropriate measures.

Keywords: Hospital infections, Antibiotics, Antibiotic resistance

P178 - 870: FREQUENCY AND SUSCEPTIBILITY PATTERN OF THE NON FERMENTATIVE GRAM NEGATIVE BACTERIA IN TWO EDUCATIONAL HOSPITALS IN SARI.

Zahra Norouzibazgir[1], Bahman mirzaei[2]

1. (Corresponding author (MSc Student of Microbiology, Faculty of Medicine, Mazandaran University of Medical Sciences, Student Research Committee
2. Assistant Professor of Microbiology, Faculty of Medicine, Mazandaran University of Medical

Background and Aim: Non-fermentative gram negative bacteria as an opportunistic strain because of multi drug resistant patterns has been reported as the main concern in hospital wards in worldwide. Screening of the non- fermentative bacteria and susceptibility pattern were the main objectives of this study.

Methods: In this study, following to the isolation and identification of non-fermentative gram negative bacteria (Pseudomonas aeroginosa and Acinetobacter baumanni) by using biochemical recipes from clinical specimen referred to the Zareh an BooAli hospitals in Sari, susceptibility pattern of mentioned bacteria was assessed according to the CLSI guidelines taking advantage of Disc Diffusion method.

Results: Out of 1792 clinical specimens, 412 (22.99%) were identified. Prevalence of the isolates was as follow: 166 (40.29%) P. aeroginosa and 238 (57.76%) A. baumanni. Susceptibility patterns was shown, 95.78% of P. aeroginosa isolates were resistant against cephalexin (97.8% in Boali, 93.3% in zare). This value for A. baumanni strains when subjected to the imipenem observed as 98.7% (100% in boali, 97.4% in Zare) resistant for imipenem too.

Conclusion: In conclusion because of high prevalence of carbapenem resistant strains in mentioned hospitals designing the new procedure for antibiotic trophy and designing new protocols to remove the mentioned bacterial agents are essential.

Keywords:P. aeroginosa, A. baumanni, clinical sample, susceptibility testing.

P179 - 872: URINARY TRACT INFECTION CAUSED BY EXTENDED-SPECTRUM BETA-LACTAMASE–PRODUCING BACTERIA AND INTEGRONS

hossein hosseini nave[1], Zahra Golestani[2]

1. Departmant of medical microbiology, Kerman of university, Iran
2. B.Sc. in Cellular & Molecular Biology, Cellular & Molecular Biology Department, Higher Education Center of Estahban

Background and Aim: Urinary tract infection (UTI) is one the most common type of bacterial infections worldwide. Generally, Escherichia coli is the most frequent Gram-negative bacteria causative of UTI (70-95%) and one of the most commonly isolated organisms in clinical microbiology laboratories. For the clinical treatment of Escherichia coli, drugs such as β-lactam and quinolone are commonly used but nowadays antimicrobial resistance (AMR) is a serious global public health issue worldwide. Lateral gene transfer (LGT) and Extended-spectrum β-lactamases (ESBLs) cause antimicrobial resistance (Class I Integrons are located on transposable plasmids are known to transfer AMR through an assortment of gene cassettes and Extended-spectrum β-lactamases (ESBLs) are also known to encode genes located on integrons and transposons.

Methods: Antimicrobial susceptibility testing was performed using the disk diffusion method Which is very common and low cost than other methods. To determine whether the E. coli isolates carried integrons, the conserved regions of the int genes were amplified with the degenerate primer pair hep35-hep36.

Results: Here, we characterized some of the most common loci which can play a key role in antimicrobial resistance such as SHV, TEM, CTX-M, VEB, PER, BEL-1…(The most common ESBLs) and aadA2-1, aacA4, aadA1, aadA2 (gene cassettes).

Conclusion: There is a need for further exploration of the urinary tract infection, and how the Extended-Spectrum Beta-Lactamase–Producing Bacteria and integrons cause antimicrobial resistance (mechanism of causing antimicrobial resistance)

Keywords: Urinary tract infection , ESBL, integron, AMR

P180 - 877: DETECTION OF B -LACTAMASE ACTIVITY IN VARIOUS CLINICAL COAGULASE NEGATIVE STAPHYLOCOCCI AND ITS CORRELATION WITH DRUG RESISTANCE

Mahsa Ebrahimi[1], Teena Dadgar[2], Hadi Koohsari[3]

1. Department of biology, Goran Branch, Islamic Azad University, Gorgan, Iran
2. Department of biology, Goran Branch, Islamic Azad University, Gorgan, Iran
3. Department of Microbiology, Azadshahr Branch, Islamic Azad University, Azadshahr, Golestan, Iran

Background and Aim: Staphylococcus epidermidis, the most important member in the coagulase- negative Staphylococci.Beta lactams are the most widely used antibiotics for treatment of staphylococcal infections and β lactamase enzymes are the greatest source of resistance to these antibiotics. The aim of this study was to assess the frequency of β-lactamase positive bacteria and antibiogram pattern in Coagulase Negative Staphylococci isolated from various clinical samples and healthy carriers.

Methods: Bacterial identification was performed with microbiological methods ,antibiogram pattern was performed with Kirby Bauer method to five beta-lactam antibiotics(Rosco.co) . β–lactamase production was performed with two methods Iodometric and Acidometric methods .

Results:A total of 170 isolates of Staphylococcus epidermidis isolated from various clinical samples and 80 nasal isolates of healthy carriers. Results obtained from the antibiogram showed that the isolates exhibited the high resistance to Penicillin and y. Iodometric and acidometric methods indicated presence of beta-lactamase in 75.55 and 59.99% of the S. epidermis isolates, respectively. 76.33 and 27.77% of the isolates resistant to Penicillin tested positive in the iodometric and acidometric tests, respectively . β–lactamase production was performed with Acidometric method and antibiogram pattern was performed with Kirby Bauer method .

Conclusion: Use of the antibiogram method on beta-lactam antibiotics showed that this method was only unsuitable for determining the treatment strategy for infection caused by these organisms, The iodometric test was a better method for determine β–lactamase production CONs strains , which can be useful in selecting the suitable antibiotic.

Keywords:β-lactamases, drug resistance, coagulase negative staphylococci

P181 - 880: ANTIBACTERIAL EFFECT OF AILANTHUS ALTISSIMA EXTRACT ON SOME BACTERIA IN SWIMMING POOLS IN COMPARISON WITH ANTIBIOTICAL EFFECT

Razieh Taghavizad[1], Sepideh Farazandeh[2], Shiva Khalil_moghaddam[3]

1. Associate professor of the Department of Biology, Yadegar -e- Imam Khomeini (RAH) Shahre-Rey Branch, Islamic Azad University, Tehran, Iran
2. M.Sc. Student of Microbiology, Yadegar -e- Imam Khomeini (RAH) Shahre-Rey Branch, Islamic Azad University, Tehran, Iran.
3. Associate professor of the Department of Biology, Yadegar -e- Imam Khomeini (RAH) Shahre-Rey Branch, Islamic Azad University, Tehran, Iran.

Background and Aim: Swimming pools are infected with bacteria such as Staphylococcus aureus, Pseudomonas aeruginosa, Proteus vulgaris that enter the pool through body open pores due to inaccuracy and non-compliance with sanitary regulations.

Methods: In this research, a fast-growing plant of Ailanthus altissima was used that is now considered as an ecological problem. The leaves were collected and powdered in the shade. The aqueous, hydroalcoholic and methanolic extracts were prepared by maceration and condensed by rotary. Four concentrations of 20, 30, 40 and 50 mg/ml of extracts were used. For the effectiveness of extracts, the agar well method and nutrient agar medium were used and each effect was replicated three times. Chloramphenicol antibiotic was used as a positive control.

Results: Halo diameter of lack of microbial growth was proportional to the concentration of extract. The results showed that methanolic A. altissima extract with a concentration of at least 30 mg/ml had the highest halo of lack of microbial growth for all three bacteria. The most effectiveness of methanolic extract of A. altissima was on P. vulgaris (with halo diameter of lack of microbial growth of 19-20 mm).

Conclusion: Although the lower concentration of antibiotics has the same result, the use of a plant extract with a higher concentration, will be uncomplicated, or of at least minimal complication.

Keywords: Proteus vulgaris, Pseudomonas aeruginosa, Staphylococcus aureus

Applied and Environmental Microbiology

P182 - 9: WHEAT GROWTH PROMOTING TRAITS OF FREE NITROGEN FIXING BACTERIA OBTAINED FROM A FIELD IN KERMAN DISTRICT

Najmeh Yazdan panah[1], Farokh Rokhbakhsh-Zamin[2]

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

Background and Aim: Application of biofertilizers, especially nitrogen fixing bacteria, is one of the most important plant nutrition strategies for sustainable agriculture. Accordingly, the use of biofertilizers containing plant growth-promoting rhizobacteria (PGR), has been strongly considered recently.

Methods: Nitrogen fixation tests, phosphate and zinc solubilization, indole acetic acid test, hydrogen cyanide production, ammonia production, nitrogen reduction, and resistance to salinity and temperature tolerance were checked about all isolated bacteria.

Results: In this research, after sampling of wheat plant, 17 bacteria were identified and named with the codes as IAUK3011-3027. They all could grow from 5 to 43oC, salt tolerance was observed from 0.5 to 5%, and growth was from 4 to 8% NaCl. Pot experiment was performed about three rhizobacteria as 3018, 3021 and 3023 with three replications. Based on the results, it was found that stem length, root length, fresh and dry weight of the stem, and fresh and dry weight of the roots were significantly affected by isolated rhizosphere bacteria positively.

Conclusion: The findings indicate that the selected rhizobacteria can be considered as putative alternatives for chemical fertilizers with potential to increase the growth of wheat or may be other plants.

Keywords: Wheat, Nitrogen fixation, Plant Growth promoting rhizobacteria, pot experiment

P183 - 17: PROBABLE LINK BETWEEN ISOLATION OF NOCARDIA SPP. FROM ENVIRONMENT AND HUMAN NOCARDIOSIS

Masoud Keikha[1]

1. M.Sc. student of Medical Microbiology and student Research Committee, Isfahan University of Medical Sciences, Isfahan, Iran

Background and Aim: Nocardia spp. are gram-positive, aerobic, filamentous, partial acid-fast bacteria which saprophytic lives in the environmental resources and can enter to human body through inhalation and cutaneous inclusion which cause several infection that proposed as nocardiosis in patients with underlying conditions and healthy people. The aim of this study was evaluation of relationship between isolation of Nocardia from environmental resources and clinically cases of nocardiosis in Iran.

Methods: We obtained several Iranian reports of environmental and clinical studies of Nocardia spp. since 2000-2018 years, except of case reports. Then we calculate probable association of environmental and clinical original article using Chi Square (p-value <0.05) in SPSS ver20 software; Moreover, the frequency of Nocardia spp. was also compared between this two groups.

Results: We found that this hypothesis (circulation of Nocardia spp. between environment and patients) was proved (p=0.001). Clinical studies was showed that N. asteroides was the most frequent nocardial species which isolated from Iranian patients followed by N. farcinica, N. cyriacigeorgica, N. nova complex and N. otitidiscaviarum; similar to clinical studies; in the Iranian environmental studies was showed that Nocardia asteroides complex followed by Nocardia cyriacigeorgica, N. asteroides, N. otitidiscaviarum, N. kroppenstedtii and N. pseudobasiliensis was most frequent Nocardia spp. which isolated from hospital and environmental samples.

Conclusion: The genus Nocardia are relatively slow growing bacteria (between 3-30 days) which can be survive and adapted with harsh environmental conditions. Based on our results this hypothesis was proved.

Keywords: Nocardia spp.; nocardiosis, Nocardia asteroides complex

P184 - 24: EFFECT OF SYMBIOSIS INTERACTION OF MYCORRHIZAE ARBUSCULAR ON MINERAL UPTAKE IN WHEAT (PISHTAZ CULTIVAR)

Farhad Rejali[1], Ashraf Esmaeilizadeh[2], Hadi Asadi Rahmani [3], Hossein Kari Dolatabad[4]

1. Member of scientific staff, Soil & Water Res Institute
2. Soil & Water Res Institute
3. Member of scientific staff, Soil & Water Res Institute
4. Soil & Water Res Institute

Background and Aim: Mycorrhizal fungi form a close symbiotic relationship with plant roots and help the roots to draw nutrients from the soil .

Methods: In order to study the effect of symbiosis interaction of Mycorrhizae Arbuscular on mineral uptake in wheat (Pishtaz cultivar), a greenhouse test with 11 treatments (2 species of Glomus mossea, 2 species of G. intraradices, 2 species of G. clarum, 1 species of G. etanicatum, 1 species of G. caledonium, 1 species of G. claroideum, 1 control treatment without mycorrhiza inoculation, a mix treatment with different species was done in greenhouse of biology department of Soil and Water Research Institute in completely randomized design.

Results: Result showed that root colonization percentage was significantly (1% probability) increased in harvest time of wheat and reached to 50% of root system. Maximum shoot dry weight was in T7 (G. claroideum) and it was 11.89 g per pot. Wheat root symbiosis with fungi, increased uptake of P, K, Zn and shoot dry weight (5% probability). Maximum P uptake was in T4 (G. intraradices) and it was 29.9 mg per pot. Maximum K uptakes were in T7 (G. claroideum) and T11 (mix treatment with different species), they were 175.95 and 173.41 mg per pot respectfully. Maximum Zn uptake was in T11 and it was 0.947 mg per pot.

Conclusion:T11 had better results in most of measured parameters comparing to other treatments.

Keywords: Mineral nutrition, Root colonization, Mycorrhiza, Shoot dry weight

P185 - 25: APPLICATION OF CARBOXIN THIRAM FUNGICIDE AND AZOSPIRILLUM GENUS ON MINERALS NUTRIENT UPTAKE OF WHEAT PLANT

Ashraf Esmaeilizadeh[1], Farhad Rejali [2], Hadi Asadi Rahmani [3], Hossein Kari Dolatabad[4]

1. Soil & Water Res Institute
2. Member of Scientific staff, Soil & Water Res Institute
3. Member of Scientific staff, Soil & Water Res Institute
4. Soil & Water Res Institute

Background and Aim: Azospirillum bacteria increase plant growth by establishing an associative relationships with the plant in various ways, the ability to nitrogen fixation and biosynthesis of plant growth hormones that stimulate plant growth.

Methods: Performing green house test, the effect of Carboxin thiram fungicide in 2 use (2 gr Carboxin thiram in 1000 gr wheat) and non-use levels on wheat plant (Chamran Cultivar) association relationship between five Azospirillum species (A. abrasilense, A.lipoferum, A. halopraeferens, A. irakense, A.sp), in two formulations (powder and liquied) separately, on uptake of K, P, Mn, Zn, Fe and Cu elements and also on Shoot Wet and Dry Weight and number of Tiller were studied.

Results: The results showed that the interaction of Azospirillum bacteria formulations and fungicide, uptake of P and Mn elements, and on shoot dry weight ($p < 0.01$) and shoot wet weight ($p < 0.05$), were significant, so that at the level of use Fungicide, the highest uptake percentage of Mn and P in liquid A. brasilense treatment (3.27%), and powder A. lipoferum treatment (19.51%), respectively were obtained. Also the highest percentage of Shoot Wet and Dry Weight were shown in powder A.lipoferum (24.44%) and powder A. halopraeferense (48.4%) respectively than non-inoculated control treatment

Conclusion: Therefore, a further study on the use of a mixture of these strains is recommended to increase the uptake capacity of all these elements and increase the yield of the test plant.

Keywords: Azosperillum, Carboxin thiram, Wheat

P186 - 32: COMPARING DETERMINISTIC AND PROBABILISTIC METHODS IN RISK ASSESSMENT OF INFECTIVE ENTEROVIRUSES FOR CONSUMPTION OF LETTUCE IRRIGATED WITH WASTEWATER EFFLUENT

Malihe Moazeni[1], Mahnaz Nikaeen[2], Mahdi Hadi[3], Sharareh Moghim[4]

1. Student Research Committee and Department of Environmental Health Engineering, School of Health, Isfahan University of Medical Sciences, Isfahan, Iran
2. Department of Environmental Health Engineering, School of Health, Isfahan University of Medical Sciences, Isfahan, Iran
3. Center for Water Quality Research (CWQR), Institute for Environmental Research (IER), Tehran University of Medical Sciences, Tehran, Iran
4. Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran

Background and Aim: Deterministic risk assessment estimates a single point of risk while probabilistic risk assessment evaluates a range of risk with use of probability distribution functions. Application of risk assessment when wastewater effluent is used in agricultural activities is important because of the potential transmission of infective enteroviruses to crop consumers. The aim of this study was to compare the deterministic and probabilistic risk methods in risk assessment of enteroviruses infections for consumption of wastewater effluent-irrigated lettuce.

Methods: In this study, 15 wastewater effluent samples were taken from a municipal wastewater treatment plant. The concentration of enteroviruses was measured with cell culture method. Risk assessment was studied with deterministic and probabilistic methods and results were compared with the WHO guideline of 10-3 infection risk per person per year (pppy).

Results: Enteroviruses were detected in 40% of samples. Deterministic risk assessment was estimated enteroviruses infection risk with a mean of 0.1424 pppy, although the probabilistic risk assessment was determined the mean enteroviruses infection risk of 0.0448 pppy. In the probabilistic method, based on the sensitivity analysis, Lettuce consumption and enteroviruses concentration in the effluent were important parameters in the increasing risk.

Conclusion: Results of this study showed that the estimated risk with deterministic method was higher than the probabilistic method. However, the estimated risk with two methods was more than of the WHO guideline therefore, control approaches should be used for the reduction of enterviruses infection risk for wastewater usage in agricultural activities.

Keywords: Deterministic risk assessment, Probabilistic risk assessment, Infection enterovirus, Effluent wastewater, Irrigation

P187 - 76: USING CONDUCTOMETRY SYSTEM TO FAST DETECTION OF STAPHYLOCOCCUS BACTERIA

Mehrdad Enami[1], mansour amin[2], pejman shabani[3], mansour yousefimanesh[4]

1. Department of Electrical and Computer, Mahshahr Branch, Islamic Azad University, Mahshahr, Iran
2. Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences , Ahvaz, Iran
3. Department of Electrical and Computer, Mahshahr Branch, Islamic Azad University, Mahshahr, Iran
4. clinical labratory, hospital of petroleum industrials, mahshahr, iran

Background and Aim: The popular methods for identifying pathogenic bacteria existing in human urine are mainly time consuming and require extensive costs. The most reliable method of identifying the infections of urinary tract is culturing urine samples that require minimum of 48 hours to diagnose pathogenic factors.

Methods: In order to do the conductometry and detect the infectious bacteria, laboratory work has been the suitable system to measure the electrical conductivity caused by the change of infectious bacteria concentration.

Results: This process requires max. of 1 hour, which is considered a fast and reliable method as compared to the popular commercial methods such as culturing the bacteria that usually takes 48 hours.

Conclusion: By conductometry, this study dealt with identifying pathogenic bacteria in the urine sample of an ill person. Thus, a suitable measuring device was made primarily to measure conductivity.

Keywords:bacteria; urine; conductivity

P188 - 95: IDENTIFICATION AND PURIFICATION OF MODERATE THERMOPHILIC BACTERIA ISOLATED FROM SARCHESHMEH COPPER MINE

REYHANEH TABREZI MOSAFA[1], REYHANEH TABRIZI MOSAFA[2], Ashraf Kariminik[3]

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: Bioleaching is one of the simplest and most effective technology for extraction of metals from low grade ore minerals and concentrates.

Methods: The purpose of this study was to isolate and identify moderate thermophilic bacteria in soil and water samples from Sarcheshmeh copper mine in summer and autumn of 2016 .After preparing and constructing a dedicated liquid culture medium of thermophilic bacteria and inoculation of water and soil samples growth of bacteria was compared in different synthetic media .The PCR method was used to identify bacteria using universal bacterial primers.. The PCR products was sequenced and then the phylogenic tree was drawn

Results: The results showed that thermophilic bacteria after incubation at 50˚C in their environment showed a good and rapid growth in solid media and the bacteria identified is Stenotrophomonas.

Conclusion: This bacterium can be used in the bioavailability of metal from waste water, which is important.

Keywords: Moderate thermophilic bacteria, Sarcheshmeh mine, PCR

P189 - 96: NEW CULTURE MEDIUM FOR MODERATE THERMOPHILIC BACTERIA ISOLATED FROM SARCHESHMEH COPPER MINE

REYHANEH TABREZI MOSAFA[1], REYHANEH TABRIZI MOSAFA[2], Ashraf Kariminik[3]

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: The application of microorganisms in the dissolution of sulfide methods has a long history. Bacteria especially moderate thermophilic organisms play an important role in the process of the addition of metal sulfides to accelerate the dissolution of valuable metal species from sulfide ores.

Methods: The purpose of this study was to find a suitable culture medium for the growth and isolation of the valuable bacteria capable in dissolution of sulfide methods. So, water and soil samples from the cold and hot season from Sarcheshmeh copper mine in 2016-2017 screened and several culture media for this purpose have been prepared. After incubation at 50˚C and isolation of bacteria, the PCR method was carried out

Results: The result showed DSM 665 culture media was determined as the golden media. In this experimental study, it was proved that the culture media that do not create high temperature in the stability of the environment and contain a lot of Fe2+, yeast extract and sodium thiosulfate are very suitable compound for the growth of these bacteria.

Conclusion: The DSM 665 culture media for isolation of moderate thermophilic bacteria from copper mines is recommended

Keywords:DSM 665 culture media,copper mine, Moderate thermophilic bacteria, PCR

P190 - 99: FEASIBILITY STUDY OF PREPARATION OF CO-AGGLUTINATION COMPLEX FOR RAPID DETECTION OF VIBRIO CHOLERA IN VACCINE RESEARCH AND LABORATORY BY USING STAPHYLOCOCCUS AUREUS PROTEIN A

Shahin Hadadian[1], Ardeshir Hesampour[2], pegah aryafar[3], Mina sepahi[4], Seyedeh marzieh Hosseini [5]

1. nano biotechnology department ,Pasteur institute of Iran
2. central Tehran branch,Islamic azad university,tehran,Iran
3. central Tehran branch,Islamic azad university,tehran,Iran
4. nano biotechnology department ,Pasteur institute of Iran
5. Islamic azad university,tehran,Iran

Background and Aim: Vibrio cholera is a gram-negative bacterial pathogen that causes lethal diarrheal disease cholera. From the first attempting to produce vaccine and in continue up to now a rapid method to recognition of vibrio were required. In this study, we try to present a rapid test to detection of vibrio cholera in laboratory and vibrio vaccine process and in process quality control in biotechnology or food manufactories .

Methods: New Zealand White rabbits were first immunized with Vibrio cholera Ogawa and Inaba whole cell. Mono-specific gamma globulin was obtained, purified and concentrated by ammonium sulfate precipitation method. These antibodies were fixed on Staphylococcus aureus Cowan 1 NCTC-8325 whole cell. Rectal swab sample were inoculated into an enriched Alkaline Peptone Water medium "pH 8.6" incubated for 5 h at 37 °C. One drop of each sample was mixed to with a drop of vibrio cholerae mono-specific co-agglutination reagent and results read in 2-3 minutes When 35 specimens were tested, the sensitivity and specificity compared with standard culture methods, were 93.33 % and 100%, respectively.

Results:co-agglutination test is a simple, rapid, and reliable method to detect Vibrio cholerae in fecal specimens would assist in the management of cases of severe diarrhea, especially since most such cases occur in areas with minimal laboratory facilities.

Conclusion:the results show that the co-agglutination method is sensitive, specific, easy, fast and inexpensive method for diagnosis of vibrio cholera, which is available with low-availability laboratory equipment. It is also an appropriate method to control and diagnose cholera.

Keywords: Complex, Protein A, Staphylococcus aurous, vibrio cholera, Co agglutination

P191 - 112: GENETIC ANALYSIS OF NONRIBOSOMAL PEPTIDE SYNTHESIS GENES (NRPSS) IN THE FRESH WATER CYANOBACTERIAL OF THE LAVASAN LAKE

Ghazale Soltani[1], Bahareh Nowruzi[2], Abbas Akhavan Sepahi[3]

1. Department of Biology, School of Basic Science, Science and Research Branch, Islamic Azad University, Tehran, Iran.
2. Department of Biology, School of Basic Science, Science and Research Branch, Islamic Azad University, Tehran, Iran.
3. ٢Department of Microbiology, Islamic Azad University, Tehran North Branch, Tehran, Iran

Background and Aim: Among the photosynthetic microorganisms, cyanobacteria are regarded as good candidates for drug discovery, with applications in agriculture, industry and especially, in pharmaceuticals. To date, the majority of bioactive metabolites isolated from cyanobacteria have either been polyketides, non-ribosomal peptides, or a hybrid of the two.

Methods: In this study, efforts have been undertaken to investigate of ten cultured fresh water cyanobacteria strains of the Lavasan Lake. These strains were identified based on the sequence of ١٦SrRNA gene and found that these strains belong to the Nostocaceae, Scytonemataceae and Rivulariaceae. The antibiogram bioasyas were screened in phototrophic condition using a paper disc method. The results showed that maximum antifungal activity was seen in Nostoc sp. Ft salt and Scytonema sp. F١٨ against Aspergillus niger and Fusarium sp. Nostoc sp. F٣ and Nostoc sp. F٤ were the only strains that showed good activity against Bacillus cereus. Lastly, we conduct a NRPS PCR, using molecular techniques, in order to sequence and phylogenetic analysis the genes responsible for the production of secondary metabolites from ten cyanobacterial strains. Moreover, Adenylation domain substrate specificity predictions for NRPS enzymes, the signature sequence and the name of the compound, were made using NRPSpreditor٢.

Results: Sequence analysis indicates the enzymes encoded by these genes may be responsible for the production of different secondary metabolites, such as antibiotics. The sequences of the genes presented in this study have been deposited in GenBank.

Conclusion: The presented results prove that fresh water cyanobacterial of Iran are a promising source to yield chemical and pharmaceutical interesting compounds.

Keywords: Peptide synthetase genes (NRPSs), Fresh water cyanobacterial, Genetic analysis.

P192 - 127: MOLECULAR DETECTION OF HUMAN GROUP A ROTAVIRUSES IN URBAN AND HOSPITAL SEWAGE SYSTEMS AND RIVER WATER SAMPLES IN ALBORZ PROVINCE

Zahra Torfeh[1], Naser Harzandi[2], Mostafa Ghaderi[3]

1. M.Sc. Student of Microbiology, Department of Microbiology, Faculty of Sciences, Karaj Branch, Islamic Azad University, Karaj, Iran
2. Assistant of Microbiology, Department of Microbiology, Faculty of Sciences, Karaj Branch, Islamic Azad University, Karaj, Iran
3. Assistant of Virology, Department of Microbiology, Faculty of Sciences, Karaj Branch, Islamic Azad University, Karaj, Iran

Background and Aim: Waterborne pathogens and related diseases are a major public health concern worldwide. Human group A rotaviruses are the most important cause of acute gastroenteritis in infants and among children <5 years of age worldwide. The aim of this study was molecular detection of human group A rotaviruses in urban and hospital sewage systems and river water samples in Alborz province.

Methods: This descriptive cross-sectional study was carried out on 76 samples collected from 4 sewage treatment systems, hospital sewage, Karaj and Baraghan rivers in Alborz province. All samples were concentrated using pellet method. Then human group A rotaviruses were identified with RT-PCR method. Primers Beg9 and End9 were used for amplifying of 1062 bp VP7 specific segment of group A rotaviruses.

Results: In total, rotaviruses were identified in 6 samples (7.89%). The frequency of rotavirus detection in summer, autumn and winter was 16.66%, 50% and 33.33%, respectively. No statistically significant difference was found between presence of rotavirus distribution and monthly distribution (P=0.886).

Conclusion: Our research on environmental dispersion of rotaviruses in sewage and river samples indicates the presence of this intestinal virus in these water sources. Since pathogens in water are still a major cause of severe illness and mortality, it is necessary to constantly monitor sewage treatment systems. Therefore finding new methods of sewage treatment to remove enteric viruses such as rotavirus is necessary.

Keywords: Human group A rotaviruses, Acute gastroenteritis, Urban sewage, RT-PCR

P193 - 129: STUDY OF ANTIBACTERIAL ACTIVITY MEDICINAL PLANTS IN THE TREATMENT OF HELICOBACTER PYLORI INFECTIONS

Nahid Dezvaree[1]

1. Ms.c Petrology

Background and Aim: Helicobacter pylori is one of the most common worldwide human infections. It is estimated over half of the Earth's population are infected with this bacterium. This pathogen is a causative agent for many gastroduodenal diseases, peptic ulcers and gastric cancer. In recent years, emerging resistant to antibiotics limits their use in the treatment of this infection. However, eradication is not always successful and the use of these antibiotics occasionally causes emergence of resistant clones and various harmful adverse effects. Thus, development of new effective therapeutic agents could represent a significant advance in treatment of these infections.

Methods: This study is a systematic review based on internal databases including SID, Iranmeddex, Scopus, PubMed, as well as articles and reviewed the letters that have met the inclusion criteria, were examined.

Results: As a result, many natural products have been studied to find new effective alternative drugs against difficult to treat H. pylori giving special attention to plants used traditionally for a long time against gastrointestinal disorders. This review presents the potential of many medicinal plants to serve as promising sources for new and alternative anti-H. pylori agents.

Conclusion: As reviewed in this paper, it is obviously, there are numerous traditional plants potentially valuable sources of novel anti-H.pylori agents. However, most reports are on crud extracts, which gives general evaluation on the potency of these plants as anti-H. pylori agents but do not provide enough data on the complexity of these natural products to serve as drugs as well as the in vivo clinical studies.

Keywords: Medicinal plants, Anti-bacterial activity, Helicobacter pylori.

P194 - 138: SUBMERGED FERMENTATION OF AURICULARIA AURICULA FOR BIOMASS STIMATION

Arghavan Rahimian[1], Sanaz Jafari[2], Ali Sheykhinejad[3]

1. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran ,Iran, Ar.rahimian66@yahoo.com
2. Department of Biotechnology, Iranian Research Organization for Science & Technology (IROST), Tehran, Iran.
3. Department of Biotechnology, Iranian Research Organization for Science & Technology (IROST), Tehran, Iran.

Background and Aim: Background: Auricularia is a genus of jelly fungi in the family Auriculariaceae. Most Auricularia species are edible and are grown commercially. Auricularia auricula, the Jelly Ear Fungus, is mainly seen in winter and spring. It grows mainly on dead elder trees and on fallen branches, but occasionally you may also find it growing on other kinds of hardwood. Auricularia species are widely distributed in Kerala's Western Ghats, and recently, Auricularia auricula-judae, A. polytricha, and A. mesenterica have been reported.

Methods: Methods: In this research, submerged fermentation media containing whey and potato extract was used.

Results: Results: In this study, results shows that the value of production of Auricularia auricula biomass in submerged fermentation medium containing 5% potato extract is higher than whey media

Conclusion: Conclution: Media containing high carbohydrate source, nitrogen source are required for the growth of fungi, because potato extract media in comparison with whey media has higher C/N ratio.

Keywords: Auricularia,submerged fermentation media,biomass

P195 - 139: BIOMASS PRODUCTION OF AURICULARIA AURICULA IN SOLID SUBSTRATE

Arghavan Rahimian[1], Mahnaz Mazaheri Assadi[2], Mehran Kianirad[3]

1. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran ,Iran, Ar.rahimian66@yahoo.com
2. Professor of Industrial and environmental biotechnology, Iranian Research Organization for Science & Technology (IROST), Tehran, Iran,
3. Assistant Professor of biotechnology department, Iranian Research Organization for Science & Technology (IROST), Tehran, Iran,

Background and Aim: Background: Auricularia auricula, known as the Jew's ear, wood ear, jelly ear or by a number of other common names, is a species of edible Auriculariales fungus found worldwide. The fruiting body is distinguished by its noticeably ear-like shape and brown colouration; it grows upon wood, especially elder. The fungus can be found throughout the year in temperate regions worldwide, where it grows upon both dead and living wood.

Methods: Methods: This process consists of depositing a solid culture substrate, such as rice or wheat bran,corn cube, wheat straw , saw dust and tea waste.

Results: Results: According to the results, solid culture bed containing 90 percent of sawdust and 10 percent rice bran has the highest amount of biomass production in the Auricularia fungus.

Conclusion: Conclution: All the results presented here suggest that Auricularia auricula can grow in saw dust solid media better than the other media because this fungus has a lignin peroxidase, so it can degradate the lignin in this solid state.

Keywords: Auricularia,solid state,biomass

P196 - 154: ISOLATION OF BLACK YEASTS FROM OIL FIELDS OF AHVAZ; POTENTIAL BIOREMEDIATION CANDIDATES

Somayeh Dolatabadi[1], Ahmad Allahabadi[2], Marziyeh Zeydabadi[3], Azar Sharifian[4]

1. Faculty of Engineering, Sabzevar University of New Technologies, Sabzevar, Iran
2. Faculty of Health, Sabzevar University of Medical Sciences, Sabzevar, Iran
3. Faculty of Health, Sabzevar University of Medical Sciences, Sabzevar, Iran
4. Faculty of Health, Sabzevar University of Medical Sciences, Sabzevar, Iran

Background and Aim: Black yeasts are highly resistant against environmental stresses such as drought, and extreme temperature. They belong to different fungal kingdoms like: Chaetothyriales, and Eurotiales. They are ecologically diverse and can be seen in oil polluted lands. Black yeasts isolated from polluted lands show potential for remediation of toxic compounds, present in the same field and could be applied in bioremediation studies.

Methods: Soil samples from oil fields of Ahvaz were collected. From each soil sample, ten gram was diluted in PBS buffer and shaked for half an hour. From the upper layer, 0.5 ml was transferred to PDA media containing 0.05 mg/l chloramphenicol and mycosel agar. Plates were incubated at 27° C for two weeks and monitored routinely for presence of any black colony. Isolates were identified by morphological characters. Molecular method using ITS sequencing was applied and strains were completely identified at species level.

Results: From 25 soil samples, 15 strains were isolated and purified. These strains were identified by molecular methods. The ITS sequences were blasted in https://www.ncbi.nlm.nih.gov/ and were identified as Exophiala xenobiotica.

Conclusion: Exophiala xenobiotica was named after its properties for degradation of xenobiotics. These strains were isolated from oil fields of Ahvaz and identified as E. xenobiotica. The isolates as achieved from contaminated lands, show promises for being able to grow in those lands and to be applied as a new bioremediation strategy. Black yeast fungi have many advantages over bacteria which have been used in soil bioremediations as they can grow in more harsh environments.

Keywords: Black yeast, soil remediation, Exophiala xenobiotica, ITS sequencing

P197 - 182: EFFECT OF ULTRASOUND ON CYANOTOXIN DESTRUCTION

Nakisa Nikoee[1], Nima Bahador[2]

1. Dept. Microbiology, College of Science, Agriculture and Modern Technology, Shiraz Branch, Shiraz, Iran
2. Dept. Microbiology, College of Science, Agriculture and Modern Technology, Shiraz Branch, Shiraz, Iran

Background and Aim: Cyanobacteria are photosynthetic organisms with a very simple structure. Although, most of the cyanobacterial groups have capability to produce toxins and the toxins has destructive effect on living organisms, therefore, the present study try to screen cyanobacteria with ability to produce toxins and then evaluate effect of ultrasound on the same.

Methods:30 water samples have been collected Kor River. Then serially diluted and cultivated on BG 11 Agar under light and dark conditions .The colonies were analyzed using microscopic and molecular identification by specific primers for the toxins. Then ultrasonic transducer operated at 23-48 kHz equipped with a 40 mL reaction vessel which is fitted with a Teflon window. The reaction vessel was centered at a distance of 4.50 cm . Since modest heating is observed during ultrasonic irradiation, the entire assembly was submerged in an ice bath to maintain a constant temperature of 4 °C throughout the reaction process. Then the toxins destruction was monitored by HPLC with photodiode array detector

Results: The results indicated that out of 4 isolates 3 were produced the microcystin and 2 were produced cylindrospermopsin. The isolates were belong to: Geminocystis ،Cyanobacterium sp. KSU-AQIQ-3 ، Synechocystis aquatilis and Cyanobacterium stanieri The degradation of the extracted toxins was confirmed by HPLC

Conclusion: Although cyanotoxins are important for human health the ultrasound could be effective for destruction of the toxins

Keywords: Cyanobacteria, Kor River, Ultrasound

P198 - 202: DECOLORIZATION OF REMAZOL RED B BY HALOMONAS SP. PTCC1417 ISOLATED FROM URMIA LAKE: OPTIMIZATION BY TAGUCHI METHODOLOGY

Nasrin Froedin[1], Mehran Kookalani Khaletabad[2], Sosan Froedin[3]

1. nasrinfuroedin@yahoo.com
2. mmehrann@gmail.com
3. nasrinfuroedin@gmail.com

Background and Aim: Azo dyes account as the most dyes of all textile dyestuffs produced, and are the most common dye in textile industry. Azo dyes-containing effluents from these industries have caused serious environment pollution.Compared with chemical/physical methods, biological processes have received more interest.

Methods: In this study, we investigated effects of four factors including temperature, pH, dye concentration, salt concentration on decolorization of Remazol Red B by Halomonas sp. PTCC1714. The optimization of dye decolorization in 16 experiments with different conditions was statistically analyzed using Taguchi design in Qualitek-4 software.

Results: The results showed that Halomonas sp. PTCC1714 was able to decolorize Remazol Red B in varying salt at 5–20% (w/v), pH at 5-9, dye concentration at 100-5000 ppm and temperature 31-40 ˚C. The optimum factor levels were a dye concentration of 100 ppm, salt concentation 5 % (w/v) and pH 9 and temperature 31˚C. The predicted value obtained for dye decolorization under these conditions was about 94%.

Conclusion: We can conclude that Halomonas sp. PTCC1714 has a high potential for decolorization of Remazol Red B from textile wastewater in different conditions.

Keywords: Halomonas, Azo dyes, Rimazol Red B, Decolorizatin

P199 - 208: ISOLATION MOLCULAR AND IDENIFICATION OF MYCOBACTERIUM PORCINUM AND MYCOBACTERIUM CELERIFLAVUM FROM MARKAZI PROVINCE ENVIRONMENTAL RESOURCES AND ANALYSIS OF THEIR POLYCYCLIC AROMATIC HYDROCARBONS' BIODEGRADATION ACTIVITY

Davoud Azadi[1], zagra Rezaei[2], Thereh Motalebirad[3]

1. Department of Laboratory Sciences and Anesthesia, Khomein University of Medical Sciences, Khomein, Iran
2. Department of Laboratory Sciences and Anesthesia, Khomein University of Medical Sciences, Khomein, Iran
3. Department of Laboratory Sciences and Anesthesia, Khomein University of Medical Sciences, Khomein, Iran

Background and Aim: Polycyclic aromatic hydrocarbons are one of the prevalent oil pollutant. Nowadays these carbohydrates due to their Toxicity, mutagenesis, carcinogenicity, and also environmental stability caused by hydrophobia character and low solubility are considered as one of the preferences of environmental protection agancy. Therefore, clearance of the regions polluted with these compounds are of significance. Biodegradation of these compounds is a safe and affordable method of environmental clearance. In this research, we described the molcular isolation and identification of the mycobacteruim's strains abling to degrade polycyclic aromatic hydrocarbons in vitro.

Methods:a total of 30 environmental samples colected from the contaminated sites of Markazi province have been analysed by using the combined microbiologic and molcular methods such as PCR and Genetic makers sequencing of 16SrRNA, hsp65 and rpoB. The growth rate in presence of pollutants, chromatography and turbidity have been applied In order to determine the biodegradation activities of the isolates.

Results:6 isolates of mycobacteruim (20%) have been isolated from 30 samples which 4 and 2 isolates appertained to 2 species of mycobacteruim porsinum and mycobacteruim selifravom respectively. The strains of mycobacteruim porsinum and seflivarom could degrade 50% and 70% of PAH in concentration of 1 mg PAH, successfully.

Conclusion: The results achived in this research illustrated that the isolated strains of mycobacteruim porsinum and mycobacteruim selriflavom have a high ability to biodegrade the polycyclic aromatic hydrocarbins. Hence, additional investigations are recomended for isolation and applicationally use of the bacteria's strains for biological deletion of polycyclis aromatic hydrocarbons from contaminated environments.

Keywords: Mycobacterium, Bioremediation, 16S rRNA sequencing, Phylogeny

P200 - 227: BIODEGRADATION OF PHENOL USING STAPHYLOCOCCUS SP. ISOLATED FROM HOUSEPLANT POTTING SOIL

Mohsen Shahriari moghadam[1]

1. Department of Environmental Sciences, Faculty of Natural Resources, University of Zabol, Zabol, Iran

Background and Aim: Environmental pollution is one of the major today's challenges. Phenolic compounds are environmental pollutants and found in the effluent of various industrial operations. The objective of this study was to isolate and characterize phenol degrading bacteria from houseplant potting soil.

Methods: About 5g of soil was transferred to a flask containing mineral salts medium with 1000 mg/l phenol as the sole carbon and energy source and incubated (120 rpm and 30˚C) on an orbital shaker. After detecting bacterial growth, 1 ml of medium was transferred to a new flask and this process was repeated three times. At the end of enrichment, bacterial strains were isolated by serial dilution on nutrient agar plates and purified strains were identified using 16S rDNA gene sequence analysis. Colorimetric method was used to measure phenol concentration in mediums.

Results: Among the isolated strains a bacterium strain showed a higher phenol degradation ability and according to molecular analysis showed 99% similarity to Staphylococcus sp. Isolated strain degraded about 46% of medium phenol after 3days.

Conclusion: In a nutshell, we isolated and characterized Staphylococcus sp. from houseplant potting soil. The results revealed the significant ability of this strain to utilize phenol as the only carbon and energy sources. Obviously, this strain may be used in bioremediation projects.

Keywords: Staphylococcus sp., phenol, bioremediation, pollution

P201 - 246: IS THE AIR SAMPLES APPROPRIATE TO ISOLATE THE DENITRIFYING BACTERIA?

Taranom Yarandpour[1], Parisa Mohammadi[2], Ezat Asgarani[3]

1. MSc Student, Department of Microbiology, Faculty of Biological Sciences, Alzahra University, I.R.Iran
2. Associate Professor, Department of Microbiology, Faculty of Biological Sciences, Alzahra University, I.R.Iran
3. Associate Professor, Department of Biotechnology, Faculty of Biological Sciences, Alzahra University, I.R.Iran

Background and Aim: In recent years, air pollution has emerged as a problem in mega cities of the developing countries. Because of this reason, the application of the biological procedures is significant due to its cost-effectiveness, low side contamination and high efficiencies. One of the most harmful air pollutants is nitrogen oxides. Nitrogen oxides also impose environmental impacts such as the ozone production, global warming and acid precipitation. In addition, it reveals harmful effects on human health.The purpose of this experiment is to find the denitrifying bacteria from air samples that can convert these oxides into dinitrogen (N2).

Methods: For this reason, after air sampling according to impingment method, serial dilution prepared in screening medium (SM), and the sample was cultured onto the bromothymol blue (BTB) medium to identify the colony of the denitrifying bacteria. Then nitrate broth was used to ensure that N2 gas was produced.

Results: The results showed that none of isolates produced nitrogen gas.

Conclusion: Consequently, the air was not proper samples to isolate the denitrifiers. It should be carried out more investigation on soil or sewage samples to find these kind of bacteria.

Keywords:air pollution, denitrifying bacteria, nitrogen oxides

P202 - 276: OPTIMIZATION OF TRICHODERMA CULTURE MEDIUM USING DIFFERENT CARBON SOURCES TO INCREASE XYLANASE ENZYME PRODUCTION.

Neda Afzali[1], Bahareh Rahimian Zarif [2], Nahid Hagh Nazari [3]

1. Department of biology , sanandaj branch , Islamic azad University SANANDAJ , Iran.P.O.Box:618
2. Department of biology , sanandaj branch , Islamic azad University SANANDAJ , Iran.P.O.Box:618
3. Department of biology , sanandaj branch , Islamic azad University SANANDAJ , Iran.P.O.Box:618

Background and Aim: Trichoderma is one of ascomycete mesophile fungi, which exist in all soils and are part of the majority of soil's cultivable fungi. Xylanases are part of hydrolases and possess single chains of glycoproteins whose weighs range from 6 to 8 KD. In this study, we try to. optimization of Trichoderma culture medium using different carbon sources to increase Xylanase enzyme production.

Methods: We provided the standard Trichoderma reesei strain from the microbe collection of Iranian Research Organization for Science and Technology.Then,we measured the activity of its Xylanase enzyme using the standard method of DNSA. Next, for the sake of optimization, different parameters of the medium like carbon, examined.

Results: The parental strain of Trichoderma reesei is featured by the xylanase enzyme activity of 2/59 U. the strain at the present of wheat cabran, respectively as the carbon, and at 7/5 pH and with the average of 35 °C had the most amount of production.

Conclusion: Xylanase enzyme is one of the most important enzymes used in diverse industries but unfortunately is not produced in our country. As it can be seen from the results of this study, we can optimize the conditions for cultivating different organisms so as to increase the industrial production of various enzymes which are not produced in Iran. We hope, thereby, to make such a production easier at the industrial scale.

Keywords: Trichoderma reesei, Xylanase, medium optimization Different sources of carbon

P203 - 281: PERFORMANCE EVALUATION OF BIOFILTER IN REMOVING AMMONIA AND HYDROGEN SULFIDE GASES AT LABORATORY SCALE AS A MODEL IN INDUSTRIAL CATTEL

Sahar Karami rubati[1]

1. Islamic Azad University of Ahar

Background and Aim: Compound such as Ammonia and Hydrogen Sulfide are pollutant gases.Large amounts of NH3 and H2S are generated and released from industrial processes, such as metallurgy, food preparation, livestock farming, leather manufacturing, waste-water treatment and treatment of fuels.There are different methods to remove these troublesome compounds.These methods are often expensive and produce other pollutant as well.That is why ammonia and hydrogen sulfide removal in industrial are restricted.These days using biofilters has been taken into consideration by expert because of its advantages such as low cost, low energy consumption, no chemical usage and no production of contaminated by products.

Methods: This research was done in 2013 at Environmental lab of Iranian Ghaza Azmaa. Biofilter cylinders are30 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 arranges .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 .

Results: Among the four cylinders ,the ones that were filled with Peat soil, Leaves soil and straw recorded 100% elimination in comparison with others.

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- Hydrogen Sulfide- Ammonia

P204 - 283: INVESTIGATION THE ELIMINATION OF MICROBIAL CONTAMINATION IN GLASS CLEANER FORMULATIONS

Mohammdfazel Abedini[1], fatemeh Mashhadi[2], maryam mirzazadeh[3]

1. Paknam company
2. Paknam company
3. Paknam company

Background and Aim: In this study, the effect of different type of alcohol in elimination of microbial contamination in glass cleaner has been investigated. Different formulations have been chosen base on specification table in ISIRI 3305.

Methods: Glass cleaner formulations with the different percentage (w/w) of ethanol and isopropanol with total 10% (w/w) prepared, and with blend of microorganism Escherichia coli , Pseudomonas aeruginosa , Candida albicans contaminated. After that samples were studied with test method base on ISIRI 11804 and ISIRI 5875.

Results: Results show that isopropanol in glass cleaner with the Lowers percentage have the highest effect in elimination of microbial contamination. Also blend of ethanol and isopropanol in glass cleaner formula are more effective than ethanolic glass cleaner in elimination of microbial contamination. Ethanolic formulations with lower than 10 percent ethanol need preservative for elimination of microbial contamination

Conclusion: As regards in reversion of ISIRI 3305, the solvent concentration was reduced from 15% to 9% . This study was demonstrated, it is not necessary using of preservative for controlling the microbial contamination at 15% dosage of ethanol. Because of using glass cleaner for cleaning accessible glassy surface, it is necessary to produce this kind of detergent without any contamination. Base on this study microbial check in the standard test method of this product is suggesting.

Keywords:elimination ,microbial contamination ,microorganism, Escherichia coli , Pseudomonas aeruginosa , Candida albicans

P205 - 320: ISOLATION OF THERMOPHILIC SULFOBACILLUS THERMOSULFIDOOXIDANS FROM SARCHESHMEH COPPER MINE IN KERMAN, IRAN

Fatemeh Hosseinzadeh Parizi[1], Farokh Rokhbakhsh Zamin[2], Zahra Manafi [3]

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
3. MSc Biohydrometalorgy unit R & D department of Sarcheshmeh Copper mine, Kerman, Iran

Background and Aim: Thermophilic bacteria produce important industrial enzymes but there is not sufficient information about this group. Accordingly, in this research, modified heat stable solid and liquid media were used for isolation and purification of thermophilic bacteria from copper mine.

Methods: Thermophilic bacteria were isolated from Sarcheshmeh Copper mine in Kerman, Iran. Different identification tests were performed as biochemical and molecular methods. The 16S rDNA sequence of the isolate was compared with databases in GenBank using the program BLASTN by selecting the optimization parameter to highly similar sequences (Megablast). The evolutionary relationships of this isolate with standard ones were studied by phylogenetic tree.

Results: Isolated bacterium was non-motile Gram positive bacillus. It was observed individually, in pairs or short chains in microscopic examination. Grown colonies were yellow turning to reddish brown on modified solid medium containing Fe2+. It was thermophilic with a growth temperature up to 60oC and acidophilic with pH range of 1.5-5.5. Phylogenetic analysis based on 16S rRNA gene sequences alignment revealed the highest similarity between isolated strain with other standard species of the genus Sulfobacillus.

Conclusion: Modified Solid and liquid media (Data not shown) were used. Out of the total isolates obtained from the Sarcheshme copper mine, one isolate was found to sustain temprature up to 60oC. The ability of the bacterium to grow in this state revealed to be thermophile. This mixotroph and chemothroph bacterium was identified by molecular test as Sulfobacillus thermosulfidooxidans. This strain like other thermophilic bacteria may have the ability to be used for bioleaching and production of thermostable enzymes.

Keywords: Thermophilic bacteria, Sulfobacillus thermosulfidooxidans, Sarcheshmeh Copper mine, 16SrRNA, Phylogenetic tree

P206 - 331: ASSESSMENT THE PHYSICOCHEMICAL PROPERTIES, STRUCTURE AND FUNCTION OF FUNGAL STRAINS LIGNIN PEROXIDASE PHANEROCHAETE CHRYSOSPORIUM

Nasrin Sanayipoor[1], Aliakbar Haddad-Mashadieizeh[2], Samaneh Dolatabadi[3]

1. Department of Biology, Islamic Azad University, KhorasanRazavi, Neyshabur, Iran
2. Department of Cellular and Molecular Biology, Faculty of Science and Institute of Biotechnology, Ferdowsi University of Mashhad, Mashhad, Iran
3. Department of Biology, Islamic Azad University, KhorasanRazavi, Neyshabur, Iran

Background and Aim: Phanerochaete chrysosporium is a fungal strain with high metabolism competence aromatic hydrocarbons based on synthesis and secretion of lignolitic enzymes including lignin proxidase . Lignin proxidase as glycoprotein enzyme with high redox potential and resistance in low pH. Therefore, identification the functional and structural properties of this enzyme and its isoforms in different strains is a crucial step in bioremediation of environmental pollutions or development new anti-cancer food drugs.

Methods: Selective protein sequence with access number AF140062 was obtained from NCBI database and physicochemical properties of them were. The relationship among fungal and non-fungal strains were determined via MAGE.6 program through PAM250- BLOSUM62 matrices. Structural modeling of selected enzyme with homology method using SWISSMODEL and Modeler program, active site was determined after quality evaluation was performed RAMPAGE and MOE tests. thermal stability of enzyme was performed with a molecular dynamics simulation in industrial temperature using GROMACS test. Finally, functional capability of enzyme was determined by molecular docking test ratio aromatic hydrocarbons obtained from PUBCHEM database.

Results: The results of this study led to the achievement of the structure of enzymes and homolog while it was good quality, binding affinity and different functionality they showed against aromatic hydrocarbons . So that, on average between 11 hydrocarbon selective binding affinity with Dibenzo (a, i) pyrene highest and the lowest was Anthracene.

Conclusion: However, the ability favorable physico-chemical and thermal stability of the mother enzyme and structural optimization, synthesis and subsequent tests were on the agenda.

Keywords: Bioremediation, food drugs, Phanerochaete chrysosporium, aromatic hydrocarbons, lignin proxidase.

P207 - 338: ISOLATION AND CHARACTERIZATION OF POTASSIUM SOLUBILIZING BACTERIA FROM RHIZOSPHERE SOIL AND DIFFERENT PARTS OF SAFFRON

Mansoor Zamanifar[1], mosa karimi[2]

1. author
2. presenter

Background and Aim:potassium is an essential nutrient to promot growth and production crops by plants. extensive use of potassium chemical fertilizer to fix the plants need to it caused pollution of bio environmental and decrease of human's health some soil bacteria, can promote growth plants by supply the required elements of them therefore use of these bacteria as bio fertilizer can reduce the high usage of chemical fertilizer

Methods:different sample of Rhizosphere soil and complete saffron plant collected from several agriculture lands. The bacteria Isolated by dilution method and selected beneficial bacteria by forming big halo zone on aleksandrov agar plate Biochemical tests Performed to characterization of selected bacteria. In vivo test best bacteria on saffron plants did to measurement of its effect on plant growth and yield of them

Results:one hundred and ten bacteria isolated from rhizosphere and different part of saffron plant .selected fourteen bacteria that forming big halo zone on alecksandrov plate agar which indicates the high power of the bacteria in the solution of potassium. pH and temperature test showed that six bacteria had the best growth sustainability in abnormal conditions. In compared with plants without any fertilizer, saffron plant inoculated with selected bacteria had be increasing in dry weight of stigma, petal and number of corm.

Conclusion: Isolated bacteria with Potassium solubilising power can be alternative other to potassium chemical fertilizer

Keywords:bio fertilizer-human health- agriculture

P208 - 345: ISOLATION OF STREPTOMYCES BY ANTIDERMATOPHYTIC EFFECTS FROM SHORGHALE SOIL

Azin Akbaei[1], Behin Omidi[2], Nastarn Asghari moghadam[3]

1. M.Sc of Microbiology, Islamic Azad University, Central Branch, Tehran, Iran
2. Assistant professor of Biology Group, Islamic Azad University, Central Branch, Tehran, Iran.
3. Assistant professor of Biology Group, Islamic Azad University, Central Branch, Tehran, Iran.

Background and Aim: Todays drug resistance are increasing. "Researchers are looking for alternative to replace common drug. One of this alternatives are Streptomyces. Streptomyces are filamentous bacteria that includes more than 500 species that isolation from soil and water. Some species of them can secretion antibiotics or other metabolites that kill or inhibit the growth of other microorganism. In this study we were screening for Streptomyces that had antidermatophyte effect on Microsporum canis from shorghale soil.

Methods: For isolation of Streptomyces sample soil were tested by serial dilution method and culture in starch casein agar then incubated in 280c for 7 day. Gypsum and powder colonies were detected. For metabolite produced isolated bacteria were cultured in ISP2 broth in 28 0c and 150 rpm for 7 day. Then centrifuged and the same volume, ethyl acetate was added and incubated in 280c for 5h. Then liquid transfered to Separatory funnel. The supernatant phase was transferred to distiller. This liquid were used for anti dermatophyte effect. Microsporum canis was cultured in SCC agar. Antifungal effects studied by disk diffusion method and was compared with terbinafine and itraconazole.

Results: Sixty Streptomyces were isolated from shorghle soil. One of them has shown a very good antifungal effect. The diameter of the non-growth zone was 29±1.24 , Results from 16srRNA indicate that this bacteria is 99.9% similar to Streptomyces albidochoromogenes.

Conclusion: Streptomyces have high ability to produce antimicrobial metabolites. By purification and formulation these metabolites, they can be used of them as an alternative to common antibiotics or antiagents.

Keywords: Streptomyces , dermatophytic , soil

P209 - 359: INVESTIGATING THE MICROFLORA OF IRANIAN TRADITIONAL SOURDOUGH

Maryam Rafiee Damaneh[1], Samira Yazidi[2], Jamshid Fooladi[3]

1. Alzahra University, Faculty of Basic Sciences
2. Alzahra University, Faculty of Basic Sciences
3. Alzahra University, Faculty of Basic Sciences

Background and Aim: Sourdough contains flour, water and other additives (such as NaCl), which is fermented by a heterogeneous population of microorganisms including yeast and Lactic acid bacteria (LAB). The aim of this study is to investigate the microflora of traditional sourdough of Taftoon bread and to describe the chemical features of sourdough. By using methods based on cultivation of microorganisms and chemical analyses (the final titratable acidity and pH), the bacterial and yeast populations of sourdough and its chemical features have been investigated and described. In general, just 3 types of bacterial colonies and 25 yeast strains were isolated from sample of traditional Taftoon sourdough.The total number of bacterial colonies was 1.8*106 colony in each sample gram (cfu/gr), while the total number of yeasts was much lower, about 5.6 * 102cfu/gr. pH sourdough was 3.24 and its final titratable acidity(TTA) was 23.8 ml from 0.1 normal NaOH on 10-grams sample of sourdough.

Methods: Data collection:Sourdough sample. pH determination:Digital pH METER.

Results: Chemical features of traditional sourdough: Average pH of sourdough was 3.24 and its average final titratable acidity was 23.8 ml via normal 0.1 NaOH on 10g sourdough. LAB count and yeast: The total number of LAB colonies in sourdough was 1.8*106 cfu/g, while the total number of yeasts was much lower and approximately 5.6*102cfu/g. In general, 18 LAB strains and 25 yeast strains were isolated from this sample.

Conclusion: The density of microorganism in Iranian traditional sourdough is less than sourdough of European breads,that is the difference of these two types of sourdoughs.

Keywords: sourdough, yeast, LAB, final titratable acidity, pH

P210 - 368: ISOLATION AND IDENTIFICATION OF MERCURY RESISTANT BACTERIA FROM THE HENDIJAN'S BEACHES AND EVALUATION OF THEIR EFFICIENCY IN BIOREMEDIATION OF MERCURY CONTAMINATED ENVIRONMENTS

Zahra Noroozi asl[1], Hossein Zolgharnein [2], Soheila Matroodi [3], Kamal ghanemi [4], Hossein Motamedi [5]

1. Marine Biotechnology, Department of Marien Biology, Faculty of Marine science and Oceanography, Khorramshahr University of Marine Science and Technology , Khorramshahr, Iran (z.noroozi2015@gmail.com)
2. Department of Marine Biology, Faculty of Marine science and Oceanography, , Khorramshahr University of Marine Science and Technology , Khorramshahr, Iran(Zolgharnein@kmsu.ac.ir
3. Department of Marine Biology, Faculty of Marine science and Oceanography, , Khorramshahr University of Marine Science and Technology , Khorramshahr, Iran (S_matroodi@yahoo.com)
4. Department of Marine Biology, Faculty of Marine science and Oceanography, , Khorramshahr University of Marine Science and Technology , Khorramshahr, Iran (kamalghanemi@gmail.com
5. Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Ahvaz, Iran . Biotechnology and Biological Science Research Center, Shahid Chamran University of Ahvaz, Ahvaz, Iran(motamedih@scu,ac,ir)

Background and Aim: With regards to increasing environmental pollution by heavy metals including mercury, bioremediation using heavy metal resistant bacteria has been paid attention as environmental friendly approach. The purpose of the present study was to isolation and identification of the mercury resistant bacteria from the Hendijan's beaches.

Methods: In this study, 3 sampling stations were selected. Isolation and purification of the Hg resistant bacteria were done through cultivation on Hg containing Nutrient Agar medium. The appeared colonies were identified basedon biochemical tests and sequencing of 16S rRNA gene. The growth curve of resistant bacteria was studied at 600 nm and he minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) of Hg for purified isolates were also investigated. Hg removal rate of the most Hg resistant isolate was also determined through measuring the amount of remained mercury in culture medium.

Results: As a result, the selected strain with the most resistance to mercury was identified as Bacillus cereus with 99% similarity to registered sequence in gene bank.The MIC and MBC of Hg for this isolate was 50 ppm and 200ppm, respectively This isolate was able to remove 92% of Hg from culture medium containing 10 ppm mercury.

Conclusion: These findings suggest that the isolated bacterium in this study had a good resistance to mercury and can be a suitable option for bioremediation of Hg contaminated wastewaters

Keywords: Mercury, Heavy Metals, Bioremediation

P211 - 369: ISOLATION AND IDENTIFICATION OF LEAD RESISTANT BACTERIA FROM WASTEWATER OF THREE PETROCHEMICAL COMPANIES IN BUSHEHR PROVINCE.

Zahra Noroozi asl[1], Hossein Zolgharnein [2], Soheila Matroodi [3], Kamal ghanemi [4], Hossein Motamedi [5]

1. Marine Biotechnology, Department of Marien Biology, Faculty of Marine science and Oceanography, Khorramshahr University of Marine Science and Technology , Khorramshahr, Iran (z.noroozi2015@gmail.com)
2. Department of Marine Biology, Faculty of Marine science and Oceanography, Khorramshahr University of Marine Science and Technology , Khorramshahr, Iran(Zolgharnein@kmsu.ac.ir)
3. Department of Marine Biology, Faculty of Marine science and Oceanography, , Khorramshahr University of Marine Science and Technology , Khorramshahr, Iran (S_matroodi@yahoo.com)
4. Department of Marine Biology, Faculty of Marine science and Oceanography, , Khorramshahr University of Marine Science and Technology , Khorramshahr, Iran (kamalghanemi@gmail.com)
5. 3Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Ahvaz, Iran. Biotechnology and Biological Science Research Center, Shahid Chamran University of Ahvaz, Ahvaz, Iran (motamedih@scu,ac,ir)

Background and Aim: Lead is the most extensive heavy element in the environment. Resistant bacteria to this heavy metal are an approach in bioremediation. Isolation and identification of these resistant strains is the first step in bioremediation purposes. The aim of this study was to isolation and identification of lead-resistant bacteria and evaluation of their lead bioremediation potential.

Methods: For this purpose, sampling was done from wastewater of three petrochemical companies in Bushehr. The samples were diluted and then cultured on Nutrient Agar medium containing 100ppm Lead nitrate. The tolerance of isolates was determined based on their MIC to lead and the most resistant strain was selected. The growth curve of the resistant strain at different concentrations of lead was obtained at 600 nm absorbance. The rate of lead removal was evaluated by Atomic Absorption analysis. Identification of the resistant bacteria was done by based on biochemical tests and sequencing of 16S rRNA gene.

Results: The biochemical tests and sequencing results have confirmed the selected strain as Proteus mirabilis with 99% similarity. The MIC of lead for this isolate was 1500ppm and the removal rate of lead was measured as 94 % in the medium containing 100ppm.

Conclusion: Based on these results it can be suggested that this isolate is a good candidate for further studies in bioremediation purposes for lead removal from contaminated environments.

Keywords: Lead, Heavy Metals, Bioremediation

P212 - 376: ISOLATION AND IDENTIFICATION A PROTEASE PRODUCING BACTERIUM FROM THE FLORA OF TERMITES

Reihaneh Assari[1], Ahmad Asoodeh[2]

1. M.Sc. Student of Biochemistry,Department of Chemistry, Faculty of Science,Ferdowsi University of Mashhad, Mashhad, Iran
2. Professor, Department of Chemistry, Faculty of Science,Ferdowsi University of Mashhad, Mashhad, Iran

Background and Aim: Microbial proteases cover 65 percentof industrial enzyme's market and about %25 of the total production of enzymes.Proteases are used in different industries such as detergent additives,photography,food,dehairing in leather and pharmaceutical industries.The aim of the present study was isolation and identification of bacteria from digestive system of termites producing proteases and determination optimal conditions to reach the maximum of protease production.

Methods: Initially, a few termites were washed carefully with sterile water,their abdomenswere removed using a sterile syringeand transferred to a plate containing nutrient agar and incubated at 37 °C in incubator. After separating colonies, their protease activities were evaluated bythe skim milk agar. The selected colony was identified by 16SrDNA. Finally, optimal growth conditions regarding carbon and nitrogen sources,various substrate,temperature and pH rangeswereexamined.

Results: Among 5 colonies one colonyproducing a transparent clear zonewas selected. Molecular analysis showed that the isolate belonged to bacillus family and named as Bacillus sp. CH96. Lactose and ammonium chloride was the best sources of carbone and nitrogen while casein (1%) has the highest enzyme production. Temperature 37 °C and pH 8 showed the most enzyme production.

Conclusion: The isolate ofBacillus sp. CH96 in current study possessed potential protease that may be used in some industries.

Keywords: Protease, Bacillus, termits, enzyme production

P213 - 392: EFFECT OF DIFFERENT CELL DISRUPTION METHODS ON PROTEIN EXTRACTION OF SPIRULINA

Mina Mehdie shishavane[1], Hamideh Ofoghi[2], Saeid Mirdamadi[3]

1. Department of Biotechnology, Iranian Research Organization for Science and Technology (IROST), Tehran, Iran.
2. Department of Biotechnology, Iranian Research Organization for Science and Technology (IROST), P.O. Box: 3353-5111, Tehran, Iran. Tel: +98 (21) 56276326-7. Fax: +98(21) 56275510. Ofoghi@irost.ir
3. Department of Biotechnology, Iranian Research Organization for Science and Technology (IROST), Tehran, Iran.

Background and Aim: Microalgae have valuable compounds such as lipids, proteins, polyunsaturated fatty acids, carotenoids, valuable pigments and vitamins that can be used in food, feed, cosmetics, pharmaceuticals industries. Spirulina is an edible (GRAS), photosynthetic and multicellular cyanobacteria (blue-green algae) appertaining to the Oscillatoraceae family. It has several biological activities useful for the body. It has received considerable attention due to its high protein content (50-70%). In order to use proteins, the cell wall has to be break. Spirulina has a relatively fragile cell wall, mainly composed of murein and no cellulose. Many cell disruption techniques to break the cell wall of microalgae such as bead milling, ultrasonication, microwave radiation, enzymatic treatment, cell homogenizer and high-pressure cell disruption have been used.

Methods: In this study Spirulina has been grown in Zarrouk medium under conditions 28±2 0C, 2.5 LUX, light/dark cycles 16/8, 120 rpm agitation. Spirulina were harvested by centrifugation during the exponential growth phase. Ultra sonication, bead milling and soaking in distilled water (3, 24, 48, 72 hours) have been investigated to evaluate release of proteins, After centrifugation the supernatant was analyzed for proteins with Lowry method. A calibration curve was prepared using bovine serum albumin.

Results: The content of proteins in three cell disruption methods along with a control in distilled water (0 hour) are: 13.7 % control, 63% ultrasonication, 45% bead milling and 41% soaking in D.W. (at different hours did not differ significantly).

Conclusion: Therefore Ultrasonication was efficient method to break the cell wall of Spirulina and to release the proteins into the aqueous phase.

Keywords: Microalgae, Spirulina, ultrasonication, Zarrouk medium ,

P214 - 439: EVALUATION OF MICROBIAL AND PHYSIOCHEMICAL CHARACTERISTICS OF INFLUENT AND EFFLUENT WATER ENTERING TO POINT OF USE WATER TREATMENT SYSTEMS IN GOLSAR COMPLEX, RASHT.

Esmaeil Roohbakhsh[1], Daryush naghipour1[2], , Masood Watan Doust2[3]

1. School of Health, Guilan University of Medical Sciences, Rasht, Iran
2. School of Health, Guilan University of Medical Sciences, Rasht, Iran
3. School of Health, Guilan University of Medical Sciences, Rasht, Iran

Background and Aim::Drinkingwater can be contained necessary, unnecessary and noxious constituents. Good water treatment process should be able to preserve necessary ingredients and remove others. The purpose of this study was to evaluate point of use water treatment systems in providing above purposes.

Methods: Random sampling was conducted from 8 blocks in GolsarComplex (Guilan, Rasht) for 3 months. Physiochemical and microbial analyses were conducted for systems influent and effluent. Also, statistical analyses were performed on obtained results.

Results: Average of turbidity, total hardness and TDS in effluents were0.26 NTU, 56.4 mg/L and 78.9 mg/L, respectively. Although the systems could decrease turbidity (necessary to remove), but they remove total hardness and TDS (necessary for humans) to unsafe levels. Also, average of total coliforms, fecal coliforms an HPC in effluents were 0.9, 0.2 and 324, respectively. The use of activated carbon for removal of organic and inorganic contaminants, can be used as microbial beds and deteriorate microbial quality of effluents.

Conclusion: Point of use water treatment systems could remove both unnecessary (turbidity, Fe, Mn) and necessary constituents of water (total hardness, TDS, fluoride and residual chloride), unselectively. So, the selection of systems steps should be controlled to gain a safe water in effluent.

Keywords: Point of use water treatment systems, Turbidity, Total coliforms, Fecal coliforms, Heterotrophic plate count

P215 - 455: EFFECTS OF DIETS SUPPLEMENTED WITH POLYSACCHARIDE EXTRACT FROM ALGAE, PADINA AUSTRALIS ON GROWTH, ANTIOXIDANT AND NONSPECIFIC IMMUNE STATUS OF SHRIMP, LITOPENAEUS VANNAMEI

Zahra Aminikhoei[1]

1. Agricultural Research Education and Extension Organization (AREEO), Iranian Fisheries Science Research Institute (IFSRI), Offshore Research Center, Chabahar, Iran

Background and Aim: This study was conducted to investigate the effects of different levels of water-soluble polysaccharide extract from brown algae, Padina australis (WPP) on growth, antioxidant enzymes activities and nonspecific immune responses of shrimp, Litopenaeus vannamei .

Methods: Three replicate groups of shrimp (1 ± 0.1g) were fed four isonitrogenous and isolipidic diets containing four levels, 0 or control, 0.5, 1.0, and 1.5 g kg-1 of WPP for 8 weeks.

Results: Results show that the diet containing 1.0 g kg-1 of WPP had significant positive effect on growth performance of shrimp. In addition, the activities of antioxidant enzymes including superoxide dismutase, glutathione peroxidase, catalase and malondialdehyde improved by feeding 0.5 and 1 g kg-1 of WPP. Also, the lysozyme and phenoloxidase activities in those of shrimp fed 0.5 and 1 g kg-1 of WPP were significantly higher than those fed control and 1.5 g kg-1 WPP.

Conclusion: These results suggested that the use of 1.0 g kg-1 of water-soluble polysaccharides of P. australis can be beneficial for growth, antioxidant and nonspecific immune of L. vannamei.

Keywords: Water-soluble polysaccharides, Padina australis, Litopenaeus vannamei, Antioxidant enzyme and Immune response

P216 - 457: ISOLATION AND CHARACTERIZATION OF PHOSPHORUS SOLUBILIZING BACTERIA

mosa karimi[1], mansoor zamani far[2]

1. presenter
2. author

Background and Aim: Phosphorus is one of the vital elements for living and growth of all plants. Due to deficiency of the available soil phosphorus to plants, utilization of phosphorus fertilizers is an inescapably Necessity. Perilous side effects of continuity usage of chemical fertilizers are undeniable. Phosphorus solubilizing bacteria are able to disposal phosphorus that was trapped in the soil to plants. Therefore; the application of this bacteria as bio-fertilizer can be the best solution to reduce or stop the high usage of chemical fertilizers.

Methods: Samples of the soil were collected from different agricultural lands in bagharz. Bacteria of the soil were isolated by serial dilution method. These bacteria were classified according to the physicochemical tests. To determination of the phosphorus solubilizing bacteria, the YED-P medium was used. The Bacteria with forming big halo zone on the YED-P medium were chosen. To the selection of the most appropriate bacteria, pH and thermal tests were done.

Results: At first, 108 bacteria were separated. Thirteen bacteria were able to form a clear zone on the YED-P medium. Two of the thirteen bacteria that capable to make a big clear zone was chosen, and then pH and thermal test were done to them. Results showed that selected bacteria had good stability in different pH and thermals conditions.

Conclusion: Phosphorus solubilizing bacteria can be the best option that we have natural agriculture free of chemical materials. They are able to provide P to the plants in the absorbable forms without any toxicity.

Keywords:natural agriculture, bio-fertilizer, soil bacteria.

P217 - 461: EVALUATION OF ENTRAPMENT APPROACH FOR SPORE LACCASE IMMOBILIZATION

Mojtaba Khakshour sini[1], Ali Makhdoumi[2], Ahmad Asoodeh[3], Mohammad Reza Housaindokht[4]

1. Applied and Environmental Microbiology Laboratory, Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran.
2. Applied and Environmental Microbiology Laboratory, 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.
4. Department of Chemistry, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran.

Background and Aim: Laccase enzymes (1,4-benzenediol: oxygen oxidoreductases, EC 1.10.3.2) are copper-containing proteins that oxidase a variety of aromatic substrates. They possess great potentials for biotechnological and environmental applications. Enzyme immobilization was defined as confining the enzyme molecules to a solid matrix different from the one in which substrate are present. The main aim of immobilization is to obtain stable and reusable enzymes with resistance to different environmental factors.

Methods: In the current study we applied entrapment approach to immobilize the spore laccase from Bacillus sp. KC2. Different concentration of sodium alginate (0.1, 0.5, 1.0, 1.5, 2, 2.5, and 3.0 %w/v), calcium chloride (0.1, 0.15, 0.2, 0.25, 0.3 M), zinc sulfate (0.1, 0.15, 0.2, 0.25, 0.3 M) and, copper sulfate (0.025, 0.05, 0.1, 0.15, 0.2 M) were varied to determine the best immobilized system with the activity in different pH and temperatures. Laccase activity was measured colorimetricaly based on the oxidation of ABTS (0.1 mM, at 420 nm).

Results: The highest immobilization efficiency were found to be as 89%, 83% and 80% in the beads formed by mixing 2% (w/v) alginate with 0.3, 0.2, and 0.05 M, Zn2+, Ca2+, and Cu2+, respectively. In the optimum pH (4.5 for all beads), and temperatures (35°C for Cu, 50°C for Zn and Ca beads) conditions the enzymes activity of entrapped spore laccase were equal to 10, 3.3 and 2.8 mU/bead in the Zn, Ca, and Cu beads, respectively.

Conclusion: The results showed the entrapment approach have great potentials to produce immobilized laccase system with activity in various conditions.

Keywords: Laccase, Immobilization, Bacillus

P218 - 463: DECOLORIZATION OF INDIGO CARMINE BY THE IMMOBILIZED SPORE LACCASE SYSTEMS

Mojtaba Khakshour sini[1], Ali Makhdoumi[2], Ahmad Asoodeh[3], Mohammad Reza Housaindokht[4]

1. Applied and Environmental Microbiology Laboratory, Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran.
2. Applied and Environmental Microbiology Laboratory, 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.
4. Department of Chemistry, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran.

Background and Aim: It is estimated that approximately 7 × 105 -1 × 108 tons dyes were produce annually and one-tenth of these dyestuff penetrate the environment through industrial wastes. Dyes have several health and environmental hazards. While physical and chemical methods do not have much success due to their high cost and production of secondary toxic waste, biodegradation of dyes by laccase enzyme is a promising method. The advantages of immobilized systems like improved stability and the reusability of biomolecules, encourage their applications in the bioremediation process.

Methods: The spore laccase were obtained from Bacillus strain and entrapped in the three type beads including: alginate-Ca, alginate-Cu, and alginate-Zn. Decolorization processes were performed in the mixture containing of acetate-sodium buffer (0.1 M), dye (25 mg/L), ABTS (0.1 mM), and 30 beads. All mixtures were incubated mildly shaking (150 rpm) at 30 °C. Decolorization rate was determined spectrophotometrically by the relative decrease in absorbance at λmax (610 nm) of dye.

Results: The first round complete decolorization was achieved after 150, 300 and 1440 min for the Zn, Cu and Ca beads, respectively. Regarding to reusing the immobilized systems, Zn and Cu beads showed two and twelve decolorization cycles stability. Interestingly for the immobilized system based on alginate-Ca the colorization were proceeded at the higher speed than the first round. The complete decolorizations were observed after 1080, 600, 300, 300, and 240 min for the second, third, fourth, fifth, sixth rounds of reused beads.

Conclusion: The results showed the potentials of immobilized laccase systems for bioremediation process.

Keywords: Laccase, Dye decolorization, Indigo carmine, Immobilization

P219 - 464: IDENTIFICATION AND ASSESSMENT OF POTENTIAL BIOLOGICAL CONTROL OF SUGAR BEET RHIZOSPHERIC BACTERIA ON RHIZOCTONIA CROWN AND ROOT ROT DISEASE

Zhaleh Khanibagi[1], Nabi khezrinejad[2]

1. Department of Plant Protection, Mahabad branch, Islamic azad univercity, Mahabad, Iran
2. Department of Plant Protection, Mahabad branch, Islamic azad univercity, Mahabad, Iran

Background and Aim: Rhizoctonia crown and root rot of sugar beet occurs by soil born multi nucleus fungi Rhizoctonia solani (Thanatephorus cucumeris (A. B. Frank) Donk.

Methods: In order to investigate potential biocontrol of the disease by rhizospheric bacteria, infected sugar beet samples were collected from southern area of West Azerbaijan province and disease causal agent were isolated, purified and identified. Also in order to isolation and identification of sugar beet rhizospheric bacteria healthy sugar beet samples were taken from Mahabad, Bokan, Miandoab and Piranshahr cities. Suspension of rhizosphere soil serially diluted and cultured on NA medium. To screening and assessment potential antagonistic ability of bacterial strains, dual culture test between bacterial strains and pathogen were conducted on plates containing PDA+NA media sealed with plastic wraps.

Results: After few days inhibitory zone diameters were measured. Among 71 isolates, 26 had inhibitory zone. 10 bacteria with more zones were selected for biochemical and physiological tests and phenotypic characterization were determined. On this basis, H12 isolate identified as Enterobacter sp. B11, D7 and T4 isolates identified as Pseudomonas putida. D13, D3, D2, H18, H20 isolates identified as Pseudomonas flourescens and M4 identified as Pseudomonas flourescens bv.5.

Conclusion: Microorganisms living in rhizosphere of plants are suitable candidates for biological control and bacteria are the main member of root colonizing microbial population. Identified strains are belong to Pseudomonadaceae and Enterobacteriaceae families that found in any habitats and tolerable to different environments. The strains had good result in case of biological control of disease in vitro condition.

Keywords: Biological control, Rhizosphere, bacteria, soil born

P220 - 469: OPTIMIZATION OF MEDIA AND CULTURE CONDITION OF PSEUDOMONAS BACTERIA TO INCREASING THE DEGRADATION OF POLYETHYLENE.

Zhale Moradì[1], bahare rahimian zarif[2]

1. department of biology faculty of science .sanandaj branch b.islamic azad university .sanandaj .iran
2. department of biology faculty of science .sanandaj branch b.islamic azad university .sanandaj.iran

Background and Aim: Today ‘growing of plastic consumption in iran is over 2 million tons in each year .Therfore,it cause differnt problems in the environment.Thus,the purpose of current study was to optimization of media and culture condition of pseudomonas bacteria to increase the degradation of polyethylene as one of the main components in plastic products.

Methods: The standard strain of pseudomonas aeruginosa (PTCC 1562) was grown in 100 ml of the inorganic medium (based on the McFarland standard).After adding 100 mg of low-density polyethylene nylon slices (2cm.2cm),culture incubated for 10 days and then the slices was washed by SDS .Finally, lost weight was measured and the culture condition was optimized.

Results: Our results indicated that Polyethylene was degradaded by 2%in the initial conditions by the standarad bacterial strain .Also the highest polyethylene breakdown(PH7)was 2% weight loss at a temperature of 30C,3.4% at 30 days incubation time,4.4 % at 120rpm of shaker,2.7% in the presence of yeast extract with an 3.8% estimated weight loss.Finally, the removal of polyethylene in set of optimized conditions by pseudomonas aeruginosa PTCC1562 was 7.4%.

Conclusion: The result of this study showed that this effective strain can be used for removal of polyethylene.

Keywords:polyethylene ‘pseudomonas aeruginosa‘plastic biodegradation

P221 - 471: PRODUCTION OF BACTERIAL CELLULOSE USING SUGARCANE VINASSE

Mehran Ataei[1], Hossein Motamedi[2]

1. Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Ahvaz, Iran
2. 1Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Ahvaz, Iran 2Biotechnology and Biological Science Research Center, Shahid Chamran University of Ahvaz, Ahvaz, Iran. *Corresponding author: Hossein Motamedi, Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Golestan Blvd., Daneshgah sq., Ahvaz, Khouzestan, Iran. Tel/fax: +98-6133331045- Email: motamedih@scu.ac.ir, hhmotamedi@yahoo.com

Background and Aim: In comparison with chemically synthesized polymers, biopolymers due to their physicochemical properties have been paid attention Cellulose is one of the most applied polymers that has a broad range of applications from High-strength paper and diet foods production to medical applications such as soft tissue replacement and artificial blood vessels production. The aim of this study was to use sugarcane vinasse as low cost and available substrate for cellulose production.

Methods: For this purpose Gluconoacetobacter xylinus PTCC 1734, the type species for cellulose production was inoculated in to sterile pure as well as 5 and 10 % concentrations of vinasse and incubated at both static and shaking conditionsat 30°C for 8 days. Simultaneously, hestrin schramm medium was used with same incubation conditions. The produced cellulose was washed by distilled water and treated with 0.1M NaOH. Cellulose production was confirmed according molish and benedict tests and the dry weight of cellulose was calculated.

Results: As a result the highest cellulose production was achieved at pure vinasse in static condition as 0.201 g while in case of hestrin schramm the cellulose yield was0.097 g.

Conclusion: These results suggest that vinasse which is a waste byproduct of sugarcane industry have the potential to be used as substrate for cellulose biopolymer production. It will reduce production costs and hence promote commercial production of this biopolymer.

Keywords:biopolymers, bacterial cellulose, G.Xylinus, sugarcane, vinnase

P222 - 476: ISOLATION AND CHARACTERIZATION OF A BACTERIUM WITH FREE GLUTAMINASE L-ASPARAGINASE II FROM THE PERSIAN GULF

Saloomeh Shoaei Naeeni[1], Omid Ranaei Siadat[2], Gholamhossein Ebrahimipour[3], Bijan Bambai[4]

1. Faculty of Life Sciences and Biotechnology, Shahid Beheshti University, G.C., Evin, Tehran, P.O. Box: 1983969411, Iran
2. 2Protein Research Center of Shahid Beheshti University, G.C., Evin, Tehran, P.O. Box: 1983969411, Iran
3. Faculty of Life Sciences and Biotechnology, Shahid Beheshti University, G.C., Evin, Tehran, P.O. Box: 1983969411, Iran
4. National Institute of Genetic Engineering & Biotechnology, Karaj Highway, P.O. Box: 14965/161, Tehran, Iran

Background and Aim:L-asparaginase enzyme has various applications, particularly in medicine and food industry. Given some side effects and adverse possession of a minor amount of glutaminase activity, the search for new sources of microbes producing glutaminase-free L-asparaginase type II is underway.The present study aimed to isolate a bacterium from the Persian Gulf that produces glutaminase-free L-asparaginase type II. It is also aimed to measure the amount of this enzyme and the condition under which it increases.

Methods: In order to assess the capability of extracellular asparagine production, the isolated bacteria from the seawater were cultured in M9 medium containing phenol red and asparagine. Those bacteria with positive asparaginase test were cultured in M9 medium containing glutamine and phenol red to assess their glutamine activity. The bacterium isolate producing asparaginase was identified using morphological and biochemical means and 16 SrDNA. L-asparaginase enzyme activity of the isolate was explored with a colorimetric method. The effect of anaerobic condition on the amount of L-asparaginase type II activity was explored by culturing under aeration condition and with no aeration.

Results: The result showed that the isolated bacterium was Rhizobium nepotum strain SHN1. The asparaginase enzyme activity and the specific activity of this bacterium were 0.467 IU/mL and 0.015 IU/mg, respectively. These characteristics increased to more than 50% in anaerobic condition.

Conclusion: The results indicated that microbial flora from the Persian Gulf flora could be a remarkable source of glutaminase-free L-asparaginase enzyme.

Keywords:L-asparaginase enzyme, Rhizobium nepotum, glutamination

P223 - 481: ALGINATE PRODUCTION USING A NATIVE PSEUDOMONAS SP. ISOLATED FROM SOIL

Marjan Tayyebi[1], Prof. Hossein Motamedi[2]

1. Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Ahvaz, Iran
2. Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Ahvaz, Iran . Biotechnology and Biological Science Research Center, Shahid Chamran University of Ahvaz, Ahvaz, Iran.

Background and Aim: Alginates are polysaccharides that are produced by brown seaweeds, some red algae and Gram negative bacterial genera. These are used in various industries including foods, cosmetics, pharmaceuticals, drug delivery, medicine and tissue engineering. The purpose of this study was isolation of native alginate producer strains from soil in Ahvaz.

Methods: Soil samples were harvested from plant decomposing region. Ten g of sample was added to 90 ml of physiological saline and incubated at 27 °C with continuous shaking. Following precipitation of suspended particles,10 µl of supernatant was cultured on Mueller Hinton agar medium and the appeared colonies were screened on Cetrimide agar for Pseudomonas spp. isolation. Nitrogen fixation ability of isolates were investigated through Döbereiner assay. Pseudomonas spp. were identified by biochemical tests. Alginate was extracted through sequential stages such as centrifugation, sedimentation by ethanol and drying in vacuum and confirmed through Carbazole analysis assay with borate. The quantitative assay of produced alginate was done through absorbance measurement at 530 nm and comparison with standard alginate solution absorbance.

Results: The selected Pseudomonas sp. was able to produce alginate of 7.40 w/w with yield and a 0.926 mg/ml concentration in Nutrient broth medium while in the modified salt medium (MMSM) with 5% Vinasse, the yield of alginate production was 50.485 w/w with 1.09 mg/ml concentration.

Conclusion: The results revealed that vinasse as a cheap and available substrate can be used for alginate production by isolated Pseudomonas sp. and further studies are needed to develop this process for optimized alginate production.

Keywords: Alginate, biopolymer, Pseudomonas spp., Carbazole assay, Vinasse

P224 - 491: CLONING AND EXPRESSION OF L-ASPARAGINASE II GENE EXTRACTED FROM RHIZOBIUM NEPOTUM STRAIN SHN1 IN ESCHERICHIA COLI BL21

Saloomeh Shoaei Naeeni[1], Omid Ranaei Siadat[2], Gholamhossein Ebrahimipour[3], Bijan Bambai[4]

1. Faculty of Life Sciences and Biotechnology, Shahid Beheshti University, G.C., Evin, Tehran, P.O. Box: 1983969411, Iran
2. Protein Research Center of Shahid Beheshti University, G.C., Evin, Tehran, P.O. Box: 1983969411, Iran
3. Faculty of Life Sciences and Biotechnology, Shahid Beheshti University, G.C., Evin, Tehran, P.O. Box: 1983969411, Iran
4. National Institute of Genetic Engineering & Biotechnology, Karaj Highway, P.O. Box: 14965/161, Tehran, Iran

Background and Aim: Asparaginase as an enzyme catalyzes hydrolyze L-asparagine to aspartic acid and ammonia and has various applications in medicine and food industry. As a medication, it is used to treat acute lymphoblastic leukemia, acute myeloid leukemia, and non-Hodgkin's lymphoma. Due to some side effects including neurotoxicity, clotting, hepatitis, allergic reactions and adverse possession of a small amount of transglutaminase activity, the search for new sources of microbial transglutaminase lacking enzyme dysfunction is underway.

Methods: In this study, L-asparaginase extracellular activity extracted from Rhizobium nepotum strain SHN1 (isolated from the Persian Gulf water) with no transglutaminase activity was measured. In order to assess the capability of extracellular asparagine production, this strain were cultured in M9 medium containing phenol red and asparagine and then were cultured in M9 medium containing glutamine and phenol red. L-asparaginase enzyme activity of the isolate was explored with a colorimetric method.

Results: The asparaginase enzyme activity and the specific activity of this bacterium were 0.467 IU/ml and 0.015 IU/mg, respectively. These characteristics increased to more than 50% in anaerobic condition. Gene expression of this enzyme was cloned in pET21a vector and its expression host in E. coli BL21 well stated. The protein molecular weight of 32 kD and enzymatic activity of L -asparaginase in host expression of 10.46 IU/ml unregulated to 56% L- asparaginase enzyme's production.

Conclusion: The results of the present study suggest that R. nepotum strain SHN1 may be a reliable source for the free glutamine L-Asparaginase.

Keywords:L-asparaginase enzyme, Rhizobium nepotum, glutamination, pET21a, E. coli BL 21

P225 - 505: DEGRADATION OF LONG CHAIN ALKANES BY NEWLY ISOLATED BACTERIA

Mohammad javad Mozaffari poor[1], Fatemeh Davoodi Dehaghani[2], Mohammad Barshan-tashnizi[3]

1. Department of Biology, Faculty of Basic Sciences, Central Tehran Branch, Islamic Azad University, Tehran, Iran
2. Department of Biology, Faculty of Basic Sciences, Central Tehran Branch, Islamic Azad University, Tehran, Iran
3. Department of Life Sciences Engineering, Faculty of New Sciences and Technologies, University of Tehran. Tehran, Iran

Background and Aim: Long chain alkanes are significant proportion of the oil. Soil and water pollution with these compounds, have many environmental consequences. Separation of microorganisms with the ability to decompose these alkanes, as followed in this research, is a suitable and biocompatible method for solving environmental problems of the oil industry.

Methods: Soil was removed from a depth of 20 cm in a contaminated area of Abadan and it analyzed by Gas chromatography-mass spectrometry. 0.5 gr of soil was added to 100 mL of nutrient broth containing two anti-fungal antibiotics; nystatin and cycloheximide, each at a concentration of 50 mg/L, and incubated in a shaking incubator at 30°C overnight. Then, n-Dodecane (C12H26), n-Tetradecane (C14H30) and n-Icosane (C20H42) were separately added to mineral salt medium (MSM), in the presence of 0.5%w/v SDS. The flasks were inoculated with 2% bacterial stock and incubated at the same condition. Each experiment was repeated twice. Absorption in 660 nm was considered as a scale of the bacterial growth with alkane consumption.

Results: According to the GC-MS results, C12 ,C14 ,C16 and C20 in the soil sample was 2.5%, 2.2%, 1.9% and 2.3%w. Mean absorption of the growth media with three carbon sources i.e. C12 ,C14 and C20 after two weeks was 0.15, 0.13 and 0.95.

Conclusion: It could be hoped that the isolated bacteria would have the potential for bioremediation of oil polluted areas.

Keywords: Hydrocarbons, Bioremediation, Mineral Salt Medium

P226 - 508: ISOLATION OF PAH DEGRADING BACTERIA FROM OIL CONTAMINATED SOIL OF DARKHOVEYN

Mohammad javad Mozaffari poor[1], Fatemeh Davoodi Dehaghani[2], Mohammad Barshan-tashnizi[3]

1. Department of Biology, Faculty of Basic Sciences, Central Tehran Branch, Islamic Azad University, Tehran, Iran
2. Department of Biology, Faculty of Basic Sciences, Central Tehran Branch, Islamic Azad University, Tehran, Iran
3. Department of Life Sciences Engineering, Faculty of New Sciences and Technologies, University of Tehran. Tehran, Iran

Background and Aim: Polycyclic aromatic hydrocarbons (PAHs) are the most toxic and carcinogenic pollutants and cause serious damage to humans and the environment. Soils contaminated with petroleum compounds usually have bacteria that degrade these compounds, which grow on PAHs as carbon and energy sources. This study aimed to find such bacteria.

Methods: Soil contaminated with oil was collected near one of the wells in Darkhoveyn, 40 km from Abadan, and analyzed by high performance liquid chromatography (HPLC). 0.5 gr of this soil was added to 100 mL of nutrient broth with nystatin and cycloheximide, each at a concentration of 50 mg/L. flasks were incubated in an incubator shaker at 30°C overnight. Then mineral salt medium (MSM) with 0.5%w/v SDS was used to grow bacteria and 10 gr/L of naphthalene, anthracene and phenanthrene were added to the flasks as carbon sources, separately. After two weeks, OD660 was considered as a measure of the bacterial growth.

Results: The total amount of soil aromatics was 1855 µg/kg. The various compound concentrations were: Naphthalene 134, Phenanthrene 425, Anthracene 3.8, Fluoranthene 170, Pyrene 263, Benz[a]anthracene 190, Chrysene 508, Dibenz[a,h]anthracene 71 and Benzo[ghi]Perylene 45 µg/kg. The mean absorption at 660nm for naphthalene, anthracene and phenanthrene was respectively 0.4, 0.12 and 0.15 with two replications.

Conclusion: According to the findings, these bacteria can use naphthalene, anthracene and phenanthrene as the only carbon source and they are capable bacteria in bioremediation.

Keywords: Polycyclic aromatic hydrocarbons, Carbon source, Biodegradation

P227 - 512: DIBUTYL PHTHALATE DEGRADATION USING DEINOCOCCUS SPP. ISOLATED FROM LOUT DESERT OF IRAN

Hosna Abbasi[1], Mojtaba Mohseni[2], Omeleila Nazari[3]

1. myself. H.Abasi@stu.umz.ac.ir
2. Department Microbiology, Faculty of Science, University of Mazandaran, Babolsar, Iran
3. Department of Inorganic Chemistry, Faculty of Chemistry, University of Mazandaran, Babolsar, Iran

Background and Aim: Dibutyl phthalate is colorless and odorless, with very low solubility in water; it is used as a plasticizer in most polymer products. Phthalates have gained attention due to their high levels of toxicity, carcinogenicity, Endocrine disorder and the emergence of multiple diseases in humans and living organisms. Assessment of dibutyl phthalate biodegradation (DBP) using Deinococcus spp. isolated from Lout desert of Iran was the aim of this study.

Methods: The strains were inoculated into TSB medium and incubated at 30 °C for 24 hours. Then 5 ml of growth medium was transferred to 100 ml of fresh minimal salt medium with 1 ml of sterile 7% DBP as a sole carbon and energy source. The flasks were incubated on an orbital shaker at 30 °C and 150 rpm for 24-48 hours. Biodegradation of DBP was investigated by two assessment methods including optical density using spectrophotometer (wavelength at 600 nm) and high-performance liquid chromatography (HPLC).

Results: The results demonstrated that both native Deinococcus strains, LD4 and LD5, started degradation after 6 hours then reached to a maximum after 24 hours of incubation. The results of growth assessment in the culture medium containing DBP showed that optical density of growth medium was increased in both LD4 and LD5 from 0.211 to 0.751 and 0.226 to 0.763, respectively.

Conclusion: The results of this research revealed that the native Deinococcus strains isolated from Lout desert are suitable for the degradation of phthalates in industrial wastewater and contaminated sites.

Keywords: Dibutyl phthalate, biodegradation, Deinococcus

P228 - 523: EFFECT OF TEMPERATURE ON GROWTH AND ANTIOXIDANT CONTENT OF THE MICROALGA MONORAPHIDIUM SP.

Asyah Aghababaei[1], Parichehr Hanachi[2], Mostafa Noroozi [3]

1. biology sciences, Alzahra University, Thehran, Iran
2. Department of Biochemistry,Alzahra University, Thehran, Iran
3. Department of Biotechnology ,Alzahra University, Thehran, Iran

Background and Aim: Monoraphidium it is a single-cellular algae, since microalgae is one of the major sources of new compounds with medicinal properties.The purpose of this study was to investigate the effects of three different temperatures (23, 28, 34˚c) on the growth, antioxidant property, total phenolic and flavonoid content at the end of the logarithmic stage monoraphidium, to increase the production of these valuable compounds was studied.

Methods: For this purpose, samples were cultured in 2 L bottles containing 1.5 L of culture medium Bolds Basal Medium ; and under different temperatures treatment. Antioxidant assays were performed 16 days after the start of culture. After lyophilized, 10 mg of powder obtained, the cell mass was extracted by methanol solvent.

Results: The results showed that the peak population density was obtained at 28 ˚c. The most antioxidant property in the frap method and the total phenol content at 28˚c were 127.65 µmol Fe2+ g-1± .036 antioxidant and8.06mgGAE g -1 ± .046 phenolic compounds, respectively. The maximum amount of flavonoids was reached at a temperature of 33 ˚c, at a rate of 54.37 mg quercetin g-1± .017. Although the temperature of 33 ˚c reduced the amount of biomass, but the percentage of flavonoids differs slightly from other temperatures.

Conclusion: The findings of this study showed that increasing the temperature to 28˚c resulted in improved growth and increased antioxidant and total phenolic content. Based on the results of this research, temperature stress can be used to increase the production of antioxidants

Keywords: Monoraphidium, Antioxidant property, Phenolic content, Flavonoid

P229 - 538: INVESTIGATING THE EFFECT OF ANTAGONISTIC BACTERIA ON CONTROL OF PHYTOPHTHORA ROOT ROT OF CUCUMBER IN WEST AZERBAIJAN PROVINCE

Sahel Bange Zare[1], Nabi Khezrinejad[2]

1. 1- Graduate Student, Department of Plant Protection, Faculty of Agriculture, University of Mahabad
2. 2- Department of Plant Protection, Mahabad Branch, Islamic Azad University, Mahabad, Iran

Background and Aim:phytophthora root and crown rot of cucumber is one of the most important soil born disease worldwide. This study was carried out to identify and investigate the potential antagonistic bacteria for control of disease in West Azerbaijan province.

Methods: For this purpose, pathogen was isolated on a semi-selective culture medium of CMA-PARP. 20 isolates recovered from various parts in West Azerbaijan province. isolates were identified as Phytophthora drechsleri on the selective medium based on morphological and growth characteristics in different temperatures. for isolation and identification of cucumber rhizospheric bacteria healthy cucumber samples and their rhizospheric soil were taken from different cities. Samples immediately transferred to laboratory. One gram soil of rhizosphere added to 9 ml sterile distilled water. Suspension serially diluted and cultured on NA. single colonies were selected basis on morphology and purified. Antagonistic effect of the strains was evaluated based on their growth inhibitory of pathogen.To screening and assessment bacterial strains potential antagonistic ability, dual culture test were conducted on PDA+NA media. After 24 hours fungal disc transferred to center of plate containing bacteria and sealed. After few days inhibitory zone diameters were measured.

Results: Among 45 isolates, 6 had strong inhibitory zone. Based on phenotypic characteristics the strains B1, B2, B8, B10, B15 and B20 were identified as Bacillus sp., Pseudomonas putida, B. cereus, Achromobcater sp., P. fluorescens and Paenibacillus polymyxa, respectively.

Conclusion: Biological control by bacteria was reported formerly, In this study good results obtained in vitro condition and bacteria includes gram positives and gram negatives.

Keywords:biological control, soil born disease, public safety

P230 - 548: DISTRIBUTION OF FUNGAL CONTAMINATION IN INDOOR BAZAARS- ZANJAN

Arezoo Tavakoli[1]

1. Assistant Prof, Department of Nursing, Islamic Azad University, Eghlid Branch

Background and Aim: Indoor air pollution is one of the challenging cases in the health community created by biological and non-biological agents. Fungi are biological contaminants that produce many symptoms such as allergy, asthma and respiratory disorders. Bioaerosols of fungal origin, consisting of spores and hyphal fragments that inhaled easily and lead to bronchial irritation, immune diseases.

Methods: The community composition and concentration variation pattern of airborne fungi were investigated in Sep (2017) to March (2018) in two marketplaces in Zanjan. The first sampling place is Zanjan bazaar known as a longest roofed bazaar in Iran. The second place is a fruit and vegetable market. Air sampling is done weekly with SKC sampling pump with airflow of 14.5 lit/min for a period of 10 min. The samples were transferred on Sabouraud Dextrose Agar (SDA) media containing 50 µg/mL kanamycin and then incubated at 25ºC.

Results: The type and concentration of fungi species were determined. The most common fungi were Aspergillus, Penicillium, Cladosporium and Alternaria spp and less population of Rhizopus sp Candida sp determined. The concentration of fungi shows the variable pattern in different part of the bazaar, especially during autumn.

Conclusion: The environmental factors such as temperature, humidity affected the results. Additionally, the age of a building, ventilation rate, the length of a bazaar, and type of shopping have considerable effects on the isolates. The fungi population and concentration in Fruit market were higher than other places. In the middle of the bazaar, the pattern of fungi distribution was different from the entry.

Keywords: Fungi, Air , Contamination, Market, Zanjan

P231 - 550: IDENTIFICATION OF APPLE FRUIT BACTERIA AND EVALUATION OF THEIR BIOCONTROL POTENTIAL AGAINST APPLE BLUE MOLD (PENICILLIUM EXPANSUM (IN WEST AZERBAIJAN PROVINCE

Nahideh Sigari[1], Nabi Khezrinejad[2]

1. 1- Graduate Student, Department of Plant Protection, Faculty of Agriculture, University of Mahabad
2. 2- Department of Plant Protection, Mahabad Branch, Islamic Azad University, Mahabad, Iran

Background and Aim: Apple blue mold (Penicillium expansum Link) is the most important postharvest disease worldwide. it has numerous mycotoxins. Fungicide resistance development and concern for public safety from fungicide residues on fruits has led to the search for alternative control measures including biocontrol for the management of storage diseases of pome fruit. the study aimed to identification and evaluate biological control potential of bacteria associated with apple fruits against apple blue mold.

Methods:apple Red and Golden cultivars were taken from Mahabad, Urumieh, Shahin Dezh and Miandoab cities cold storages during 2016 – 2017. Due to bacterial isolation and identification, apple healthy samples were selected. Suspension serially diluted and cultured on NA. To screening and assessment bacterial strains potential antagonistic ability, dual culture test between bacteria and fungus was conducted on plates with PDA+NA media. After few days inhibitory zone diameters were measured.

Results: Among 60 isolates, 16 had inhibitory zone. Among them 10 bacteria with bigger inhibitory zones were selected for biochemical and physiological tests and their phenotypic characterization were determined. among selected isolates 4 of them are Gram negative and 6 are gram positive, all are oxidase and catalase positive and their hypersensitivity reaction test are negative on geranium leaves. on the basis of biochemical, physiological and nutritional tests the isolates identified as Pseudomonas fluorescens, Bacillus subtilis And Bacillus licheniformis.

Conclusion: Biological control by bacteria and yeasts was reported formerly, In this study good results obtained in vitro condition. gram positives were more effective and common than gram negatives.

Keywords:biological control, postharvest disease, public safety

P232 - 565: ISOLATION OF MAGNETOTACTIC BACTERIA FROM AQUATIC ENVIRONMENTS AND THEIR POTENTIAL IN THE PRODUCTION OF IRON NANOPARTICLES

Nafise Shamsabadi[1], Mojtaba Mohseni[2], Hassan Taghavi[3]

1. Department Microbiology, Faculty of Science, University of Mazandaran, Babolsar, Iran
2. Department Microbiology, Faculty of Science, University of Mazandaran, Babolsar, Iran
3. Department of Marine Biology, Faculty of Environmental and Marine Sciences, University of Mazandaran, Babolsar, Iran

Background and Aim: Magnetic bacteria are a diverse group of motile and gram-negative aquatic prokaryotes with the ability to produce iron nanoparticles enclosed with membranes, called magnetosomes which consist of magnetite iron oxide crystals (Fe3O4) or greigite iron sulfide crystals (Fe3S4). The purpose of this study is to isolate magnetic bacteria from aquatic environments and evaluate the ability of these bacteria to produce magnetic nanoparticles.

Methods: The samples were collected from different areas at depths of 10-100 cm and stored at ambient temperature and low light for several days. Then the magnetotactic bacteria (MTB) were isolated using the capillary racetrack method. In order to grow the MTB and synthesize the iron nanoparticles, the sample containing MTB was inoculated into a special liquid culture medium of magnetic bacteria and incubated at 28 °C for one month.

Results: Magnetic activity and bacterial movement were investigated using hanging drop method by use of an optical microscope. The results of gram staining technique showed that the MTB isolates were gram negative. After extraction of nucleic acids from isolates using standard method, polymerase chain reaction and sequencing of 16S rRNA gene were used for the identification of magnetic bacteria. Also, the morphology of the bacteria and their magnetosome were investigated using transmission electron microscopy.

Conclusion: The results of this study demonstrated that the MTB isolates was able to produce magnetic nanoparticles.

Keywords:MTB - Magnetosome – Magnetotaxis - Magnetite

P233 - 568: SELECTION A MULTI-METAL RESISTANT BACTERIA FROM ENVIRONMENTAL SAMPLES FOR BIOREMEDIATION PURPOSES

Fatemeh Yaghoobizadeh[1], Mohammad Roayaei Ardakani[2]

1. Biotechnology and bioscience research center ,Shahid Chamran University of Ahvaz, Ahvaz,Iran
2. 1. Shahid Chamran University, faculty of science, biology department 2. Biotechnology and bioscience research center ,Shahid Chamran University of Ahvaz, Ahvaz,Iran

Background and Aim: Mercury and selenate are among the most toxic elements and can give rise to the irreversibly damage to the CNS and abnormalities. As the various forms of them are stable in environment, many of microorganisms have developed resistance systems and can play role in bioremediation. Thus the aims of this research are isolation and multi-metal resistance capability of bacteria and finally identification of the best bacteria.

Methods: At the beginning, isolation of mercury-resistant bacteria in mLB agar medium containg HgCl2 was performed. The best isolates were selected using Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC) methods at the range of 25-800ppm HgCl2. Following, selenate resistance capacity of one isolate was evaluated at the range of 32.5-1200mM. Identification of metal resistant isolate are doing.

Results: By culturing collected environmental samples on suitable medium, above 50 colonies were isolated. Using predefined tests, an isolate was selected; MIC and MBC of this isolate was 400ppm to mercury and 600mM and 1200mM to selenate, respectively. The primary identification test showed that this isolate was gam negative bacteria belonging to Enterobacteriacae family.

Conclusion: Bioremediation can be used to clean unwanted substances from air, soil, water and raw materials from industrial processing. It should be noted that furthur studies such as detection of sorption mechanism and process optimization need to be done. Moreover, it could be noticed that if metal resistant genes of this isolate determine, cloning of them can help for designing biofilters.

Keywords: Multi-metal resistance, bacteria, biofilter

P234 - 590: ISOLATION AND PURIFICATION OF SELENIUM-LEACHING BACTERIA FROM COPPER REFINERY ANODE SLIME

Mobina Bayatian[1], Mohammad Reza Soudi[2], Parisa Tajer-Mohammad-Ghazvini[3]

1. Department of Microbiology, Faculty of Biological Science, Alzahra University, Tehran, Iran; bayatianmobina@gmail.com.
2. Department of Microbiology, Faculty of Biological Science, Alzahra University, Tehran, Iran; msoudi@alzahra.ac.ir
3. Materials and Nuclear Fuel Research School, Nuclear Science and Technology Research Institute, Tehran, Iran; ptajer@aeoi.org.ir

Background and Aim: Anode slime from copper electro-refining normally contains various metals such as selenium, tellurium, copper, silver, nickel, platinum group metals (PGM), barium, iron, gold, lead that has a high commercial value. Generally anode slimes are processed to recover silver, gold, selenium and tellurium. Bioleaching is an effective technology for metal recovery that is performed by microorganisms. Selenium is a strategic element which is essential for all organisms and has a wide range application in industry.

Methods: The current work attempts to isolate strains from copper refinery anode slime which are capable of selenium bioleaching. In order to achieve this aim, Tryptic Soy Broth and Luria-Bertani media with anode slime incubated at 30˚C for three weeks. During this time, samples from these media cultured on Tryptic Soy Agar and Nutrient Agar. Then bioleaching tests carried out by the isolated and purified bacteria and leach liquor analyzed by Inductively Coupled Plasma-Optical Emission Spectroscopy (Perkin Elmer Optima 7300DV).

Results: In this research, four Gram-positive and one Gram-negative rod-shaped bacteria were isolated. On average, these bacteria had the ability to solubilize 6.66 mg/l selenium from copper anode slime.

Conclusion: Copper anode slime contains toxic forms of elements, so leaching-bacteria should be able to grow in this rough condition. Screening from anode slime has the advantage of isolating resistant bacteria to harsh condition of this slime. Thus, each of the isolated bacteria can be a suitable candidate for selenium bioleaching processes from secondary resources due to the unique resistance of these bacteria.

Keywords: Copper anode slime, Bioleaching, Selenium, Metal extraction

P235 - 607: DEVELOPING A NOVEL COST-EFFECTIVE CHROMOGENIC CULTURE MEDIUM FOR DETECTION AND ISOLATION OF SALMONELLA SPECIES

Hassan Salimi[1], Vafa Mayahi[2]

1. Zist Kavosh Iranian Co. (Ibresco), Karaj, Alborz, Iran
2. Zist Kavosh Iranian Co. (Ibresco), Karaj, Alborz, Iran

Background and Aim: Salmonella species as salmonellosis infection agent invade gastrointestinal tracts leading to gastroenteritis (diarrhea, abdominal cramps, and fever) to enteric fevers (including typhoid fever), which is still a major health problem. Moreover, isolation of Salmonellae from dairy products has caused great destructive impacts on dairy industry. So far various commercial detection media have been proposed for Salmonellae isolation from clinical samples, yet chromogenic culture media led to more specific results with higher recovery rates. But the commercial chromogenic media are very expensive due to application of antibiotics and chromogenic substrates.

Methods: Here, we focused on developing a new accurate and efficacious chromogenic media to diagnose and isolate Salmonella strains. Thus we used specific Salmonellae chromogenic substrates, in addition to inhibitors of Proteus, Pseudomonas and Gram-positive strains. Detection of coliforms was also conducted using this method.

Results: Though cost-effective, results obtained from observation of clinical samples cultured on the proposed chromogenic medium revealed the high recovery rate of Salmonella species colored in magenta, while coliform strains were isolated in blue-green.

Conclusion: Hence, we developed a novel chromogenic medium for Salmonellae, which is also accurate, effective, and cost-effective with rapid identification and high recovery rates for Salmonella and coliform strains in clinical samples.

Keywords: Salmonella, Chromogenic media, Detection, Salmonellosis, Gastroenteritis

P236 - 612: ISOLATION OF N2 FIXING AND PHOSPHATE SOLUBILIZING RHIZOBACTERIA FROM DIFFERENT FIELDS IN KERMAN DISTRICT, IRAN

Mahla Farajzadeh Mazandarani[1], Farokh Rokhbakhsh-Zamin[2]

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: Phosphorous is the most critical element for plant nutrition. Phosphate solubilization in soil can be achieved by using rhizobacteria with ability to enzymatic reactions such as phosphatase production or by soil acidification by acid production. Accordingly, in this study it is important to find new powerful phosphate solubilizing and nitrogen fixing rhizobacteria.

Methods: Rhizospheric soil samples were randomly collected from different plants and immediately transferred to the lab by using ice box. About one gram of soil was poured into the bottle containing Thompson's medium. After shacking, it was placed horizontally and incubated for seven days at 30oC. Then, a streak plate was made on nitrogen free, iron free agar to obtain different colonies. An aliquot (10 µl) of each suspension with approximately 1×107 colony forming units/ml (CFU/ml) from a 2-day culture was spot inoculated on sperber agar. A clear zone around each spot during 1 week at 28oC was considered positive evidence of phosphate solubilization.

Results: Twenty seven bacteria were isolated from soil samples. Nitrogen fixation abilities of all strains were confirmed by their growth on different nitrogen free media such as Ashby, Burk and jensen's media. On the other hand, nine isolates showed significant activities about phosphate solubilization and Their solubilization efficiencies (SE) were observed and calculated as 110.5,112.5,120.0,121.4,133.3,135.7,142.8, 166.6, 200.0.

Conclusion: Isolated strain as IAUK7059 showed very promising results about nitrogen fixation and phosphate solubilization and it has a very good potential to be used in further experiments for biofertilizers construction.

Keywords: Rhizobacteria, Phosphate Solubilization, Nitrogen fixation, PGPR, In vitro screening

P237 - 659: INVESTIGATING THE EFFECT OF ENVIRONMENTAL PARAMETERS ON PIGMENTATION OF SOME TALAROMYCES STRAINS.

Parisa Yousefi[1], Mohammad ali Amoozgar[2], Azam Haddadi[3]

1. Department of Microbiology, Karaj Branch, Islamic Azad University Karaj, Iran.
2. Microorganisms Bank, Iranian Biological Resource Center, Alborz provience, Iran.
3. Department of Microbiology, Karaj Branch, Islamic Azad University Karaj, Iran.

Background and Aim: The high production yields of pigments by the genus Talaromyces and their high thermal stability have implied that industrial application interests may appear in the food and textile industries. New sources of natural pigments are getting particular research interests due to the toxicity produced by synthetic colouring agents. Fungi may provide a readily available alternative source of natural pigments. In this study, we isolated a fungal strain from soils around of Lake Urmia. The growth and pigment production of the fungi was optimized to obtain highest yield. The present study aimed to assess the potential application of the pigments produced by Talaromyces spp.

Methods: In this study, we examined one strain of Talaromyces stipitatus which was supplied from IBRC by the following deposition number:IBRC30060.To investigate effect of different temperature on growth and production of pigment , the media were incubated at different temperatures for 7 days. After 7 days the radial growth rates were measured. The effect of about 3% different sources of carbohydrates were examined on pigment production.

Results: In this study, The fungi grew best and produced maximum pigment, when the temperature was maintained at 28°C. Starch was also found to be the most suitable carbohydrate source for the fungi.

Conclusion: The native strains are widely available in natural environments. These results indicate that the selected fungal strains can serve as novel sources of pigments that have important industrial applications.

Keywords: Talaromyces , pigmentation, optimization.

P238 - 661: BIOLOGICAL ACTIVITY AND STRUCTURAL CHARACTERIZATION OF A NOVEL EXOPOLYSACCHARIDE ISOLATED FROM A FOREST FUNGUS IN NORTH OF IRAN

Tayebeh Fooladi[1], Mohammad Reza Soudi[2]

1. Department of Microbiology, Faculty of Biological Sciences, Alzahra University, Vanak Village Street-1993893973,Tehran, Iran
2. Department of Microbiology, Faculty of Biological Sciences, Alzahra University, Vanak Village Street-1993893973,Tehran, Iran

Background and Aim: Fungal exopolysaccharides (EPSs) have been recognized as high value biomacromolecules with strong bioactivity. In the present study, a fungal strain, designated SF1344, producing a high level of extracellular biopolymer was isolated from forest area of Golestan province, North of Iran.

Methods: The biopolymer was purified by the sequential precipitation via solvent extraction. Paper chromatographic analysis (TLC) and FT-IR spectrum were used to structural analysis of the EPS. GC-MS along with derivizataion procedure was applied for complementary characterization. Antioxidant and antimicrobial activity were evaluated base on DPPH and MIC method, respectively.

Results: Structural analysis of the growth-dependence EPS (2.73 g/l ± 0.02), revealed the presence of hydroxyl, carboxyl, N-acetyl and amine groups. analysis of the methylated EPS showed the presence of D-glucose, D-xylofuranose and D-galactofuranose with approximate mass-to-charge-ratio of m/z 405, 475 and 441, respectively, based on GC-MS library compared to the standard sugars treated with the same reactions. Antioxidant activity based on DPPH method, suggested that EPS from SF1344, strongly scavenged radicals about (80.6%) compare to ascorbic acid (0.5 mM) as the positive control. Antimicrobial activity of the EPS was highlighted by disc diffusion (diameter of inhibition zone) and broth micro-dilution method (minimum inhibitory concentration). The best activity against S. typhimurium ATTC (14023), S. paratyphi A ATCC (1230) and S. aureus ATCC (25022) with MIC of 100 µg/ml, 50-100 µg/ml and 50-100 µg/ml, respectively, was provided by biopolymer obtained from SF1344.

Conclusion: The fungal EPS with unique structural composition exhibited strong invitro bioactivity which is powerful resources of medicinal applications.

Keywords: Antioxidant, Antimicrobial, Biopolymer, GC-MS, minimum inhibitory concentration (MIC)

P239 - 666: EFFECT OF UV RADIATION ON THE SACCHAROMYCES CEREVISIAE FOR IMPROVING ITS TOLERANCE AGAINST 1- BUTANOL

Fatemeh Sheikhi[1], Khosrow Rostami[2], Mehrdad Azin[3], Mohammad Ali Asadollahi[4], Payam Ghiaci[5], Mansour Ebrahimi[6]

1. Sugarcane Training and Research Institute of Khuzestan
2. Iranian Research Organization for Science and Technology
3. Iranian Research Organization for Science and Technology
4. Industrial Biotechnology, University of Isfahan
5. University of Gothenburg, Goteborg GU with expertise in Biotechnology, Molecular Biology, Systems Biology
6. Bioinformatics Research Group, Green Research Center, University of Qom

Background and Aim: Butanol is a class of chemicals, which has several applications such as fuel, industrial solvent, etc. Saccharomyces cerevisiae, in particular, is a well-studied organism with a long history of industrial use; e.g. in brewing and ethanol production. Different isomers of butanol exhibit different extents of toxicity. 1-butanol being the most toxic with concentrations above 1.5-2% (v/v), is inhibitory for most cells including the native 1-butanol producers. One of the reasons for this is probably that 1-butanol is a hydrophobic molecule with the strongest ability to permeate and/or interact with the cellular membrane components. Random mutagenesis by physical mutagens such as UV radiation seems to be an uncomplicated method for yeast strain improvement.

Methods: 0.1 ml of a suspension of about 1.7× 108 cells/ml of industrial strain "Ethanol red" of Saccharomyces cerevisiae was plated on YEPD-1-butanol agar medium, containing (g/l): yeast extract,10; peptone, 20; dextrose, 20; 1-butanol, 2%, 2.25% and 2.5% (v/v); agar, 20; pH 5.5. The plates were exposed to short wavelength U.V. light, (280 nm) from a distance of 20cm by using a 30W germicidal U.V. lamp in different times up to 180 seconds, until a survival of about 0.01% was obtained.

Results: Mutants that were resistant against 1-butanol (2%, 2.25% and 2.5%) were selected.

Conclusion: In this research, the procedures of creating a novel mutant of Saccharomyces cerevisiae which was screened from a mutated population of yeast, which was treated by UV light and screened in different concentration of 1-butanol is described.

Keywords: Saccharomyces cerevisiae ,UV radiation ,1- butanol tolerance

P240 - 679: THE STUDY AND IDENTIFICATION OF DETERIORATING FUNGI ON DOCUMENTS IN GOLESTAN PALACE

Melika Hajimoniri[1], Hossein riahi[2], Somayeh keypour[3]

1. Masters student
2. Professor
3. Assistant Professor

Background and Aim: Paper works are an important part of the cultural , artistic and social history of human societies,and many of these papers are lost every year due to biological damage. For this reason, the prevention of these changes, is one of the most important duties of protectors. Fungi are the most important microrganisms in degradation of cellulose based products. Fungi can produce and release a wide variety of enzymes, pigments and acids, as well as the ability to live and grow in low moisture. This study was conducted to identify cellulose degrading fung in Golsetan Palace documents. In external environments mushrooms and lichens are the most important destructive factors of historical habitates and sculptures made of rock,mortar and gypsum.

Methods: Sampling from contaminated documents was carried out using conventional deionised water and sterilized swab method and transferred to PDA(Potato Dextrose Agar) medium and in laboratory was kept in incubator at a temperature of 25+_ 3 and identify with the help of reference books.

Results: The results show that the degrading fungi of the contaminated documents are penicillium chrysogenum, P.digitatum,alternaria alternata,cladosporium cladosporioides.

Conclusion: The best strategy for protecting contaminated documents is prevention.the internal climate conditoins, which are indicated by temperature, relative humidity and absolute humidity are important factors for the growth of the fungus It is recommended to prevent fungal contamination in control centers to control the air condition and and clean the documents repeateadly.

Keywords: Deteriorating fungi, Documents, Identification, Golestan palace

P241 - 686: STUDY OF PATHOGENIC BACTERIA ISOLATED FROM FLIES IN SARI CITY, NORTH OF IRAN.

Masoumeh Eslamifar[1], Farzad Motevali Haghi[2], Mohammad Ahanjan [3], Jamshid Yazdani-Charati [4], Khalil Akbari Mohammadi[5]

1. Ph.D. Student of Microbiology, Department of Environmental Health Engineering, Faculty of Health, Mazandaran University of Medical Sciences, Sari, Iran.
2. Assistant professor of Department of Entomology, School of Health, Mazandaran University of Medical Sciences, Sari, Iran. Email: Haghi77@yahoo.com
3. Associate Professor, Department Microbiology, Faculty of Medicine, Mazandaran University of Medical Sciences, Sari, Iran. Email: ahanjan2007@gmail.com
4. Associate Professor Department of Biostatistics, School of Health, Mazandaran University of Medical Sciences, Sari, Iran. Email: Jashid_1380@yahoo.com
5. Msc of Biology, Department of Environmental Health Engineering, Faculty of Health, Mazandaran University of Medical Sciences, Sari, Iran. Email: khak43@yahoo.com.

Background and Aim: Flies are found worldwide, occurring nearly every place inhabited by human. They may transmit disease organisms to people. This study was done to isolate some of bacteria from medically important flies (Lucilia sericata & Musca domestica genera) in Sari City and determine their antibiotic susceptibility pattern.

Methods: In this experimental study, totally 2020 house flies (Musca domestica) and 600 blow flies (Lucilia sericata) were collected from 3sites of Sari city. Bacteria on the external surface and digestive system of each fly were identified by using standard tests based on Bergay, s technique. Antibiotic susceptibility test was performed by disc diffusion method based on CLSI.

Results: Most of isolated bacteria from Lucilia Sericata & Musca domestica in the current study are pathogenic. The most common isolated bacteria were E. coli (19% in M. domestica & L. sericata) and Staphylococcus aureus (15.8 % in L. sericata & 8.45% in M. domestica). Antibiotic resistance was found in isolated.

Conclusion: This study showed that flies can spread pathogenic bacteria with antibiotic resistance in human being, directly or as a vector. Therefore, their population should be controlled in North of Iran.

Keywords: Musca domestica ,Lucilia sericata, Medically important, Antibiotic resistant Bacteria, Iran.

P242 - 695: ISOLATION OF SALT TOLERANT RHIZOBACTERIA WITH PHOSPHATE SOLUBILIZATION AND NITROGEN FIXATION TRAITS FROM SOME DIFFERENT FIELDS IN KERMAN, IRAN

Marjan Saber[1], Farokh Rokhbakhsh-Zamin [2]

1. Department of Microbiology, Faculty of Science, Kerman Branch, Islamic Azad University, Kerrman, Iran.
2. Department of Microbiology, Faculty of Science, Kerman Branch, Islamic Azad University, Kerrman, Iran.

Background and Aim: Plant Growth Promoting Rhizobacteria (PGPR) are highly diverse and this research in the subject of Microbial biotechnology in agriculture focus on the saline resistant indigenous bacteria with beneficial effects on plant growth because native rhizobacteria in our arid and semi-arid regions adapted to abiotic stresses.

Methods: Soil samples were collected from rhizosphere of plants of fields in Kerman. 5 grams of rhizosphere soil samples were suspended to 45 ml sterile saline. Following serial dilution technique and using Luria agar, different colonies were obtained. The ability of isolates to fix atmospheric nitrogen was confirmed by growth of spot inoculated isolates on nitrogen free media as Burk, Jensen and Ashby's media. 10 µl aliquot of each suspension with 1×107 CFU/ml was spot inoculated on sperber agar. A clear zone around each spot was considered positive evidence of phosphate solubilization. Luria broth tubes were prepared in different NaCl concentrations as 0.5 to 9.0%. Inoculated tubes were incubated at 30oC for 7 days and growth was measured by O.D. at 660 nm.

Results: Out of 20 isolates, 5 resistant rhizobacteria to 9% NaCl were selected. They showed considerable phosphate solubilization as (SE: 3229, 3216, 3219, 3223 and 3226). Their abilities to grow on nitrogen free media also revealed nitrogen fixation trait.

Conclusion:selected rhizobacteria showed very promising results on phosphate solubilization, nitrogen fixation and salt resistance and they have very good potential to be used in further experiments for molecular identification and may be biofertilizer construction.

Keywords: Phosphate solubilization, Nitrogen fixation, NaCl resistance, Rhizobacteria, PGPR

P243 - 698: MOLECULAR ISOLATION OF RHIZOPUS ORYZAE STRAINS WHICH PRODUCE LIPASE FROM NATURAL SOURCES.

mahdizadeh Zahra[1], mahdizadeh Zahra. *[2], Hatef Ajoudanifar2[3]

1. * MSc student of biotechnology, Islamic Azad University, Damghan, Iran, Email1*: zahramehdizade1531@gmail.com
2. Faculty member of Islamic Azad University, Damghan , Iran , Email: ajoudanifar.hatef@gmail.com

Background and Aim: Introduction and objectives: Aspergilla genus includes fungi which are applied industrially. Some of the strains of this genus lead to the infection of agricultural crops like pistachio, corn and other crops and besides to the reduction of cultural crops' quality, they have led to the poisoning and mutagenesis of other creatures like human. The goal of this study is molecular isolation of Rhizopus oryzae strains which are producing lipase from natural sources.

Methods: The prepared samples were cultured on PDA medium. To produce these enzymes, mineral medium was used for solid-state fermentation. In following, the effects of carbon source, the initial pH of the medium and incubation temperature on the production of enzyme were assayed. After production of spore suspension, solid state fermentation was carried out. The enzymes were isolated after the fermentation and their enzymatic activities were evaluated. ...

Results: The Rhizopus oryzae genus showed high enzymatic activity for lipase in most of its strains and are able to produce lipase enzyme and regarding the vast expansion of this fungus in this country, it can be an important genus for biotechnology and industry driven activities. Based on the present screening, most of the local strains are able to produce the lipases ...

Conclusion: The fungi have a significant biotechnological potential in the production of enzymes and some of them are able to produce the enzymes in large industrial scale. The results about the lipase activity of ...

Keywords: Enzyme, DNA extraction, Lipase, Aspergillus, Isolation

P244 - 718: ISOLATION AND IDENTIFICATION OF IRON RESISTANT BACTERIA FROM PARDIS MOUNTAIN IN JAM AREA AND FAJR JAM GAS REFINERY COMPANY WASTEWATER AND STUDY OF HEAVY METAL BIOREMEDIATION BY THEM

Maryam Ahmadzadeh[1], Zarrindokht Emami-Karvani[2], Gholamreza Amiri[3]

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

Background and Aim: Fe (iron) is an essential element for human and other organism's cell activity but in high concentration have toxic effects on biosystemes. Heavy metals even at low concentration in environment, soil and water, due to their pollution effects could been harmful for humans, animals and plants.

Methods: Heavy metals tolerant micro-organisms can bioremediate heavy metals from their environment. in this study 21 iron tolerants strains of micro-organisms were isolated from water of subterranean canal and soil of Pardis mountain in Jam area and Fajr Jam Gas Refinary Company (F.J.G.C) wastewater.

Results:they were tolerant to high concentration of iron (up to 140 gr /lit) and they could remediate high perecent of iron. 4 strains of these micro-organisms have selected for identification. 16 Sr DNA identification results of these strains showed that 2 striains (LG3B1 and LG52B) that isolated from wastewater of (F.J.G.C) were the same and identified as (Bacillus paramycoides. NH24A2(T)) and (KP2A1 and KP4B2) isolated from Pardis mountain were as (Pseudomonas stutzeri ATCC 17588(T) and Pseudomonas songnenensis NEAU-ST5-5(T) respectively.

Conclusion: Iron and other metal enter human and all living cells through the uptake pathways by siderophore, so iron resistance micro-organisms could be used for pollutants bioremediation. It could be used the consercium of these 21 strain for heavy metal bioremediation.

Keywords:bioremediation, Heavy metals,iron, Pseudomonas stutzeri, Pseudomonas songnenensis, Bacillus paramycoides

P245 - 720: ISOLATION AND IDENTIFICATION OF HEAVY METALS RESISTANCE BACTERIA FROM PARDIS MOUNTAIN IN JAM AREA AND STUDY OF LEAD BIOREMEDIATION BY THEM

Maryam Ahmadzadeh[1], Zarrindokht Emami-Karvani[2], Gholamreza Amiri[3]

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

Background and Aim: Pb (Lead) is one of the heavy metals. Heavy metals resistance in micro-organisms result from their exposure with these compounds. Environmental contaminations of soil, water and air by heavy metals are mainly produced by industrial activities. Human exposure with lead is very dangerous and it's toxicity depends on the dosage and the route of exposure.

Methods: Bioremediation by heavy metals resistance micro-organisms is the best technique that is very simple, fast and inexpensive. In this research 21heavy metals tolerant micro-organisms were isolated from Fajr Jam Gas Refinary Company (F.J.G.C) wastewater and water of subterranean canal and soil of Pardis mountain in Jam area that they can remediate high perecent of lead.

Results:4strains of these micro-organisms were selected for molecular identification by 16 Sr DNA sequencing. The results showed that the strains (KP2A1 and KP4B2) isolated from Pardis mountain were (Pseudomonas stutzeri ATCC 17588(T)) and (Pseudomonas songnenensis NEAU-ST5-5(T)) respectively. KP2A1 could tolerant to lead nitrate up to 15mM concentration and had the ability to removed 72.8% of lead nitrate and KP4B2 could tolerant to lead nitrate up to 13mM concentration and removed 56.7% of lead nitrate. 2striains (LG3B1 and LG52B) that isolated from wastewater of (F.J.G.C) determined as (Bacillus paramycoides NH24A2(T)) by molecular identification. This strain could tolerant lead up to 15mM concentration and they removed 67.2% and 65.1% of lead nitrate respectively.

Conclusion: It is recommended to perform these experiments at a wider scale and use consortium of these 21 strains for lead bioremediation.

Keywords:bioremediation, Heavy metals ,lead, Pseudomonas stutzeri, Pseudomonas songnenensis, Bacillus paramycoides

P246 - 725: A METHOD FOR PREPARATION OF COMPETENT RALSTONIA EUTROPHA CELLS AND GENE TRANSFORMATION

Mohaddeseh Mohsenpour[1], Zahra Noormohammadi[2], Shiva Irani[3], Nour Amirmozafari[4]

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 Microbiology, Faculty of Medicine, Iran University of Medical Science and Health Services, Tehran, Iran

Background and Aim: Ralstonia eutropha have a broad prospects applying in biodegradation and bioremediation because its ability of produce Polyhydroxyalkanoates (PHAs). The aim of this study was to access a suitable method for preparation R. eutropha competent cells as a key stage for genetically modification and the study of its ability for exogenous transformation.

Methods: In this study two factor was conducted to investigate the effects of CaCl2 concentration (20mM, 50mM, and 100mM) and bacterial growth (log-phase levels: OD= 0.2, 0.4, 0.6, and 0.8) in the preparation and transformation efficiency of the R. eutropha competent cells. The pBI121 vector was transformed into prepared R. eutropha competent cell as sample plasmid vector. The accuracy of gene transformation was confirmed by colony PCR.

Results: The results showed that concentration of 20 mM CaCl2 and OD: 0.8 are two important factors affecting the transformation efficiency in R. eutropha.

Conclusion: The method that we optimized in this study for R. eutropha competent cells preparation is simple and time consuming. Due to R. eutropha is a versatile microorganism and because of biotechnological interest, optimization of a transformation method for introducing exogenous gene, can be used for R. eutropha genome editing and modification of this interest bacteria traits.

Keywords: Competent cell, Ralstonia eutropha, Gene transformation

P247 - 751: INVESTIGATION OF BIOREMEDIATION POTENTIAL AND BIOPOLYMER PRODUCTION OF PSEUDOMONADS ISOLATED FROM PETROLEUM HYDROCARBON-CONTAMINATED AREAS

Mohammad Tabatabaei[1], Mohammad Hadi Eskandari[2], Ali Goudarztalejerdi[3], Darioush Mowla[4]

1. Department of Pathobiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
2. Department of Food Science and Technology, College of Agriculture, Shiraz University, Iran.
3. Department of Pathobiology, Faculty of Veterinary Science, Bu-Ali Sina University, Hamedan, Iran
4. Environmental research center in petroleum and petrochemical industry, Shiraz University, Iran

Background and Aim: Bacteria are diverse and abundant in soils, but only a few bacteria have known to growth on hydrocarbon contaminated areas and utilize complex carbon source such as crude oil for the synthesis of Polyhydroxyalkanoate (PHA) (bioremediation potential and the ability to produce important biopolymer). Bioremediation is the conversion of chemical compounds by living organisms, especially microorganisms, into energy, cell mass and biological waste products. Some of the most important of these bioremediation products are PHA, which are a family of biopolymers produced by some bacteria and accumulated intracellularly as carbon and energy storage material.The main objective of this study was to investigate bioremediation potential and biopolymer production of Pseudomonads isolated from petroleum hydrocarbon-contaminated areas of different regions of Iranian South-Western refineries.

Methods: From 45 isolated Pseudomonads, Fifteen PHA-producing strains were identified and their morphological, physiological, genomic, and 16S rRNA gene sequence properties were studied. Screening for PHA production was carried out by incubating the isolates in PHA production medium supplemented with 2% (v/v) Gachsaran crude oil. The repeated monomer composition of the copolymer was determined by GC–MS.

Results: Approximately 1/3 of the isolates were able to produce PHA using petroleum as a carbon source and produced biopolymer composites contained monomers of: C8 (3-hydroxyoctanoate), C10 (3- hydroxydecanoate), C12 (2-hydroxydodecanoate), C14 (3-hydroxytetradecanoate) and C16 (3- hydroxydecahexanoate) which are known as biopolymers.

Conclusion: This study indicates that stressed environments like oil-contaminated sites can be potential sources for PHA producers and these isolates could be used in future bioremediation of hydrocarbons.

Keywords:bioremediation, biopolymer , PHA, Pseudomonads

P248 - 756: EXAMINATION OF PHYSICOCHEMICAL CHARACTERIZATION OF CELL SURFACES PROPERTIES OF STAPHYLOCOCCUS AUREUS.

Fariba Farniya[1], Ailar Jamalli [2], Teena Dadgar[3]

1. MS.c Gorgan Branch Islamic Azad University Gorgan Iran
2. Laboratory Sciences Research Center Golestan University Of Medical Sciences Gorgan IR Iran
3. Gorgan Branch Islamic Azad University Gorgan Iran

Background and Aim: Bacterial attachment to inert surfaces is influenced by the properties of both, substratum and bacterial cell, such as charge, hydrophobicity surface rough ness, the presence of fimbriae, flagella and production of exopolysaccharids (EPS). The properties of the bacterial cells are affected by the environmental conditions (temperature, PH or composition of the culture medium), hence, alterations in these conditions can affect the bacterial adhesion. The adhesion process of bacterial to the surfaces include interactions, such as van der waals, Lewis acid-base, hydrophobic and electrostatic interactions. Staphylococcus areus is a human phatogen that causes both chronic and nosocomial infection many of wich are mediated by their ability to adhere to medical devices and to form biofilms.

Methods: The MATS test (microbial adhesion to solvents) was performed to evaluate the Lewis acid-base properties and the hydrophilic / hydrophobic nature of bacterial surfaces under different percentages of serum of human blood (growth media). The pairs of solvents used were: chloroform (an acidic solvents) and hexadecane (apolar), ethylacetate (a basic solvent) and hexane (apolar). The percentage of bound cells to each solvent was calculated by the equation: % Adh = (1-A/A0)×100 where A0 was the absorbance of the bacterial suspension before mixing and A was the absorbance after mixing.

Results: This study has shown that under different percentage of serum of human blood staphylococcus aureus (ATCC 25923) has different interactions

Conclusion: The cells were grown on BH1 (BRAIN HEART INFUSION) include 10% serum of human blood have Low characteristic of electron-donor.

Keywords: Bacterial adhesion.hydrophobicity.

P249 - 761: SCALE UP OF RHAMNOLIPID-TYPE BIOSURFACTANT PRODUCTION BY PSEUDOMONAS AERUGINOSA MA01 IN A 5-L BIOREACTOR

Atefeh Bodagh[1], Habib Abbasi[2], Hossein Shahbani Zahiri[3], Kambiz Akbari Noghabi[4]

1. National Institute of Genetic Engineering and Biotechnology (NIGEB), P.O. Box 14155-6343, Tehran, Iran,
2. Jundi-Shapur University of Technology, Dezfol, Iran
3. National Institute of Genetic Engineering and Biotechnology (NIGEB), P.O. Box 14155-6343, Tehran, Iran,
4. National Institute of Genetic Engineering and Biotechnology (NIGEB), P.O. Box 14155-6343, Tehran, Iran,

Background and Aim: We report here the fermentative production of a rhamolipid-type biosurfactant by Pseudomonas aeruginosa MA01 from shake flasks to a bench-scale bioreactor using sunflower oil as a sole source of carbon at 30°C. Rhamnolipid biosurfactant retained its properties including surface activity, CMC, lower toxicity, high foaming, and etc. throughout fermentation in a 5-L bioreactor.

Methods: The conditions under which the study was set entailed agitation speed of 300 rpm, aeration rate 1.5 vvm, pH 7, temperature 30°C, and sunflower oil 3.5%.

Results: When the bacterium reached its maximum growth extent, it began producing rhamnolipid biosurfactant under shaking after a process time of 168 hours.

Conclusion: The highest amount of rhamnolipid biosurfactant produced by Pseudomonas aeruginosa was found to be 40 g/l which was more than 38% of the shake flask.

Keywords: Biosurfactant; Rhamnolipid; Pseudomonas aeruginosa….; Scale-up; Bioreactor

P250 - 762: INVESTIGATING THE BIOPOLYMER CAPACITY OF BACTERIA IN COAGULATION AND FLOCCULATION OF WATER TREATMENT AND SEWAGE TREATMENT

ZABIHOLLAH YOUSEFI[1], Elaheh Shanehchi[2], Seyed Noroddin Mousavinasab[3], poorya Gill [4], Mehdi Rasouli [5], Massomeh Eslamifar[6]

1. Mazandaran University of Medical Sciences , Sari, Iran,
2. Mazandaran University of Medical Sciences , Sari, Iran,
3. Mazandaran University of Medical Sciences , Sari, Iran,
4. Mazandaran University of Medical Sciences , Sari, Iran,
5. Mazandaran University of Medical Sciences , Sari, Iran,
6. Mazandaran University of Medical Sciences , Sari, Iran,

Background and Aim: In this study, biopolymers released from selected bacteria from a sewage treatment system, known as active sludge, are extracted according to the characteristics of flocculation and its characteristics. The biopolymers as a coagulant is a substitute for common chemicals in the sewage purification industry and the treatment of contaminated water.

Methods: Firstly, the biological bacteria producing bacteria from sludge produced by the municipal wastewater treatment plant are identified and separated. Different types of culture medium and differential tests are used to isolate bacteria. In the following steps, the bacterial flocculation activity is measured using extrapolated bile polymers, and the ability of the bacteria is evaluated for the highest degree of flocculation activity. The extraction and purification of the bioflocculant is carried out further. Thermal tolerance of the bioflocculant is measured. To determine the clotting properties of extracellular polymeric materials and bio-polymer specimens, the effect of bioflocculant dose and pH of the solution is tested.

Results: The purified bioflocculant from bacteria was evaluated. The study showed that extraction bioflocculant have a thermal bearing and retain their flocculation activity after having tolerated 100 ċ for more than 90% of the flocculation property. The chemical analysis shows that biofloquoland consists of 56.74% polysaccharide, 2.066% protein. FTIR spectroscopy confirms the presence of hydroxyl groups, carboxyl groups and amine groups.

Conclusion: The results of this study showed that bioflocculant produced by bacteria could be an appropriate flocculation option for water and sewage treatment, considering its biodegradability.

Keywords: Biopolymer, bioflocculant, water Treatment

P251 - 775: BIOREMEDIATION OF AZO DYES BY NEWLY ISOLATED BACTERIA FROM CONTAMINATED SOIL OF NAJAFABAD

Farnaz Kalani[1], Fatemeh Davoodi Dehaghani[2]

1. student of master of science
2. Department of Biology, Faculty of Basic Sciences, Islamic Azad University Central Tehran Branch, Tehran, Iran

Background and Aim: Azo dyes are important contaminants of water and soil. In recent years, decolorization using microbial cells has been widely used. In this study the ability of isolated bacteria to use Pigment Red 48:2, Pigment Yellow 13 or Pigment Blue 15:3 as carbon source was investigated.

Methods: Dye contaminated soil samples were collected near a textile factory in Najafabad. The ability of biodegradation was studied in Mineral Salt Medium (MSM) with 50mgL-1 of each azo dye. The initial pH was adjusted at 6.5. The medium was dispensed in 50 mL quantities into 250 mL erlenmeyer flasks. The flasks were cultivated in a shaker incubator at 200 rpm and 30°C. Thereafter, the optical density in 660nm were monitored at five hour intervals.

Results: With increasing incubation time, a gradual increase in decolorization was observed. Pigment Red 48:2 was decolorized in the first 2 hours. Pigment Yellow 13 completely decolorized within 5 days and Pigment Blue 15:3 was completely decolorized within 7 days.

Conclusion: These results are particularly showing the effectiveness of newly isolated bacteria for biodegradation of Pigment Red 48:2. Their decolorization power is better than many previous studies. The different results between the removal rates of dyes can be related to the structural differences of the dyes and metabolic pathways of bacteria in the bacterial consortium.

Keywords:bioremediation, azo dyes, bacterial consortium, Mineral Salt Medium

P252 - 789: QUALITATIVE SCREENING AND LIPID EXAMINATION OF BACTERIAL CELLS BY COLORING USING A NILE RED

Susan Solati[1], Keivan Behshti Maal[2], Ahmadreza Massah[3]

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, Khorasgan branch, Islamic azad university, Isfahan, Iran

Background and Aim: Coloring with Nile red as a method for determining the qualitative amount of lipid in many studies has been used on lipid accumulation in microorganism cells. But application of this technique has not been reported so far to investigate the production of lipid in fat producing cyanobacteria strain cell to produce biodiesel. This study is aimed to provide a quick and practical method for fat producing cyanobacteria strain screening process.

Methods: To prepare a Nile red solution for coloring, solution of 33% gr / lit was prepared in acetone solution of this material. In order to color using Nile red 1 ml of cell suspension was centrifuged at 5000 rpm and washed twice with 1 ml of phosphate buffer solution, again 1 ml of buffer solution was added to it. After homogenization, 10 micro-liters of Nile red solution was added to it. Obtained suspension was placed in dark for 5 minutes at 37 ° C and then it was observed using a fluorescent microscope.

Results: Coloring with Nile red to investigate the production of intracellular cyanobacteria cell oil, was conducted to produce biodiesel. The location of intracellular lipid accumulation was determined by golden fluorescence color, which was caused by emission of light from fluorescent color of Nile red after binding to oily compounds produced in fat-producing cyanobacteria cells.

Conclusion:: Screening fat producing cyanobacteria strains using a coloring method with Nile red fluorescent has a very good efficiency.

Keywords: Biodiesel, Cyanobacteria, Nile red coloring

P253 - 790: EVALUATION OF THE EFFECT OF SOIL BACTERIA AND TEXTILE WASTEWATER BACTERIA ON DECOLORIZATION OF RUBIN DYPRESY AND METHYL RED COLORS

Leila Darvishi[1], Azizollah. Ebrahimi[2], Mohammadreza.Mahzounieh[3]

1. university of shahrekord.Faculty of Veterinary Medicine. Department of pathobiology.Master of bacteriology
2. university of shahrekord.Faculty of Veterinary Medicine. Department of pathobiology.Assistant Professor of Microbiology
3. university of shahrekord.Faculty of Veterinary Medicine. Department of pathobiology. Professor of Microbiology

Background and Aim: Azo dyes, are the most commonly used colors, in textile industry. These colors are considered as environmental pollutant. These colors with industrial wastewater, enter the environment and pollute the ecosystem. The purpose of this study, was to isolate and identify of bacteria with ability of biodegradation of Methyl Red and Roubin Dyprsy colors from wastewater of dyeig workshops.

Methods: In this study were used of samples like: soil and two wastewater of dyeing workshops. The samples were cultivated on a nutrient agar (N.A) medium containing the colors. After checking, many bacterial colonies were isolated. After purification of colonies, 100 µl of bacteria stoks was inoculated into the medium containing nutrient broth (N B) with pH= 7 and the colors with concentration of 200 ppm . Then the samples were incubated at 30° C for 6-7 days. The samples were separate and check after centrifuged, in appropriate wavelength for each color (450 nm for Roubin Dyprsy and 490 nm for Methyl Red) and decolorization percentage of samples were measured by specterophotometr device.

Results: The eight of isolates gram-positive cocci and cocobacil, showed the highest ability to decolorization of colors. The highest decolorization was observed 46.84% for Ruby Dipersy color by O3 isolate and for Methyl Red color 80% by Y4 isolate.

Conclusion: The results showed that native strains under applicable condition, can be used for biodegradation of industrial dyes.

Keywords: Wastewater, Soil, Bacteria, Decolorization, Azo Dyes, Rubin Dyprsy, Methyl Red.

P254 - 792: QUALITATIVE INVESTIGATION OF CYANOBACTERIA STRAIN OIL PRODUCTION USING IR TECHNIQUE

Susan Solati[1], Keivan Behshti Maal[2], Ahmadreza Massah[3]

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, Khorasgan branch, Islamic azad university, Isfahan, Iran

Background and Aim:biodiesel is a renewable fuel that can be produced biological oils derived from plants, animals or microbes.

Methods: One of the appropriate techniques to demonstrate the production of convertible oil to biodiesel is IR technique. Principle of this method is to establish a peak in a certain range of developed spectrum based on unit cm-1. Production of lipid in the strain of cyanobacteria separated from urban wastewater was analyzed using IR technique and a perkinElmer model device. The investigated range of device was adjusted from 400 cm-1 to 4000 cm-1.

Results: Creating a peak in each particular region represents a specific operative group. Presence of known operative groups in biodiesel combination includes the presence of a peak at 1099 cm-1, 1164 cm-1, and 1236 cm-1 of C-O-C bond, which indicated ester factor, and long peak in 1747 cm-1 region represents carbonyl group and peaks between 2855 cm-1 and 2928 cm-1 indicate aliphatic compounds. All peaks in specified points prove the type of convertible oil to biodiesel.

Conclusion:IR technique was used as a cheap, accurate and fast method to analyze the lipids produced by cyanobacteria strain in order to produce biodiesel.

Keywords: Biodiesel,IR technique, renewable

P255 - 799: PRECISION OF HELICOBACTER PYLORI SEROLOGY IN COMPARISON TO STOOL ANTIGEN TEST

ALKA HASANI[1], Afshin Ghodrati[2], Asghar Elli Arbatan[3], Leila Dehghani [4], Akbar Hasani[5]

1. Tabriz University of Medical Sciences,Tabriz, I.R.Iran
2. Tabriz University of Medical Sciences,Tabriz, I.R.Iran
3. Tabriz University of Medical Sciences,Tabriz, I.R.Iran
4. Tabriz University of Medical Sciences,Tabriz, I.R.Iran
5. Tabriz University of Medical Sciences,Tabriz, I.R.Iran

Background and Aim: Helicobacter pylori is a bacterium allied with peptic ulcer disease, gastric adenocarcinoma, and chronic gastritis. In Iran estimated prevalence varies in different parts and with various modalities used. The clinical efficacy of noninvasive diagnostic tests varies with the age of the population studied. Immunoglobulin A (IgA) and IgG serologic tests are considered less reliable in children than adults, while other researchers supported the use of IgM. Thus, to implement diagnostic or control strategies accuracy in diagnostic tools is mandatory. We aimed to compare the efficacy of serology over stool antigen detection for H. pylori.

Methods: This study was carried out in the diagnostic laboratory of the University teaching hospital, Tabriz September 2016 to December 2017. Helicobacter pylori-specific ELISA for the presence of IgG, IgA, and IgM antibodies was done on the sera of 350 cases. H. pylori stool antigen test was performed by ELISA on fresh stool obtained from each case. Using Stool antigen test as the gold standard, sensitivity, specificity, positive predictive value (PPV), negative predictive value (NPV), and accuracy were calculated with 95% confidence intervals for IgG, IgA, and IgM.

Results: IgG demonstrated the highest sensitivity (50.5%) and was significantly more specific in children than adults. Overall, IgM demonstrated low sensitivity (36.0%) in comparison to IgG but with no statistical difference between children and adults. IgA sensitivity (17.7%) was unacceptably low. IgG correlated better with stool antigen test than IgA or IgM.

Conclusion: The results obtained suggest to use different cutoff values by age.

Keywords:H.pylori; Serology ; Stool-antigen test; Diagnosis

P256 - 813: INVESTIGATION OF FLUORENE BIODEGRADATION USING THE SPRAY PLATE METHOD

Ehteram sadat Rahimi[1], Jamshid Fooladi[2], Gholamhossein Ebrahimipour[3], Mohammad Reza Soudi[4]

1. Department of Microbiology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
2. Department of Biotechnology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
3. Department of Microbiology and Microbial Biotechnology, Faculty of Biological Sciences and Technology, University of Shahid-Beheshty, Tehran, Iran
4. Department of Microbiology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran

Background and Aim: Fluorene (Flu.), a tricyclic PAH with two benzene rings fused to a cyclopentane ring, is formed during the combustion of fossil fuels, such as in the oil refinery process, and in automotive tailpipes. This xenobiotic compound and its derivatives are a major environmental concern associated with petroleum and oil spills, waste incineration, and industrial effluents. Fluorene is one of the compounds on the EPA Priority Pollutants List.

Methods: After sampling and enrichment of surface sediment, 100 ml of diluted enrichment culture, spread on the surface of an mineral salt medium(MSM) agar plate without any carbon source. After 15 minutes, a solution of fluorene was sprayed on the surface of the plate, and the plate was incubated at 30°C for 10 to 14 days.

Results: Colonies showing degradation of fluorene were surrounded with yellow zones on MSM agar plates. Solid fluorene had disappeared from cleared areas.

Conclusion: This method was applicable to detection of bacteria able to assimilate fluorene.

Keywords: Biodegradation, Fluorene, PAHs, Spray plate method

P257 - 814: PREVALENCE AND RAPID DIAGNOSIS OF ERYTHRASMA IN A UNIVERSITY DIAGNOSTIC LABORATORY OF NORTH WEST IRAN: ROLE OF CULTURE VS. DIRECT EXAMINATION

Afshin Ghodrati[1], Alka Hasani[2], Leila dehgani[3], Fouzye farzane[4]

1. Tarbiat modares Univercity
2. Tabriz univercity of medical science
3. Tabriz univercity of medical science
4. Tabriz univercity of medical science

Background and Aim: Erythrasma is a chronic superficial infectious disorder affecting the major skin folds or the intertriginous areas of the skin. The incriminated organism is usually the bacteria however, fungal morphology also plays vital role. The disease exhibits coral-red fluorescence under Wood light or is diagnosed by gram stain. The aim of this study was to determine the frequency of erythrasma and the microorganisms implicated in adult patients with superficial or intertriginous lesions.

Methods: This prospective study enrolled out-patients possessing either superficial erythematous patch or intertriginous area of involvement. Smear was made by scraping the affected area and specimen collected was examined after gram's stain as well as subjected to culture on Sabouraud dextrose agar and blood agar.

Results: Of 108 patients enrolled, 26 (24.07 %) were diagnosed with erythrasma based gram's staining observation, which showed presence of epithelial cells covered with tiny gram positive bacilli resembling Corynebacterium spp. or yeast like cells. The disease was more common in women 73 (67.59%) and the mean age of the patients was 36.5 years. The main clinical findings were scaling and maceration. On bacterial culture Corynebacterium spp. was isolated in 12 (11.1%) cases while 8 (30.7%) cases were positive for following microorganisms: Candida spp. (16.6 %) and dermatophytes (12.5 %).

Conclusion: Erythrasma is a common condition and it persists if not treated appropriately. Rapid diagnosis is easily obtained by gram's staining, while culture is laborious. The coexistence of erythrasma with dermatophytes and Candida spp. should be considered when bacterial morphology is absent.

Keywords: Erythrasma;gram;Corynebacterium;Candida;Dermatophytes

P258 - 866: CONSTRUCTION OF AN ALGINATE BASE HYDROGEL AND EVALUATING HEALING ACTIVITIES OF MENTIONED COMPONENT AS LOCAL OINTMENT WERE THE MAIN OBJECTIVES OF THE CURRENT STUDY.

Bahman Mirzaei[1], Somayeh Etemadian[2], Hamid Reza Goli[3], Sara Bahonar[4], Sanaz Amirgholami[5], Parisima karami[6], Mojgan Farhadi[7], Rahmatollah Tavakoli[8]

1. Department of Medical Microbiology and Virology, Faculty of Medicine, Mazandaran University of Medical Sciences, Sari, Iran.
2. Department of Medical Engineering, Faculty of Engineering Maziar University, Noor, Iran
3. Department of Medical Microbiology and Virology, Faculty of Medicine, Mazandaran University of Medical Sciences, Sari, Iran.
4. Department of Medical Microbiology and Virology, Faculty of Medicine, Mazandaran University of Medical Sciences, Sari, Iran
5. Department of Medical Microbiology and Virology, Faculty of Medicine, Mazandaran University of Medical Sciences, Sari, Iran
6. Department of Medical Microbiology and Virology, Faculty of Medicine, Mazandaran University of Medical Sciences, Sari, Iran
7. Department of Medical Microbiology and Virology, Faculty of Medicine, Mazandaran University of Medical Sciences, Sari, Iran
8. The Health of Plant and Livestock Products Research Center, Mazandaran University of Medical Sciences, Sari, Iran

Background and Aim: Developing a strategy for making the alginate base hydrogel components against burned wound infections could be promising for healing the mentioned wounds followed by elimination of the biofilm forming bacteria colonization.Construction of an alginate based hydrogel and evaluating healing activities of the mentioned component as local ointment were the main objectives of the current study.

Methods: Following the collection of the honey from three different provinces of Iran, the components and structures of the collected materials were analyzed taking advantage of INSO-92 procedure subsequently, antibacterial effect of diluted three different kinds of honey against wild-type bacterial species got evaluated via agar well diffusion method. An alginate base hydrogel was prepared by the use of calcium chloride as a linker between the alginate and honey functional groups. Then, component was structurally analyzed by Fourier Transform Infrared spectroscopy (FTIR). Afterward, under in vivo conditions, the healing activities of prepared ointment were studied in infected burned rat models.

Results: According to the antibacterial effect of the honeys, 75% diluted thymol based honeys collected from Damavand province were the most efficient ones. Furthermore, it was the healing activity of mentioned ointment was proven in vivo studies. The difference between 1600-1800 wave numbers in constructed alginate-based hydrogel alginate and honey because of C=O bond variations structurally confirmed proper construction of hydrogel. The hydrogel was the better healing activity in rats burned wound too.

Conclusion: In conclusion the promising efficiency of alginate-based hydrogel in an elimination of bacterial infections was confirmed as the main aim of the current survey.

Keywords:burned wound infections ,honey, alginate based hydrogel

Biotechnology and Microbial Nanotechnology

P259 - 69: ANTI HELICOBACTER ACTIVITY OF AMOXICILLIN CONJUGATED WITH GOLD NANOPARTICLE

Nahid Yarian[1], Alireza ghanbari[2], Ali javadi[3]

1. Department of Microbiology, Islamic Azad University, Qom, Iran
2. Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran.
3. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran.

Background and Aim: Helicobacter pylori is a main causes of peptic ulcer. unfortunately, drug resistance in this bacterium has made treatment difficult; therefore new treatment methods are of importance. Using nanotechnology in medicine may be able to help humans in this field in the future Our goal is to construct gold nanoparticles and to conjugate them with commonly used therapies and investigate their anti-helicobacter effect.

Methods:gold nanoparticles were synthesized by Turkevich method and analyzed by a spectrophotometer, and electron microscope device; then nanoparticles of gold and amoxicillin were conjugated and the conjugate compounds were reanalyzed. After confirming the conjugation, the antimicrobial effects of gold nanoparticles and the free drugs alone were compared with their conjugated state by disc method.

Results: The maximum absorption wavelength of the gold nanoparticles was 522 nm. These particles were seen in almost spherical shape in the electron image and the largest amount was found in the solution of 10.0 nm. In practice, conjugation changed the solution's color from red to purple and the maximum absorption wavelength of gold nanoparticles to 670 in the conjugated amoxicillin, In analysis with FT-IR, conjugate spectrum changed compared to the free state of antibiotics. Regarding antimicrobial tests, The inhibition zone in conjugate state increased in all antibiotics relative to free mode.

Conclusion: According to the findings, gold nanoparticles alone had no antimicrobial effects at low concentrations, but could increase the activity of conjugated antibiotics against Helicobacter pylori, with optimal effect on both sensitive and resistant isolates of Helicobacter pylori.

Keywords: Anti Helicobacter ,amoxicillin,gold nanoparticle

P260 - 72: ANTI HELICOBACTER ACTIVITY OF CLARITHROMYCIN CONJUGATED WITH GOLD NANOPARTICLE

Aliraza ghanbari[1], Nahid Yarian[2], Ali javadi[3]

1. Department of Microbiology, Islamic Azad University, Qom, Iran
2. Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran.
3. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran.

Background and Aim: Helicobacter pylori is a main causes of peptic ulcer. unfortunately, drug resistance in this bacterium has made treatment difficult; therefore new treatment methods are of importance. Using nanotechnology in medicine may be able to help humans in this field in the future Our goal is to construct gold nanoparticles and to conjugate them with commonly used therapies and investigate their anti-helicobacter effect.

Methods:gold nanoparticles were synthesized by Turkevich method and analyzed by a spectrophotometer, and electron microscope device; then nanoparticles of gold and clarithromycin were conjugated and the conjugate compounds were reanalyzed. After confirming the conjugation, the antimicrobial effects of gold nanoparticles and the free drugs alone were compared with their conjugated state by disc method.

Results: The maximum absorption wavelength of the gold nanoparticles was 522 nm. These particles were seen in almost spherical shape in the electron image and the largest amount was found in the solution of 10.0 nm. In practice, conjugation changed the solution's color from red to purple and the maximum absorption wavelength of gold nanoparticles to 670 in the conjugated clarithromycin, In analysis with FT-IR, conjugate spectrum changed compared to the free state of antibiotics. Regarding antimicrobial tests, The inhibition zone in conjugate state increased in all antibiotics relative to free mode.

Conclusion: According to the findings, gold nanoparticles alone had no antimicrobial effects at low concentrations, but could increase the activity of conjugated antibiotics against Helicobacter pylori, with optimal effect on both sensitive and resistant isolates of Helicobacter pylori.

Keywords: Anti Helicobacter ,clarithromycin,gold nanoparticle

P261 - 109: IN SILICO FUSION OF ALPHA AND ALPHA TOXIN GENES OF CLOSTRIDIUM PERFRINGENS TYPE A AND CLOSTRIDIUM SEPTICUM.

Ali Haghroosta[1], Reza Pilehchian langroudi[2], Hossein Goudarzi [3], Ebrahim Faghihlo[4], Zohre Ghalavand[5], Mohammad mahdi Ranjbar [6], Marziyeh Kamalirousta[7]

1. Department of Anaerobic Bacterial Vaccines Production, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization(AREEO), Karaj, Iran.Department of Microbiology, School of Medical, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
2. Department of Anaerobic Bacterial Vaccines Production, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization(AREEO), Karaj, Iran.
3. Department of Microbiology, School of Medical, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
4. Department of Microbiology, School of Medical, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
5. Department of Microbiology, School of Medical, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
6. Department of Poultry Virology Research, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization(AREEO), Karaj, Iran.
7. School of science, Kharazmi University, Karaj, Iran.

Background and Aim: Recombinant DNA technology is an in vitro molecular techniques to isolate and manipulate DNA fragments. Using this technique, construction chimeric molecules, called recombinant DNA molecules. The chimeric fusion protein technology represents the strategy to achieve rapid, cheap and efficient expression of proteins. Designing and producing a fusion construction is the most important problem of producing large quantities of functional protein. This construction should have all necessary components of a real gene. The aim of this study was designing and producing fusion of Clostridium perfringens types A and Clostridium septicum alpha-alpha toxin genes in silico.

Methods: Clostridium perfringens type A alpha gene nucleotide sequence (cpa) and Clostridium septicum alpha gene (csa) were retrieved from GenBank. Then, to produce chimeric fusion protein, alpha-alpha fusion gene was designed. Secondary and tertiary structures and characteristics of the fusion protein was determined by online software. At last the fusion protein was validated by Rampage and ProSSA software.

Results: Designed alpha-alpha fusion gene construction have 2334bp in length which nucleotides 1 to 1194 is alpha complete toxin of C.perfringens type A, nucleotides 1195 to 1230 (36 bp) is linker sequence which is optimized for E. coli and residue sequence is alpha activated toxin of C. septicum. Rampage and ProSSA software showed the fusion protein is validation and functional.

Conclusion: The designed fusion gene construction is suitable to clone and expression in a suitable host cell, which could be used for producing of a recombinant alpha-alpha fusion protein vaccine.

Keywords: Clostridium perfringens, Clostridium septicum, Alpha toxin, Fusion gene.

P262 - 210: EFFECTS OF ELECTROMAGNETIC FIELDS EXPOSURE ON THE MAGNETOSOME PRODUCTION, ELIMINATION OF FREE RADICALS AND ANTIOXIDANT DEFENSE SYSTEMS IN MAGNETOSPIRILLUM GRYPHISWALDENSE MSR-1

Leila Hatami giklou[1], mohsen abolhassani[2], masoud ghorbani[3], Seyyed Nezamodin Hosseini[4], Behzad Ghareyazie [5], leila mamanei[6], Seyed. Fazlollah Mousavi [7]

1. Dept. of Research and Development, Research & Production complex, Pasteur Institute of Iran, Karaj, Iran
2. Hybridoma Lab., Dept. of immunology, Pasteur Institute of Iran, Tehran, Iran
3. Dept. of Research and Development, Research & Production complex, Pasteur Institute of Iran, Karaj, Iran
4. Dept. of Research and Development, Research & Production complex, Pasteur Institute of Iran, Karaj, Iran
5. Agriculture Biotechnology Research Institute of Iran (ABRII), Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran.
6. Agriculture Biotechnology Research Institute of Iran (ABRII), Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran.
7. Dept. of Microbiology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Magnetotactic bacteria integrate magnetosomes, which are unique organelles that contain nanometer-sized crystals of biogenic magnetic iron minerals with the ability to a response to the external magnetic fields. The biogenic magnetic nanoparticles (magnetosomes) was featuring tunable magnetism and high biocompatibility have been attracting much interest in medical applications especially as scavengers to eliminate intracellular reactive oxygen species. However, the physiological significance and other possible functions of these magnetosomes has not been explored in detail.
Methods: In this study, we have investigated the biological functions of magnetosomes with respect to their ability to scavenge reactive oxygen species (ROS) in Magnetospirillum gryphiswaldense MSR-1. To assess the changes in ROS levels under different magnetic field intensity conditions, cells were cultured under the microaerobic condition in medium containing the high and low intensity of magnetic field.
Results: The result showed that the antioxidant enzyme activity for eliminating of free radicals was increased by 38% when a magnetic field treatment with intensity 500 mT was added to the magnetosome biomineralization process of magnetotactic bacteria during of 50 h. The purpose of this study was to highlight the impact of magnetosome formation and antioxidant defense systems in the suppression of oxidative stress and elimination of free radicals in the magnetotactic bacteria cells.
Conclusion: This is the first study to demonstrate that the magnetic field with inducing the magnetosomes production play an important role in decreasing or eliminating ROS. This is the first study to demonstrate that the magnetic field assisted magnetosome formation and antioxidants defense systems in Magnetospirillum gryphiswaldense MSR-1.

Keywords:elimination of ROS, antioxidant enzymes activity, magnetic field, magnetosome, Magnetospirillum gryphiswaldense MSR-1

P263 - 213: BACTERIAL MAGNETIC NANOPARTICLES CONJUGATED WITH MONOCLONAL ANTIBODY AS AFFINITY-MAGNETIC MATRIX AND APPLICATION IN AFFINITY MAGNETIC SEPARATION

Leila Hatami giklou[1], mohsen abolhassani[2], masoud ghorbani[3], Seyyed Nezamodin Hosseini[4], Behzad Ghareyazie [5], leila mamanei[6], Seyed. Fazlollah Mousavi [7]

1. Dept. of Research and Development, Research & Production complex, Pasteur Institute of Iran, Karaj, Iran
2. Hybridoma Lab., Dept. of immunology, Pasteur Institute of Iran, Tehran, Iran
3. Dept. of Research and Development, Research & Production complex, Pasteur Institute of Iran, Karaj, Iran
4. Dept. of Research and Development, Research & Production complex, Pasteur Institute of Iran, Karaj, Iran
5. Agriculture Biotechnology Research Institute of Iran (ABRII), Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran.
6. Agriculture Biotechnology Research Institute of Iran (ABRII), Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran.
7. Dept. of Microbiology, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: Biogenic magnetic nanoparticles (MNPs) synthesized by magnetotactic bacteria due to their individual features and have great potential in biomedical applications recently fascinated great attention. Bacterial magnetosomes have been used experimentally as the carriers for enzymes, nucleic acids, antibodies and anticancer drugs since 1991. In addition to the unique applying properties of biogenic magnetic carriers, magnetosomes also show superiority as multifunctional targeting nanoscale drug carriers, which is hardly matched by synthetic magnetic particles. Conjugation of monoclonal antibodies to magnetosome nanoparticles is an effective method for macromolecules diagnosis and purification.

Methods:. In this study, the monoclonal antibodies against 24 kDa surface antigen of hepatitis B viruses were conjugated to super biogenic paramagnetic iron oxide (magnetosome) nanoparticles using Sulfo-LC-SPDP and Sulfo SMCC method in order to separate the HBsAg.

Results: The magnetic separation of this conjugated monoclonal antibody was found to be 28% higher than affinity chromatography method that can be used to the best alternative method instead of it's for the isolation and purification of recombinant HBsAg from yeast for vaccination. Also, studies with a Zeta Potential Analyzer showed that the magnetosomes-Ab complex had hydrated radii significantly smaller than those of WT magnetosomes and zeta potentials less than −40 mV, indicating that the magnetosome-Ab colloids were relatively stable.

Conclusion: Observed magnetosome-Ab conjugation efficiencies were as high as 71.24 µg Ab per mg magnetosomes nanoparticles, and the conjugated Abs retained most of their activity.

Keywords:magnetosome, Magnetospirillum gryphiswaldense MSR-1, affinity magnetic separation, cojugation. monoclonal antibody

P264 - 254: ENHANCING PROTEOLYTIC ACTIVITY OF LYSOBACTER ENZYMOGENES BY UV MUTAGENESIS

Reyhaneh Jafary Kelahroudi[1], Vahideh Valizadeh[2], Dariush Norouzian[3], Seyed Mohammad Atyabi[4], Reza Ahangari Cohan [5]

1. Islamic Azad University, Science and Research Branch, Tehran
2. Pasteur institute of Iran, Nanobiotehnology department
3. Pasteur institute of Iran, Nanobiotehnology department
4. Pasteur institute of Iran, Nanobiotehnology department
5. Pasteur institute of Iran, Nanobiotehnology department

Background and Aim: Increasing the amount of protease enzymes from microbial sources is in the center of attention nowadays. Random mutagenesis is a cost effective procedure for reliable short-term strain improvement and is the method of choice. In this study, UV mutagenesis was done in order to achieve a mutant Lysobacter enzymogenes strain which shows higher production rate of protease enzyme.

Methods: Random mutagenesis by UV radiation was performed at the distance of 20 cm from light source. The overnight cultures of Lysobacter enzymogenes were transferred to sterile Petri plates, which were exposed to UV light for 100, 150 and 200 seconds. Then the dilution of mutated bacteria was cultured in nutrient agar medium to obtain single colonies. The mutated isolates were randomly cultured from the nutrient agar medium to casein agar plate, as a selective media. Screening was performed by comparing the diameter of the halo zone in the skimmed milk agar plates of wild type with the mutated strains. Further, the protease activity of selected strains was quantitatively evaluated by Lowry method.

Results: The results showed that UV radiation was not hampering the growth of the bacteria even in the 200 second exposure. After screening procedure we could find some mutated strains which showed a larger halo zone diameter and increased enzymatic activity compared to the wild-typed bacteria.

Conclusion: Random mutagenesis by physical method (UV radiation) was a facile and effective way for increasing protease production in Lysobacter enzymogenes.

Keywords: Lysobacter enzymogenes, proteolytic activity, random mutagenesis, ultraviolet radiation

P265 - 258: DESIGNING A NANOBIOSENSOR FOR DETECTION OF BRUCELLA ABORTUS BASED ON POLYCLONAL ANTIBODY AND SILICA NANOPARTICLES

Arash Shams[1], Bahareh Rahimian Zarif[2], Mojtaba Salouti[3], Bahram Amini[4], Reza Shapouri[5], Sako Mirzaie[6], Ali Einloo[7], Hamidreza Taheri[8]

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 Biology, Zanjan Branch, Islamic Azad University, Zanjan, Iran.
4. Department of Biology, Zanjan University, Zanjan, Iran.
5. Department of Biology, Zanjan Branch, Islamic Azad University, Zanjan, Iran.
6. Department of Biology, Sanandaj Branch, Islamic Azad University, Sanandaj, Iran.
7. Department of Biology, Zanjan Branch, Islamic Azad University, Zanjan, Iran.
8. Department of Biology, Zanjan Branch, Islamic Azad University, Zanjan, Iran.

Background and Aim: Brucellosis is caused by the livestock, meat and dairy products contaminated with Brucella spp. Currently, there are several methods for the diagnosis of Brucella spp., but none of them have enough sensitivity and specificity. Therefore, providing a new diagnostic way with high performance seems to be necessary. In this study, detection of Brucella abortus was investigated based on polyclonal antibody against Brucella abortus and Blue silica.

Methods: Initially, blue silica nanoparticles were synthesized. Then, it was conjugated to the polyclonal antibody. After functionalization, the nanoparticles were added to the microbial suspension containing Brucella abortus. Subsequently, dye was to be released from the complex. Finally, the sensitivity and the specificity of nanobiosensor were investigated in various concentrations of Brucella abortus and other bacterial strains such as E.coli, Salmonella, Shigella, Staph aureus and Pseudomonas, respectively.

Results: Based on the results, sensitivity was determined 1.5 × 103 CFU mL-1. Also, specificity was confirmed in the presence of other bacteria.

Conclusion: The results of this study showed that, this technique has a high ability to fast detection of brucellae.

Keywords: Brucella abortus, Detection, Silica nanoparticles, polyclonal antibody.

P266 - 261: INCREMENT OF LYSOBACTER ENZYMOGENES PROTEASE ACTIVITY BY EMPLOYING COLD ATMOSPHERIC PLASMA

Faranak Faraji Tabar[1], Vahideh Valizadeh[2], Seyed Mohammad Atyabi[3], Malihe Keramati[4], Reza Ahangari Cohan [5]

1. Islamic Azad University, Science and Research Branch, Tehran
2. Pasteur Instite Of Iran, Nanobiotechnology department
3. Pasteur Instite Of Iran, Nanobiotechnology department
4. Pasteur Instite Of Iran, Nanobiotechnology department
5. Pasteur Instite Of Iran, Nanobiotechnology department

Background and Aim: Cold atmospheric plasma (CAP) is an ionized gas that has recently been extensively studied. It has mutagenic effect which can be used as a method of random mutagenesis in order to obtain improved strains at the industrial scale. In the present study, the effect of CAP was assessed for the first time on the growth and physiological characteristics of Lysobacter Enzymogenes which is the bacteria known for producing endopeptidases. Moreover, screening was done to define isolates with higher production rate of protease enzyme.

Methods: The L. Enzymogenes , ATCC 29487 was cultured in the nutrient agar medium for 48 hours at 33° C. Duration of exposure to CAP was increased gradually for 20, 45, 60, 90, 120, 150, 180 seconds in a total volume of 400 microliters of the overnight culture of the bacteria. Then the dilution of mutated bacteria was cultured in nutrient agar medium to obtain single colonies. Screening was performed using casein agar and by measuring the diameter of the halo zone in the skimmed milk agar. Then the protease activity of selected strains was determined by Lowry method.

Results: The results showed that CAP was not hampering the growth of the bacteria even at the exposure of 180 second. After screening, some mutated strains showed a larger halo zone diameter and increased enzymatic activity compared to the wild-typed bacteria.

Conclusion:CAP didn’t showed destructive effect on the bacteria growth and acted as a physical mutagen for obtaining enhanced L. Enzymogenes strains which showed higher protease production rate.

Keywords: Lysobacter Enzymogenes, Physical mutagenesis, cold atmospheric plasma (CAP), Endopeptidase

P267 - 274: THE EXPERIMENTAL MODEL OF NECROTIC ENTERITIS IN CHICKENS INDUCED BY LIVE COCCIDIOSIS VACCINE ALONG WITH CLOSTRIDIUM PERFRINGENS

Mohammad Fatemi Motlagh[1], Leyla Yahaghi[2], Seyed Latif Mousavi Gargari[3]

1. Department of Biology, Faculty of Basic Sciences, Shahed University, Tehran, Iran
2. Department of microbiology, Diako Teb Azma institute
3. Professor, Department of Cell Biology, Faculty of Basic Sciences, Shahed University, Tehran, Iran

Background and Aim: Necrotic enteritis (NE) is one of the most important enteric diseases in poultry and is a high cost to the industry worldwide. The economic impact of the disease is estimated to be US$ 2 billion annually due to mortalities and poor performance and the cost of prevention and treatment. The aim of this research is to design an efficient, applicable and repeatable necrotic enteritis model for therapeutic studies.

Methods:78 one-day-old SPF (Ross 308) broilers were divided to 13 groups including control, three B groups for challenging with three CFU clostridium perfringens, three P groups for challenging with 3 doses of coccidiosis vaccine and three BP groups challenged with six dosages of bacteria and parasite vaccine in different days. The B groups challenged by 0.5, 1 and 2×108 at days 17-20 and three times a day. The P groups challenged by 100, 150 and 200-fold of the coccidial vaccine on day 28th. The BP groups were received both bacteria and parasite vaccine. The dose and time of administration were similar to that of B and P groups. Small intestine lesions of all groups were assessed and scored following euthanized of chickens.

Results: Scoring showed lesion score 1, 2 and 5 for B, P and BP groups respectively.

Conclusion: The results showed that clostridium perfringens alone can't induce necrotic enteritis and needs predisposing agents like coccidia vaccine for induction of the model. The chickens that administered with coccidial vaccine only, showed moderate ulcer but chickens challenged with both clostridium perfringens and coccidial vaccine, induced the model significantly.

Keywords:necrotic enteritis, coccidiosis, Clostridium perfringens, Eimeria, vaccine

P268 - 275: IN SILICO DESIGNING AND ANALYSIS OF A CHIMERIC VACCINE AGAINST CLOSTRIDIUM PERFRINGENS AND EIMERIA SPP

Mohammad Fatemi Motlagh[1], Jafar Amani[2], Seyed Latif Mousavi Gargari[3]

1. Department of Biology, Faculty of Basic Sciences, Shahed University, Tehran, Iran
2. Applied Microbiology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran
3. Professor, Department of Cell Biology, Faculty of Basic Sciences, Shahed University, Tehran, Iran

Background and Aim: In poultry, necrotic enteritis (NE) is caused mainly by α toxin and the pore-forming toxin NetB of Clostridium perfringens. The ability of the bacterium to cause disease is linked to several predisposing factors that affect intestinal conditions and create a favorable environment for proliferation of bacteria. Perhaps the most important of these factors is the incidence of coccidiosis. NE incidence and the mortality rates are higher when chickens are co-infected with Eimeria (coccidiosis). The aim of this research is in silico design a bivalent vaccine against both diseases.

Methods: Amino-acid sequences of NetB, α toxin, and AMA1 (from Eimeria) were obtained from UniProt. To determine their antigenic potency, solubility and localization of proteins were analyzed separately and together as a chimer, using VAXIJEN, PROSO II, and TMHMM databases. The recombinant gene was optimized with codon optimization tools for expression in prokaryotic systems. The mRNA structure and stability were analyzed. The stability and 3-D structure of the chimeric protein (using ITASSAR) with an appropriate linker was also determined.

Results: According to our in silico analyses, the chimeric protein was stable with high antigenicity and immunogenicity.

Conclusion: In conclusion, this stable immunogenic construct could generate a potent immune response against Clostridium perfringens and Eimeria spp and may be considered as a bivalent NE and coccidiosis vaccine candidate for in vitro studies.

Keywords:necrotic enteritis, coccidiosis, Clostridium perfringens, Eimeria, bioinformatics

P269 - 301: GREEN MEDIATED SYNTHESIS AND CHARACTERIZATION OF SILVER NANOPARTICLES USING TEUCRIUM POLIUM LEAF EXTRACT AND EVALUATION OF ITS ANTIFUNGAL POTENTIAL

Solmaz Ghojavand[1], Solmaz Ghojavand and mahboobeh madani [2], Javad Karimi[3]

1. -
2. Department of Microbiology, Falavarjan Branch, Islamic Azad university, Isfahan, Iran
3. Department of biology, Faculty of Science and Technology, University of Shahid Ashrafi Isfahani, Isfahan, Iran

Background and Aim: Silver nanoparticles play an integral part in the evolution of new antimicrobials against the broad ranges of pathogenic microorganisms. The aim of this study was to produce silver nanoparticles by green methods, characterized these structures and assess their antifungal activity against Fusarium oxysporum

Methods:: In this study, we report the synthesis of nanoparticles using Teucrium polium extract. The silver nanoparticles have been characterized by UV-vis absorption spectroscopy, X-ray diffraction, Fourier transform infrared spectroscopy, and scanning electron microscopy. Also antifungal activity was determined by the well diffusion method.

Results: Results showed that the synthesized AgNps have a spherical shape and a size ranging from 37 to 122 nm. Also silver nanoparticles showed antifungal activity against Fusarium oxysporum

Conclusion: So silver nanoparticles may represent a new therapeutic option for the treatment of fungal infections.

Keywords: Silver nanoparticles; Antifungal activity; Teucrium polium

P270 - 303: ISOLATION AND IDENTIFICATION OF NATIVE XYLITOL PRODUCING YEAST STRAIN AND OPTIMIZATION OF MICROBIAL PRODUCTION

Solmaz Ghojavand [1], mahboobeh madani[2], Marjan Enshaeieh[3]

1. . Young Researchers and Elite Club, Falavarjan Branch, Islamic Azad University, Isfahan, Iran
2. Department of Microbiology, Falavarjan Branch, Islamic Azad university, Isfahan, Iran
3. Department of Biotechnology, Iranian Research Organization for Science and Technology (IROST), Tehran, Iran

Background and Aim: Among Plyols, xylitol is the sweetest poly-alcohol and due to high thermal resistance, is used as a dietary and pharmaceutical supplement. Xylitol usually is produced by chemical reduction of xylose or hemicellulotic compounds rich in xylose. Bioconversion of xylose to xylitol through micro-organisms does not need toxic catalists, is somhow easy and environmentally safe and is high valued according to defects of chemical method.

Methods: In this stdudy efforts were done to isolate yeast from soil samples, tree leaves, flowers and vegetables, then identification of native yeast with the highest xylitol production was done through PCR method. Xylitol was analysed using HPLC method. Optimization of xylitol production was done using experimental design called as Taguchi method

Results: The yeast, Rhodotorula glutinis had highest xylitol production equivalent to 12.5 g/L. The yeast in medium conditions as rpm 150, temperature 23º C, pH= 6 and incubation period 72h had highest production. Chemical conversion of xylose to xylitol is difficult; because the yield is low and product recovery need highly costed functions to separate them

Conclusion:. As a result, biological production of xylitol using microorganisms is highly regarded nowadays and isolation and optimization of xylitol production using yeasts has great importance.

Keywords:xylitol, Taguchi method, HPLC, PCR method

P271 - 304: MYCOSYNTHESIS OF SILVER NANOPARTICLES BY FUSARIUM OXYSPORUM AND ITS APPLICATION AGAINST ASPERGILLUS AND FUSARIUM

Firooze Nasr azadani[1], Firooze Nasr azadani and mahboobeh madani[2], Javad Karimi[3]

1. -
2. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran
3. 3Department of biology, Faculty of Science and Technology, University of Shahid Ashrafi Isfahani, Isfahan, Iran

Background and Aim: The microbial synthesis of nanoparticles is a green chemistry approach that combines nanotechnology and microbial biotechnology. The aim of this study was to obtain silver nanoparticles (SNPs) using aqueous extract from the filamentous fungus Fusarium oxysporum as an alternative to chemical procedures and to evaluate its antifungal activity agains Aspergillus & Fusarium.

Methods:: In this study, we report the synthesis of nanoparticles using F. oxysporum biomass. The silver nanoparticles have been characterized by UV-vis absorption spectroscopy, X-ray diffraction, Fourier transform infracted spectroscopy and scanning electron microscopy. Also antifungal activity was determined by the well diffusion method.

Results: Results showed that the synthesized AgNps have a spherical shape and a size ranging from 25 to 100 nm. Also silver nanoparticles showed antifungal activity against Fusarium and Aspergillus.

Conclusion: So silver nanoparticles may represent a new therapeutic option for the treatment of fungal infections.

Keywords:: Silver nanoparticles; Antifungal activity; Fusarium; Aspergillus

P272 - 305: BIOINFORMATICS DESIGN AND PRODUCTION OF RECOMBINANT CHIMERIC ANTIGENS OF E.COLI O157:H7 AND BRUCELLA ABORTUS AND EVALUATION OF ITS STRUCTURE

Nika Aeinechi[1], Jafar Amani[2], Hossein Fahimi[3]

1. Faculty of Advanced Sciences & Technology, Pharmaceutical Sciences Branch, Islamic Azad university
2. Microbiology Research Center, System Biology and Poisonings Institute , Baqiyatallah University of Medical Sciences , Tehran , Iran.
3. Department of Molecular and Cellular Sciences, Faculty of Advanced Sciences & Technology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, 194193311, Iran. h.fahimi@iaups.ac.ir.

Background and Aim: Diarrhea remains a major health problem for human societies and Livestock breeding systems. Intestinal bacteria which can produce intestinal poisons, plays an important role in the development of these diseases. Escherichia coli hemorrhage's shiga Toxin (EHEC), is known to cause intestinal infections in developing countries. Also, Brucella spp. are facultative intracellular Gram-negative bacteria and an important etiological agent that cause zoonotic diseases.

Methods: EspB 150-312 and Omp3161-201 were attached together with suitable linker. These multi genes were synthesized with codon optimization for E.coli host and were fused together by the application of three repeats of five hydrophobic amino acids as linkers. The structure of the synthetic construct gene, its mRNA and deduced protein and their stabilities were analyzed by bioinformatic software. Furthermore, the immunogenicity of this multimeric recombinant protein consisting of three different domains was predicted.

Results: The chimeric gene was synthesised and subcloned into pET28a by related company , then we expressed in E.coli BL21 (DE3) and purified succesfully with Ni- NTA agarose. Expression of recombinant chimeric protein was confirmed by Western blot. Concentration of recombinant protein was assayed by Bradford. The produced recombinant protein was purified by mixed mix chromatography.

Conclusion: Results from circular dichroism,with some difference, these structures can be detected in the second structure of the protein.

Keywords:E.coli O157:H7, EspB , Brucella Abortus , Omp31

P273 - 309: GREEN SYNTHESIS OF SILVER NANOPARTICLES BY STREPTOMYCES SP. OSIP1 AND ITS ANTIBACTERIAL ACTIVITY

Ali Bakhtiari sardari[1], Bahar Shahnavaz[2], Mansour Mashreghi[3], Hossein Eshghi[4]

1. msc student, Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
2. Assistant Professor,Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
3. Professor, Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
4. Professor, Departments of Chemistry, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran.

Background and Aim: Due to the unique features of the nanoparticles, they are applying in biotechnology, medical imaging and catalysts. Silver nanoparticles (AgNPs) are among the most widely used nanoparticles that show a broad spectrum of antibacterial and antiviral activity.

Methods: Production of silver nanoparticles by psychrotolerant strain of OSIP1 and antibacterial properties was investigated. The strain was cultured in TSB medium and incubated at 20 °C for 3 days. 1 mM silver nitrate solution was added to the supernatant of medium culture. The colorless solution of silver nitrate changed to deep brown, indicating the formation of AgNPs. The UV-visible and XRD spectroscopy were used to determine the purity and size of the nanoparticle. The antimicrobial property of silver nanoparticles was evaluated using ELISA. The antibacterial activity of biosynthesized AgNPs was tested on two pathogenic bacteria namely Pseudomonas aeruginosa and Bacillus subtilis. The tested bacteria were exposed to different concentrations of biosynthesized AgNPs (ranging from 1000 to 1.9 µg/ml) in Muller Hinton broth medium and incubated at of 37 °C for 24 hours.

Results: The results showed one peak (400-500 nm) was detected for silver nanoparticles in the UV-visible spectrometer indicated the presence of silver nanocrystals. This result was proved using the XRD method with nanocrystals size of 22 nm. Silver nanoparticles have a minimum inhibitory concentration (MIC) of 250 µg/ml and 31.25 µg/ml for Pseudomonas aeruginosa and Bacillus subtilis, respectively.

Conclusion: This eco-friendly method could be an alternative method for synthesis of green nanoparticle and thus has a potential to use in biomedical applications.

Keywords:: biosynthesis, UV-visible, XRD, MIC

P274 - 310: SYNTHESIS, CHARACTERIZATION AND ANTIBACTERIAL PROPERTIES OF SILVER NANOPARTICLES BY A PSYCHROTOLERANT STRAIN

Ali Bakhtiari sardari[1], Bahar Shahnavaz[2], Mansour Mashreghi[3], Hossein Eshghi[4]

1. msc student, Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
2. Assistant Professor,Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
3. Professor, Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
4. Professor, Departments of Chemistry, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran.

Background and Aim: Because of the ever-increasing resistance of pathogenic microorganisms, requires new treatments. Bacterial resistance to silver is rare; therefore, this property can be used for antibiotic-resistant bacteria.

Methods: In this study, the potential of extracellular production of silver nanoparticles by psychrotolerant strain of OSNP14 and antibacterial properties was investigated. The strain was cultured in TSB medium and incubated at 20 °C for 3 days. After time, the culture medium was centrifuged and 1 mM silver nitrate (1 M concentration) was added to the supernatant. Reduction of Ag+ to Ag0 was confirmed by the colour change of culture medium. The UV-visible and XRD spectroscopy were used to determine the purity and size of the nanoparticle. The antimicrobial property of silver nanoparticles was evaluated using microdilution method using ELISA. The pathogenic bacteria of Escherichia coli and Staphylococcus aureus were exposed to different concentrations of silver nanoparticles in Muller Hinton broth medium and incubated at of 37 °C for 24 hours. The results showed one peak (400-500 nm) was detected for silver nanoparticles in the UV-visible spectrometer indicated the presence of silver nanocrystals.

Results: This result was proved using the XRD method with nanocrystals size of 53 nm. Silver nanoparticles have a minimum inhibitory concentration (MIC) of 62.5 mg/l and 125 mg/l for Staphylococcus aureus and Escherichia coli, respectively.

Conclusion: This study showed that psychrotolerant strains are suitable for nanoparticles production due to the physicochemical properties of nanoparticles including size, zeta potential, surface morphology and crystalline structure of the elements that can inhibit bacterial pathogens.

Keywords:psychrotolerant, silver nanoparticle, antibacterial, MIC

P275 - 311: BIOSYNTHESIS OF SILVER NANOPARTICLES FROM RUMEX ALVEOLATUS AND INVESTIGATION OF THEIR POTENTIAL IMPACT ON ASPERGLLUS NIGER

Aniseh Defaei[1], Aniseh Defaei[1], Mahboobeh Madani*[2], javad karimi[3]

1. -
2. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran
3. Department of Biology, Faculty of Science and Technology, University of Shahid Ashrafi Isfahani, Isfahan, Iran

Background and Aim: Nanoparticle synthesis using plants is an alternative to conventional physical and chemical methods.

Methods: The present study describes a rapid and eco-friendly synthesis of AgNPs using Rumex alveolatus leaf extract, characterizing and the study of antifungal activity against Aspergillus niger. The synthesized AgNPs were characterized using UV-visible spectroscopy, FTIR and Scanning electron microscopy.

Results: The obtained crystaline structure of silver nanoparticles ranged in size from 50 to 90 and was mostly spherical in shape. Synthetized silver nanoparticle by Rumex alveolatus showed antifungal activity against Aspergillus niger.

Conclusion: These results provide insight into the development of new antimicrobial agents against fungi.

Keywords: Silver nanoparticle; Antifungal activity; Rumex alveolatus; A.niger

P276 - 317: RANDOM MUTAGENESIS BY NTG TO INCREASE PROTEASE ACTIVITY OF LYSOBACTER ENZYMOGENES

Malihe Amirkhani[1], Dariush Norouzian,[2], Vahideh Valizadeh,[3], Seyed Mohammad Atyabi[4], Malihe Keramati[5]

1. Islamic Azad University, Science and Research Branch, Tehran
2. Pasteur Instite Of Iran, Nanobiotechnology department
3. Pasteur Instite Of Iran, Nanobiotechnology department
4. Pasteur Instite Of Iran, Nanobiotechnology department
5. Pasteur Instite Of Iran, Nanobiotechnology department

Background and Aim: Proteases are a large group of enzymes which have many uses in medicine and industry. These enzymes could be extracted from various microorganisms. Today, strain improvement of producer strains is in the center of attention in the commercial scale. Endopeptidase Lyse C extracted from Lysobacter enzymogenes, is widely used in the sequencing of proteins. So in the present study, random mutagenesis by chemical method was employed in order to enhance protease production of L.enzymogenes strains.

Methods:L. enzymogenes strain ATCC 29487 was obtained and cultured on the nutrient agar medium at 33 °C for 48 h. A mutagenic technique using the chemical mutagen nitrosoguanidine (NTG) was applied to isolate mutants with more protease production rate. The bacterial strains were exposed to various concentrations of NTG (100, 150 and 200 µg/ml) for 20 and 40 min. In the next step, screening was done by culturing L. enzymogenes on the nutrient agar medium containing casein. The enzyme production was determined by measuring the halo zone diameter caused by casein lysis via protease enzymes, and quantitatively examined with Folin & Ciocalteus phenol reagent.

Results: It was found that NTG mutagenesis was effective for increasing the production of protease enzyme in some mutated isolates.

Conclusion: Random mutagenesis by chemical method (NTG) was an effective way for increasing protease production in Lysobacter enzymogenes.

Keywords: Lysobacter Enzymogenes, chemical mutagenesis, nitrosoguanidine (NTG)

P277 - 327: CLONING AND SOLUBLE OVER-EXPRESSION OF HUMAN GROWTH HORMONE(TRX-HIS6-HGH) IN ESCHERICHIA COLI

Seyed Mohammad Hasanpour matikolaee[1], S.Mortaza Robatjazi[2], Valiollah Babaeipour[3], Hamideh Rouhani Nejad[4]

1. Department of Science and Biotechnology, Malek Ashtar University of Technology, Tehran, Iran
2. Department of Science and Biotechnology, Malek Ashtar University of Technology, Tehran, Iran
3. Department of Science and Biotechnology, Malek Ashtar University of Technology, Tehran, Iran
4. Department of Science and Biotechnology, Malek Ashtar University of Technology, Tehran, Iran

Background and Aim: Human growth hormone is a 22kDa polypeptide which consists of 191 amino acids and two disulfide bonds. This hormone has therapeutic applications. E.coli is the preferred host since hGH has no need to post translational modification. Often the protein over-expression in E.coli is led to inclusion bodies (IBs) formation, this form has some disadvantages such as misfolding of target protein, solubilization and refolding in downstream process. The expression of hGH fused with Trx, NusA, or FH8 tags make it soluble and folded in E. coli. In this study, Trx-His6-hGH was expressed in soluble form in E.coli Rosettagami strain.

Methods: The designed gene cassette, from 5́ to 3́, consists of Trx, His6, enterokinase and hGH respectively. The cassette is first cloned in the pET-32a(+) plasmid and then transferred to E.coli DH5α and afterward transferred to the E.coli Rosettagami. The expression of hGH was performed in Luria Bertani(LB) and Terrific Broth(TB) in 25℃ in shaking flask. Results were analyzed by SDS-PAGE and confirmed with western blot.

Results:SDS-PAGE analysis showed that 58% and 55.5% of total protein expressed belongs to Trx-His6-hGH in LB and TB respectively. As the amount of biomass is important for next downstream processes, the results from TB was accepted. Of 55.5% of hGH expressed 33.7% and 18.8% expressed in soluble and IBs form respectively.

Conclusion: According to the results of this study, over-expression of soluble hGH in cytoplasm of E.coli can be achieved appropriately when fused with Trx tag.

Keywords: Recombinant Human Growth Hormone, rhGH, Trx-hGH, Cytoplasmic over-expression of rhGH, Cloning of Trx-His6-hGH,Trx-His6-hGH

P278 - 330: PURIFICATION OF SOLUBLE OVER-EXPRESSED HUMAN GROWTH HORMONE(TRX-HIS6-HGH) IN ESCHERICHIA COLI WITH NI-NTA CHROMATOGRAPHY SHOWED CLASSI NATIVE PROTEIN CONTAMINANTS.

Seyed mohammad Hasanpour matikolaee[1], S.Mortaza Robatjazi[2], Valiollah Babaeipour[3], Hamideh Rouhani Nejad[4]

1. Department of Science and Biotechnology, Malek Ashtar University of Technology, Tehran, Iran
2. Department of Science and Biotechnology, Malek Ashtar University of Technology, Tehran, Iran
3. Department of Science and Biotechnology, Malek Ashtar University of Technology, Tehran, Iran
4. Department of Science and Biotechnology, Malek Ashtar University of Technology, Tehran, Iran

Background and Aim: Human growth hormone(hGH) is a 22kDa polypeptide consists of 191 amino acids and two disulfide bonds. This hormone has therapeutic applications. E.coli is the preferred host since hGH has no need to post-translational modification. Often Trx, NusA, FH8 tags are used to express soluble protein in E.coli. By using Ni-NTA chromatography very little amount of the target protein in the protein mixture can be purified with high purity in just one step. In this study Trx-His6-hGH was purified with Ni-NTA chromatography.

Methods: The gene cassette was designed. It consists of, from 5́ to 3́, Trx, His6, enterokinase and hGH respectively. The cassette is first cloned in the pET-32a(+) plasmid and then transferred to E.coli DH5α and afterward to E.coli Rosettagami and expression was performed in Terrific Broth(TB) in 25℃. Then cleared cell lysate was applied to Ni-NTA column. The purification was done on imidazole concentrations of 5mM, 20mM and 50mM and the results were analyzed by SDS-PAGE.

Results:SDS-PAGE results showed no purity in purification with 5mM of imidazole in equilibration buffer. The purity was approved with 20mM but there were some proteins that co-purified with the Trx-His6-hGH at the elution step. The purity was significantly approved with 50mM and protein contaminants were decreased significantly. The average purity of purified Trx-His6-rhGH was 86% with the yield of 37.5%.

Conclusion: According to the results, purification of over-expressed soluble hGH in E.coli can be achieved appropriately by using His6 tag and Ni-NTA chromatography. The protein contaminants co-purified in this study belongs to worst class(Class I).

Keywords: Recombinant Human Growth Hormone, rhGH, Trx-His6-hGH, Ni-NTA Chromatography, ClassI native protein contaminants in His6-hGH Purification, Purification of Trx-His6-hGH using Ni-NTA Chromatography

P279 - 332: CLONING AND EXPRESSION OF TRUCATED FORM OF SERRALYSIN ENZYME IN ESCHERICHIA COLI

Atousa Aghai[1], *Vahideh Valizadeh[2], Maryam Rouhani[3], Reza Ahangari cohan[4], Dariush Norouzian[5], Mahsa Kavousi[6]

1. Department of Biology , East Tehran Branch , Islamic Azad University , Tehran , Iran
2. pasture institute of iran Nanobiotechnology department
3. pasture institute of iran Nanobiotechnology department
4. pasture institute of iran Nanobiotechnology department
5. pasture institute of iran Nanobiotechnology department
6. Department of Biology , East Tehran Branch , Islamic Azad University , Tehran , Iran

Background and Aim: Serralysin is a proteolytic enzyme with anti-inflammatory, fibrinolytic and anti-biofilm activity. Nowadays due to spread of the antibiotic resistance, the roll of serralysin for destroying biofilms is highlighted. The big length of the protein which hampers its penetration is the main drawback of it. It was suggested that the main strategy for increasing its biological efficiency is altering the structure without destroying the catalytic activity. Therefore, this study is planned in order to design and express the truncated form of serralysin enzyme in E.coli

Methods: Based on the bioinformatics studies the truncated form was designed and suitable primers were synthesized. The cloning procedure was done by using NcoI and XhoI restriction enzymes and pET28a expression vector. Recombinant plasmid was transformed into E.coli DH5a as a cloning host and then sub cloned into E.coli BL21 as an expression host. Cloning was confirmed by colony PCR and double restriction enzyme digestion. The recombinant enzyme expression was confirmed by SDS-PAGE and western blot analysis. Then the target protein was purified using Ni-NTA chromatography.

Results:: Cloning and expression of the recombinant truncated serralysin was confirmed by detecting the protein band on the expected size. The optimal conditions of expression was detected in the LB broth, at 37° C, IPTG 1 mM , OD600: 0.6 and expression for 4 hours.

Conclusion:: Based on the results, the designed truncated form of the serralysin was successfully expressed and purified as a recombinant protein in the E. coli. Additional analysis should be accompanied to evaluate its activity and other characteristics.

Keywords: Serralysin, Truncated form, Recombinant protein, Anti biofilm.

P280 - 337: PRODUCTION OF ANTIBIOTIC GRISEOFULVIN (GSF) FROM NATIVE NIGROSPORA SP.

Negar Ahmadi[1], Seyed abolhasan Shahzade Fazeli[2], Mahdi Moshtaghi Nikou[3]

1. University of Science and culture, Faculty of Basic Sciences and Advanced Technologies in Biology
2. University of Science and culture, Faculty of Basic Sciences and Advanced Technologies in Biology
3. Microorganisms Bank, Iranian biological Resource Center (IBRC), ACECR

Background and Aim: Production of antibiotic GSF from endophytic fungi, Nigrospora has been investigated in this project. GSF is a non-toxic antibiotic showing activity against pathogenic bacteria and fungi. This is a first report of griseofulvin producing native and endophytic Nigrospora sp. which was isolated from Iran.

Methods: The strains were supplied from Iranian Biological Resource Center (IBRC) by the following deposition numbers: IBRC30242, IBRC30268, IBRC30269 and IBRC30199 and identified based on the morphological characterizations and ITS-rDNA sequence comparison. To produce GSF, fungi mycelia were inoculated in to 500 ml Erlenmeyer flasks containing 100 ml potato dextrose broth and incubated at 25 ºC on a rotary shaker (200 rpm) for 21 days. For harvesting mycelia, the fermentation broth was centrifuged at 5000g for 15 min. For extraction of GSF, The biomass was subjected to 100 ml ethyl acetate for 3h on rotary shaker (220 rpm).

Results: The liquid phase was recovered by filter paper Whatman No. 41 and then concentrated under low oxygen pressure. Also the presence of GSF in the extract was confirmed by spectrophotometry at 290 nm. Activity of extract was evaluated against S. aureus, E. coli and phytopathogenic fungus Fusarium sp. by agar disc diffusion method.

Conclusion:GSF is one of the first antifungal natural products which used for treatment of mycotic disease such ringworm infections. This antifungal antibiotic has a wide variety of biological activities. It's anticipated that endophytic fungi comes to be a superb sources for bioactive compound.

Keywords: Endophytic, Nigrospora, Secondary metabolite, Antifungal antibiotics, Griseofulvin

P281 - 340: GREEN SYNTHESIS OF ZINC OXIDE NANOPARTICLES BY LACTOBACILLUS ACIDOPHILUS

Saeedeh Morovati[1], Mohammad Reza Zolfaghari1[2], Behin Omidi[3]

1. M.Sc of Microbiology, Islamic Azad University, Qom Branch, Qom, Iran
2. Associate professor of Micribiology Group, Islamic Azad University, Qom Branch, Qom, Iran.
3. Assistant professor of Biology Group, Islamic Azad University, Central Branch, Tehran, Iran

Background and Aim: In recent years zinc oxide nanoparticles (ZnO-NPs) as an important ceramic materials. Its used in skin conditions, textile and automotive industries, and have anticancer, antibacterial propertiest. Zinc oxide nanoparticles was synthesized by physical and chemical methods but this method have been toxic effect The another method is Green synthesis that used plants, and microorganisms. Some microorganisms was used but the most of them had pathogenic effects. In this study we used Lactobacillus acidophillus as a probiotic to biosynthesis of ZnO-Np

Methods:: Lactobacillus acidophillus (PTCC1643) was cultured in MRS broth and incubated in 37 ̊c and 5%co2 for 24 h Then its centrifuged in 4000 rpm for 20 min. Supernatant was filtered (by 0.45 micron) then supernatant was added to zinc nitrate 0.001M and incubated in 37c for 1 week. was used uv-vis spectrophotometer, XRD, XRF, AAA and TEM

Results: Result was shown that Lactobacillus acidophillus could biosynthezed ZnONp. Strong Peak was observed at 374nm in UV-Vis spectrophotometer, XRD and XRF results shows that ZnO-NPs has been produced. Size of This ZnO-Nps was 45±0.12nm and their concentration was 150.75ppm.

Conclusion: According to results, we have successfully extracellular synthesized of ZnO-NPs by Lactobacillus acidophillus supernatants. This way is simple, safe, low cost, effective and ecofriendly. In other hand Lactobacilluses are the major group of probiotics, then this bacteria are safe and without pathogenic effects. So we can used of them in medical and pharmacology purposed.

Keywords: Lactobacillus acidophilus- Biosynthesis- Zinc oxide nanoparticles

P282 - 358: INVESTIGATING THE ANTIMICROBIAL EFFECTS OF NANOPARTICLES BACTERIA ISOLATED FROM AGRICULTURAL TERRITORYS OF URMIYE , IRAN

Asadi Mohammad[1], elnaz abedini[2]

1. shahid beheshti univercite
2. 19 mayis universite

Background and Aim: The use of microorganisms in the synthesis nanoparticles is known as an eco-friendly method. Moreover, because of the ability of microorganisms to synthesize nanoparticles of various sizes, shapes and morphologies, this method has gained extreme attentions in recent years. The aim of this study was, therefore, to investigate the antimicrobial effects of nanoparticles synthesized by bacteria isolated from agricultural territorys of Urmiye , Iran.

Methods: This study was carried out in 2017. nanoparticles were characterized by SEM, EDS and XRD analyzes. The antimicrobial effects of nanoparticles were also assessed against some pathogenic bacteria.

Results: Of the 40 nanoparticle producing bacteria, the strains that were able to produce nanoparticles with high antimicrobial activity yielded under different environmental conditions, were selected. The results of scanning electron microscopy (SEM) confirmed the presence of nanoparticles with a spherical shape. EDS analysis showed that silver content of the particles was about 60 wt %. Sequence alignment and phylogenetic tree results showed that M9 and B7 strains are closely related to Bacillus cereus and Pseudomonas argentinensis, respectively, with 99% homology.

Conclusion: The results showed that the M9 and B7 strains can synthesize nanoparticles with high antimicrobial effects under different environmental conditions.

Keywords: Biosynthesis, nanoparticles, Bacillus Cereus, Antimicrobial effect

P283 - 361: LACTIC ACID PRODUCTION BY LACTOBACILLUS DELBRUECKII FROM AGRICULTURAL WASTE: ROLE OF C:N RATIO AND DIFFERENT CARBON AND NITROGEN SOURCES

Amirhossein Ghadiri[1], Saeed Veysi[2], Shideh Pourkhalili[3], Afshin Taravati[4]

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 Biology, Rasht Branch, Islamic Azad University, Rasht, Iran
4. Department of Veterinary Science, Rasht Branch, Islamic Azad University, Rasht, Iran

Background and Aim: Lactic acid and its derivatives are widely used in the food, pharmaceutical, leather and textile industries. There are two main routes for producing lactic acid; synthetic route through hydrolysis of lactonitrile and microbial route through fermentation of carbohydrates using lactic acid bacteria (LAB). The aim of this study was to investigate the effect of C:N ratio and different carbon and nitrogen sources on lactic acid production by lactobacillus delbrueckii from agricultural waste.

Methods: Lactobacillus delbrueckii PTCC 1333 was obtained from the Iranian Research Organization for Science and Technology (IROST). In this work, design of experiments (DOE) methodology using full factorial design was applied to evaluate the influence of C:N ratios (10, 20 and 30), different carbon sources (corn, rice and potato waste) and nitrogen sources (ammonium sulfate, ammonium nitrate, peptone and yeast extract) on lactic acid production. The fermentation process was held at a temperature of 37 °C for 48 hours. Lactic acid contents in fermentation broth were analyzed by high pressure liquid chromatography (HPLC) system.

Results: The highest Lactic acid production (61.18 g/l) was achieved in C:N ratio of 10:1, corn waste as a carbon source and yeast extract as a nitrogen source.

Conclusion: The results showed that C: N ratio is another important factor that affects lactic acid production that needs to be optimized in the main component of the medium. Also, corn waste due to natural sources of protein and high starch content is a good and cost-effective substrate for lactic acid production.

Keywords: Lactobacillus delbrueckii, Yeast extract, Agricultural waste, HPLC

P284 - 364: PRODUCTION AND OPTIMIZATION OF PHYTASE IN THE SOLID-STATE FERMENTATION BY ASPERGILLUS NIGER

Shahab Nazari Shad[1], Amirhossein Ghadiri[2], Mahdi Shahriarinour[3]

1. Department of Microbiology, Rasht Branch, Islamic Azad University, Rasht, Iran
2. Young Researchers and Elite Club, Rasht Branch, Islamic Azad University, Rasht, Iran
3. Department of Microbiology, Rasht Branch, Islamic Azad University, Rasht, Iran

Background and Aim: Phytase (Myo-inositol hexaphosphate phosphohydrolase) catalyzes the hydrolysis of phytate to inositol phosphates, myo-inositol, and inorganic phosphate. Phytase is widely distributed as an additive in industrial feed production in monogastric animals such as poultry and pig, playing a significant role in increasing the bioavailability of nutrients and reducing the accumulation of phosphorus in the environment. The aim of this study was to investigate the production and optimization of phytase by Aspergillus niger in a solid-state fermentation containing rice bran.

Methods: Aspergillus niger PTCC 5010 was obtained from the Iranian Research Organization for Science and Technology (IROST). In this work, design of experiments (DOE) methodology using Response surface was applied to evaluate the influence of carbon sources (maltose and sucrose) and nitrogen sources (yeast extract and peptone) on phytase production. Measurement of the enzyme activity was carried out by measuring optical density at 660 nm.

Results: The highest phytase activity (69.21 U/g) was observed in the medium containing 17.83 g/l maltose, 17.05 g/l sucrose, 9.04 g/l yeast extract and 12.24 g/l peptone.

Conclusion: Currently, phytase emerges as world's most widely used feed enzyme. In this study phytase production in SSF containing rice bran supplemented with different carbon and nitrogen sources was studied. The results showed that rice bran can be used efficiently as a nutrient source for phytase production by Aspergillus niger.

Keywords:phytase, rice bran, Aspergillus niger, solid state fermentation

P285 - 370: CHITOSAN GEL-EMBEDDED SIMVASTATIN NIOSOMES AN EFFICIENT ANTIMICROBIAL SYSTEM FOR WOUND INFECTIONS

Iman Akbarzadeh[1], saeedeh ahmadi[2], haleh bakhshandeh[3]

1. Department of Chemical and Petroleum Engineering, Sharif University of Technology, Tehran, Iran,imanakbarzadeh71@yahoo.com
2. Department of Biophysics, Islamic Azad University, Tehran, Iran, saeedeh_ahmadi@rocketmail.com
3. Department of Nanobiotechnology, Pasteur Institute of Iran, Tehran, Iran, h.bakhshandeh@gmail.

Background and Aim: Simvastatin is known as an anti-hyperlipidemic drug and is a 3-hydroxy-3-methylglutaryl coenzyme A (HMG-COA) reductase inhibitor. The inhibition of HMG-COA reductase imposes other effects other than lipid lowering such as antibacterial properties. Due to rise of bacterial resistance to traditional antibiotics introducing new drug and delivery systems is really important to control of infection specially wound infections. Niosomes are a special type of vesicular drug delivery system based on non-ionic and cholesterol surfactants which create microscopic lamellar structures.

Methods: In this study, the chitosan gel-embedded simvastatin niosomes was prepared and Its antimicrobial effects (MIC) in comparison with free drug were investigated on two effective bacterial species (Staphylococcus aureus and Pseudomonas aeruginosa) in wound infection.

Results: It was revealed that simvastatin solution and niosomal-gel formulation of simvastatin have inhibitory effects at 31.5 mg/ml and 15.25 concentrations respectively on Staphylococcus aureus growth, while drug concentrations in niosomal formulation has no inhibitory effects on Staphylococcus aureus growth. results showed that simvastatin has no inhibitory effects on gram-negative bacteria (Pseudomonas aeruginosa) growth.

Conclusion: Based on the results, it can be concluded that chitosan gel-embedded simvastatin niosomes has significant inhibitory effect on Staphylococcus aureus in comparison with simvastatin solution and therefore has a more effective effect in controlling wound infections.

Keywords:simvastatin; Niosome; Staphylococcus aureus ; Pseudomonas aeruginosa

P286 - 397: PROPIONIC ACID: METHODS OF PRODUCTION AND CURRENT STATE

Zahra Pilevar[1], Hedayat Hosseini[2]

1. Student Research Committee, Department of Food Science and Technology, National Nutrition and Food Technology Research Institute, Faculty of Nutrition Sciences and Food Technology, Shahid Beheshti University of Medical Sciences, Tehran, Iran
2. Department of Food Science and Technology, National Nutrition and Food Technology Research Institute, Faculty of Nutrition Sciences and Food Technology, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: Bio-production of propionic acid by Propionibacterium has been received considerable attention, however, there are some drawbacks and limitations for application, thereby strategies are proposed in order to increase production yield.

Methods: This review contributes to a comprehensive overview of important biotechnological aspects of propionic acid (PA) production as a common ingredient in food and biotechnology industries. Major available PA production processes, focusing mostly on biological production, were discussed.

Results: Important PA producers, principally Propionibacterium as the most prevalent one, and a wide range of reported straightforward and complex growth/production mediums were summarized. Furthermore, bioprocess variables, which could influence the production yield are described. Also, possible methods of extraction and analysis of PA as well as the introductions of different strategies in order to overcome limitations of competitive microbial production from the economical point of view are proposed.

Conclusion: Appropriate pre-adaptation of the microorganism and application of metabolically engineered mutant may lead to increased production yield of biomass and acid. The most significant factors influencing the production of PA in submerged fermentation are temperature and pH control that directly influence the high yields.

Keywords: Fermantation; Glycerol; Propionibacterium; Propionic acid; Propionic acid production; Propionic acid productivity

P287 - 421: ANTIFUNGAL EFFECTS OF GREEN SYNTHESISED SILVER NANOPARTICLES AGAINST CANDIDA GLABRATA AND CANDIDA DOUBLINIENSIS

Marzieh Jahangiri[1], Malahat Rezaee[2], Mahboobeh Madani[3]

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

Background and Aim: Candida spp. represent one of the most common pathogens which are responsible for fungal infections. Administration of antifungal drugs is often accompanied by various complications such as toxicity, drug interactions and yeast resistance to antifungal therapy.

Methods: In this study, silver nanoparticles (AgNPs) were synthesized using Zataria multiflora extract. The nanoparticles stynthesis were performed in optimized parameters of temperature, plant extract and silver nitrate concentration. Characterization of the biosynthesized nanoparticles was carried out using Zetasizer for determination of particle size and polydispersity index, X-ray diffraction, FTIR and TEM. In-vitro antifungal activity of green synthesized AgNPs was evaluated by MIC and MFC assays against Candida glabrata and Candida doubliniensis.

Results: The result showed that the particles were in size ranging between 25 and 50 nm and had polydispersity index of 0.324. X-ray diffraction (XRD) spectrum of the silver nanoparticles exhibited 2θ values corresponding to the silver nanocrystal. The FTIR results also showed interaction between the plant extract and Ag-NPs due to the similarity in the peak patterns. The results show that the silver nanoparticles effectively inhibited the growth of the tested yeasts at the concentrations of 31.25 mg/ml and 62.5 mg/ml for Candida glabrata and Candida doubliniensis, respectively.

Conclusion: AgNPs were successfully synthesized from silver nitrate solution through a simple green route, using Zataria multiflora extract as a reducing agent. In addition, the results represented that the green synthesized AgNPs has a good capability to use as antifungal agents.

Keywords: Ag nanoparticles, Antifungal effect, Candida glabrata, Candida doubliniensis, Zataria multiflora

P288 - 433: EXPRESSION OF CONSERVED DOMAIN OF P1 PROTEIN OF M. PNEUMONIAE IN E.COLI

Mahdieh Mahmoodi[1], Parvaneh Saffarian[2], Majid Esmaelizad[3]

1. Islamic Azad University, Department of Biology, Science and Research Branch, Tehran; Iran
2. Islamic Azad University, Department of Biology, Science and Research Branch, Tehran; Iran
3. Central laboratory department, Razi vaccine and serum Research institute, Agricultural Research, Education and Extension Organization(Areeo), Karaj, Alborz, Iran

Background and Aim: Mycoplasma pneumoniae is a common pathogen that causes upper and lower respiratory tract infections in people of all ages, responsible for up to 40 % of community-acquired pneumonias. It also causes a wide array of extra pulmonary infections and autoimmune phenomena. P1 protein is a surface protein on the M. pneumoniae which are functional in receptor recognition, as the probable adhesion protein.

Methods: Full length of P1 protein were analysed by bioinformatics tools. All of 93 P1 protein sequences available in NCBI data base were compared by multiple alignment tools. Consensus and hypervariable regions of P1 proteins were identified. Bioinformatics analysis identified four conserved and three hypervariable regions in 1628aa of P1 protein. All of important B-cell and T-cell epitopes were located only in two conserved b and d regions. So we chosed a highly conserved region residues 580 to 840 for experimental. For suitable expression in E. coli, all Codons were optimized in complete coding target peptide with 360 aa. Nucleotide sequence was cloned to pET32a+ vector. Expression of conserved domain of p1 protein of Mycoplasma pneumoniae was optimized in E. coli.

Results: Results showed that the recombinant partial p1 protein fusion with TRX tag sequence was expressed in Bl21 strain of E. coli successfully.

Conclusion: This peptide might be useful to developing a elisa diagnostic test.

Keywords: Mycoplasma pneumoniae- P1 protein- Expression- elisa

P289 - 440: EXPRESSION OF RECOMBINANT P48 PROTEIN OF MYCOPLASMA BOVIS IN E. COLI, APPLICABLE TO ELISA TEST

Saeideh Khakpour oqani[1], Parvaneh maghami[2], Majid Esmaelizad[3]

1. 1Islamic Azad University, Department of Biology, Science and Research Branch, Tehran; Iran;
2. 1Islamic Azad University, Department of Biology, Science and Research Branch, Tehran; Iran;
3. Central laboratory department, Razi vaccine and serum Research institute, Agricultural Research, Education and Extension Organization(Areeo), Karaj, Alborz, Iran

Background and Aim: Mcoplasma bovis causes a range of diseases in cattle throughout of the world including arthritis, pneumonia and mastitis. Early diagnosis of Mcoplasma bovis infection is important to effective treatment and control of disease.

Methods: In first step, all of nucleotide and protein sequences of p48 were collected from GenBank. The pattern of Iranian p48 protein were compare with available sequences from other regions. Based on bioinformatics tools a specific protein sequences was selected with high population coverage in Iran. For suitable expression in E.coli, all Codons were optimized in complete coding target sequence. Complete coding sequences of P48 protein was cloned to pET28a+ vector. Expression of recombinant P48 protein was optimized in Bl21 strain of E. coli.

Results: Results showed that the recombinant p48 protein of mycoplasma bovis was expressed in Bl21 strain of Ecoli successfully.

Conclusion: In this study, we attempt to design a construct for expression of recombinant P48 protein of Mycoplasma bovis as an antigen for application in diagnostic elisa test.

Keywords: Mcoplasma bovis- P48 protein- Expression- elisa test

P290 - 488: ASAIA BACTERIUM AS A POTENTIAL TOOL TO COMBAT AGAINST MALARIA AND OTHER VECTOR BORNE DISEASES

Majid Asgari[1], Abasali Raz[2], Mahdokht Ilbeigi khamseh nejad[3], Javad Dadgar Pakdel [4], Navid Dinparast D.jadid[5]

1. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran, Tehran, Iran.
2. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran, Tehran, Iran.
3. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran, Tehran, Iran.
4. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran, Tehran, Iran.
5. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran, Tehran, Iran.

Background and Aim: Malaria is a vector borne diseases which considered as one of the priorities of WHO for many years. Different strategies have been suggested to control the malaria disease. Paratransgenesis is one of the solutions for vector control. In this strategy, symbiont microorganisms are used for disrupting the parasite life cycle or vector fitness. Asaia is a bacterium from acid acetic alpha proteobacterium which stably associated with some mosquitos like several Anopheles. Asaia has some specific characteristics that make it as a potent candidate for paratransgenesis such as: cultivation in cell-free media, colonization in different parts of the vector body, easy transformation and vertical and horizontal transmission to larvae.

Methods: Different larval samples of Anopheles were collected from three provinces of Iran: Siastan and baluchestan, Hormozgan and Fars. Samples were transferred to National Insectary of Iran. Bacteria were isolated from larval and adult midguts and cultured in specific media of Asaia. Morphological and biochemical analysis were performed on samples. Molecular confirmation was performed by 16s rRNA PCR with genus specific primers.

Results: Based on the specific culture situations and molecular test, we isolated Asaia bacteria from the collected samples from the three aforementioned provinces.

Conclusion: Paratransgenesis is kind of a “Trojan Horse” avenue for achieving the control and transmission blocking of the disease. In general, Asaia has some basic characteristics such as: no pathogenicity for human, simple genetic manipulating, vertical and horizontal transmission, culture on non-expensive media. Therefore, Asaia can be considered as a very potent agent for developing a robust paratransgenesis tool to control malaria disease.

Keywords: Asaia, Malaria, paratransgenesis, Anopheles, 16s rRNA

P291 - 518: CLONING OF PHBC GENE, ENCODING PHB POLYMERASE ENZYME, IN ALCALIGENES EUTROPHUS PTCC 1615

Farzaneh Barati[1], Ezat Asgarani[2], Sara Gharavi[3]

1. M.Sc. Student of Microbial Biotechnology, Depratment of Biotechnology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran.
2. Associate Professor, Depratment of Biotechnology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran. (Corresponding Author Email: asgarani@alzahra.ac.ir)
3. Associate Professor, Depratment of Biotechnology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran.

Background and Aim: Alcaligenes eutrophus PTCC 1615 is well known for its polyhydroxybutyrate production capability. PHB polymerase which encoded by phbC gene is a key enzyme in PHB biosynthesis in A. eutrophus.

Methods: For isolation of the target DNA including phbC gene, its promoter and terminator region, primers were designed with Oligo7 and Gene runner software and then evaluated by NCBI Primer Blast. pET28(a) vector which isolated from E. coli DH5α, cleaved by BamHI/HindIII and ligated with the double digested target DNA fragment. Ligation product was transferred in to A. eutrophus PTCC 1615 by CaCl2 and heat shock method. Transformants were selected on LB-agar plate containing kanamycin (200 µg/ml). Plasmid DNAs were isolated from some colonies and PCR was performed for identifying of recombinant plasmids.

Results: The size and sequence of isolated DNA fragment were confirmed by agarose gel electrophoresis and the sequencing data, respectively. Also, according to the results of PCR and sequencing, the colonies harboring recombinant DNA molecule were identified.

Conclusion:PHB polymerase which encoded by phbC gene, is the most critical enzyme in PHB biosynthesis pathway. Many studies have been indicated that overexpression of phbC gene in PHB producing bacteria, resulted in increased PHB accumulation. In this study, the isolated phbC gene was introduced in to the parent A. eutrophus PTCC 1615 by transformation process. The existence of promoter and terminator regions in isolated DNA fragment is appropriate for overexpression in A. eutrophus at the same time with its own phbC gene, without using an inducer.

Keywords:cloning, PHB polymerase, PHB, Alcaligenes eutrophus.

P292 - 530: INVESTIGATION THE EFFECT OF SELENATE ON PHYCOCYANIN CONTENT OF SPIRULINA PLATENSIS

Fatemeh Yaghoobizadeh[1], Mohammad Roayaei Ardakani[2], Hamid Rajabi Memary[3]

1. Biotechnology and bioscience research center ,Shahid Chamran University of Ahvaz, Ahvaz,Iran
2. 1. Shahid Chamran University, faculty of science, biology department 2. Biotechnology and bioscience research center ,Shahid Chamran University of Ahvaz, Ahvaz,Iran
3. Shahid Chamran University, faculty of Agriculture

Background and Aim: Spirulina platensis is well known to have antioxidant properties, due to the presence of molecules as Phycocyanin (PC) and allophycocyanin (APC) which are the major photosynthetic accessory pigments in S. platensis. They have been used as nutrients. Selenium supplementation was found to be an effective in reducing the incidence of cancer. Nowadays, there are many interests to make Se-enriched products. Therefore, the elucidation of exact process contributed to the reactions of S. platensis to Se has great importance. For produce Se-enriched S. platensis in a large scale, the impact of different concentrations of selenate on its metabolic process need to be assessed. The aim of this study was to investigate the effects of selenate on phycocyanin content of S. platensis as an important food pigment.

Methods: In the current study, Spirulina platensis was exposed to increasing concentrations of selenate (and without selenate as control). After incubation of miroalgae at predefined time for interaction by this oxyanion, effect of its toxicity was investigated on the amount of essential pigment's content especially phycocyanin. Phycocyanin content was measured according Sharma et al (2014).

Results: The results showed that concentration of 10 mg l-1 Se improved the growth rate as compared to the control. Increasing levels of selenate cause changes of PC concentrations.

Conclusion: Microalgae assimilate selenite and selenate efficiently into selenoprotein, volatile compounds and Se-amino acids. More precise studies are needed to find the exact physiological and molecular mechanisms invalved in plant reactions to Se.

Keywords:S. platensis, selenate, phycocyanin

P293 - 531: ANALYSIS OF ALPHA AMYLASE ENZYME IN IRANIAN THERMOPHILIC STRAINS

Narges Soleimani Tabar[1], Sara Gharavi[2], Zahra Moosavinejad[3], Mahboubeh Zarrabi[4]

1. MSc. Student of Microbial Biotechnology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
2. Departmental of Biotechnology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
3. Departmental of Biotechnology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
4. Departmental of Biotechnology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran

Background and Aim: Amylase is one of the most important enzymes in biotechnology. Among amylase, alpha amylase] EC:3.2.1.1] is of more important due to its extensive application in industries and accounts for about 25% of the enzyme market. This enzyme causes the hydrolysis of the starch Glycosylated α (1-4) and produces maltose and glucose. Thermostable heat-resistant enzymes, which are mainly isolated from thermoplastic microorganisms, have large commercial applications. Alpha amylase is used in different sectors such as detergent and paper industries, bread and alcohol production and etc.

Methods: Using soil samples of a corn field and the enzymes Logel which cultivated at 50 ° C on the 1% containing starch environments, the bacteria were isolated from the alpha-amylase enzyme. Then, to select the best strain of the enzyme production, some quantitative and qualitative methods were done on Denitrosalicylic acid reagent and the suitable strain was selected. Finally, for Phyllogenetic studies of this bacterium the 16S RIBOSOMAL RNA gene primers were used.

Results:23 strains of alpha amylase enzyme were isolated in this study. After qualitative and quantitative investigations, it was found that Z3 strain has the least amount of km with the highest activity. Bioinformatics studies showed that this strain has 98% similarity with Bacillus subtilis

Conclusion: The results of this study indicate that the selected strain has the alpha-amylase enzyme, which is suitable for the industry use.

Keywords: Alpha-amylase, Thermostable, Starch

P294 - 534: TREATING KLEBSIELLA PNEUMONIAE -MEDIATED LOBAR PNEUMONIA IN MICE BY A SPECIFIC BACTERIOPHAGE

Mahboubeh Soleimani sasani[1], Fereshteh Eftekhar[2]

1. 1. Department of microbiology and microbial biotechnology, faculty of life sciences and biotechnology, Shahid Beheshti University , Tehran, Iran
2. 1. Department of microbiology and microbial biotechnology, faculty of life sciences and biotechnology, Shahid Beheshti University , Tehran, Iran

Background and Aim: Multidrug-resistant Klebsiella pneumonia, which is very common in hospital environments, causes infections in humans especially in immunocompromised patients. Phage therapy, which is an alternative antibacterial therapies, is now under serious consideration and one possible option therapies to treat bacterial infections. In our study, we isolated a lytic bacteriophage from wastewater sample and study the ability of bacterial viruses to treat mice challenged with K. pneumoniae.

Methods:A specific phage with lytic activity for K. pneumoniae ATCC10031 was isolated from sewage samples and characterized, and its potential as a therapeutic agent was evaluated in an experimental model of K. pneumoniae-mediated lobar pneumonia in mice. Mice were challenged by intranasal inoculation(i.n) with bacteria (108CFU/ml). A single intraperitoneal injection of 1010PFU/ml (MOI 100) and 109PFU/ml (MOI 10) of isolated phage administered immediately after i.n. In 2 groups, injection of this phage was delayed up to 24 h post infection and phage and bacterial numbers counting in mice blood and lungs after mice euthanasia.

Results: The results of this study suggest that Treatment by a single injection of Phage simultaneous with bacterial infection and Delayed Phage Treatment, clearance of bacteria from the mice can obtain due to phage therapy. This phage thus have the potential to be used for phage therapy. Surveys of bacterial counts for mice treated with isolated phage by the intraperitoneal route (in MOI 10 and 100) provided significant protection in infected mice from both blood and lungs tissue.

Conclusion: These results demonstrate the isolated phage can be used for the treatment of K. pneumoniae infections.

Keywords: Bacteriophage, lung infection, Klebsiella pneumoniae, lobar pneumonia

P295 - 539: APPLICATION OF CORN STEEP LIQUOR AS FACTORY OVERPLUS PRODUCTS AND NITROGEN SOURCE FOR OPTIMIZATION PROCESS OF BACTERIAL CELLULOSE PRODUCTION USING RESPONSE SURFACE METHODOLOGY

Ali Abdollahi[1], Mansour Mashreghi[2]

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 Biotechnology Research Group, Institute of Biotechnology, Ferdowsi University of Mashhad, Mashhad, Iran Center of Nano Research, Ferdowsi University of Mashhad, Mashhad, Iran

Background and Aim: Bacterial cellulose (BC) that is produced by various species of bacteria especially genus Gluconobacter have certain properties and different applications. High purity, appropriate tensile strength, water absorbance and maintenance also biocompatibility and biodegradability are some of BC unique characteristics. Examples of BC applications include substrate for preparation of bioscafolds and targeted drug delivery. Therefore, increasing BC production efficiency is highly demanded. In this research, a cheap and overplus factory products (corn steep liquor or CSL) have been used as nitrogen source for BC production. BC production was then optimized along with other factors using response surface methodology (RSM).

Methods: In this study, optimization process was performed in 3 levels using Acetobacter xylinum BPR2001. Five detrimental factors including pH (5, 6, 7), 20 g/L fructose-glucose ratios (1:1, 1:3 and 3:1), bacterial inoculation quantities (5%, 10%, 15%), ethanol (0%, 1% and 2%) and finally inexpensive extra factory products CSL (40, 80 and 120 ml/L) were considered in 46 designed experiments which all incubated at 28oC for 7 days in static cultures

Results:RSM analysis showed that pH 5, fructose-glucose 1:3 ratio, 2% ethanol; bacterial inoculation quantity 15% and 120 ml/L CSL increased BC production efficiency from its basic level in standard culture (Hestrin- shrime) which was 8 g/L to 11.55 g/L.

Conclusion: Overplus factory CSL in comparison to commercial CSL (Sigma-Aldrich) not only is more affordable but also can increase BC production efficiency up to 40%. Therefore it is suggested for BC mass production.

Keywords: Bacterial cellulose, Overplus factory products, Corn steep liquor, Response surface methodology

P296 - 544: SEQUENCING OF A LACCASE GENE FROM POLYETHYLENE- DEGRADING BACTERIUM

Marzieh Partozadeh[1], Sara Gharavi[2], Ezat Asgarani[3], Mahboubeh Zarrabi[4]

1. MSc Student 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 Biotechnology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran
4. Department of Biotechnology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran

Background and Aim: Environmental pollution is one of the major and most important problems of the modern world. Polyethylene is widely used for various applications that lead to a large quantity of plastic waste causing serious environmental problems. Laccase is involved in biodegradation of polyethylene. This enzyme can help in the oxidation of the hydro-carbon backbone of polyethylene.

Methods: In this study, sequencing of a laccase gene from a bacterium, isolated from PE waste depot was carried out. The isolate was cultured in a medium with PE as the sole carbon source. Before this step the molecular identification of the isolate had been done and the phylogenic tree determined that Acidovorax ebreus was the closest species. The FASTA sequences of laccase genes of 52 acidovorax species was received from NCBI database, then was aligned with MEGA7 software. After analyzing of conserved sequences 3 forward and 3 reverse primers were designed with these data. The primers were synthesized by sinaclon company. Bacterium extracted genome were amplified by the primers Pairwise. PCR optimization was carried out. To cover the entire gene sequence another primer design and PCR was done.

Results: The agarose gel depicted the size of the PCR product was about 900bp.

Conclusion: There are only a few reports on enzymes degrading synthetic plastics. Cloning of the genes encoding PE-degrading enzyme are under study.

Keywords: Polyethylene , biodegradation, laccase.

P297 - 552: HYALURONIC ACID PRODUCTION BY CORYNEBACTERIUM GLUTAMICUM

Mahshid Yousefian shahabeddini[1], Dr. Mohammad Barshan Tashnizi[2], Dr. Kasra Esfahani[3]

1. Department of Life Sciences Engineering, Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran
2. Department of Life Sciences Engineering, Faculty of New Sciences and Technologies, University of Tehran, Tehran, Iran
3. Department of Plant Biotechnology, National Institute of Genetic Engineering and Biotechnology, Tehran, Iran

Background and Aim: Hyaluronic acid(HA), is a glycosaminoglycan composed of repetitive disaccharide units of D-glucuronic acid and N-acetyl glucosamine, polymerized by hyaluronan synthase(HAS). HA has been shown to be an important biopolymer according to its unique properties such as high hygroscopicity, biocompatibility and non-immunogenicity that made it applicable to widespread use in medicine, pharmaceuticals and cosmetics. Due to the pathogenicity of the bacteria which make hyaluronic acids for capsule formation, microbial production of HA is tending to development of engineered bacteria which are generally recognized as safe(GRAS).

Methods:hasA(HAS coding gene) was optimized and synthesized, followed by subcloning in pEKEx2 vector which is an expression shuttle vector for E. coli/ C. glutamicum. C. glutamicum was transformed by pEKEx2-hasA by electroporation. After the extraction of produced HA, production of developed strain was examined by CTAB turbidity method.

Results: The result of double digestion of pEKEx2-hasA, showed a 1284 bp band on gel electrophoresis. colony PCR on C. glutamicum by designed primers, showed 750 bp band, amplified a region located at the middle of the gene, as expected. Comparison of the results of CTAB turbidity method, between the developed strain and the wild type, showed the presence of hyaluronic acid in extracted media.

Conclusion: In the present study, C. glutamicum ability for HA production has been investigated. The results showed a successful production of hyaluronic acid after the expression of hyaluronan synthase. Recording to C. glutamicum advantages such as fast growth, inexpensive medium and being lack of hyaluronidase, C. glutamicum can be a suitable choice for this purpose.

Keywords:hyaluronic acid, hyaluronan synthase, corynebacterium glutamicum

P298 - 553: AUGMENTATION OF BACTERIAL CELLULOSE PRODUCTION BY VARIOUS TREATMENTS AND DENSITY ALTERATION OF CORN STEEP LIQUOR AND BEET MOLASSES

Ali Abdollahi[1], Mansour Mashreghi[2]

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 Biotechnology Research Group, Institute of Biotechnology, Ferdowsi University of Mashhad, Mashhad, Iran Center of Nano Research, Ferdowsi University of Mashhad, Mashhad, Iran

Background and Aim: Nowadays bacterial cellulose (BC) because of its outstanding properties and increased applications has become more attractive than plant cellulose. However one of the major issues in BC production is the expenses of substrates (carbon and nitrogen sources). Biowastes such as plant wastes are incredible resources for many industrial products. Therefore in this research beet molasses were used for BC production.

Methods: Acetobacter xylinum BPR2001 was used for BC production as main bacterial strain. Different ratios of beet molasses and CSL were designed in 27 experiments. Experiments were included with the 50 ml/L of diluted beet molasses in water (1:4 ratio) in combination with 10 ml/L CSL (without diluting, diluted in the ratios of 1:1 and 2:1) in 3 levels (non-pretreatment, heat- pretreatment, H2SO4 and heat pretreatment). Parameters such as pH 6, ethanol 2% and bacterial inoculation quantity 10% were the same for all experiments. All experiments were conducted in triplicate at 28oC for 7 days in static cultures.

Results: Outcomes revealed that the highest amount of dry BC (5.1 g/L) can be produced from the media of heat-pretreatment molasses and non-pretreated undiluted CSL. Also the amount of 4.63 g/L dry BC was obtained from the heat-pretreatment molasses with H2SO4 and heat pretreated CSL (2:1) media. Finally, in Hestrin-Shramm standard medium with the same conditions the amount of 4 g/L dry BC was produced.

Conclusion: Pretreatment of molasses and CSL with heat and H2SO4 could improve the bacterial cellulose production as a beneficial and efficient method.

Keywords: Bacterial cellulose, Biowaste, Beet molasses, Corn steep liquor, Pretreatment

P299 - 591: THE EFFECT OF ANTIBACTERIAL POLYVINYL ALCOHOL/FE3O4@CARBON NANOTUBES NANOCOMPOSITE AGAINST PSEUDOMONAS AERUGINOSA

Hadis Hassanvand[1], Vahid pezeshkpour[2], farzaneh fasihi[3]

1. Cellular and Molecular Research Center, Yasuj University on Medical Sciences, Yasuj, Iran
2. Cellular and Molecular Research Center, Yasuj University on Medical Sciences, Yasuj, Iran
3. Cellular and Molecular Research Center, Yasuj University on Medical Sciences, Yasuj, Iran

Background and Aim: Burn wound is a suitable site for infections and drug resistant P. aeruginosa is the most common bacteria causing these infections. Therefore, research on finding effective drugs seems to be necessary. The aim of this study was to determine antibacterial bio-Nano-bio-organic structures on the burn wound infections due to P.aeruginos.

Methods: In this research study, the polyvinyl alcohol/Fe3O4@carbon nanotubes (PVA/Fe3O4@CNTs) nanocomposite was prepared by electrochemical-assisted synthesis method, characterized by FT-IR, UV–vis, FE-SEM, TEM, BET and XRD techniques, and subsequently applied for the ultrasound-assisted removal of methylene blue (MB) dye from aqueous solution and as antibacterial agent in vitro investigation against Pseudomonas aeruginosa (PAO1) bacteria by MIC, MBC, ZOI metodes.

Results:PVA/Fe3O4@CNTs at the concentration of 50 mg/ml showed the highest inhibitory effect on the growth of P. aeruginosa, whereas, at the concentration of 200 mg/ml the most lethal effect were observed.

Conclusion: Overall, the results of the study showed that the PVA/Fe3O4@CNTs have antimicrobial properties against P. aeruginosa. Therefore, using them in the treatment of infections caused by these bacteria is useful and also be used as disinfectant.

Keywords: Antibacterial, PVA/Fe3O4@CNTs, P. aeruginosa

P300 - 592: THE EFFECT OF ANTIBACTERIAL ZN4NO3 NANOPARTICLE AGAINST PSEUDOMONAS AERUGINOSA

Farzaneh Fassihi[1], Vahid pezeshkpour[2], Hadis hasnvad[3]

1. Cellular and Molecular Research Center, Yasuj University on Medical Sciences, Yasuj, Iran
2. Cellular and Molecular Research Center, Yasuj University on Medical Sciences, Yasuj, Iran
3. Cellular and Molecular Research Center, Yasuj University on Medical Sciences, Yasuj, Iran

Background and Aim: Burn wound is a suitable site for infections and drug resistant P. aeruginosa is the most common bacteria causing these infections. Therefore, research on finding effective drugs seems to be necessary. The aim of this study was to determine antibacterial bio-Nano-bio-organic structures on the burn wound infections due to P.aeruginos.

Methods: In this research study, the Zn4No3 Nanoparticle nanocomposite was prepared by electrochemical-assisted synthesis method, characterized by FT-IR, UV–vis, FE-SEM, TEM, BET and XRD techniques, and subsequently applied for the ultrasound-assisted removal of methylene blue (MB) dye from aqueous solution and as antibacterial agent in vitro investigation against Pseudomonas aeruginosa (PAO1) bacteria by MIC, MBC, ZOI metodes

Results: Zn4no3 Nanoparticle at the concentration of 100 mg/ml showed the highest inhibitory effect on the growth of P. aeruginosa, whereas, at the concentration of 200 mg/ml the most lethal effect were observed.

Conclusion: Overall, the results of the study showed that the Zn4No3 Nanoparticle have antimicrobial properties against P. aeruginosa. Therefore, using them in the treatment of infections caused by these bacteria is useful and also be used as disinfectant.

Keywords: Antibacterial, Zn4No3 Nanoparticle, P. aeruginosa

P301 - 597: ISOLATION, IDENTIFICATION AND OPTIMIZATION OF MICROBIAL OIL PRODUCTION AND EVALUATION OF THE ANTIBACTERIAL EFFECT

Fatemeh Khosravani por[1], mahboobeh madani[2], Marjan Enshaeieh[3]

1. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran
2. 1. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran
3. Department of biotechnology,Iranian Reasearch Organization for science andTechnology (IROST),Tehran,Iran

Background and Aim: Oleaginous yeasts have attracted much attention because of being single cells, lack of endotoxin and the possibility of large-scale biotechnological production. Oleaginous yeasts that are classified as GRAS (safety microorganisms) are suitable for single cell oil production

Methods: Evaluating of fatty acid profiles before and after optimization process using gas chromatography-mass spectrometry and finally evaluation of its antibacterial properties, were conducted. The best yeast strain was identified as Cryptococcus heimaeyensis using PCR method. After optimization of lipid production with Taguchi method, lipid production and lipid yield were reached to 8.05 g/L and 58.33%, respectivel. Esterified lipid composition contains linoleic acid, oleic acid and palmitic acid, as the most fatty acids in the fatty acid profile of the yeast. Oil extractions from yeasts have very similar fatty acid profile to vegetable oils and showed antimicrobial effect.

Results: Isolation, identification and optimization of microbial oil production and evaluation of the antibacterial effect was studied in this study

Conclusion:: Finding of native strains with high potential of lipid production and optimization through experimental design method is of great importance in the fields of biotechnological productions

Keywords:microbial lipid, anti-bacterial effect, gas chromatography-mass spectrometry

P302 - 602: SONOCHEMICAL INCORPORATED OF CYTOSINE IN CU-H2BPDC AS AN ANTIBACTERIAL AGENT AGAINST STANDARD AND CLINICAL STRAINS OF PROTEUS MIRABILIS WITH RSBA GENE

Vahid Pezeshkpour[1], farzaneh fasihi[2], Hadis hasnvad[3], hajar naseri[4]

1. Cellular and Molecular Research Center, Yasuj University on Medical Sciences, Yasuj, Iran
2. Cellular and Molecular Research Center, Yasuj University on Medical Sciences, Yasuj, Iran
3. Cellular and Molecular Research Center, Yasuj University on Medical Sciences, Yasuj, Iran
4. Cellular and Molecular Research Center, Yasuj University on Medical Sciences, Yasuj, Iran

Background and Aim: Burn wound is a suitable site for infections and drug resistant Proteus mirabilis is the most common bacteria causing these infections. Therefore, research on finding effective drugs seems to be necessary. The aim of this study was to determine antibacterial bio-Nano-bio-organic structures on the burn wound infections due to Proteus mirabilis.

Methods: The cytosine embedded copper based metal–organic framework (Bio-MOF) was synthesized by facile one-step sonochemical method by simply mixing of 4–4, biphenyldicarboxylic, cytosine and copper nitrate (Bio-Cu-H2bpdc-Cy). The prepared bio-MOF was characterized by XRD, FTIR and FE-SEM techniques. The effect of Cu-H2bpdc-Cy on the expression of the rsbA gene was evaluated in the clinical and standard Proteus mirabilis and study of MIC of Cu-H2bpdc-Cy by microdilution against them that have the rsbA gene. According to different concentrations of MIC, MBC concentrations was cultured on blood agar culture medium. Regarding to the concentration of MIC, gene expression changes were obtained by real-time PCR.

Results:MIC for standard and clinical strains of Proteus mirabilis was 1.6 and 1.8 mg/ml, and also MBC was obtained to be 1.8 and 2.0 mg/ml, respectively. Finally, in the real time PCR method, expression of the rsbA gene in presences of bio-Cu-H2bpdc-Cy was reduced, but has no effect on the gene expression of the Housekeeping DNA Gyrase-B gene

Conclusion: Considering the effect of Cu-H2bpdc-Cy on the rsbA gene in Proteus mirabilis bacteria, it is possible to use of Cu-H2bpdc-Cy agent as a therapeutic supplement against this bacterium.

Keywords: Proteus mirabilisCu-H2bpdc-CyrsbA geneReal time PCRSonochemical method

P303 - 633: CLONING THE MUTATED PYRAZINAMIDE ENZYME OF MYCOBACTERIUM TUBERCULOSIS IN ESCHERICHIA COLI BL21

Saeedeh Khaleghnejad[1], Farahnoosh Doustdar[2], Faramarz Mehrnajad[3]

1. Shahid Beheshti Uni of Med Sci
2. Shahid Beheshti Uni of Med Sci
3. University of Tehran

Background and Aim: Pyrazinamide (PZA) is one of first line drugs for tuberculosis treatment. It should be metabolized into its active form by the M. tuberculosis pyrazinamidase (PZase). It has been shown that resistance to PZA could be related to mutations in the PZase enzyme. Therefore the understanding of the effect of mutations on the structure of PZase and its relation with the function of the enzyme can be useful in designing better anti tuberculosis drugs. In this study one of the most important mutation which has reported in most studies were selected for study.

Methods: Using gene runner software and designing related primers and performing PCR, V155G mutation was developed in the sequence of PZase gene. Then the gene was cloned in expression vector pET21a (+). For the recombinant enzyme overexpression, the Escherichia coli BL21 (DE3) cells were transformed by the constructed vector. After induction, the recombinant PZase was purified using the Ni_NTA sepharose column and confirmed by sodium dodecyl sulfate polyacrylamide gel electrophoresis and western blotting.

Results: After cloning, expression and purification process the band of purified protein was observed with a molecular mass of 20 kDa in SDS-PAGE and in western blotting the band of enzyme was confirmed using Anti his tag antibody.

Conclusion: Using expression vector pET21a (+) and Escherichia coli BL21 (DE3) is a suitable cloning system for cloning and production of recombinant PZase and preparing the enzyme for further structural and functional studies.

Keywords: Pyrazinamidase enzyme, Mycobacterium tuberculosis, Cloning, mutation.

P304 - 642: SOLID LIPID NANOPARTICLES OF KHORASANI PROPOLIS EXTRACT: PREPARATION, CHARACTERIZATION, AND ANTIBACTERIAL ACTIVITY

Fatemeh Shahab navai[1], Fatemeh Shahab navaei[2], Ahmad Asoodeh [3]

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

Background and Aim: Propolis has been known for its antibacterial properties in medicine and cosmetics. The consumption of raw propolis restricts these benefits due to low bioavailability and low solubility. Different Nano encapsulation technologies are used to increase water solubility of propolis extract. The aim of this study is to synthetize solid lipid nanoparticles (SLNs) of khorasani propolis ethanol extract (EEP) and determine its antibacterial activity against Escherichia coli,Staphylococcus aureus,Bacillus subtilis and Pseudomonas aeruginosa.

Methods:SLNs prepared by ultra-sonication method. Briefly, 0.1 g of EEP was add to 80µl Tween-80 and 2 ml deionized water. The mixture ultrasonic for 2min (20w at 25°c) and then immediately, 15 ml cold water was added to the mixture to form SLN. The synthesized SLN size determined by dynamic light scattering (DLS). The minimum inhibitory concentration (MIC) of synthetized propolis ethanol extract SLN (PEESLN) against four pathogenic bacteria was evaluated by broth microdilution method in a range of 0.5-4mg/ml.The MBC was determined by the lowest concentration that kills 99.9% of the initial bacterial population.

Results:DLS result showed that PEESLN has less than 100nm particle size. The MIC values of PEESLN against E. coli, S. aureus, B. subtilis and P. aeruginosa, were calculated 1,1,0.5 and4 mg/ml, respectively. The MBC values of EEP was same as MIC except for E.coli (2mg/ml). The results exhibited that, PEESLN had better inhibitory effect on gram positive bacteria than gram negative bacteria.

Conclusion: Synthetized PEESLN showed good water stability and antimicrobial activity. It could be considered as an antimicrobial agent in several materials such as wound band,toothpaste and etc.

Keywords: Propolis, Solid Lipid Nanoparticles,Antibacterial activity, DLS

P305 - 664: GRAPHITIC CARBON NITRIDE NANOPARTICLE AS A SAFE AND EFFICIENT PHOTOSENSITIZER FOR PHOTODYNAMIC THERAPY OF METHICILLIN RESISTANT-STAPHYLOCOCCUS AUREUS

Esmaeil Darabpour[1], Nasim Kashef[2], Ghasem Shiravand[3], Alireza Badiei[4]

1. Department of Biology-Faculty of Science-Shahid Chamran University of Ahvaz-Ahvaz-Iran
2. Department of Microbiology, School of Biology, College of Science, University of Tehran, Tehran, Iran
3. School of Chemistry, College of Science, University of Tehran, Tehran, Iran
4. School of Chemistry, College of Science, University of Tehran, Tehran, Iran

Background and Aim: The antibiofilm efficacy of PDT as a promising therapeutic option in the management of biofilm-associated infections can be improved by nanoplatform-based photosensitizers. Certain nanoscale materials such as graphitic carbon nitride (g-C3N4) have the ability to generate reactive oxygen species (ROS), due to their unique optical absorption properties, so allowing them to behave as photosensitizers. The aim of this work was to investigate the in vitro antibiofilm photodynamic efficacy of g-C3N4 nanoparticles against methicillin resistant-Staphylococcus aureus (MRSA).

Methods: Three-dimensional (3D) nanostructures of g-C3N4 were successfully synthesized by one-pot thermal polymerization of dicyandiamide under nitrogen atmosphere. The biofilms were incubated with g-C3N4 nanoparticles and then irradiated with a white light-emitting diode (LED) light (emission range 400-800 nm). Also, we have investigated the in vitro cytotoxicity and phototoxicity of g-C3N4 nanoparticle on human dermal fibroblasts.

Results: Atomic force microscopy (AFM) measurements confirmed the nanometric size of the prepared g-C3N4 particles. Graphitic carbon nitride mediated-PDT showed significant photoinactivation against 24h-old biofilm of MRSA (>3.8 log10 CFU reduction). At the same experimental conditions, only 29.2% of the fibroblasts were photo-inactivated.

Conclusion: In conclusion, g-C3N4 nanoparticle may be a potential photosensitizer for the treatment of staphylococcal biofilm-associated infections which are accessible to light.

Keywords: Photo-inactivation, Wound infection, Nanotechnology

P306 - 667: ISOLATION AND IDENTIFICATION OF PHENOL DEGRADING YEASTS FROM CONTAMINATED SAMPLES

Kimiya Ghavami langroudi[1], shaghayegh nasr[2], Hamid Moghimi[3]

1. Department of Microbial Biotechnology, Science and Research branch, 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 Microbial Biotechnology, School of Biology, College of Science, University of Tehran, Tehran, Iran

Background and Aim: Phenol is a major environmental pollutant in wastewater of various industries including oil refineries, pharmaceuticals, and plastic industries. The biodegradation of phenols is an environmentally friendly and cost-effective technology.

Methods: Twenty-five contaminated soils and wastewaters samples were collected for isolation of high potential phenol degrading yeasts. Bushnell Hass Mineral Salts medium (BHMS) supplemented with 100, 200 and 250 mg/L phenol was used during three steps enrichment process. The screening of phenol degrading strains was carried out on solid BHMS medium and the maximum tolerance of different concentration of phenol (250, 500, 1000, 1500 mg/L) was assessed. Analysis of 26S rDNA and ITS were performed for the taxonomic characterization of isolated strains.

Results:A total of 29 yeast strains were isolated as phenol degrading strains based on their ability to growth on solid media containing 250 mg/L of phenol. Different morphotypes were identified by sequencing of universal marker genes as Candida tropicalis, Candida blankii, Rhodosporidium paludigenum, Solicoccozyma aeria, Rhodotorula paludigenum and Exophialia oligosperma. The highest level of phenol tolerant was observed by Rhodotorula toruloides at 1500 mg/L. Candida tropicalis is previously known as a potent utilizer of high initial phenol concentration up to 2000 mg/L. However, to the best of our knowledge, there was not a previous record of phenol degradation for any of above mentioned species.

Conclusion: These results indicated that the isolated strains possess a potential ability for removal of phenol pollution from wastewater and contaminated soil.

Keywords: Phenol, Bioremediation, Soil, Waste water, Yeast

P307 - 688: ANTIBACTERIAL EFFECTS OF CEFTIZOXIME COMBINED WITH METAL NANOPARTICLES AGAINST NEISSERIA GONORRHOEAE

Pouria Sheikhi[1], Somayeh Hosseini khomeirani[2], Amirhosseini Ghadiri[3], Saeed Veysi[4], Gholamreza safari[5]

1. Department of Genetic, Rasht Branch, Islamic Azad University, Rasht, Iran.
2. Department of Microbiology, Pharmaceutical Sciences Branch, Islamic Azad University.,Tehran, Iran .
3. Young Researchers and Elite Club, Rasht Branch, Islamic Azad University, Rasht, Iran.
4. Young Researchers and Elite Club, Rasht Branch, Islamic Azad University, Rasht, Iran.
5. Department of Biology, Rasht Branch, Islamic Azad University, Rasht, Iran

Background and Aim: Neisseria gonorrhoeae is the second most prevalent bacterial sexually transmitted infection (STI) worldwide, and the etiological agent, N. gonorrhoeae has developed resistance to all antimicrobials used as first-line treatments. The aim of this study was to formulate CuO and Ag nanoparticles Coated by Ceftizoxime and determine its antibacterial effects in comparison with common antibiotics against N. gonorrhoeae.

Methods:N. gonorrhoeae PTCC 1773 was obtained from the Iranian Research Organization for Science and Technology (IROST). The nanoparticles were prepared using chemical reduction method. The morphology of the nanoparticles was observed using an XRD and SEM. Antimicrobial effect of Nano formulations were investigated using well diffusion method. Minimum Inhibitory Concentrations (MIC) were determined by monitoring the growth of bacteria at 600 nm after 24 hours incubation at 35°C.

Results: In this study, the antimicrobial activity of nanoforumulation for N. gonorrhoeae was measured by well diffusion method. Antibiotic conjugation with nanoparticles shows a higher antibacterial function than any of the formulations alone.

Conclusion: The antibacterial activity of Ceftizoxime was enhanced in presence of metal nanoparticles against N. gonorrhoeae. This allows more efficient therapy compared with the antibiotic original form. Ceftizoxime@metal nanoparticles could be used as an adjuvant with antibiotic therapy, either for topical use or as a coating for biomaterials, to treat N. gonorrhoeae.

Keywords: Metal Nanoparticles, Ceftizoxime, Neisseria gonorrhoeae

P308 - 728: STUDYING THE ANTIBACTERIAL PROPERTIES OF CHITOSAN NANOPARTICLES ALONG WITH ORIGANUM ESSENTIAL OIL TO INCRESE THE NEPHROPIDAE SHELF LIFE AT REFRIGERATOR TEMPERATURE

Zohre Saeidi[1]

1. Dr. Amir Ali Anvar

Background and Aim: Along with the increasing growth of Nanotechnology use in producing antimicrobials and improving properties of nanoscale comparing with raw materials,the need to use this new knowledge is felt in order to increasing the shelf-life of food products that are prone to corruption.

Methods: The purpose of this research is to study antimicrobial properties of chitosan nanoparticles along with the Origanum essential oil to increase the shelf life of shrimp at refrigerator temperature. In this research the essential oil with concentration of 1&2% and nanoparticles of chitosan with concentration of 2% which is provided by the EPI method, are used.The samples are evaluated in 6 different treatments during a 14-day period in terms of microbial(Total Bacteria Count, Coliform and Staphylococcus Aureus)and chemical properties(TVN,TBA,PH)and sensory evaluation.

Results: The results show meaningful difference between control sample and treatments in terms of Total Bacteria Count,Coliform and Staphylococcus Aureus($P<0.05$).Two treatments which involve nanoparticles of chitosan along with concentrations of 1&2% of essential oil,have better microbial and chemical factors among the others.

Conclusion: Although these coatings are able to meaningfully decrease the amount of Staphylococcus Aureus and Coliform colonies,the highest decrease is observed in Total Count on the fourth day.This means that the limitation of storing samples in the refrigerator in terms of microbial and chemical factors shouldn't be more than 5days.The sensory evaluation also shows that there is a meaningful difference between the control and treated samples and the treatment involving a concentration of 1%of chitosan nanoparticles and 1% essential oil has scored more than the others.

Keywords: Chitosan nanoparticles, Nephropidae, Shelf life, Origanum essential oil, Antimicrobial properties

P309 - 765: IRANIAN NATIVE HONEY AS A ROBUST AGENT IN GREEN SYNTHESIS OF SILVER NANOPARTICLES WITH ANTIBACTERIAL FEATURES

Sadegh Khorrami[1], Fatemeh Jafari[2], Ali Zarrabi[3]

1. Department of Biotechnology, faculty of Advanced Technologies and Sciences
2. Department of Biotechnology, faculty of Advanced Technologies and Sciences
3. Department of Biotechnology, faculty of Advanced Technologies and Sciences

Background and Aim: Honey, as a precious gift from nature, has historically been involved in the human diet. Although this natural product has a high potential to combat a variety of diseases, especially infectious diseases, use of this substance in therapeutic processes directly, faces some limitations.

Methods: In this study the potential of Astragalus gossypinus honey in the green synthesis of silver nanoparticles has been investigated, as the interface of agricultural science, nanotechnology, and biomedicine. UV-Vis, XRD, DLS, FE-SEM, and FT-IR were used to the physicochemical characterization of products

Results: Based on the result, Astragalus honey plays an efficient role in the synthesis and stabilizing of silver nanoparticles (spherical, 42.7 nm), although it doesn't show significant antibacterial activity against investigated strains. The resulted nanoparticles have significant antibacterial activity against E. coli, P. aeruginosa, and S. aureus bacterial strains even at low concentrations (MIC= 24.5 µg/mL) and their activity is concentration dependent as well.

Conclusion: The results of this investigation revealed that Astragalus honey as a Natural Agent plays an efficient role in the synthesis and stabilizing of monodisperse silver nanoparticles. This green synthesis method is eco-friendly, low cost and applicable, in addition, silver nanoparticles synthesized by this method have good physicochemical properties and antibacterial behavior, although Astragalus honey doesn't show significant antibacterial activity in this study.

Keywords: Iranian Native Honey, Green Synthesis, Silver Nanoparticles, Antibacterial Agent

P310 - 781: OPTIMIZATION OF CARBON AND NITROGEN SOURCES FOR THE PRODUCTION OF LYSINE IN CORYNEBACTERIUM GLUTAMICUM BY COLORIMETRIC METHOD

Hadis Akbarian[1], Jamshid fooladi[2], Seyyedehzahra Mousavi Nejad[3]

1. Biotechnology group, Biology Science Department, Alzahra University, Tehran, Iran
2. Biotechnology group, Biology Science Department, Alzahra University, Tehran, Iran
3. Biotechnology group, Biology Science Department, Alzahra University, Tehran, Iran

Background and Aim: The use of microorganisms in production of economically and functionally valuable materials is taken into consideration in recent years. Amino acids are valuable substances that can be used in various industrial fields, including the pharmaceutical industry, healthcare products, food and feed. Lysine is essential amino acid in animal foods and used as a supplement to livestock, pigs and poultry.

Methods: In this study, increasing the production of lysine by C. glutamicum was investigated and quantitative production checked by Colorimetric method .So carbon and nitrogen source to production of lysine by changing a factor method was optimized.

Results: The results showed that the highest amount of lysine was produced in high fructose corn syrup as carbon source and ammonium sulfate as nitrogen source in 96 h incubation at pH=7,temptaure=30 °C and 150 rpm.

Conclusion: Today, the biotechnology production amine acids due to their extensive usage is remarkable. By optimizing various factors in the production of them by microorganisms, production efficiency can be increased.

Keywords: Optimization, Production, Lysine, Colorimetric method

P311 - 807: THE EFFECT OF MAGNETIC NANOPARTICLES ON THE GROWTH OF LUMINESCENT BACTERIA

Shadab Jabbarzadeh[1], Mehdi Zeinoddini[2], Saman Hosseinkhani[3], Azadeh Azizi [4]

1. Malek Ashtar University of Technology
2. Malek Ashtar University of Technology
3. Malek Ashtar University of Technology
4. Malek Ashtar University of Technology

Background and Aim: Magnetic nanoparticles are one of the most important nanoparticles that have been identified in microbiology by their effects on growth, morphology, and the yield of different bacteria. From 1995 to 2013, the EPA (U.S. Environmental Protection Agency) confirmed the performance of nearly 500 innovative environmental technologies for measuring water pollution. Exposure time for specimens varies from 5 minutes to 2 hours. One of these methods is the use of bioluminescence bacteria as biological markers that date back to the 1950s. Therefore, optimizing of these bacteria is very important for the measurement of water pollution. One of the optimization methods is use of Fe3O4 magnetic nanoparticles.

Methods: Two strains of Vibrio Fischeri and Vibrio Harvey cultured in a swa medium with different concentrations of 20 nm nanoparticles of nano-us (50,100,150 and 200 µg / ml) at 25 ° C and 200 rpm. The growth rate and light emission of bacteria was measured using spectrophotometer and luminometer in 2 hours intervals, respectively.

Results: Results The data was shown that light emission of V.fischeri and V.harvey in two different concentration of 150 microgram per ml and 50 microgram per ml, have positive effects on growth rate and cause more stability of light from bioluminescence activity, respectively.

Conclusion: Optimizing luminescence bacteria improves the efficiency of measuring water pollution. Therefore, more precise measuring kits can be designed.

Keywords:luminescent, optimization, Vibrio, light emission

P312 - 815: STUDY OF THE EFFECT OF SILVER NANOPARTICLES ON GRAM NEGATIVE BACTERIA ISOLATED FROM RESISTANT URINARY TRACT INFECTION

Armaghan Azimi[1], Taqipour. Sh[2]

1. Lahijan Free University
2. Lahijan Free University

Background and Aim: Urinary tract infection is one of the most common human infections. Due to antibiotic resistance, using a nanoparticle can eliminate a wide range of bacteria. When the silver becomes smaller in size to nanometres, silver increases its microbial properties, which is why it is important in medicine to investigate its effects.

Methods: From 250 clinical specimens collected from the pathophysiological laboratory of Lahijan, 131 gram negative bacterial agents were isolated from UTI. The bacteria that were grown were identified by biochemical methods. Antimicrobial tests were performed according to the CLSI standard. The isolated gram negative bacteria were exposed to different concentrations (50 ppm, 200 ppm, 400 ppm) and the diameter of the non-growth hole was measured.

Results: The results showed that E. coli were the most common bacteria responsible for UTI, with the frequency of 73.62%, Klebsiella 17.25%, Enterobacter 6.85%. Other isolates including Pseudomonas, Proteus, Citrobacter, providencia, Serratia and Morganella had the lowest incidence of 2.28%. All samples were sensitive to silver nanoparticles at concentrations of 100 ppm and 200 ppm. Enterobacter aerogenes was highest at 800 ppm concentration and Proteus vulgaris showed a lowest inhibition zone at 50 ppm.

Conclusion: This study showed a direct correlation between the concentration of nanoparticles and the percentage of bacterial elimination, as the concentration of silver nanoparticles increased, more bacteria were lost.

Keywords:UTI, Nanoparticles, Antibiotics resistance

P313 - 847: COMPARISON OF ANTIBACTERIAL ACTIVITY OF GRAPHEN OXIDE- SILVER NANOCOMPOSITE SYNTHESIZED BY TWO DIFFERENT GREEN APPROACHES

Sadegh Khorrami[1], Zahra Abdollahi[2], Ghazaleh Eshaghi[3], Ali Zarrabi[4]

1. Department of Biotechnology, Faculty of Advanced Sciences and Technologies, University of Isfahan, Isfahan, Iran
2. Department of Biotechnology, Faculty of Advanced Sciences and Technologies, University of Isfahan, Isfahan, Iran
3. Department of Biotechnology, Faculty of Advanced Sciences and Technologies, University of Isfahan, Isfahan, Iran
4. Department of Biotechnology, Faculty of Advanced Sciences and Technologies, University of Isfahan, Isfahan, Iran

Background and Aim: There are many disagreements on the antibacterial behavior of Graphene Oxide (GO). However, GO was used as an ideal substrate for tethering metal nanoparticles to overcome their drawbacks, because of its unique properties, such as biocompatibility. Hence, exploration of the antibacterial properties of graphene-based nanocomposites has been one of the most important research fields.

Methods: In this study, Ag-GO nanocomposites were green synthesized by using Walnut extract at two different approaches: 1) GO + silver nitrate + extract, and 2) GO + extract + silver nitrate. Physicochemical properties of the final products were characterized by UV-Vis, FT-IR, XRD, and FE-SEM. Subsequently, the antibacterial activity of the products was assessed on both gram-positive (Staphylococcus aureus) and gram-negative (Pseudomonas aeruginosa) bacterial strains and their activity compared with silver nanoparticles and Tetracycline.

Results: According to the results, GO did not reveal any antibacterial activity and Tetracycline had high activity only against S. aureus. Moreover, Antibacterial activity of products could be summarized as AgNPs > nanocomposite 2 > nanocomposite 1. In the both of the approaches, AgNPs were well dispersed on GO sheets. However, FE-SEM pictures revealed that in approach 1, AgNPs are placed between GO sheets. While in approach 2, AgNPs covere the surface of sheets. Therefore, it seems at approach 2 AgNPs decorated on GO sheets had more interaction with bacterial cells than approach 1 products.

Conclusion: It is concluded that the composition of AgNPs and GO could lead to controlled antibacterial activity and their stability, depending on the synthetic approach.

Keywords: Silver nanoparticles, Graphene Oxide, Nanocomposite, Antibacterial Agent

P314 - 869: DESIGNING AND EXPRESSION OF THE ENGINEERED SERRALYSIN ENZYME

Sogol Pourasghar[1], *Vahideh Valizadeh [2], Maryam Rouhani[3], Reza Ahangari Cohan[4], Dariush Norouzian Shamassebi[5]

1. Department of Biology, Tehran North Branch, Islamic Azad University,Tehran,Iran. Nano-biotechnology Department, Pasteur Institute of Iran.
2. Nano-biotechnology Department, Pasteur Institute of Iran
3. Nano-biotechnology Department, Pasteur Institute of Iran
4. Nano-biotechnology Department, Pasteur Institute of Iran
5. Nano-biotechnology Department, Pasteur Institute of Iran

Background and Aim: Serralysin is a bacterial metalloprotease which is associated with virulence in Serratia mercessence, strain E15. Serralysin is useful in the treatment of pain and inflammation. Serralysin appears to have synergistic effect with antibiotic drugs and augment their antibacterial properties. The serralysin enzyme comprised of 470 amino acids in length with no disulfide bond in the structure. The large structure and possible degradation in the intestines (due to lack of tightened intra-molecular bond) has been cited to possible reduce the bioavailability of the enzyme and large protein structures may not be absorbed well. Therefore, this study is planned in order to design and express the engineered form of serralysin to amend these limitations.

Methods: The engineered form of the enzyme with one disulfide bond was designed based on bioinformatics studies and suitable primers were synthesized. Cloning into pET28a expression vector was performed and confirmed by colony PCR and double restriction enzyme digestion. The expression of recombinant protein was confirmed by SDS-PAGE and western blot analysis. Finally the target protein was purified using affinity chromatography method.

Results: Amplifying, cloning and expression of the engineered enzyme were accomplished successfully. The protein band was detected on the expected size (approximately 40 KDa) and confirmed with western blot analysis. Purification process leads obtaining properly purified protein.

Conclusion: The engineered serralysin was expressed and purified as a recombinant protein in the E. coli properly. However, further analysis should be conducted to evaluate its activity and determining other characteristics.

Keywords: Engineered serralysin, Cloning, Expression, and Purification

Clinical Infection and Vaccine

P315 - 35: PREVALENCE OF BLOOD INFECTION BY GRAM NEGATIVE BACTERIA IN PATIENTS ADMITTED TO SHAHID RAJAEE HOSPITAL OF KARAJ

Sara Ghozati[1]

1. Graduate Student, Islamic Azad University, Varamin-Pishva Branch, Faculty of Life Sciences, Department of Microbiology

Background and Aim: Septicemia or blood infection is one of the most important causes of mortality in patients hospitalized in different parts of hospitals, which is considered as an emergency medical emergency. This study was conducted to investigate the role of Gram-negative bacteria in the development of blood infection in Rokhayee hospital in Karaj.

Methods: This study was performed on 3500 patients with septicemia suspicious symptoms admitted to Shahid Rajaee Hospital. Samples were taken from patients for blood culture. The bacteria developed in blood cultures were isolated and identified using conventional bacteriological methods.

Results: Out of 3500 patients under study during one year, 70 cases of Gram-negative bacteria were isolated in blood cultures, 13 of which were in the first six months of the year and 57 of them were in the second six months. In total, six types of Gram-negative bacteria were isolated from Escherichia coli, Enterobacter, Pseudomonas, Acinetobacter, Yersinia, and Klebsiella patients. Escherichia coli was the most common bacteria responsible for the infection of the blood.

Conclusion: The results of this study showed that gram negative bacteria were the main causes of blood infection and mortality and the prevalence of blood infection in the second month of the year was higher.

Keywords: Septicemia, bacteremia, hospital infection, hospitalized patients

P316 - 83: OPRI MODIFIED GENE CLONING FROM PSEUDOMONAS AERUGINOSA BACTERIA IN E.COLI

TINA SADRI[1], MOHAMMAD HADI FAKOOR[2]

1. Department of Microbiology, Hidaj Branch, Islamic Azad University, Hidaj, Iran.(Student of MSc microbiology)
2. Department of Microbiology, Hidaj Branch, Islamic Azad University, Hidaj, Iran. (faculty member of Islamic Azad University).

Background and Aim: The Pseudomonas aeruginosa bacteria has a lots of disease factors and because of these factors creates infection in many parts of the body. Such as in lungs, burned-wounds and case of hospital infection. On the other hand, the resistance to antibiotic drugs is increasing. Perhaps, choosing the right vaccine can solve the problem. So, we suggest other membrane protein I (OprI) modified.

Methods: Bioinformatics studies were performed on Pseudomonas aeruginosa strain PAO1. Extraction of oprI gene from Pseudomonas aeruginosa PAO1, primer design, PCR and cloning of this gene in the plasmid pET 28a and its transfer to Escherichia coli BL21 were performed. Then, using three confirmatory methods including universal primer PCR and enzymatic digestion.

Results: In this studies with bioinformatics software, High conservation and strong antigenic propertis of OprI protein was demonstrated in Pseudomonas aeruginosa strains. In the laboratory experiments, the oprI was cloned in Escherichia coli BL21. And approval tests were positive.

Conclusion: Cloning ability of this gene is suitable for the evaluation of the target vaccine.

Keywords: Pseudomonas aeruginosa, oprI, vaccine, Cloning

P317 - 87: EVALUATION OF ANTI-VARICELLA ANTIBODY IN YOUNG WOMEN BEFORE THEIR MARRIAGE: A SERO-EPIDEMIOLOGIC STUDY IN SOUTH OF IRAN

Abdolreza Sotoodeh[1], Morteza pourahmad[2]

1. Department of microbiology, Jahrom University of Medical Sciences, Jahrom, Iran
2. Department of Internal Medicine, Jahrom University of Medical Sciences, Jahrom, Iran

Background and Aim: Chickenpox during pregnancy can cause severe complications in both the mother and her baby. However, no complications will occur in a mother with proper immunity. Therefore, physicians and health systems can make better decisions when they know the immunologic status of the women in a community.

Methods: This cross-sectional descriptive study was carried out on 334 young women who intended to marry between 2006 and 2008. The subjects' VZV-immunoglobulin G (IgG) and demographic characteristics were evaluated.

Results: The mean age of the subjects was 20.5+/-4.9 years and their mean anti-varicella value was 86.22+/-71.05 U ml(-1). Of 333 young women studied, 242 (72.7%) were positive, 89 (26.7%) were negative for anti-varicella antibody and two were equivocal (0.6%). The rate of immunity increased with increasing age; all of the subjects over 35 years of age were immune to varicella. The positive predictive value (PPV) for self-reported history of chickenpox in subjects was estimated to be 79.5% and the negative predictive value (NPV) of a negative or uncertain disease history was 30.5%. A higher immune ratio was seen in women with more siblings.

Conclusion: The mean age at first pregnancy in Iran is 25.7 years and the results of our study indicate that more than one-fourth of these women are not immune to varicella. We therefore recommend vaccination in women, especially those who are under 35 years of age. Number of siblings and positive history of varicella infection may be the indicators to determine the immunity level of a pregnant woman who has had contact with a patient with chickenpox.

Keywords:varicella zoaster, seroprevalence, women

P318 - 89: ENDOBRONCHIAL TUBERCULOSIS AND BRONCHIAL ANTHRACOFIBROSIS: A CASE REPORT

Meinoosh Sha'bani[1], Zahra Doosti[2], Fatemeh Abbasi[3]

1. Infectious Diseases and Tropical Medicine Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
2. Infectious Diseases and Tropical Medicine Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. Infectious Diseases and Tropical Medicine Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: Endobronchial tuberculosis (EBTB) is defined as tracheobronchial tree involvement by Mycobacterium tuberculosis. It is seen in 10 to 40 percent of patients with active pulmonary tuberculosis. More than 90% of the patients with EBTB have some degree of bronchial stenosis. Bronchial anthracofibrosis is defined in patients without underlying pneumoconiosis and history of smoking, diagnosed by endobronchial endoscopy revealing dark pigmentation (anthracosis) of the bronchial mucosa.

Methods: Here we aim to report a 73-year-old woman with fever, persistent cough and hemoptysis, who was finally diagnosed as anthracosis and tuberculosis together.

Results: Bronchial anthracofibrosis should be suspected in non-smoker, middle-aged women with history of biomass products exposure and compatible clinical and radiographic features.

Conclusion: Due to this report and previous ones, as there is potential association between tuberculosis and anthracosis, bronchoscopic investigation should be done in cases of negative sputum evaluation and also to exclude other diagnoses.

Keywords: Mycobacterium Tuberculosis, Anthracosis, Bronchoscopy

P319 - 90: EVALUATION OF NLRP1 GENE EXPRESSION IN PATIENT WITH SEPTICEMIA AND CONTROLS

Hamid Mosahasankhani[1]

1. Department of Microbiology,kerman branch,Islamic Azad university, kerman,Iran.

Background and Aim:NLRP1 is intracellular receptor that recognition the microorganism dependent molecular patterns. Septicemia is a condition in which the infection has entered the patient's blood stream. The main intracellular mechanism of anti-septicemia is still being investigated. Therefore, in this study, NLRP1 gene expression was evaluated in septicemia subjects in comparison with control subjects.

Methods: The expression of NLRP1 gene in 40 patients with septicemia was mediated by Real time PCR was evaluated. The bacterial agents present in the blood of septal patients were determined by blood culture.

Results: Results showed that expression of NLRP1 gene in the mRNA level in patients was significantly increased compared to healthy controls. Blood culture results were infected by reporting four bacteria of Escherichia coli, Staphylococcus aureus, Acintobacter Bumanni and Pseudomonas aeruginosa. The expression of NLRP1 genes in patients with different bacterial infections did not differ.

Conclusion: Based on the results, it seems it appears that NLRP1 is the main intracellular immunity against bacteria during sepsis they can be investigated for their role in stimulating the immune system through the activation of inflammatory cytokines, Interleukin 1 and 18. It is hoped to help medico with new therapies for sepsis, including immunotherapy, cell therapy and gene therapies.

Keywords: Septicemia, NLRP1 , Gene expression.

P320 - 116: STUDY OF URINARY TRACT INFECTION IN DIABETIC PATIENTS AND THEIR ANTIBIOTIC RESISTANCE PATTERN IN THE ABBAS ABAD

Maryam Shahrdami[1], Zahra Arab[2], Fatemeh Tazari[3]

1. biochemistry undergraduate student, Department of biology, Andishesazan Institute of Higher Education, Neka, Iran
2. Microbiology undergraduate student, Department of biology, Andishesazan Institute of Higher Education, Neka, Iran
3. Instructor of Department of biology, Andishesazan Institute of Higher Education, Neka, Iran

Background and Aim: Diabetes including the most common endocrine disorders. Diabetic neuropathy is also due to the defect in the bladder complete discharge cause a urinary tract infection. Complications of urinary tract infection in patients with diabetes are more and due to different effects need for appropriate antibiotic treatment. The aim of this study is to determine the urinary tract infection in diabetics and nondiabetics and determine the sensitivity of their antibiotic.

Methods: This cross-sectional study on 300 samples of patients in the town of Abbas Abad. Subjects are based on symptoms of infection and the answer of urine culture was studied in the two groups of people with and without infection. The results analyzed using the software.

Results:A total of 69% of samples related to women and 4% related to men with urinary tract infection that of the 3.8% of women with diabetic were diagnosed with urinary tract infection. Study on the diabetic female patients ages over 40 years and lower than 20 years dedicated the minimum and maximum percentage of the urinary tract infection. The most common of pathogens identified in diabetics includes E. coli, Staphylococcus aureus, Staphylococcus saprophyticus. The most amount of their resistance towards cotrimoxazole, amikacin, ciprofloxacin and the lowest amount of resistance was to gentamicin, norfloxacin, nitrofurantoin.

Conclusion: As a result, it is necessary to pay more attention in the identification of pathogens of infection urinary tract, the appropriate use of antibiotics and doing periodic activity to identify the pattern of drug resistance of patients with diabetes.

Keywords: Antibiotics resistance, Diabetes, UTI affection

P321 - 128: THE IMPACT OF THE HELICOBACTER PYLORI TREATMENT ON THE QUALITY OF LIFE IN THE PATIENTS WITH CHRONIC IDIOPATHIC URTICARIA

Maryam Taburak[1]

1. Student Kermanshah University of Medical Sciences, Kermanshah, Iran

Background and Aim: Chronic Urticaria (CU) is one of the most common skin diseases with prevalence ranging between 15 and 25%. This disease takes more than 6 weeks and is often associated with angioedema. In many cases, the cause remains unknown and seems to be an idiopathic disease and may have a profound influence on patients' quality of life. Despite a general agreement that bacteria infection and parasitic infestations can be involved in the pathogenesis of CIU, proven evidence of these relationships is lacking. The aim of this study is to assess the efficacy of Helicobacter pylori infection eradication in improvement of quality of life in patients with CIU.

Methods: In this clinical trial study, 60 CIU patients were enrolled. The patients suffering from chronic urticaria were randomly divided into two groups: cases the patients infected with Helicobacter pylori received Omeprazole, Metronidazole, Clarithromycin (OMC) for 2 weeks and controls (placebo). The patients' quality of life was compared using Chronic Urticaria Quality of Life Questionnaire (CU-Q2oL) before the treatment and one month after the treatment. The data were analyzed using SPSS 22.

Results: There was no significant difference between two groups receiving OMC or placebo treatments regarding the quality of life before the treatment ($P>0.05$). However, one month after the treatment a significant difference was observed ($P<0.05$).

Conclusion: The results showed that the prescription of OMC was not effective in improving the quality of life of the patients suffering from chronic urticaria.

Keywords: Chronic Urticaria Idiopathic (CIU), Helicobacter Pylori Infection, Quality of Life, CU-Q2oL.

P322 - 135: OPRM CLONING OF PSEUDOMONAS AERUGINOSA BACTERIA IN ESCHERICHIA COLI AFTER BIOINFORMATICS CONFIRMATION AS A CANDIDATE FOR VACCINE.

Hamidreza Kalantari[1], Mohammad Hadi Fakoor[2]

1. Department of Microbiology, Hidaj Branch, Islamic Azad University, Hidaj, Iran.(Student of MSc microbiology)
2. Department of Microbiology, Hidaj Branch, Islamic Azad University, Hidaj, Iran. (faculty member of Islamic Azad University).

Background and Aim: Pseudomonas aeruginosa is an opportunistic pathogen that infects immunosuppressed individuals and compromised tissues such as burn wounds, damaged corneal tissue, and the trachea of intubated patients or patients with cystic brosis. On the other hand, the resistance to antibiotic drugs for this bacteria is increasing. Perhaps, choosing the right vaccine can solve the problem. So, we suggest other membrane protein M (OprM).

Methods: Bioinformatics studies were performed on Pseudomonas aeruginosa. Primer design, PCR (Polymerase Chain Reaction) and cloning for oprM in the plasmid pET 32a done. Then, its transfer to Escherichia coli BL21 were performed. Finally, it was approved by universal primer PCR and enzymatic digestion methods.

Results: The bioinformatics studies shown high conservation and strong antigenic properties for OprM protein. In the laboratory experiments, the oprM was cloned in Escherichia coli BL21. And approval tests were positive.

Conclusion: Cloning ability of this gene is suitable for the evaluation of the target vaccine.

Keywords: Pseudomonas aeruginosa, oprM, vaccine, Clonning

P323 - 189: EVALUATION OF TNF-A CYTOKINE PRODUCTION IN PATIENTS WITH TUBERCULOSIS COMPARED TO HEALTHY PEOPLE

Arezou Mirzaei[1], Hassan Mahmoudi[2]

1. Islamic Azad University, Hamadan Branch, Hamadan, Iran
2. Department of Microbiology, Hamadan University of Medical Sciences, Hamadan, Iran.

Background and Aim: Mycobacterium tuberculosis (TB) is one of the most important causes of human mortality. Approximately, 1⁄3 of the world populations are infected with TB and 5-10 % of them develop the active form of the disease. Cytokines play a major role in the host defense process against Mycobacterium infections. Among these cytokines, tumor necrosis factor (TNF-α) has a prominent role in defense and pathological responses to tuberculosis.

Methods: This case-control study was carried out during one year from May 2016 to June 2017. In the study, 45 cases of tuberculosis patients with the diagnosis of tuberculosis (smear and positive culture) as case group and 45 healthy subjects as control group were studied. The serum levels of TNF-α cytokine were determined with the use of the enzyme-linked immunosorbent assay (ELISA) method.

Results: The results of this study showed that concentration of TNF-α in patients with TB increased significantly ($P<0.05$). Also, the finding showed that between the control group and the patient in the age groups of 20-30, 50-60 years, there was a significant difference.

Conclusion: The results of this study showed that cytokines can be useful as a probable marker for the diagnosis of tuberculosis. As well as, due to increase the significance level of TNF-α cytokine production of in the patient group, the measurement of serum levels of this cytokine with the main methods for identifying tuberculosis. Based on this study, we can conclude that the level of serum TNF-α is increased in patients with pulmonary tuberculosis.

Keywords: Mycobacterium tuberculosis, Tumor Necrosis Factor, Cytokine

P324 - 195: MOLECULAR DETECTION AND SEROTYPING OF STREPTOCOCCUS PNEUMONIAE IN MENINGITIS SUSPECTED CHILDREN IN 2014-2018, BOJNURD, IRAN. WHICH TYPE OF VACCINE IS MORE SUITABLE FOR THIS REGION?

Sepideh Abdoli[1], Saghar Safamanesh[2], Mahsa Khosrojerdi[3], Amir Azimian[4]

1. Department of Biotechnology and Molecular Sciences, Faculty of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
2. Department of Pathobiology and Laboratory Sciences, Faculty of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
3. Department of Pediatrics, Faculty of Medicine, Semnan University of Medical Sciences, Semnan, Iran.
4. Department of Pathobiology and Laboratory Sciences, Faculty of Medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.

Background and Aim: To date, we know more than 90 Streptococcus pneumoniae capsular serotypes based on their polysaccharide component. The prevalence of these serotypes is varied based on geographical area and presumable vaccination program. Owing to the lack of regular vaccination programs for S. pneumoniae in infants in developing countries, serotyping of the prevalent isolates can be useful in true vaccine selection.

Methods: All suspected Cerebro Spinal Fluid (CSF) samples for bacterial meningitis in Imam Reza Hospital- Bojnurd were collected during 2014-2018. Because of a high rate of false negative culture results, we used PCR Method for detection of lytA and psaA genes of S. pneumoniae and also modified Marrimon's Multiplex PCR method for serotyping of this bacteria.

Results:106 of 901 samples were positive for S. pneumoniae using PCR while 92 cases were positive with conventional methods. Serotyping was performed using modified Marrimon's Multiplex PCR method. Serotypes 23F, 19F, 1, 14, 19A and serogroup 6 were the most common types in our samples. serogroups 18 (C), 15(A/F/B/C), 9(A/V), 7(A/F), 11(A/D/F) and 22(A/F) were also detected in our isolates. 2.8% of samples were non-typable.

Conclusion: In last two years, some serogroups including 9(A/V), 15(A/F), 7(A/F), 1, 11(A/D/F), 22(A/F) have been increased in our samples. Based on results, it seems that the PCV-13 is the best candidate for the coverage of our common serotypes of meningitis-related S. pneumoniae strains. This vaccine covers 77.13% of our common serotypes. The results of this study will help the design of an appropriate vaccination program for this region.

Keywords: Streptococcus pneumoniae, capsule, polysaccharide, serotype, molecular, Vaccine

P325 - 196: PREVALENCE OF URINARY TRACT INFECTIONS AND ITS CAUSATIVE AGENTS IN IMAM REZA HOSPITAL, BOJNURD, IN 1396

Amirreza Khoshniat[1], Parisa Khoshniat[2], Saghar Safamanesh[3], Sara Nojoomi[4], Amir Azimian[5]

1. Arvin Scientific Association, Faculty of Medicine, North Khorasan University of Medical Sciences
2. Arvin Scientific Association, Faculty of Medicine, North Khorasan University of Medical Sciences
3. Department of Pathobiology and Laboratory Sciences, faculty of medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
4. Laboratory, Imam Reza Hospital, North Khorasan University of Medical Sciences, Bojnurd, Iran.
5. Department of Pathobiology and Laboratory Sciences, faculty of medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.

Background and Aim:bacterial infections are the most common infectious diseases in the urinary system and are able to engage the upper and lower urinary tract. Given the importance of urinary tract infections in this study the prevalence of and factors involved in urinary tract infection in Imam Reza Hospital were evaluated.

Methods: Culture of urine samples received at the laboratory of Imam Reza Hospital was performed to determine the bacterial species. Isolates were identified using conventional biochemical tests.

Results: In 1396 a total of 1754 urine culture were performed, of which between 193 (11%) were positive. Of the positive cases 79.8% were Escherichia coli, 4.1% were Staphylococcus aureus ,3.6% were Pseudomonas aeruginosa, 3.1% were Enterobacter aerogenes, 2.6% were Staphylococcus epidermidis, 2.6% were Streptococcus viridians, 2.1% were enterococci and also 2.1% were Proteus mirabilis.

Conclusion: The results indicated that the overall rate of positive urine culture is lower than previous studies and E. coli is the leader agent. The relatively low percentage of cases with Proteus and Enterobacter in comparison with gram-positive bacteria, including Enterococci, Streptococci and Staphylococcus epidermidis shows the evolution of the common causes of urinary tract infections.

Keywords: Urinary tract ,infection, bacteria,

P326 - 197: A CASE OF HUMAN WRIST SYNOVIAL INFECTION CAUSED BY ACCIDENTAL INJECTION OF ANIMAL VACCINE

SEYYED AHMAD HASHEMI[1], Mohsen Abad [2], Reza Ganji [3], Amir Azimian[4]

1. Department of Infectious Diseases, Faculty of Medicin, 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 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 the 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 the physician because of wrist pain. He didn't have systemic symptoms of brucellosis.

Results: Microscopic examination of abscess discharge showed a large number of gram-negative bacilli and also a large number of neutrophils. PCR showed the 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, the culture was negative and vaccine strain couldn't produce systemic symptoms such as fever, sweat, ague and weight. Our patient didn't have the 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

P327 - 215: INVESTIGATION THE SENSITIZATION OF ASTHMATIC PATIENTS TO A.ALTERNATA, BY IGE-IMMUNOBLOTTING

Azar Sabokbar[1], Mohammad Hadi Fakoor [2], Somayeh Talebi [3]

1. Associate Professor of Mycology, Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran.
2. Department of Microbiology, Hidaj Branch, Islamic Azad University, Hidaj, Iran.
3. Ph.D of Microbiology, Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran

Background and Aim: There is evidence to demonstrate an association between fungal sensitization and asthma. Several studies have shown saprophytic fungi such as Alternaria, species are the most prevalent fungal allergens in the worldwide.

Methods: Forty-eight patients with asthma (23 male, 25 female) and Forty-eight healthy controls (23 male, 25 female) were collected. Glass beads and liquid nitrogen was used to disrupted the cell wall of cultured fungi. SDS-PAGE was used to isolation of protein fractions. IgE immunoblotting against the patients and controls sera were performed to isolation of protein bands after electrotransfering into the nitrocellulose membrane.

Results: Our results demonstrated the most allergenic bands consist to A. alternata with 17 bands (44.7%) and we found that asthmatic patients 41 to 70 years old were more sensitive when compared to others age groups.

Conclusion: Our results showed that A. alternata had more power in sensitizing the patients.Also the protein bands with high molecular weight can be considered as an index of sensitizing in immunoblotting assay.

Keywords: Asthma, Asthmatic patients, Alternaria alternate, IgE-immunoblotting

P328 - 248: IDENTIFICATION OF CAPSULAR TYPES K1 AND K2 IN CLINICAL ISOLATES OF KLEBSIELLA PNEUMONIAE PRODUCING BIOFILM AND NON-PRODUCING BIOFILM

Parisa Roshani Asl[1], Elahe Tajbakhsh[2]

1. M.Sc, Department of Microbiology, Faculty of Basic Sciences, Shahrekord Branch, Islamic Azad University, Shahrekord, Iran
2. Associated Professor, Department of Microbiology, Faculty of Basic Sciences, Shahrekord Branch, Islamic Azad University, Shahrekord, Iran

Background and Aim: Klebsiella pneumoniae is a Gram-negative opportunistic pathogen commonly causes health-care associated infections. Biofilm formation and capsule play major role in development of K. pneumoniae infections. Capsular serotypes K1 and K2 of this bacterium can cause severe diseases in human. The purpose of this study was to determine the serotypes K1 and K2 and biofilm formation among K. pneumoniae isolates collected from medical diagnosis laboratories in Shahrekord, Iran.

Methods: This study was performed on 50 clinical samples of K. pneumoniae. The ability of biofilm formation was investigated by Microtiter Plate assay. DNA was extracted by boiling. The 16srRNA gene, K1 and K2 serotypes were determined by PCR method. Data analysing was carried out using Chi-square test and SPSS software version 18.

Results: The 16srRNA gene was observed in all strains. 44 (88%) isolates were biofilm producer and 6 (12%) isolates were non-producing biofilm. Serotype K1 and K2 existed in 13 (26%) and 6 (12%) isolates respectively. Data analysing by Fisher test showed a statistically significant relationship between the capsular serotype and biofilm formation (P> 0.05).

Conclusion: The findings indicate that serotype K1 is one of the most important capsular serotypes in K. pneumoniae. Due to potential risk of these serotypes in hospital settings, identification of these serotypes is essential and important.

Keywords: Klebsiella pneumoniae, capsular serotype, biofilm.

P329 - 255: ASSESSMENT OF ORNITHOBACTERIUM RHINOTRACHEALE INFECTION IN COMMERCIAL CHICKENS SUBMITTED TO POULTRY CLINIC OF RAZI INSTITUTE AND SLAUGHTERHOUSES OF KARAJ CITY

Seyedgholamreza Mirzaei[1], Banani M[2], Nouri A[3]

1. Department of Avian Diseases, Research & Diagnosis, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization, Tehran, Iran
2. Department of Avian Diseases, Research & Diagnosis, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization, Tehran, Iran
3. Department of Avian Diseases, Research & Diagnosis, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization, Tehran, Iran

Background and Aim: Ornithobacterium rhinotracheale (ORT) has been associated with other respiratory pathogens in poultry and turkeys, and although the pathogenicity of the bacterium has been proven to be primary, but in most cases, along with other pathogens, it causes severe economic damage and causes respiratory symptoms, decreased growth, decreased Egg production and increased mortality and elimination of slaughter. The best vaccine is an autogenous vaccine prepared from local strains, and on the other hand, the latest isolates are required for research work.

Methods:for bacterial isolation, after sampling from 60 herds at slaughter age. Samples were cultured in Blood agar containing gentamicin for 24h in 37°C at 5% CO2 then suspicious colonies examined by Gram staining for Pleomorphic and Gram negative bacterium. Confirmatory identification followed by biochemical test ،including determination of oxidase (most strains Oxidase positive and probable oxidase-negative strains) and catalase reaction (Negation). The samples that were identified as ORT were subjected to DNA extraction of bacteria using standard phenol chloroform method. Then, a pair of specific primers to partial 16s RNA genome amplification fragment of 784 bp, used in PCR test.

Results: About 20 (33%) strains were isolated in this research, in comparison to other studies in Iran the prevalence of ORT still is above according to European countries.

Conclusion:so conclusively need more emphasis to implementing the hygienic measurements in poultry rising industries.

Keywords: Ornithobacterium rhinotracheale, Isolation, chicken

P330 - 269: PREVALENCE OF UREAPLASMA UREALYTICUM IN VAGINAL SWAB SAMPLES OF INFERTILE FEMALES REFERRED TO MAHDIEH HOSPITAL OF TEHRAN

Fatemeh Sameni[1], Hossein Dabiri[2]

1. 1Department of Microbiology, Pharmaceutical Sciences Branch,Ialamic Azad University
2. University of Medical Sciences, Tehran, Iran, Department of Clinical Microbiology, School of Medicine, Shahid Beheshti University of Medical Siences, Tehran , Iran

Background and Aim: Infertility is one of the most medical problems in the world. Bacterial infections are consider as one of the risk factors. Ureaplasma urealyticum colonization has been associated with stillbirth, preterm delivery, histologic chorioamnionitis, vaginitis, cervicitis, postpartum sepsis, and infertility. The aim of this study was to assess the Ureaplasma urealyticum frequency in infertile women referred to Mahdieh Hospital in Tehran in 2016-2017.

Methods: Endocervical swab samples from 65 infertile women were collected in PBS buffer. After extracted DNA from specimens, a PCR test was performed for detection of U. urealyticum in patients.

Results: Total prevalence of U. urealyticum infection in infertile women was 15 out of 65 (23.1%). There was no correlation between the history of abortion, use of OCP, education, and age, with the prevalence of Ureaplasma urealyticum infection.

Conclusion: Because of colonization of this asymptomatic infection in genital tract of women and its combination with other factors such as other microorganisms or genital imperfection may cause infertility. According to the results of this study, Ureaplasma urealyticum is considered as a risk factor in female infertility, and it can be concluded that routine control and treatment of bacterial infections, can be important in prevention and treatment of the women's infertility and community health. More investigations are needed to approve this possibility.

Keywords: Ureaplasma urealyticum, female infertility, PCR

P331 - 292: EVALUATION OF THE INCIDENCE OF BRUCELLOSIS IN A 10-YEAR PERIOD IN ASADABAD CITY, HAMEDAN PROVINCE

Fatemeh Darabi[1], Marziyeh Hesari [2], Ali Moradi [3]

1. Department of Public Health, Asadabad School of Medical Sciences, Asadabad, Iran.
2. 2. Bachelor of Public Health, Public Health, Assad Abad Medical Sciences Faculty, Assadabad, Iran
3. 3. PhD in Epidemiology, Asadabad Medical Center, Asadabad Medical Sciences College, Asadabad, Iran

Background and Aim: Brucellosis or brucellosis is a chronic and infectious zoonotic disease that occurs acutely, subacute or chronic. The disease is present in many developing countries, including Iran. The aim of this study was to evaluate the incidence of disease during the years 2007 to the first half of 1396 in Asadabad, Hamedan province.

Methods: In this descriptive study, all cases of Asad Abad population in the year 2007 to the first half of 1396, using the records of apple system and records of patients identified in the city health center based on age, gender, The year (time) of the infection and type of infection were collected and analyzed.

Results: The incidence of this disease in Asadabad city was 61 per thousand (60% female and 40% male). The highest frequency was in the age group of 30-60 years. Most infected people have been exposed to contaminated contaminated contaminants; 95% of rural patients and male farmers and women have also been housewives; the peak is in the spring. The definitive diagnostic method is LME and WRIGHT; the most severe complication is arthritis.

Conclusion: This study shows that in the city of Asadabad the most common group of women who have been exposed to the disease of brucellosis were rural housewives, they should attract public partnerships and collaborate between them to control the brucellosis in the role of health care providers and homes Consider hygiene in spillage control.

Keywords:brucellosis, rate, incidence, asadabad city

P332 - 313: PATTERN OF STAPHYLOCOCCUS SIMULANS ANTIBACTERIAL RESISTANCE IN A REFERRAL TEACHING HOSPITAL IN NORTHEAST OF IRAN

Ayda Tafazoli[1], aliahmadabadi[2]

1. Student of microbiology, Mashhad Azad University, Mashhad, Iran
2. . Surgical oncology research center, Mashhad University of Medical Sciences, Mashhad, Iran

Background and Aim:: While staphylococcus simulans is considered as the normal bacterial flora of human skin, there is some reports that it can cause severe clinical infections. Besides, there is increasing data about antibiotic and antiseptic resistance in coagulase negative staphylococci. This study was designed to investigate S.smulans antibacterial resistance pattern in a referral hospital in northeast of Iran

Methods:: this cross-sectional study was performed in Imam Reza referral hospital in years 2015-2016. All positive cultures for S.simulans extracted from Hospital Information System. Data were analyzed by SPSS version 24.

Results: There was 3823 positive cultures. In 75 patients S.simulans was cultured from blood (39), wound (12), urine (8), eye exudates (5), pleural cavity or bronchus (5), central venous catheter (3), CSF (2), and pericardium (1). The mean age of patients was 44.8±30.1 years (range: 0.1- 93). The mortality rate was 26.7%. The most positive cultures was from emergency department (31), ICUs (8) and pediatrics department (8). Isolated bacteriae were resistant to penicillin (78%), erythromycin (78%), co-trimoxazole (54%), clindamycin (46%), cefoxitin (44%), ciprofloxacin (35%), and gentamycin (33%). All of isolates were sensitive to vancomycin

Conclusion:: This study shows that S.simulans has a high level of resistance to most routinely used antibacterial agents and antibiotics must be used more cautiously in our clinical practice. High positive cultures for S.simulans in some wards, especially in emergency department may be an indicator of higher contamination in those wards. More investigations about rate of sample contamination and clinical significans of S.simulans positive cultures is warranted.

Keywords:: staphylococcus simulans, coagulase negative staphylococci, antibacterial resistance

P333 - 371: BACTERIAL PATTERN AMONG PATIENTS WITH WOUND INFECTIONS AT GHAEM HOSPITAL, MASHHAD, IRAN

Sepideh Hasanzade[1], Mahya Manouchehri[2], Majid Alizadeh[3], Narges Shekoftemehr[4], Mahboobeh Honarmand[5], Kiarash Ghazvini[6]

1. Department of Microbiology and virology, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
2. Antimicrobial Resistance Research Center, Avicenna Research Institute, Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
3. Antimicrobial Resistance Research Center, Avicenna Research Institute, Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
4. Antimicrobial Resistance Research Center, Avicenna Research Institute, Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
5. Antimicrobial Resistance Research Center, Avicenna Research Institute, Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
6. Department of Microbiology and virology, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Background and Aim: Wound infections are a major problem in health care facilities worldwide, frequently neglected in under-resourced countries. Resulting in extended length of stay infection, substantial morbidity and mortality, high excess of cost, and less frequent cause of death in the patient. Aim: To determine the prevalence of bacterial pattern among patients with wound infections at Ghaem hospital which located in Eastern part of Iran.

Methods:A year prospective study of 200 wound infection in different units of Ghaem hospital in Mashhad, was carried out. Sample were collected between March 2017 and March 2018. Conventional technique for isolation of bacteria was applied for identification to confirm primary and secondary isolates.

Results: Most bacterial isolates were Klebsiella pneumoniae (n=39, 32%), Acinetobacter spp. (n=35, 23%), E. coli (n=25, 14%), Coagulase negative Staphylococci (n=25, 14%), Staphylococcus aureus (n= 16, 9%), Pseudomonas aeruginosa (n=12, 7%), Entrobacter spp (n=11, 6%), Proteus spp. (n=7, 4%), and Enterococcus faecalis (n=6, 3%). Most of the cases were related to surgical units (23%), and then the internal unit (21%) and emergency units (17%).

Conclusion: The high prevalence rate of wound infection in the surgical units of Ghaem hospital was estimated due to prevention proceedings during and after surgery. Moreover, the levels of contamination in the most part of the hospital were above the normal.

Keywords: Prevention , Surgery, Wound infection

P334 - 379: EPIDEMIOLOGY OF HUMAN BRUCELLOSIS IN KANGAVAR CITY, KERMANSHAH PROVINCE, IRAN

Naser Nazari[1]

1. Dept of Parasitology, Medical school, Kermanshah University of Medical Sciences, Kermanshah, Iran

Background and Aim: Brucellosis is a zoonotic infection caused by the bacterial genus Brucella. The bacteria are transmitted from animals to humans by ingestion through infected food products, direct contact with an infected animal, or inhalation of aerosols. The disease is an old one that has been known by various names, including Mediterranean fever, Malta fever, gastric remittent fever, and undulant fever. Humans are accidental hosts, but brucellosis continues to be a major public health concern worldwide and is the most common zoonotic infection.

Methods:A cross-sectional study was carried out in Kangavar city, Kermanshah province, to determine the seroprevalence and risk factors associated with human brucellosis (2014-2017). A questionnaire was used to collect data on socio-demographic characteristics and human brucellosis related risk factors.

Results:A total of 182 patients were involved in the study. Blood samples from the patients were collected and screened for Brucella using Serum Agglutination Test. Human Brucella seroprevalence was (n = 182). The prevalence was highest among males (62.1 %,) than female (37.9%) and the residence in rural areas(74.8%).

Conclusion: Brucellosis is highly prevalent in Kangavar district, and therefore, an important public health problem. The transmission risk was aggravated by consumption of unpasteurized milk products, residing in rural settings. There is a need to initiate screening, treat infected humans, and educate the public about risk factors and appropriate preventive measures of brucellosis.

Keywords: Brucellosis, Epidemiology, Durood, Lorestan, Iran.

P335 - 448: FLUOROQUINOLONE RESISTANCE OF E.COLI ISOLATED FROM PATIENTS WITH URINARY TRACT INFECTION IN INTENSIVE CARE UNIT IN IMAM KHOMEINI HOSPITAL, SARAB, IRAN

Azam Valizadeh[1], Ali Bahadori[2], Khalil Maleki Chulu[3], ali sadighi[4], Kamiar Khadivi[5], Parizad Azami[6], Maryam felekari[7], Leyla Hashemi Nezhad[8]

1. M.Sc.of Microbiology, Sarab Islamic Azad University, Sarab-Iran
2. Department of Medical Microbiology, Sarab faculty of Medical Sciences, Sarab-Iran
3. Department of Nursing, Sarab faculty of Medical Sciences, Sarab-Iran
4. BSc student of Laboratory Sciences, Sarab Faculty of Medical Sciences, Sarab, Iran
5. BSc student of Laboratory Sciences, Sarab Faculty of Medical Sciences, Sarab, Iran
6. BSc student of Laboratory Sciences, Sarab Faculty of Medical Sciences, Sarab, Iran
7. BSc student of nursing, Sarab Faculty of Medical Sciences, Sarab, Iran
8. BSc student of nursing, Sarab Faculty of Medical Sciences, Sarab, Iran

Background and Aim: Urinary tract infection(UTI)is one of the most prevalent infectious diseases and Escherichia coli is its common cause.The rate of antimicrobial resistance in the ICU is several folds higher than in the general hospital setting. ICU is one of potential sources of nosocomial infections even in countries where extensive infection control measures are routinely implemented.This study was carried out to evaluate antimicrobial susceptibility patterns of E.coli isolated from patients with Urinary tract infection against Fluoroquinolones in intensive care unit in Imam Khomeini hospital,Sarab,Iran

Methods:A total of 100 E.coli isolates from 134 patients with UTI were collected. All of the isolates were identified with routine laboratory methods. Antimicrobial susceptibility pattern of isolated strains were tested by Disk Agar Diffusion (DAD) method according to CLSI standard patterns.

Results: According to the results of our study 37% of isolated serotypes were sensitive to Nalidixic acid, 67% of them sensitive to Norfloxacin, 70% sensitive to Ciprofloxacin and 75% were sensitive to Ofloxacin. Also 1% of isolates showed intermediate sensitivity to Ciprofloxacin and 3% of isolates showed intermediate sensitivity to Ofloxacin according to CLSI standard protocol.

Conclusion: Our results revealed a high level resistance against Fluroquinolons. It seems that this increasing trend is because of inappropriate antibiotic use. To overcome to this problem the use of unnessesary antibiotic therapy should be limited and use of various antibiotics should bu restricted to the results of antibiotic sensitivity patterns.

Keywords:antibiotic resistance, Escherichia coli, Urinary Tract Infection, Fluroquinolon, Sarab.

P336 - 451: PREVALENCE OF HELICOBACTER PYLORI INFECTION IN PEDIATRIC PATIENTS WITH FAMILIAL MEDITERRANEAN FEVER (FMF) AT SOTH OF TURKEY

Ali Bahadori[1], Tümgör G[2], Agin M[3], Maleki Chollou Kh[4], ali sadighi[5], Hashemi nejad L[6], Hamedfar N[7], Yousefi B[8], Pourhasan M[9]

1. Department of Medical Microbiology, Sarab Faculty of Medical Sciences, Sarab-Iran
2. Department of Pediatric Gastroenterology, Cukurova University Medical Faculty, Adana, Turkey
3. Department of Pediatric Gastroenterology, Faculty of Medicine, Van University, Van, Turkey
4. Department of Nursıng, Sarab Faculty of Medical Scıences, Sarab, Iran
5. B.Sc. student of Medical Laboratory Sciences, Sarab Faculty of medical sciences, Sarab, Iran
6. B.Sc. student of Nursing, Sarab Faculty of medical sciences, Sarab, Iran.
7. B.Sc. student of Medical Laboratory Sciences, Sarab Faculty of medical sciences, Sarab, Iran
8. B.Sc. student of Medical Laboratory Sciences, Sarab Faculty of medical sciences, Sarab, Iran
9. B.Sc. student of Nursing, Sarab Faculty of medical sciences, Sarab, Iran

Background and Aim: Familial Mediterranean fever (FMF) is an autosomal recessive disease characterized by recurrent attacks causing inflammation of the serosal membranes. Helicobacter pylori is a strong risk factor for the development of peptic ulceration, gastric adenocarcinoma, gastric mucosa–associated lymphoid tissue (MALT) and lymphoma. Studies showed that H.pylori infections can effect on the frequency and severity of Familial Mediterranean Fever attacks. In our study we aimed to determine the H.pylori infection prevalence in patients suffering from FMF to evaluate, the probability of significant relation between H. pylori infection and FMF

Methods:sample collection was performed by endoscopic route on 28 patients suffering from FMF and dyspeptic complaints at Balcali Hospital, Pediatric Gastroenterology Clinic, Adana, Turkey. DNA was extracted from gastric biopsies by DNA extraction kit. Prepared DNA utilized for PCR targeted at the urea gene of Helicobacters by using genus specific primers

Results: In this study 68% of patients were female and 32% of them were male. All of the patients had dyspeptic symptoms and presence of Helicobacter genus confirmed at 25% of cases

Conclusion: In conclusion, H. pylori positivity level in our study was 25%.This level is not particularly high and is compatible with data for childhood H. pylori positivity in Turkey but recurrent abdominal pain may be due to both FMF and H. pylori infection in children. As for today, the correlation between H. pylori infection and FMF seems unlikely; however, studies evaluating the interaction of cytokines in both diseases and their relations and roles will be needed to reach better conclusions

Keywords: Dyspepsia, Helicobacter pylori, FMF, Endoscopy

P337 - 460: EVALUATION OF CAUSATIVE BACTERIAL AGENTS IN URINARY TRACT INFECTIONS AND DETERMINATION OF ANTIBIOTIC RESISTANCE PATTERNS IN IMAM KHOMEINI HOSPITAL, SARAB, IRAN

Bager Naderi[1], Ali Bahadori[2], Khalil Maleki Chulu[3], ali sadighi[4], Kamiar Khadivi[5], Leyla Hashemi Nezhad[6], Maryam felekari[7], Parizad Azami[8], Mohammad Pourhasan [9]

1. M.Sc.of Microbiology, Sarab Islamic Azad University, Sarab-Iran
2. Department of Medical Microbiology, Sarab faculty of Medical Sciences, Sarab-Iran
3. Department of Nursing, Sarab faculty of Medical Sciences, Sarab-Iran
4. B.Sc. student of Medical Laboratory Sciences, Sarab Faculty of medical sciences, Sarab, Iran
5. B.Sc. student of Medical Laboratory Sciences, Sarab Faculty of medical sciences, Sarab, Iran
6. B.Sc. student of Nursing, Sarab Faculty of medical sciences, Sarab, Iran.
7. BSc student of nursing, Sarab Faculty of Medical Sciences, Sarab, Iran
8. B.Sc. student of Medical Laboratory Sciences, Sarab Faculty of medical sciences, Sarab, Iran
9. B.Sc. student of Nursing, Sarab Faculty of medical sciences, Sarab, Iran

Background and Aim: Urinary Tract Infections(UTI)are one of the most common infections.According to various pathogens in urinary tract infections and different patterns in different parts of the world and their sensitivity to antibiotics due to increasing consumption of antibiotics,antibiotic resistance is increasing. In this study we tried to evaluate epidemiology of UTI causing bacteria and their antibiotic resistance in outpatients.

Methods:A hospital based cross sectional study was conducted and urine samples were collected using the mid-stream“clean catch”method from 100 clinically-suspected cases of urinary tract infections .The samples tested bacteriologically using standard procedures. Antimicrobial susceptibility test was performed for the isolated pathogens using Kirby-Bauer disk diffusion method according to Clinical and Laboratory Standards Institute guidelines.Urine culture and antibiotic susceptibility to common antibiotics were determined.

Results: The most common pathogens isolated were Escherichiacoli(76%),Klebsiella pneumoniae (10%),S.epidermidis(6%),S.saprophyticus(4%),S.aureus(2%),Pseudomonas(1%)and proteus (1%).E.coli and Klebsiella pneumoniae showed the highest percentage of resistance to antibiotics.In the study of antibiotic resistance in urinary tract infections, the pathogens were most resistant to quinolones and then to Cotrimoxazole.Of all urinary tract infection pathogens, Klebsiella was resistant to a greater number of antibiotics.

Conclusion: This study finding showed that E.coli isolates were the predominant pathogens and the presence of bacterial isolates with very high resistance to the commonly prescribed drugs that in turn leaves the clinicians with very few alternative options of drugs for the treatment of UTIs.As drug resistance among bacterial pathogens is an evolving process, routine surveillance and monitoring studies should be conducted to provide physicians knowledge on the updated andmost effective empirical treatment of UTIs.

Keywords: Urinary tract infection, Hospital infections, Antibiotic resistance, Epidemiology

P338 - 563: EXPRESSION AND PURIFICATION OF AN IRON SCAVENGER RECEPTOR OF PROTEUS MIRABILIS AS A NEW TARGET AGAINST URINARY TRACT INFECTIONS

Mohammad Reza Asadi Karam[1], Mehri Habibi[2]

1. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran
2. Department of Molecular Biology, Pasteur Institute of Iran, Tehran, Iran. Email:m_habibi1362@yahoo.com.

Background and Aim: Proteus mirabilis strains are among the most common causes of urinary tract infections. Iron adsorption receptors of P. mirabilis strains have the properties of an ideal vaccine candidate against UTIs. In the present study, amplification, expression and purification of iron adsorption receptor PMI0842 of P. mirabilis was performed to evaluate its efficacy in other studies.

Methods: The amplification of PMI0842 gene in P. mirabilis HI4320 isolate was performed by using the Polymerase Chain Reaction (PCR). Then, the amplified gene was cloned and expressed in pET28a-BL21 (DE3) expression system. Purification of the PMI0842 expressed protein was performed by nickel column under the denaturation conditions. Finally, the purification of recombinant protein PMI0842 was evaluated by SDS-PAGE and Western blot.

Results: The PMI0842 gene was amplified with a size about 2000 bp in PCR. Confirmation the cloning of PMI0842 gene in pET28a vector was done using colony PCR, double enzyme digestion, and sequencing. Then, expression of PMI0842 was performed in BL21 (DE3) that SDS-PAGE and western blot showed the high purity of the eluted protein on column. The approximate size of the purified protein was about 70 KD.

Conclusion: There is currently no effective vaccine available against UTIs; therefore, development of an ideal against these infections is urgently required. Iron scavenger receptors could be among the ideal candidates against P. mirabilis that efficacy some of them were evaluated against UTIs. In this study, PMI0842 was purified for the first time and evaluation of its efficacy is under study.

Keywords: Urinary tract infection, P. mirabilis, PMI0842, Vaccine candidate

P339 - 576: FREQUENCY OF BACTERIA ISOLATED FROM ASCETIC AND PLEURAL FLUIDS IN BUSHEHR PERSIAN GULF HOSPITAL IN 1396

Zeynab Gharadaghi[1], Zeynab Gharehdaghi[2], Shaghayegh Rostami Yasuj[3], Eisa safavi[4]

1. -
2. MSc of Hematology and Blood Banking, Student of Research Committee, Bushehr University of Medical Sciences, Bushehr, Iran
3. MSc of Hematology and Blood Banking, Student of Research Committee, Bushehr University of Medical Sciences, Bushehr, Iran
4. PhD of Social Health, Bushehr University of Medical Sciences, Bushehr, Iran

Background and Aim: One of the common and valuable methods in diagnosis and staging of diseases is the study of fluid from the serous cavities of the body (pleura, peritoneum). One of the main causes of ascites and pleural effusions of the exudate type is bacterial infection, which recognizes the type of bacteria is the most important step in improving the disease. The cause of study were to investigate the type of bacteria and amount of bacterial infection in ascites and pleural effusions in Bushehr Persian Gulf Hospital

Methods: This descriptive cross-sectional study was performed on all samples of ascites and pleural effusions in the Persian Gulf Hospital. Samples were cultured on EMB, blood and chocolate agar mediums. for data analysis, SPSS21 software, Descriptive and inferential statistics were utilized.

Results: The total number of ascites and pleural effusion cultures were 84 and 108, respectively. The number of positive in ascites and pleural effusion cultures were 24(16.6% gram positive,83.4% gram negative) and 8(50% gram positive, 50% gram negative) respectively. The Types of gram negative bacteria isolated from ascites were Seratia, Entrobacter, Kelebseilla, E.coli and gram positive include Staph aureus and Strep non hemolytic. The Types of gram negative bacteria isolated from pleural effusions were and gram positive include Staph aureus and staphylococcus epidermidis and gram negative bacteria were cocci bacilli and acenitobacter.

Conclusion: This study showed that bacterial infection in ascites is more than pleural effusion in other hand One of the major causes of ascites is bacterial infection.

Keywords:pleural effusion- ascite- bacterial infection

P340 - 577: BLOOD AND PERICARDIAL FLUID CULTURE IN CARDIAC PATIENTS IN BENTOLHODA HOSPITAL OF BUSHEHR

Shaghayegh Rostami yasuj[1], zynab gharedaghi[2]

1. MSc of Hematology and blood banking, student of research committee,bushehr university of medical science, bushehr,iran
2. student of research committee,bushehr university of medical science, bushehr,iran

Background and Aim: Before and after surgery, Care and control of fever in patients undergoing cardiac surgery is essential. One of the things that is checked in these people is Infection and fever control and Blood cultures are taken from patients with high fever. some patients develop fluid around their heart, and because some bacteria cause this, pericardial fluid culture help us to prevent and control infections in the operating room. So the purpose of this study, determination of different bacteria in blood culture and pericardial fluid in patients undergoing any cardiac surgery.

Methods: This descriptive cross-sectional study which was done on cardiovascular patients who sent Blood and fluid culture for them In Bentolhoda hospital of bushehr. Blood culture and pericardial fluid culture was performed. SPSS21 software,descriptive and inferential were utilized.

Results: The statistical population included 263 patients (mail:54%,femail 46%). Blood culture and pericardial fluid culture were carried out respectively in 239 and 24 of them. The average of positive blood culture was 7.5% .gram-positive bacteria included 38.88% staphylococcus epidermidis, staphylococcus aureus, staphylococcus saprophytic and streptococcus D group were Each one 11.11% and streptococcus beta hemolytic was 5.5%. gram-negative bacteria included Ecoli was 11.11% and acinetobacter , klebsiella were Each one 5.5%. The average of positive pericardial fluid culture was %4.1 that was staphylococcus epidermidis.

Conclusion:this study showed that bacteria play a small role in the bacterial infections in cardiac patients

Keywords: Blood culture- precardial effusion- cardiovascular patients

P341 - 609: THE RELATION BETWEEN PREVALENCE OF POSITIVE ANTI-CHLAMYDIA PNEUMONIA ANTIBODY TITERS AND ATHEROSCLEROTIC DISEASES

Abbas Abdollahi[1], Payman Izadpanah[2], Sohrab Najafipoor[3]

1. Department of Microbiology, Fasa University of Medical Sciences
2. Department of Cardiology, Shiraz University of Medical Sciences
3. Department of Microbiology, Fasa University of Medical Sciences

Background and Aim: Cardiovascular disease has a significant role in increasing mortality rates in the world; one of these heart problems is related to the occurrence of atherosclerotic plaques. One of the underlying factors in this regard is bacterial infections. Many studies indicate the association between Chlamydia pneumoniae and the creation of plaques; it is one of the most important organisms in the development of coronary heart disease. The aim of this study was to investigate the association between the antibodies against Chlamydia pneumoniae and those relation with coronary atherosclerosis.

Methods: In this descriptive case-control study, serum samples were collected from two groups of patients (108 patients) and healthy subjects (108 persons). Anti-Chlamydia pneumonia antibody titers were evaluated; patients under study were diagnosed with acute myocardial infarction. Both groups were matched in terms of the age and sex to reduce possible interactions.

Results: In the evaluation of IgG antibody titers by ELISA and comparison between the two groups, the positive titers were 88.2% in the case group and 60.5% in the healthy subjects; this percentage was 74.6% in all subjects. The results of the two groups were statistically significant ($P \leq 0.005$).

Conclusion: Regarding the significance of the results in comparison between the patient and the control group, it can be argued that the presence of Chlamydia pneumonia can have a significant relationship with the development of atherosclerotic plaques. Despite the controversial findings in this regard, precise molecular studies can reveal possible mechanisms for the association of bacterial infections and the development of atherosclerosis.

Keywords: Chlamydia pneumonia, Atherosclerosis, Antibody titers, ELISA

P342 - 643: PREVALENCE OF SHIGELLA IN CHILDREN WITH DIARRHEA IN TEHRAN CHILDREN'S MEDICAL CENTER HOSPITAL

Melisa Eghbal[1], S. M.AbrishamChian Langroudi [2], , M.M.Soltan Dallal [3]

1. 1- Department of Microbiology, Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences
2. 2- Department of Microbiology, Central Tehran Pathobiology Laboratory
3. 3- Food Microbiology Research Center, Tehran University of Medical Sciences

Background and Aim: Shigellosis is a gastroenteritis caused by infection with Shigella strains of bacterial species. It is one of the most common causes of death in children in developing countries. More than one million and hundred thousand deaths occur every year around the world.

Methods: This study was conducted on 384 cases of suspected Shigella diarrhea from the Tehran Medical Center Hospital over a period of 24 months. First, using XLD culture and performing differential tests on suspicious colonies, the direction Initial diagnosis and differentiation. Then using anti-serum, Shigella isolates were confirmed and species was determined.

Results: Among identified isolates, 43 isolates were isolated using Shigella Sonei isolate (55.8%) and Shigella Flexneri isolate (44.2%) with serology kit. And Shigella boydie and dysentery were not found in this study.

Conclusion: This study suggests that in our country, the prevalence of Shigella syndrome is increasing in Iran, and according to this study, it is recommended that the necessary measures be taken to prevent the overexposure of Shigella sonnei.

Keywords: Shigella, outbreak, diarrhea

P343 - 701: PREVALENCE OF CRYPTOSPORIDIUM PARASITE IN CHILDREN OF LARESTAN IN 2017

Mohammadreza Foroutani[1]

1. Department of nursing, Larestan University of Medical Sciences, Larestan, IRAN

Background and Aim:"Cryptosporidium" parasite is from Coccidia group, that causes digestive diseases in people who have a weak security system or suffer from AIDS. This parasite has no special host. Although, the infection is usually stopped spontaneously in normal individuals, the quality of self-pollution and extension of this parasite is possible to continue the infection. The parasite can produce acute and chronic digestive infections in children. The continuation and intensity of illness can cause much harm in children. It is certainly influential for the health of the society to know about the ill children.

Methods: In this research, we collected 725 samples of fects from eight area of south of IRAN. 45 samples were watery as having diarrhea. We used the colour method(Ziehl-Neelsen's modified by Henriksen)for diagnosis.

Results: To colour these samples didn't show any sign of pollution with "Cryptosporidium" in these children. It was probably because either the facet samples were not sufficient or at the time of survey(Autumm and Winter),the rate of pollution had been less.

Conclusion: It is nevertheless a require to continue carefully this research and to find its prevalence which is a real danger for the infants' health and security.

Keywords: Cryptosporidium, Children, Iran.

P344 - 716: IN SILICO DESIGN OF A CHIMERIC HIGH IMMUNOGENIC OUTER MEMBRANE PROTEIN AS A NEW VACCINE CANDIDATE AGAINST SALMONELLA TYPHI

Ehsan Esmailnia[1], Seyed Latif Mousavi[2], Jafar Amani[3]

1. Department of Cell Biology, Faculty of Basic Sciences, Shahed University, Tehran, Iran
2. Department of Cell Biology, Faculty of Basic Sciences, Shahed University, Tehran, Iran
3. Applied Microbiology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran

Background and Aim: Enteric fever is a systemic infection caused by the Salmonella enterica serotype Typhi (S. Typhi) with a death rate of about 1%. The appearance of multidrug-resistant typhoid infections, highlights the necessity of control measures. Vaccination is an indispensable tool for the effective management of these kind of infections. With the limitations of existing S. Typhi vaccines, particularly their lack of effectiveness in young children, along with their limited availability in endemic countries, research to develop some new vaccines are needed. Previous works have shown that S. Typhi outer membrane proteins (OMPs) are highly immunogenic antigens. The aim of this study is in silico design a construct containing high immunogenic parts of two OMPs as a new vaccine candidate.

Methods: Using bioinformatics tools, a new synthetic construct comprising outer membrane fimbrial usher proteins tsaC and steB is designed. The codon optimization of recombinant gene was carried out for a prokaryotic host. The mRNA structure of the gene and its stability and traslatibility were evaluated. The immunogenicity, B-cell epitope, allergenicity, and 3-D structure of chimeric protein with an appropriate linker were also determined.

Results: In silico analyses showed that, two surface-exposed domains of selected OMPs with 569 amino acid were linked by a 4-repeated EAAAK linker. The construct was stable with high antigenicity, immunogenicity and solubility properties. Our in silico data showed that the fusion protein is not allergenic in the prokaryotic host.

Conclusion: In conclusion, this new construct from S. Typhi OMPs could generate a potent immune response and can be experimentally studied as a vaccine candidate.

Keywords: Salmonella Typhi, chimeric vaccine, outer membrane protein, steB, tsaC

P345 - 730: RECENT ADVANCES IN BRUCELLA PATHOGENESIS AND IMMUNE RESPONSE IN HUMANS

Gholamreza Hashemi Tabar[1], Ali Nemati[2], Mehrnaz Rad[3]

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: Brucella species., as animal pathogens, are small, gram-negative, non-motile, non-spore-forming, facultative intracellular coccobacilli, and cause human brucellosis those results in worldwide economic losses and human morbidity. Out of 10 classified Brucella species, B. melitensis, B. abortus, B. suis, and B. canis are pathogenic for humans and B. melitensis remains the principal cause of human brucellosis. There are no safe and licensed vaccines for prevention of human brucellosis and the bacteria do not display obvious classic virulence factors such as exotoxins, capsule, and LPS. So the present study provides a comprehensive review of Brucella pathogenesis, with the goal to cover clinical aspects of the disease in humans.

Methods: After investigating the pathogenic potential of Brucella spp. in humans, this study focused on the major mechanisms of Brucella pathogenesis, and divided them into two main categories and four steps.

Results: Invasion to host cell and intracellular survival or replication are two major virulence mechanisms of Brucella pathogenesis and their steps included: adherence, invasion, establishment, and dissemination within the host. Then, the bacteria begin to infect the phagocytic and non-phagocytic cells of the reticuloendothelial system and finally can establish a chronic infection in humans.

Conclusion: The mechanisms of Brucella pathogenesis are extremely related to its ability to enter and survive within host cells. Understanding these mechanisms can be useful not only for the development of new and improved vaccines or therapeutic methods, but also as tools for the study of components and regulation of the host immune system.

Keywords: Brucellosis, Pathogenesis, Vaccine, Immune response, Human.

P346 - 731: STUDY OF THE ABILITY OF BIOFILM FORMATION IN ESCHERICHIA COLI ISOLATES FROM URINARY TRACT INFECTIONS (UPEC) BY MICROTITER PLATE

Ali Dadvar[1], Gholamreza Hashemi Tabar[2], Mehrnaz Rad[3]

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 infections are one of the most common infections and Escherichia coli is one of the main causes of this infection. A Biofilm is actually a microbial collection that its structure makes the bacteria more resistant and reduces the treatment of these infections. The aim of this study is determine the ability of biofilm formations in E. coli isolated from urinary tract infections.

Methods: In this study, 72 samples of Escherichia coli isolated from urinary tract infections were collected from hospitals in Mashhad in 1393-1396 and were approved by Biochemical tests and then ability to biofilm formation was studied by microtiter plate and was read using an ELISA reader.

Results: Based on optical density from the 72 studied isolates, 5 isolates (7%) had the ability to form a strong biofilm, 18 (25%) isolates had the ability to form moderate biofilms, 37 (51%) isolates, had the ability to form weak biofilms and 12 (17%) isolates did not have the ability to form biofilm.

Conclusion: Considering the high percentage of biofilms formation (83%) in the isolates, it is recommended that Suitable hygiene items to be used.

Keywords: Urinary tract infection / Escherichia coli / Biofilm / Microtiter plate

P347 - 732: THE SEARCH FOR FIMA AND CSGA GENES IN ESCHERICHIA COLI ISOLATES FROM URINARY TRACT INFECTIONS (UPEC) BY MULTIPLEX PCR

Ali Dadvar[1], Gholamreza Hashemi Tabar[2], Mehrnaz Rad[3]

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: Escherichia coli is one of the most common and major bacterial agents in human urinary tract infections. Attachment factors such as fimbriae type 1 and fimbriae curli can cause colonization in the urinary tract. The aim of this study is to find and determine the fimA gene (type 1 fimbriae) and the csgA gene (curli fimbriae) in Escherichia coli isolated from urinary tract infections.

Methods: In this study, 72 samples of Escherichia coli isolated from human urinary tract infections were collected from hospitals in Mashhad in1393-1396 and the samples were approved by biochemical tests. Then with specific primers, the genes were studied by multiplex PCR assay.

Results: The results showed, all isolates (100%) had csgA gene and 56 isolates (78%) had fimA gene and 16 isolates (23%) lacked the fimA gene from 72 isolates.

Conclusion: Most of the isolates had csgA and fimA genes. According to the results, these genes should be considered for the treatment and prevention of urinary tract infections. And in order to the inhibition of attachments factors these genes should be studied further.

Keywords: Urinary Tract Infection / Escherichia coli / Multiplex PCR / fimA / csgA /

Emerging and Reemerging Infectious Diseases

P348 - 56: ANAEROBIC INFECTION:

Ali Ghorbanipour[1], Dr.saeed zaker bostanabad[2]

1. AUthor
2. Corresponding

Background and Aim: Vaginosis due to bacteroides fragilis is a rare disorder .This article describes a case of bacteroides fragilis vaginosis in a patient and review the cases of vaginosis due to this anaerobic bacterium in medical literature

Methods: Bacteroides fragilis may be isolated as a single agent, such as in blood cultures, or more typically from mixed infections. The organism is aerotolerant, but requires an anaerobic environment to propagate. Simple identification from blood cultures includes Gram stain and growth on anaerobic agar and LKV agar

Results: We emphasize that Bacteriodis fragilis is a rare agent of vaginosis and these patients should be carefully evaluated for the complications associated with this anaerobic infection.

Conclusion: Bacteroides fragilis is an anaerobic Gram-negative rod and constitutes 1% to 2% of the normal colonic bacterial micro flora in humans

Keywords: Bacteroides fragilis, Gram-negative anaerobic bacteria

P349 - 204: PREVALENCE OF BACTERIAL CONJUNCTIVITIS IN PATIENTS REFERRED TO EYE SPECIALIST HOSPITALS IN KASHAN, IRAN

Ali Nazari Alam[1], Hadis Fathizadeh[2], Mehdi Shaeri[3], Rezvan Moniri[4], Fereshteh Baddi[5]

1. Department of Microbiology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran
2. Department of Microbiology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran
3. Department of Ophthalmology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran
4. Department of Microbiology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran
5. Department of Microbiology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran

Background and Aim: Bacterial Conjunctivitis is a general non-traumatic disease of the eye characterized by pain, conjunctival hyperemia and discharge. It is an ordinary condition in children and adults and be able to be caused by a range of bacterial agents. We conducted a study to determine prevalence of bacterial conjunctivitis in patients referred to eye specialist hospitals in Kashan.

Methods: Conjunctival swab specimens were obtained from 200 conjunctivitis patients attending the Ophthalmology out-patient and in-patient department and were processed by inoculation on Blood agar, MacConkey agar and Chocolate media, Gram staining and various biochemical tests for identification

Results: Of the 200 conjunctival samples, 193 bacterial pathogens were detected; including 103(53.3%) Coagulase- negative staphylococci, 55(28.4%) Staphylococcus aureus, 6(3.1%) Pseudomonas aeruginosa, 6(3.1%) micrococcus, 5(2.5%) Streptococcus pneumoniae, 4(2.07%) Klebsiella species, 2(1.03%) bacillus cereus, 2(1.03%) diphtheroid, 2 (1.03%) Proteus mirabilis, 1(0.51%) Escherichia coli, 1(0.51%) Streptococcus viridance, 1(0.51%) streptococcus pyogenes, 1(0.51%) enterobacter, and 1(0.51%) salmonella.

Conclusion: There is a high frequency of bacterial conjunctivitis at the eye referred to specialist hospitals with the commonest causes being Coagulase- negative Staphylococci and Staphylococcus aureus.

Keywords: Conjunctivitis, Prevalence, Eye Infections- Bacterial, Staphylococcus

P350 - 214: THE EXPRESSION OF RECOMBINANT HYDI PROTEIN OF ECHINOCOCCUS GRANULOSUS IN E. COLI BL21 (DE3) STRAIN

Minoo Dasehmahmanesh[1], Hanieh Jafary[2], Zarrintaj valadkhani[3]

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. Molecular Parasitology Laboratory, Department of Parasitology, Pasteur Institute of IranTehran, Iran

Background and Aim: In Intermediate hosts such as humans and livestock where the eggs of Echinococcus granulosus develop into the metacestode (larval) stage, cause cystic echinococcosis (CE). Hydatid cyst is usually located in the liver and lungs, however rare cases showing localization of the cyst in other organs or tissues. Our objective was to investigate further the role of E. granulosus antigen B (AgB) in human early inflammatory response. An accurate diagnosis and early treatment of CE is crucial and can reduce the severity of infection. HydI is one of the antigens that can be used for detection of CE antibody in infected patients.

Methods: HydI gene was sub-cloned in expression plasmid pET31b. The recombinant plasmid was then transferred to E. coli Bl21 (DE3) strain. Then the recombinant protein expression was analyzed by SDS-PAGE.

Results: The presence of HydI gene fragment in the recombinant plasmid was confirmed by NdeI/XhoI enzymes. Sequence analysis of the correct cloning, revealed, %100 homology with the published sequence of HydI gene. SDS-PAGE analysis showed expression of protein band at 9.33 KDa in induced bacteria.

Conclusion: In conclusion, this study reported construction of a plasmid DNA encoding HydI protein of E. granulosus. We confirmed that the plasmid pET31b and the BL21 (DE3) expression host are able to direct synthesis of antigenic HydI protein.

Keywords: Echinococcosis, HydI, expression, Bl21 (DE3)

P351 - 230: DETECTION OF FOWL ADENOVIRUS E IN BROILER FLOCK IN GOLESTAN PROVINCE , 2018.

Leila Aghaiyan[1], Arash GhalyanchiLangeroudi[2], Hossein Hossein[3], Zahra Ziafatikafi[4], Reyhane Khezrdoust[5], Fateme sadat mousavi[6], Amir Modiri[7], Hosein Rezaei[8]

1. Department of Microbiology and Immunology, Faculty of Veterinary MedicineUniversity of Tehran, Tehran,Iran
2. Department of Microbiology and Immunology, Faculty of Veterinary MedicineUniversity of Tehran, Tehran,Iran
3. Department of Clinical Sciences, Faculty of Veterinary Medicine, Karaj Branch, Islamic Azad University, Alborz, Iran.
4. Department of Microbiology and Immunology, Faculty of Veterinary MedicineUniversity of Tehran, Tehran,Iran
5. Department of Microbiology and Immunology, Faculty of Veterinary MedicineUniversity of Tehran, Tehran,Iran
6. Department of Microbiology and Immunology, Faculty of Veterinary MedicineUniversity of Tehran, Tehran,Iran
7. Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran.
8. Department of Microbiology and Immunology, Faculty of Veterinary MedicineUniversity of Tehran, Tehran,Iran

Background and Aim: Inclusion body hepatitis (IBH) associated with FAdV-I (fowl adenovirus) occurs worldwide in poultry industry. It is an acute disease that mainly affects young chickens between 3 and 7 weeks of age, and is caused by several avian adenovirus serotypes. At histopathological ex-amination, the organs with the most significant lesions were the liver, intestines and lungs.

Methods: The samples were obtained from 2 weeks old broiler flock of Ross from Golestan province of Iran in March 2018. The samples (liver) were homogenized and extracted by Sina Pure DNA kit according to the protocol of the manufacturer. The 590 bp region of the hexon gene was amplified using a pair of specific primers. The reaction product were analyzed by electropho-resis. The RT-PCR product sequenced in the forward and reverse direction.

Results: The results indicated that two FAdV serotypes (11 and 8b) are high prevalence serotypes of FAdVs in Iran and are pathogenic to cause IBH in young chicks. The nucleotide sequences of hexon genes were compared with the FAdV sequences data available in the GenBank. This isolate is located in genotype E clade.

Conclusion: This is the first report of FADV in broiler farms in Golestan province. It is necessary to provide more epidemiological data to establish the prevalence of these viruses and justify the development of vaccine programs in breeders, broiler and laying hens to prevent vertical and horizontal virus infections and prevent the spread of this virus.

Keywords: Inclusion body hepatitis, Adenovirus, FADV

P352 - 333: MODELING THE POPULATION DYNAMICS OF ACQUIRED IMMUNITY TO PARASITE INFECTION

Ashkan Dehghan[1]

1. Young Researchers and Elite Club

Background and Aim:we present a model for the immunological response by the host against gastrointestinal parasites. We show that such modelling can have significant implications for real control programmes. Parasites invoke extremely complex immunological responses from their mammalian hosts.

Methods: So as to be able to construct a realistic model, we have to consider experimental observations. We introduce a variable, E, for the immune system: E=∫_(t-T)^t▒〖L(t´)dt´〗 where L(t) denotes the mean number of tissue-dwelling larvae in a host at time t with T the time-span over which the immune system retains memory of past infections. So, E is a measure of the number of larvae in the host during the time interval (t − T, t).

Results: for the biological facts we introduce an expression to describe the immune system's activity: I_αβ (E)=αE²/(β+E²) where E is the input variable,α is the maximum functional activity of the host's immune response and β provides the sensitivity of the immune system. α also reflects the nutritional status of the host. β may be host specific since it also has genetic terms.

Conclusion: According to assumption, and independent of the specific dynamical situation under consideration, the activity of the host's immune system leads to an increase in the mortality of the adult parasites. This requires an additional loss term in the dynamical equations for the mean worm burden, M(t), of the form −I M(t) < 0, where I , the strength of immunological response, works for a death rate for parasites; it depends on the level of infection.

Keywords: Mathematic modeling - dynamic-data structure - population dynmics - parasite Infection

P353 - 351: ASSESSMENT OF CATALASE AND GLIOTOXIN CYTOTOXICITY IN ASPERGILLUS FLAVUS FUNGAL

Sara Roeen[1], Parisa badei[2]

1. Department of Biochemistry, Dr Neshat's Laboratory, Shiraz, Iran
2. Professor Alborzi Clinical Microbiology Research Center, Nemazee Hospital, Shiraz University of Medical Sciences, Shiraz, Iran

Background and Aim: Aspergillus flavus is one of the most common causes of fungal infections in immunocompromised patients due to its pathogenic virulence factors such as catalase and Gliotoxin in this fungus. In this study, the catalase activities and cytotoxic effects of gliotoxin were comparedin environmental and clinical isolates of Aspergillus flavus.

Methods: Ten clinical samples of Aspergillus flavus from immunocompromised patients and ten environmental samples were collected and identified by culture and PCR-RFLP, using MwoI restriction enzyme. Catalase were extracted from spores and mycelia phase of cultures and evaluated by Amplex Red catalase assay Kit (A22180).The cytotoxicity¬ of gliotoxin on MRC-5 lung cell lines was evaluated by XTT test.

Results:: All the samples were proved as Aspergillus flavus by PCR-RFLP. Mycelia catalase measures in clinical samples were more than the ones found in environmental samples ($p>0.05$), but catalase measures from spores in both groups were equal. Mycelia catalase in all 20 species were significantly higher than spore catalase ($p<0.05$).There was no any significant difference in cytotoxicity of gliotoxinin both sample kinds ($p> 0.05$).

Conclusion: The previous studies don't enable us to determine the virulence factors of Aspergillus flavus. It has been demonstrated that Mycelial phase had more catalase activity; therefore it is more pathogenic and it can be concluded that Cytotoxicity of gliotoxin on lung cell lines in both clinical and environmental samples was identical.

Keywords: Aspergillus flavus, catalase, mycelium, spore, PCR-RFLP, gliotoxin, XTT

P354 - 632: ISOLATION OF CLOSTRIDIUM DIFFICILE FROM CDI SUSPECTED PATIENTS IN KERMAN HOSPITALS, IRAN

Mojtaba Alimolaei[1], Hamid-Reza Rahimi[2], Majid Ezatkhah[3], Sadegh Afzali[4]

1. Department of Research and Technology, Kerman branch, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran
2. Department of Toxicology and Pharmacology, School of Pharmacy, Kerman University of Medical Sciences
3. Kerman branch, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran
4. Kerman branch, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran

Background and Aim: Clostridium difficile remains the major identified cause of nosocomial diarrhea that known as C. difficile infection (CDI). This study investigated the prevalence of C. difficile isolated from CDI suspected patients (suffering from diarrhoea) in Kerman city of Iran.

Methods:A total of 151 stool specimens were collected from patients suffering from diarrhoea in Kerman city of Iran and screened for the presence of C. difficile. Fresh faecal specimens were processed and cultured on C. difficile selective agar plates, supplemented by D-cycloserine and cefoxitin. Plates were incubated in anaerobic chambers and monitored daily up to 5 days. C. difficile isolates were presumptively identified on the basis of their characteristic morphology on selective agar plates, specific horse-stable odor, Gram stain, and green- chartreuse fluorescence under a ultraviolet light.

Results: Out of investigated patients, 84 (55.63%) patients were culture positive for C. difficile. A total of 292 C. difficile isolates were recovered from stool specimens. C. difficile isolation rates from pediatrics (<18 years), adults (18–44 years), elderly adults (45-64 years), and geriatric (≥65 years) age groups were respectively 56.52%, 57.84%, 40.00%, and 50.00%, that were not significantly different ($p>0.05$).

Conclusion: This is the first report of the C. difficile isolation from hospitals in Kerman city of Iran. The results indicate that CDI might be an important nosocomial infection in hospital wards. There is little epidemiological information about CDI in Iran and it is important to pay attention to this disease. Further research is needed to determine the toxigenic C. difficile strains and types, which are scattered in this region.

Keywords: Clostridium difficile; CDI; Prevalence; Kerman; Iran

P355 - 719: FREQUENCY OF CHLAMYDIA TRACHOMATIS, MYCOPLASMA GENITALIUM, UREAPLASMA UREALYTICUM AND LISTERIA MONOCYTOGENES ISOLATED FROM VAGINAL SAMPLES OF WOMEN IN KERMAN, IRAN

Zahra Zahirnia[1], Shahla Mansouri[2], Fereshteh Saffari[3], Ghazal Mansouri[4]

1. Department of Microbiology and Virology, Kerman University of Medical Sciences, Kerman, Iran
2. Department of Microbiology and Virology, Kerman University of Medical Sciences, Kerman, Iran
3. Department of Microbiology and Virology, Kerman University of Medical Sciences, Kerman, Iran
4. Department of Obstetrics and Gynecology, Kerman University of Medical Sciences, Kerman, Iran

Background and Aim: Chlamydia trachomatis, Mycoplasma genitalium, Ureaplasma urealyticum and listeria monocytogenes are pathogens can pose serious complications during pregnancy and neonatal infection. Due to the importance of these bacteria and their lack of identification in Kerman, this study was conducted.

Methods: This study was performed on 200 women who were referred to Afzalipour Hospital that ranged from 18 to 42 years old. 124 vaginal swab specimens were for aborted women and 76 cases for pregnant. Vaginal swab specimens were placed in two enrichment transport (TSB and yeast extract with and without antibiotics). Tubes containing antibiotic were placed in the refrigerator for L. monocytogenes, but another tubes used DNA extraction. Omp, mgpa, urease and inl j genes used for U. urealyticum, C. trachomatis, M. genitalium and L. monocytogenes. The enriched specimens were cultured on Blood agar and Palcam agar. The isolates were confirmed by specific phenotypic tests for L. monocytogenes.

Results:PCR results showed that U. urealyticum, C. trachomatis and M. genitalium were higher in aborted women than in pregnant women so that 34.6% vs. 15.7% for U. urealyticum, 20.9% vs. 17.1% for M. genitalium and 15.3% vs. 10.5% for C. trachomatis. However, only for U. urealyticum the difference was significant (P= 0.0006). Cultures for L. monocytogenes were positive only about 5.5%, while PCR was positive by 29.5%.

Conclusion: The present study showed high prevalence of U. urealyticum and L. monocytogenes in aborted and pregnant women, respectively. Diagnostic test is recommended to detect these bacteria in women with high risk.

Keywords: Pregnant women, abortion, U. urealyticum, C. trachomatis, M. genitalium, L. monocytogenes

P356 - 740: A COMPARATIVE ANALYSIS ON PREVALENCE OF INTESTINAL PARASITES AMONG CANCER PATIENTS WITH A CONTROL GROUP IN HEALTH CARE CENTERS OF RASHT CITY (2017)

Mohammad Reza Mahmoudi[1], Hose-in Hasani[2], Kyehan Ashrafi[3], Zahra Atrkar Roshan[4], Meysam Sharifdini[5]

1. Cellular and Molecular Research Center, Faculty of medicine , Guilan University of Medical Sciences, Rasht- Iran
2. Faculty of medicine, Guilan University of Medical Sciences, Rasht- Iran
3. Faculty of medicine, Guilan University of Medical Sciences, Rasht- Iran
4. Faculty of medicine, Guilan University of Medical Sciences, Rasht- Iran
5. Faculty of medicine, Guilan University of Medical Sciences, Rasht- Iran

Background and Aim: Intestinal parasitic infections (IPIs) are among important threats of immunocompromised patients, especially those with cancer, and have considerable effects.

Methods: In this descriptive – cross sectional study, 761 stool samples were collected from studied groups (including 362 samples of chemotherapy patients and 399 samples from the control group) from March to September 2017. Samples were testes by direct, Formalin – Ether and Ziehl – Neelsen staining methods

Results: The overall parasitic infection rate was 11.3% in chemotherapy group and 7.3% in control group. The most prevalent infections were Blastocystis hominis (8.9%) and Strongyloides stercoralis (0.5%). Statistical analyses revealed a significant correlation between the ratio of chemotherapy frequency to scheduled frequency and parasitic infections (P = 0.001).

Conclusion: Respecting lethality of some parasitic infections such as Strongyloides stercoralis in inmmunocompromised patients, results of the present study suggested that periodic stool examinations in special parasitological laboratories should be included as a part of routine medical care in these groups of patients.

Keywords: Intestinal parasites; Dialysis; Chemotherapy

P357 - 742: TOXOPLASMA GONDII INFECTION IN CANCER PATIENTS IN GUILAN

Mohammad Reza Mahmoudi[1], Ebrahim Rajabi[2], Farshid Saadat[3]

1. Cellular and Molecular Research Center, Guilan University of Medical Sciences, Rasht- Iran
2. Faculty of medicine, Guilan University of Medical Sciences, Rasht- Iran
3. Faculty of medicine, Guilan University of Medical Sciences, Rasht- Iran

Background and Aim: Toxoplasma infection in immunocompromised individuals, such as individuals malignant patient under chemotherapy, can cause severe disease as encephalitis or systemic infections. This report is first study about prevalence of Toxoplasmosis in cancer patients in Guilan-North of Iran.

Methods: This Case control study was performed on Cancer patients referred to Educational Hospital in Rasht (North of Iran), from July 2017 to January 2018. Blood samples were collected from 148 cancer patients having different types of malignancies would like to contribute in our study, as well as 150 immunocompetent individuals as a control group, to assess the seroprevalence of anti-T.gondii antibodies.

Results: The antibodies (IgG/IgM) were measured by ELISA method. Overall, 71 cases were female and 79 cases were male. The results showed that one patients (1/148) (IgG+, IgM+) with acute phase, 94/148 (%) (IgG+, IgM-) chronic phase and 1/148 (%) (IgG-, IgM+) false positive.

Conclusion: These data showed high percent of patients were susceptible to reactivation of latent toxoplasmosis. For this reason, it is important that patients with toxoplasmosis infection are diagnosed and identified in order to refer them for early therapy or other interventions.

Keywords: Toxoplasma, ELISA,Guilan

P358 - 800: MICROSCOPY STUDY AND NESTED PCR FOR DETECTION OF CRYPTOSPORIDIUM SPP. AND MICROSPORIDIA IN REFERRED TUBERCULOSIS INDIVIDUALS AND THEIR FAMILY TO THE MASIH-DANESHVARI HOSPITAL, TEHRAN, 2016-2017

Ali Taghipour [1], taher azimi[2], Ali Haghighi [3]

1. Department of Medical Parasitology and Mycology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
2. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
3. Department of Medical Parasitology and Mycology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.

Background and Aim: Co-infection of intestinal parasites and tuberculosis (TB) in human is one of the major health problems in developing and undeveloped countries. In this study, we aimed to investigate the frequency of Cryptosporidium spp. and Microsporidia in stool samples of referred tuberculosis patients and their family to the Masih-daneshvari hospital in Tehran by using Chromotrope 2R and modified Ziehl_Neelsen staining methods and also a nested PCR technique

Methods:A total of 181 stool samples were collected from TB patients and 97 samples were obtained from their family during September 2016 to April 2017. All the 278 stool samples were stained by using Chromotrope 2R and modified Ziehl_Neelsen methods. Extracted DNA from 8 samples microscopy positive or suspected Cryptosporidium spp and Microsporidia and also 15 samples randomly negative isolates were tested by a nested PCR technique

Results: Out of 278 studied patients and their family, 6 (%2.15) stool specimens were infected with Cryptosporidium spp. 3(%1.07) and Microsporidia 3(%1.07) by nested PCR technique. Frequency of Cryptosporidium spp. in tuberculosis individuals and their family was 2(%1.10) and 1(%1.03) respectively. Frequency of Microsporidia in tuberculosis individuals and their family was 2(%1.10) and 1(%1.03) respectively

Conclusion: Findings of this research show that Cryptosporidium spp. and Microsporidia infections exist among tuberculosis individuals and their family, and emphasizes the necessity of increasing awareness among clinicians regarding the occurrence of parasite infections in these tuberculosis patients. Routine examination of stool samples for parasitic infections could significantly benefit the tuberculosis infected individuals by contributing to reduce morbidity, mortality and improved quality of life.

Keywords: Nested PCR, Cryptosporidium spp, Microsporidia, tuberculosis

P359 - 850: PHYLOGENIC ANALYSIS OF HUMAN BOCAVIRUS IN CHILDREN WITH ACUTE RESPIRATORY INFECTION IN IRAN

Mehrdad Mohammadi[1], Jila Yavarian[2], Sharareh Moghim[3], Bahram Nasr Esfahani[4], Vajihe karbasizadeh[5], Nafiseh Sadat Hosseini[6]

1. MSc student, Department of Microbiology, Isfahan University of Medical Sciences, Isfahan, Iran
2. Associate Professor, Department of Virology, School of Public Health, Tehran University of Medical Sciences.
3. Associate professor, Department of Microbiology, Isfahan University of Medical Sciences, Isfahan, Iran
4. Professor, Department of Microbiology, Isfahan University of Medical Sciences, Isfahan, Iran
5. Assistant Professor, Department of Microbiology, Isfahan University of Medical Sciences, Isfahan, Iran
6. PhD candidate, Isfahan University of Medical Sciences, Isfahan, Iran

Background and Aim: Human bocavirus (HBoV) was first described in nasopharyngeal aspirates samples from children that suffer from respiratory illness in 2005. This virus has possibility role in acute respiratory infections as well as gastroenteritis in children. This study was performed to analyze the infection frequency and confection rates of HBoV with RSV and phylogenetic analysis of the virus in children with acute respiratory infection in Iran.

Methods: During the time period 2016 to 2017, a total of 75 respiratory samples from children hospitalized with acute respiratory infection were collected. The samples were first screened for RSV by direct immunofluorescence method and then subjected to detect HBoV by PCR with primers from the NP-1 gene.

Results: The isolated HBoV were sequenced for VP2. From 75 respiratory samples, 20(26.7%) and 10 (13.3%) were positive for RSV and HBoV, respectively. The coinfection rate was 40 % ($P < 0.05$). In seasonal distribution, the winter has upmost extent outbreak ($P < 0.05$). Sequence analysis of positive samples revealed that all of them are related to HBoV 1 genotype.

Conclusion: This study demonstrated that detection of the virus in clinical samples from children with acute respiratory infection was low, and all of the detected viruses were related to HBoV genotype.

Keywords: Human bocavirus (HBoV), acute respiratory tract (ARTI) infection, RSV, Phylogenetic analysis

Food and Water Microbiology

P360 - 3: THE INHIBITORY EFFECTS OF 3 IRANIAN HONEYS IN PREVENTING TISSUE DAMAGE CAUSED BY ASPERGILLUS FUMIGATUS IN BALB/C MICE.

Ali Reza Khosravi[1], Donya Nikaein[2], Tina Hasankhani[3]

1. Mycology Research Center, Faculty of Veterinary Medicine University of Tehran, Tehran, Iran
2. Mycology Research Center, Faculty of Veterinary Medicine University of Tehran, Tehran, Iran
3. Mycology Research Center, Faculty of Veterinary Medicine University of Tehran, Tehran, Iran

Background and Aim: Occurrence of Invasive Aspergillosis (IA) has increased significantly in recent years. Although lung is the main site of aspergillosis, Aspergillus fungi can spread to other organs and cause thrombosis, hemorrhage and necrosis. Honey is a natural product with antioxidant, anti-inflammatory, immunomodulatory and antimicrobial properties. This study was designed to determine the effect of 3 Iranian honeys in prevention of tissue invasion in mice involved with invasive aspergillosis.

Methods:100 male BALB/c mice were divided into 10 groups including honey, honey/infection and negative and positive controls. Honey was administered orally (1gr/kg BW) for 10 days. On day six, mice were infected with Aspergillus fumigatus conidia (1×106/IV). On day 11, mice were euthanized and histopathological samples and tissue culture were prepared. Five mice from each group were kept for 30 days to determine survival rate.

Results: Findings showed that there were no histopathological changes in honey recipients alone. The highest rate of fungal contamination was in kidneys, and the honey/infection mice had a significant decrease in CFU/gr in comparison to the infectious group. Survival rates were also higher for Pennyroyal/Licorice and mixed honey recipient mice (p< 0/05).

Conclusion:according to our results honey can be used as an inhibitor of adverse effects of Aspergillus fumigatus on different tissues. In addition, honey consumption could prevent the invasion of fungi into different tissues and increases the survival rate. However, further studies are needed to determine the mechanism of action, most effective dosage and the exact active compounds of honey.

Keywords: Invasive Aspergillosis, honey, histopathology, mice

P361 - 13: EMERGENCE AND STABILITY OF HIGH-PRESSURE RESISTANCE IN DIFFERENT FOOD-BORNE PATHOGENS

Amin Khalili[1], alireza jahani[2]

1. master of microbial biotechnology
2. master of microbial biotechnology

Background and Aim: High hydrostatic pressure (HHP) processing is becoming a valuable nonthermal food pasteurization technique, although there is reasonable concern that bacterial HHP resistance could compromise the safety and stability of HHP-processed foods. While the degree of natural HHP resistance has already been shown to vary greatly among and within bacterial species, a still unresolved question remains as to what extent different food-borne pathogens can actually develop HHP resistance. In this study, we therefore examined and compared the intrinsic potentials for HHP resistance development among strains of Escherichia coli, Shigella flexneri, Salmonella enterica serovars Typhimurium and Enteritidis, Yersinia enterocolitica, Aeromonas hydrophila, Pseudomonas aeruginosa, and Listeria innocua using a selective enrichment approach. Interestingly, of all strains examined, the acquisition of extreme HHP resistance could be detected in only some of the E. coli strains, indicating that a specific genetic predisposition might be required for resistance development. Furthermore, once acquired, HHP resistance proved to be a very stable trait that was maintained for>80 generations in the absence of HHP exposure. Finally, at the mechanistic level, HHP resistance was not necessarily linked to derepression of the heat shock genes and was not related to the phenomenon of persistence.

Methods:0

Results:0

Conclusion:000

Keywords:0

P362 - 114: ANTIBACTERIAL EFFECTS OF KUMQUAT(CITRUS JAPONICA) ESSENTIAL OIL AGAINST SOME PATHOGENIC BACTERIA AND COMPARISON WITH SOME STANDARD ANTIBIOTICS

Sara Moosazad[1], Razzagh Mahmodi[2]

1. MSc Student of Food Safety and Hygiene, Faculty of public Health, Qazvin University of Medical Sciences, Qazvin, Iran
2. Associate Professor, Medical Microbiology Research Center, Qazvin University of Medical Sciences, Qazvin, Iran

Background and Aim:A lot of research has been done on antimicrobial properties and preservative effects of citrus and their essential oil(EOs) in food.From this we have emphasized the importance of this issue by identifying the anti-bacterial effects of kumquat EO.

Methods:: In this experimental study, the Kumquat skin EO was extracted by distillation method and the analysis of the EO was carried out using GC/MS.Minimum inhibitory concentration (MIC) and Minimum bactericidal concentration(MBC) were determined using Microdilution method and diameter of the bacteria inhibition zone by diffusion method for Staphylococcus.aureus, Escherichia.coli, Proteus.mirabilis and Pseudomonas.aeruginosa strains and compared with standard antibiotics.

Results: The yield of EO of kumquat fruit in this study was calculated to be 6.66%. Its major chemical components were 4-azatricyclo (23%), trans-Verbenol (10.94%), n-(benzylidene)2-methyl-1-propen (8.25%) and pyrido-triazole (5.25%). MIC of EO of this fruit against S.aureus, E.coli, P.mirabilis and P.aeruginosa was 0.625-0.312-0.312-0.312%, respectively. In Disk diffusion, the highest inhibition zone of growth for S.aureus, E.coli, P.mirabilis and P.aeruginosa were determined 12-10-11-18 mm respectively. Also, the results showed that Tetracycline antibiotic has a greater inhibitory effect on S.aureus, E.coli and P. .aeruginosa bacteria compared to the EO.Chloramphenicol antibiotic against S.aureus and Amoxicillin and Ampicillin antibiotics have a greater inhibitory effect on p.mirabilis than kumquat EO.

Conclusion: The antimicrobial effect of kumquat EO on the bacteria studied was significant;So it can be used as an alternative to chemical preservatives and chemical drugs offered.

Keywords:kumquat_essential oil_antimicrobial effect_pathogenic bacteria

P363 - 136: STUDY OF THE ANTIMICROBIAL EFFECTS OF METHANOLIC EXTRACT OF OLIVE LEAVES ON PATHOGENIC STRAINS UNDER LABORATORY CONDITIONS

Shabnam Torabi[1], Mohammad asghari[2]

1. Graduated from the Department of Food Science and Technology, Shahreza Azad University
2. Graduated from the Department of Food Science and Technology, Higher Agricultural and Animal Husbandry Complex, Torbat Jam Branch

Background and Aim: Olive leaf is a medicinal plant containing phenolic and oleuripine compounds, which is known as a cheap and affordable source of polyphenols. Phenolic compounds have antioxidant and antimicrobial properties. Today, with the increasing use of antibiotics and also The prevalence of resistant strains, the vacuum resulting from the use of new antimicrobials that have less side effects than antibiotics, is felt. Olive leaf is a medicinal plant that has been used extensively in ancient medicine. In this study, the effect of methanolic extract of this plant on different pathogens is investigated.

Methods: In this experimental study, olea europaea was used to evaluate its antimicrobial effects. Methanolic extracts of this plant were prepared at concentrations of 50, 100, 200, 400, 400 mg / ml, and analyzed by Escherichia coli, Pseudomonas aeruginosa, Bacillus cereus and Staphylococcus aureus. The test was to determine the minimum inhibitory concentration and minimum microbial concentration.

Results: In this study, the highest effect of methanolic extracts of olive leaves on Pseudomonas aeruginosa Varshakkey was observed at concentrations of 400 mg / ml. The inhibitory concentration of this extract on the growth of these bacteria varied from 6.25 to 100 mg / ml. The minimum germination concentration of the extract from these bacteria was also obtained from 12.5 to 200 mg / ml.

Conclusion: In this study, methanolic extracts of ovine leaves were affected by Staphylococcus aureus, Escherichia coli, and Osmosis spp., But did not inhibit Bacillus cereus.

Keywords: Vegetable extract, olive leaf, minimum inhibitory concentration

P364 - 168: INFLUENCE OF CUMINUM CYMINUM ESSENTIAL OIL ON LISTERIA MONOCYTOGENES AND ASPERGILLUS FLAVUS IN FETA CHEESE

Ali Heshmati[1]

1. Hamadan Uni of Med Sci

Background and Aim: Due to the negative effects of chemical preservatives on the health of consumers, the legal authorities and the food industry have focused on the use of essential oils and plant extracts as natural preservatives in food.

Methods: In this study, the effect of essential oils of cumin on the growth of Listeria monocytogenes and Aspergillus flavus during feta cheese storage period was studied. The methods used in this study included determination of minimum inhibitory concentration (MIC), minimum bactericidal concentration (MBC) and minimum concentration of fungicide (MFC) of essential oils.

Results: The main components of the essential oil included Alpha-terpinen-7-al (33.41%), n-dedans (21.32%), cumin aldehyde (12.35%), 1 and 8 cineole (8.98%), alpha-tropinone (4.23%) and salinin (3.4%). The MIC and MBC of the essential oil of cumin were 0.04 % and 0.08% for Listeria. Also, MIC and MFC against Aspergillus were 0.08% and 0.1%. The concentration of 0.15% essential oil prevented the production of spores by the fungus in culture media. The essential oil of cumin in the concentration of 0.2% during the storage period of cheese completely inhibited the growth of Aspergillus and reduced the Listeria population compared to the control until 6 log.

Conclusion: The results obtained from this study showed cumin essential oil has effective on growth control of Listeria monocytogenes and Aspergillus flavus in cheese

Keywords: Listeria monocytogenes, Aspergillus flavus, Cumin Cyminum, Cheese

P365 - 171: ENTROCINS PRODUCED BY THE STRAIN ENTEROCOCCUS FAECALIS T23

Tannaz Mirhadizadi[1]

1. Ferdowsi University Of Mashad

Background and Aim: We have partially characterized the bacteriocin activity of the strain Enterococcus faecalis T23. The antimicrobial activity of this strain was determined against Listeria monocytogenes, Salmonella typhimurium and closely related Lactobacilli strains. Treatment with different enzymes revealed that the active substance has a protein nature. PCR amplification resulted in detection of two bacteriocin genes:entB and entA. Bacteriocins of the studied strain were heat stable and active over a wide range of pH (3–10). Triton X-20,Triton X-80, Triton X-100, β-mercaptoetanol, Na-EDTA, SDS and NaCl did not influence the bacteriocin activity.

Methods: Identification of bacteriocin producer strain investigated by phenotypic and genotypic 16srRNA.Heat and pH treatments and biochemicals were done.entrocin genes was performed by entrocin specific primers.

Results:E.faecalis T23 presented antimicrobial activity against Listeria monocytogenes EGDe107776, Salmonella typhimurium and also closely related Lactobacilli strains, such as Lb.brevis F145, Lb. bulgaricus L340.PCR amplification with specific primers resulted in detection of two bacteriocin genes in E.faecalis T23: entB and entA. Both of identified enterocin genes encode bacteriocins, which belong to class II bacteriocins.

Conclusion: In the present study it was shown, that strain E. faecalis T23 produce antimicrobial compound with strong anti-Listerial activity.These compounds are most probably bacteriocins, as they are heat-stable and sensitive to proteolytic enzymes

Keywords:bacteriocins, enterococci, antimicrobial activity,antimicrobial peptides, enterocins.

P366 - 187: THE EFFECT OF AJOWAN OIL ON THE PHYSICOCHEMICAL, SENSORY AND MICROBIAL PARAMETERS OF YOGURT (LOW-FAT WITH MOLD)

Fatemeh Dadmarzi[1]

1. iran,tehran

Background and Aim: Ajowan oil was added to the produced yogurt in vitro in the concentrations of 20, 40, 60, 80 ppm after the starter and before packaging stages. The produced yogurt was evaluated physicochemically, microbiologically and also subjected to organoleptic studies (5 spotted hedonic) within 28 days at specified interval times. The evaluated treatments of the study included oil concentrations (20, 40, 60 and 80 ppm) and time (0, 7, 14, 21 and 28 days).

Methods: Yogurt production with ajowan oil./ Measuring pH/acidity/Organoleptic evaluation/Water Holding Capacity/Mold and yeast count/Extraction method

Results: The addition of ajowan oil controlled the acidity of the yogurt and prevented from souring across the time increasing its shelf life and so it could be possible to produce a stable product. Also, the addition of ajowan oil decreased the WHC and increased the yogurts' water. Moreover, the ajowan oil increased the shelf life of the yogurt through decreasing the number of molds and yeasts,

Conclusion: The addition of ajowan oil controlled the acidity of the yogurt and prevented from souring across the time increasing its shelf life and so it could be possible to produce a stable product. Also, the addition of ajowan oil decreased the WHC and increased the yogurts' water. Moreover, the ajowan oil increased the shelf life of the yogurt through decreasing the number of molds and yeasts,

Keywords: Ajowan oil, yogurt, physicochemical properties, organoleptic evaluations.

P367 - 201: ANTIBACTERIAL AND ANTICANCER ACTIVITY OF A BIOFLAVONOID FRACTIONATED FROM ALLIUM ASCALONICUM

Razieh Aliyan[1], Mansour Amin[2], Saeed khoshnood[3]

1. Department of Food and Drug Control, Faculty of Pharmacy, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
2. Department of Microbiology, Infection and Tropical Diseases Research Center, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, IR Iran
3. Department of Microbiology, Infection and Tropical Diseases Research Center, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, IR Iran

Background and Aim: Shallots are an important part of the diet of many populations and there is long-held belief in their health enhancing properties. Shallot extract prevent the proliferation of cancer cells and has anti-bacterial properties. The objective of this study was the evaluation of antibacterial and anticancer activity bioflavonoid fractionated from Allium ascalonicum against some bacteria and cancer cells by MIC and MTT methods.

Methods: The effect of cytotoxic extracts using MTT colorimetric assay was performed. Doxorubicin was used as a positive control sample and medium containing 5% DMSO as a negative control in cell-free extracts will be considered. Plates incubated for 48 hours in CO2 5% and then at 37 ° C. 100 ml solution of DMSO to dissolve the formazan crystals replace the previous solution and absorption at a wave length of 560 nm is read by Elisa reader. Also the effect of antibacterial extract was evaluated by MIC method.

Results: Allium ascalonicum showed antifungal and anticancer activity. C.diphtheriae was most sensitive, P. aeruginosa and S. pyogens were most resistant bacteria tested. In our study the effect of shallot extract was a dose-dependent pattern and the highest sensitivity cells was observed after 72 hours.

Conclusion: It is of interest that the extract of this plant has shown much less cytotoxicity against the normal cell line. The results of our study indicated that A. ascalonicum can be a candidate for treatment of many diseases.

Keywords: Laboratory examination, Antimicrobial effect, Anti-cancer cells, Shallot plant extract.

P368 - 236: ENTEROCOCCUS SPP. IN TRADITIONAL CHEESE: VIRULENCE TRAITS

Ali Jahansepas[1], Mohammad Aghazadeh[2], Mohammad Ahangarzadeh Rezaee[3], Alka Hasani[4], Yaeghob Sharifi[5], Toofan Aghazadeh[6], Jalal Mardaneh[7]

1. Infectious and Tropical Diseases Research Centre, Tabriz University of Medical Sciences, Tabriz, Iran
2. 1Infectious and Tropical Diseases Research Centre, Tabriz University of Medical Sciences, Tabriz, Iran. 2Department of Clinical Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran.
3. 1Infectious and Tropical Diseases Research Centre, Tabriz University of Medical Sciences, Tabriz, Iran. 2Department of Clinical Microbiology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran.
4. 1Infectious and Tropical Diseases Research Centre, Tabriz University of Medical Sciences, Tabriz, Iran. 2Department of Clinical Microbiology, Faculty of 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 Medical Genetics, Motahari Teaching Hospital, Urmia University of Medical Sciences, Urmia, Iran.
7. Department of Microbiology, School of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran.

Background and Aim: The presence of different Enterococcus spp. has been recorded in cheese; nevertheless E. faecalis and E. faecium are the most commonly isolated ones. This study goal to determine the virulence traits of Enterococcus faecalis and Enterococcus faecium recovered from traditional cheese types in North-west of Iran.

Methods: Fifty traditionally ewe or cow milk cheese samples were randomly purchased from different popular dairy markets from Urmia and Tabriz, in North-west of Iran. Samples were transported to the laboratory in an ice bag and analyzed for Enterococcus spp. Phenotypic and molecular methods at the genus and species level were applied for Identification of enterococci. Screening for Virulence Genes was determined by PCR reactions.

Results: Among all isolates, the majority was with E. faecalis with 83.33% (40/48), and the remainder included E. faecium with16.67% (8/48). In the current study, E. faecalis and E. faecium showed significant differences in the incidence of virulence factors ($P < 0.05$). A higher prevalence of virulence genes (gelE, asa1, ace and cylA) was detected in the E. faecalis isolates. The cpd (100%) was the most common virulence gene among E. faecalis isolates.

Conclusion: The presence and expression of virulence determinants and antibiotic resistance in these strains provided evidence showing that the detrimental aspects of enterococci in cheese could be a public health hazard. Therefore, this study provided the necessary criteria that could be considered in the phenotypic and molecular analysis of enterococci in the traditional cheese in order to ensure their safety by the food and sanitary control laboratory.

Keywords: E. faecalis; E. faecium; virulence factors, traditional cheese.

P369 - 238: EFFECT OF FERULA ASSAFOETIDA FRUITS ESSENTIAL OIL ON GROWTH OF ESCHERICHIA COLI 7H: 157O AND SHIGOTOXIN 2 PRODUCTION

Anna Abdolshahi[1], leila monjazeb marvdashti[2], Aliakbar Shabani [3]

1. Food Safety Research Center (salt), Semnan University of Medical Sciences, Semnan, Iran
2. 1. Department of Food Science and Technology, Faculty of Agriculture, Ferdowsi University of Mashhad (FUM), Mashhad, Iran
3. Department & Center for Biotechnology Research, Semnan University of Medical Sciences, Semnan, Iran

Background and Aim: Today awareness and concerns on the use of artificial preservatives to prevent of food infection and intoxication resulted to increase in usage of natural preservatives. Ferula assa-foetida is an ancient medical plant used for many years in Iran. Escherichia coli 7H: 157O is one of the food-borne pathogens had infectious doses in humans. The aim of this study was to investigate the effect of Ferula assa-foetida essential oil on growth of Escherichia coli 7H: 157O and production of Shigotoxin 2.

Methods: Minimum growth inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) were measured. In agar medium, essential oil injectd to the 6 mm diameter discs and the inhibition zones on the Petri dishes was determined. Moreover, production Shigotoxin-2 was evaluated by Shigotoxin assay kit. The essential oil was analyzed by gas chromatography

Results: The major component of Ferula assa-foetida essentioal oil were epi-α-cadinol (29.43%), 1-propenyl Sec butyl disulfide (14.17%) and germacrene B (13.86%). MIC and MBC of Ferula assa-foetida essential oil on Escherichia coli 7H: 157O was obtained 0.065% and 0.16%, respectively. The highest inhibition zone was obtained 35 mm for a concentration equal to MIC 0.75. The concentrations of 0.016% and 0.032% of this essential oil reduced the production of Shigotoxin 2 whereas the concentration of 0.05 inhibited toxin production

Conclusion:this essential oil is an important source of active biochemical compounds has a significant inhibitory effect on the growth and production of Shigotoxin 2 by Escherichia coli 7H: 157O

Keywords: Ferula assa-foetida, Shigotoxin 2, Escherichia coli 7H: 157O

P370 - 280: SHELF LIFE EXTENSION OF SILVER CARP DURING STORAGE USING NATURAL PRESERVATIVE

Mohamadreza Ghazizadeh[1], Ebrahim Alizadeh Doughikollaee[2], Mohsen Shahriari Moghadam[3]

1. Department of Fisheries, Faculty of Natural Resources, University of Zabol, Zabol, Iran
2. Department of Fisheries, Faculty of Natural Resources, University of Zabol, Zabol, Iran
3. Department of Environmental Sciences, Faculty of Natural Resources, University of Zabol, Zabol, Iran

Background and Aim: Today, the use of natural preservatives such as herbal extracts is increasing in marine products in order to reduce the economic losses and problems caused by bacterial pathogens transmitted through food. The aim of this study was to investigate the effect of aqueous extract of myrtle leaf on total mesophilic bacterial community (TVC) of silver carp during ice storage.

Methods: The aqueous extract of myrtle leaves powder were taken and then the fish were immersed completely (without abdominal discharges) in 0.5 and 1% solution of myrtle extract for 90 minutes. Fish were stored in two layers of ice and one layer of fish for 15 days. TVC of fish fillet was measured during storage time.

Results: The results showed that TVC were increased over time in all treatments. The highest TVC was counted in blank treatment (7.83 Log CFU/g) and the lowest (6.92 Log CFU/g) was in treatment with 1% myrtle extract at the end of storage time. A significant difference ($P<0.05$) was observed between different treatments.

Conclusion: In conclusion, it can be concluded fish immersed at 1% concentration of myrtle leaf extract is a suitable method for controlling the total mesophilic bacteria and increases the shelflife of fish during ice storage.

Keywords: Myrtle, Hypophthalmichthys molitrix, TVC, Shelf life

P371 - 286: OPTIMIZATION OF BIOLUMINESCENCE OF VIBRIO FISCHERI

Zeinab Majidzadeh moghadam[1], hamideh rouhani nejad[2], azadeh azizi[3]

1. Malek ashtar university of technology, Iran
2. Malek ashtar university of technology, Iran
3. Malek ashtar university of technology, Iran

Background and Aim: Vibrio fischeri is bacteria that produce light, mainly in seawater, marine sediments, decomposing fish, and in the intestines of marine animals. The glowing light from luminous bacteria is a specific function consist luciferase and luciferin. This bacteria regulate their conserved lux genes by the mechanism of quorum sensing with produce specific substance auto-inducer (3-oxohexanoyl-homoserine lactone), during their growth, finally induced luciferase to emit visible light. This ability of V. fischeri is useful application for researchers and laboratory tests. In this study, we want to optimization growth condition for best emitting light.

Methods: After all¬, we selected some factors can effect on bacterial growth like, temperature and culture medium¬(NaCl concentration and Arg and Cys amino acid¬). Sea water medium (5 ml) with 5 µl of V. fischeri incubated in 15, 18, 21, 24¬˚C and Room Temperature by shaking. RLU investigated in all of temperature by luminometer. For study of culture medium three concentration of NaCl (1%, 2%, 3%) and Asp and Cys (0/005 , 0/004 gr)was used.

Results: The result showed, light emitting of marine bacteria occurred in temperature of RT and 24˚C. Effects of NaCl displayed 1% NaCl and 0/005 Asp + 0/005 Cys are best concentration. Top RLU for this optimization was 24milion.

Conclusion:according to this result optimized condition for best growth and shedding light achieved. We can used these optimized V. fischeri for examination water and food toxicity(microtox).

Keywords:V. fischeri, luminous, optimization

P372 - 299: MUTAGENIC,ANTI MUTAGENIC ACTIVITIES AND ANTIBACTERIAL EFFECTS OF 3 JUNIPERUS BY AMES METHOD USING SALMONELLA TYPHIMURIUM STRAIN

Milad Mehralizadeh[1], Nahid Rahimifard[2]

1. Pharmacy student
2. associate professor in microbiology- doctorate in medicaldiagnostic laboratory sciences

Background and Aim: Today, the problems caused by the effects of synthetic and chemical drugs on the researchers have led to the investigation of the properties of various plants. All three Juniperus Sabina, Juniperus excelsa, Juniperus communis are from native species Iran and its methanolic extract has an antibacterial effect, we first developed the antimicrobial effect of these three species against Salmonella enteritidis and Yersinia enterocolitis and Campylobacter jejuni using a well plate and microplate method to determine the diameter of the inhibition zone and MIC and MBC. Also, we determined the mutagenicity and anti mutagenicity of this plant.(AIMS Test)

Methods:cross sectional,observational study,basic Applied

Results:under our experiment ,in mutagenicity test,it was not any mutagenic effect with or without s9 for j.sabina,& j.excelsa & j.communis but the antimicrobial effect of these three species against salmonella enteritidis(ATCC13111)and yersinia enterocolitis(ATCC22079)and campylobacter jejuni (ATTC 33560) is good

Conclusion:based on antimicrobial &mutagenicity (AIMS)test effect results, doing other in vivo and in vitro complementation tese are recommended for the further studies

Keywords:mutagenicity, anti mutagenicity, antibactrial activity, salmonella enteritidis ،yersinia enterocolitica ،juniperus

P373 - 300: PROTOCOL FOR THE VALIDATION OF QUALITATIVE ALTERNATIVE METHODS OF MICROBIOLOGY

Sareh Davarzani[1], Reza Soltani[2]

1. Faculty of Food Industry and Agriculture, Department of Microbiology, Standard Research Institute (SRI), Karaj, Iran
2. Faculty of Food Industry and Agriculture, Department of Microbiology, Standard Research Institute (SRI), Karaj, Iran

Background and Aim: Today, many alternative, mostly proprietary, methods exist that are used to assess the microbiological quality of raw materials and finished products and the microbiological status of manufacturing procedures. These methods are often faster and easier to perform than the corresponding standardized method.

Methods: The method comparison study is the part of the validation process that is performed in the organizing laboratory. It consists of three parts namely the following: —comparative study of the results of the reference method to the results of the alternative methodin (naturally and/or artificially) contaminated samples (so-called sensitivity study); —comparative study to determine the relative level of detection (RLOD) in artificially contaminated samples (so-called RLOD study); —inclusivity/exclusivity study of the alternative method. The sensitivity study aims to determine the difference in sensitivity between the reference and the alternative method. A comparative study is conducted to evaluate the level of detection (LOD) of the alternative method against the reference method. The evaluation is based on the calculation of the relative level ofdetection (RLOD). In the study, replicates of artificially contaminated samples are used at three ormore levels of contamination. Preferably, the levels are known as it allows calculation of the LOD.

Results: For inclusivity testing, at least 50 pure cultures of (target) microorganisms shall be tested and for exclusivity testing, at least 30 pure cultures of (non-target) microorganisms shall be tested.

Conclusion: This article determines general principle and the technical protocol for the validation of qualitative alternative methods for microbiology in the food chain.

Keywords: Validation, Alternative methods, Refrence method, Qualitative methods

P374 - 312: AN EVALUATION OF LISTERIA MONOCYTOGENES PREVALENCE IN FRESH VEGETABLES COLLECTED FROM GREENGROCERS IN BIRJAND IN 1396

Majid Zare Bidaki[1], Tayebe Zeinali[2], Ehsan Ahmadi Shahrokht[3], Yasaman Rezaee[4]

1. Infectious Diseases Research Center, Birjand Uni of Med Sci
2. Infectious Diseases Research Center, Birjand Uni of Med Sci
3. Student Research Committee, Birjand Uni of Med Sci
4. Student Research Committee, Birjand Uni of Med Sci

Background and Aim: Listeria monocytogenes is an important opportunistic and zoonotic and food pathogen causing meningitis and septicemia in infants, people with immune deficiency, and pregnants. This species is highly resistant to frost, dryness and osmotic stress and can easily grow in fresh vegetables causing contamination. The aim of this study was to investigate the prevalence of Listeria monocytogenes in fresh vegetables in Birjand.

Methods:A total of 100 samples of vegetables were randomly selected from different greengrocers in Birjand. Each sample was initially placed in LEM medium for 48 hours. Then 100 µl of inoculated LEM was transferred to selective Palm medium and incubated at 37°C for 48 hours. Grown colonies were examined morphologically and black colonies were considered as probable positive cases. Then the colony was examined by further experiments including gram staining, hemolysis, catalase and motility. All suspected isolates were conducted molecular multiplex PCR and by using to pairs of specific primers the genus of Listeria and the species of monocytogenes was confirmed.

Results: Of 100 samples of vegetable, 11 samples were suspected to Listeria in the first stage. After PCR, all cases were detected as Listeria and 7 samples were confirmed as Listeria monocytogenes.

Conclusion: The present study revealed that the prevalence of listeria monocytogenes in fresh vegetables in Birjand is about 7%. As this level of prevalence is remarkably high, it is strongly recommended to disinfect and thoroughly wash the vegetables before use.

Keywords: Listeria monocytogenes, vegetables, Prevalence, Birjand

P375 - 328: RAPID IDENTIFICATION OF SALMONELLA ENTERITIDIS IN CHICKEN SKIN USING INVA MOLECULAR MARKER

Najmeh Sodagar[1], Ahmad Reza Bahrami[2]

1. Najmeh Sodagar

Background and Aim: Salmonella is a gram-negative that can cause diarrheal illness in humans. Raw meat, especially pork, undercooked products of poultry meat, eggs and products containing raw eggs as well as unpasteurized milk are foods posing the greatest hazard to public health. If present in food, it does not usually affect the taste, smell, or appearance of the food. The bacteria live in the intestinal tracts of infected animals and humans. In the present study, we employed RCR method for screening and identification of salmonella serovar Enteritidis in skins from commercial samples in Iran.

Methods: Salmonella enterica serovars Enteritidis was grown on buffered peptone water. Artificial inoculation of chicken skin samples done. A control sample was also included to ensure that the skin was not naturally contaminated with Salmonella. DNA extracted from inoculated chicken skin samples. Amplification of the target sequence was performed using a PCR Express thermal cycler.

Results: Using the PCR assay on genomic DNA from the chicken skin, artificially contaminated with S. Enteritidis, produced a band of 796 bp in size on electrophoresis. PCR assay on these skin samples resulted in 38 (71%) positive bands of 796 bp. Detected bands corresponding to 790 bp, represent contamination of the samples to the bacteria, with different rate depending on intensity of the bands.

Conclusion:propounded the PCR assay evaluated in the current study could be used as a screening test, since results would be available in less time than with the cultural method.

Keywords: Salmonella enteritidis, invA gene, PCR assay,commercial samples

P376 - 334: SYNTHESIS OF ISOXAZOLE DRIVATIVES ON DISINFECTION OF FICAL COLIFORM BACTERIA

Fatemeh Nazemi[1], iraj khodadadi[2], freshteh mehri[3], zohreh fasihi[4], ali heshmati[5]

1. food and drug labratory of hamedan university- iran
2. food and drug labratory of hamedan university- iran
3. food and drug labratory of hamedan university- iran
4. food and drug labratory of hamedan university- iran
5. food and drug labratory of hamedan university- iran

Background and Aim: The prepared isoxazole derivatives constitute the base of some drugs. Coliforms are the most important index of water and wastewater pollution. The main objective of this research was the study of disinfection of coliform bacteria as wastewater using synthesized aromatic isoxazole derivatives.

Methods: The isoxazole derivatives were synthesized by poly(N-bromo-N-ethyl-benzene-1,3-disulfonamide) [PBBS] and N,N,N',N'-tetrabromobenzene-1,3-disulfonamide [TBBDA]. Synthesized aromatic isoxazole derivatives were added to certain amounts of wastewater. Along with disinfection, fecal coliform was detected in untreated and disinfected wastewater.

Results: The results showed that in presence of aromatic isoxazole derivatives, fecal coliform was disinfected more effectively. Maximum removal was observed in aromatic isoxazole substituted derivatives with a halogen substituent. Removal of 100% was observed at some derivatives even at 10 min.

Conclusion: Aromatic Isoxazole derivatives may be effectively applied for wastewater disinfection. because of advantages of reaction condition at room temprature and using of water as solvent, this process is a green reaction.

Keywords:isoxazole derivatives, water, wastewater, disinfection, fical coliform

P377 - 382: SURVEY AND IDENTIFICATION OF ENTEROVIRUSES IN BOTTLED WATER BY PCR-RT METHOD

Maryam Alamoti1[1], Giti Kashi[2], Farbod Pazooki3[3]

1. 1,3Bachelor Student, Environmental Health, Islamic Azad University Tehran Medical Sciences Branch, Tehran, Iran (E-mail: solehkeshvar@yahoo.com & feripazooki@gmail.com)
2. *2Associate professor, Department of Environmental Health, Islamic Azad University Tehran Medical Sciences Branch, Tehran, Iran (E-mail: g.kashi@yahoo.com) & 2Water Purification Research Centre (WPRC), Tehran Medical Sciences Branch, Islamic Azad University, Tehran, Iran (E-mail: WPRC@iautmu.ac.ir)
3. 1,3Bachelor Student, Environmental Health, Islamic Azad University Tehran Medical Sciences Branch, Tehran, Iran (E-mail: solehkeshvar@yahoo.com & feripazooki@gmail.com)

Background and Aim: In view of water health and water borne diseases prevalence, Enterovirus 71 (EV71) infections, one of the major etiologic agents of hand, foot, and mouth disease, are considered as the most important public health concern in the Asia-Pacific region including Iran country. Enteroviruses are grouped into five types. The aim of this analytical study is to identify the Enterovirus contamination of bottled water in Tehran city.

Methods: In this analytical study, random sampling is used. 22 samples are taken from different brands of bottled water of Tehran city during February to March 2018. The bottled water samples are transported in cold box and sterile condition according to procedure detailed in standard methods. Total virus numbers recovered are measured by quantitative reverse transcription-PCR (qRT-PCR).

Results: The pH, temperature, and turbidity range of 22 samples are 7.2-7.8, 14-24 ℃, and 0.4-1.3 NTU, respectively. The Enterovirus contamination range of 22 bottled water selected samples in Tehran city are 0 genome copies/L. The pH, and turbidity in all of samples present under than national standard values of bottled water.

Conclusion: Bottled water is not sterile. This method is considered as the most performance in detecting Enterovirus in bottled water. We perform quantitative detection of Enterovirus in bottled water. The low num¬ber of samples is considered as our research limitation. It is concluded that supervision on bottled water production, transporting, and storage lead to prevent water viral contamination. Growth conditions play a critical role in the recovery of Enterovirus in bottled water.

Keywords: Bottled water, Enterovirus, Genome copies, PCR-RT method, pH

P378 - 385: AMYLASE PRODUCTION UNDER SUBMERGED CULTURE OF MONASCUS PURPUREUS

Najme Gord Noshahri[1], Mina Shaban[2], Maryam Ameri[3]

1. Industrial Microorganism Biotechnology Research Department, Research Institute for Industrial Biotechnology, Academic Center for Education, Culture and Research (ACECR)-Mashhad branch, Mashhad, Iran
2. Industrial Microorganism Biotechnology Research Department, Research Institute for Industrial Biotechnology, Academic Center for Education, Culture and Research (ACECR)-Mashhad branch, Mashhad, Iran
3. Industrial Microorganism Biotechnology Research Department, Research Institute for Industrial Biotechnology, Academic Center for Education, Culture and Research (ACECR)-Mashhad branch, Mashhad, Iran

Background and Aim: Amylase has various industrial applications such as pharmaceutical, food, cosmetics and detergent. This is found in plants, animals and microorganisms. Monascus is a fungus which is well known as an extracellular enzymes producer such as amylase, glucoamylase and β-glicosidase. The aim of this study is considered Monascus pupureus for its efficiency in amylase production under submerged fermentation with various carbon sources and its correlation with fungal morphological form.

Methods: In the present study, various types of culture media by eliminating and changing the carbon sources were tested to analyze whether the enzyme is of inducing type or not; and also the effect of FeSO4 as an inducer was considered. The enzyme activity was evaluated using soluble starch and DNS reagent followed by measuring absorbance in 540 nm. Furthermore the morphology of hyphae in different production stages was observed.

Results: The results showed that the enzyme is of inducing type and FeSO4 increases its production approximately twice. Since amylase is a primary metabolite, the fungi has higher enzyme production in vegetative stage. That means the highest amylase production is in Trophophase.

Conclusion: It was demonstrated that FeSO4 plays critical role in amylase production. The most optimized condition for production of amylase enzyme from the Monascus purpureus is using soluble starch as a carbon source, 0.1% FeSO4 and incubation period of 5 days.

Keywords: Amylase, Monascus sp, Submerged fermentation

P379 - 388: EXPERIMENTAL STUDY OF THE SURVIVAL AND GROWTH OF PSEUDOMONAS AERUGINOSA IN WATER AFFECTED BY TEMPERATURE, STORAGE TIME AND TYPE OF WATER

Azin Takalloo[1], Vadood Razavilar[2], Mohammad Reza Abedini [3]

1. Departmant of Hygiene, Faculty of Veterinary Sciences, Science and Research Branch, Islamic Azad university, Tehran, Iran
2. Departmant of Hygiene, Faculty of Veterinary Sciences, Science and Research Branch, Islamic Azad university, Tehran, Iran
3. Departmant of Animal Sciences, Agriculture College, Varamin Branch, Islamic Azad university, Varamin, Iran

Background and Aim: Supply of clean drinking water is the most important public health needs and infectious diseases can easily lead to a pandemic. Pseudomonas.aeruginosa is an opportunistic pathogen that affects immunocompromised people. Some studies show that Despite chlorination, tap water is a major source of Pseudomonas.aeruginosa. In the current study, we try to evaluated effective factors on the growth of the organism in drinking water.

Methods:A multifactorial design was used to be investigate the effects of temperature, inoculation dose, and type of water as a nutrient on the growth of Pseudomonas.aeruginosa. This study was be conducted with the inoculation bacterium at the level of 104 /ml into drinking water and the factors investigated included: storage temperature of water (22 C° and 7C°), storage time of water (0, 3, 6, 12, 24, 48 days), type of mineral water (sterilized and non-sterilized) and tap water (sterilized and non-sterilized).

Results: Analyzing the survival and growth of Pseudomonas.aeruginosa in bottled mineral waters (sterilized and non-sterilized) and tap waters (sterilized and non-sterilized) at temperatures of 22 and 7 C° in storage time of 48 days after the inoculation shows that the bacterium has a noticeable growth at 22 C° ($P<0.01$) and sanitary condition of water (sterilized) ($P<0.05$) and type of water (mineral) ($P<0.01$) have a positive effect on the growth of the bacterium.

Conclusion: Results of this study show that the most important factor that facilitates Pseudomonas.aeruginosa growth in tap water is water temperature and the bacterium show the greatest growth at 22 C° ($P<0.01$)

Keywords: Pseudomonas aeruginosa, drinking water, growth, survival, temperature

P380 - 395: INVESTIGATION OF MUTAGENIC AND ANTI MUTAGENIC EFFECTS OF PORTULACA OLERACEA ON SALMONELLA TYPHIMORIUM TA100 USING AMES METHOD

Tina Sadeghi nasr[1], nahid rahimi fard[2]

1. islamic azad university of pharmaceutical sciences branch
2. iran food and drug administration

Background and Aim: The purpose of this study is to investigate the mutagenic and anti-mutagenic effects of the extract of the plant portulaca oleracea on salmonella typhimorium(TA100) and determine its effective dose. Since it is simply not possible to test these materials for eukaryotic cells, Professor Ames and his colleagues presented a low-cost, short-term, and easy bacterial test to find out the effects of mutagen substances.

Methods: In this test, genetically manipulated strains of salmonella typhimurium are used. These strains are converted into wild straw by contact with mutagenic materials. Histidine mutants with probable mutagenic substances (the extract of the plant of porulaca oleracea) are mixed on a MGA plate with some histidine and biotin; after 48 hours of incubation, the colonies are counted. due to absence of the CYT P450 enzyme system in the bacteria, rat liver enzyme is used as a buffer S9

Results: Results show that portulaca oleracea does not have any mutagenic effects on salmonella typhimorium(TA100) with or without metabolic activation, but antimutagenic effect is observed in methanolic,hydroalcholic and aqueos extracts at dilution of 71-142-258 µg/ml without metabolic activation.

Conclusion:it does not have mutagenic effect but it has anti mutagenic effect at 3 dilition of hydroalcholic and aqueos without metabolic activation.

Keywords: Ames test-portulaca oleracea-mutagen-anti mutagen-salmonella typhimorium

P381 - 411: EFFECTS OF ZIZIPHORA CLINOPODIOIDES ESSENTIAL OIL AND APPLE PEEL EXTRACT ON SHELF LIFE EXTENSION OF CAMEL MEAT DURING REFRIGERATED STORAGE

Yasser Shahbazi[1], Nassim Shavisi[2]

1. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Razi University, Kermanshah, Iran
2. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Razi University, Kermanshah, Iran

Background and Aim: Camel meat is known to be a valuable meat source for human health due to lower levels of fat and cholesterol as well as relatively higher amounts of essential amino acids, vitamins, minerals and polyunsaturated fatty acids in comparison with other red meat. The aim of the present study was application of Ziziphora clinopodioides essential oil (ZEO) and apple peel extract (APE) to increase the shelf life (microbial and chemical properties) of camel meat during refrigerated storage over a period of two weeks.

Methods: Gas chromatography-mass spectrometry was used for compound identification of ZEO. ZEO (0 and 0.5%) and APE (0 and 1%) were directly added to the camel meat. In the present study, microbial and chemical parameters of food shelf-life including total mesophilic and psychrotrophic bacteria, Pseudomonas spp., Enterobacteriaceae, total volatile base nitrogen, trimethyl-amine nitrogen, pH and peroxide value were evaluated during refrigerated storage of camel meat samples for two weeks.

Results: The main compounds of ZEO were found to be carvacrol (65.22%), thymol (19.51%), p-cymene (4.86%) and ɣ-terpinene (4.63%). The meat containing ZEO 0.5% + APE 1% significantly exhibited the lowest bacterial population for the entire of storage period ($P < 0.05$). All treated samples tended to retard the increases in total volatile base nitrogen, trimethyl-amine nitrogen, pH and peroxide value.

Conclusion: It can be concluded that ZEO 0.5% + APE 1% can be used as appropriate types of food additive to preserve camel meat during refrigerated storage up to 14 days.

Keywords: Ziziphora clinopodioides essential oil; Apple peel extract; Camel meat

P382 - 412: ANTIMICROBIAL EFFECTS OF MENTHA PULEGIUM ESSENTIAL OIL AND NISIN AGAINST STAPHYLOCOCCUS AUREUS IN COMMERCIAL BARLEY SOUP

Yasser Shahbazi[1], Nassim Shavisi[2]

1. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Razi University, Kermanshah, Iran
2. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Razi University, Kermanshah, Iran

Background and Aim:: Food-borne pathogens are causing a great number of diseases with remarkable effects on human health. Mentha pulegium has several biological uses e.g. antimicrobial, antioxidant and antispasmodics, in good correlation with the high contents of phenolic compounds. The aim of the current study was to assess the effects of Mentha pulegium essential oil (MPO) alone and in combination with nisin against Staphylococcus aureus in commercial barley soup stored at refrigerated temperature during 14 days.

Methods: Gas chromatography-mass spectrometry analysis of MPO was performed. A commercial barley soup was prepared according to the method described by producer manual. It contained barley, onion, salt, vegetable oil, parsley, yeast extract, carrot, monosodium glutamate, citric acid and spices. After preparation, the samples were inoculated with 5 log CFU/ml of S. aureus. Then, concentrations of MPO (0, 0.1, 0.2 and 0.4%) separately and in combination with nisin (0 and 100 IU/ml) were added into the barley soups.

Results: Based on our findings, pulegone (77.32%) and l-menthol (11.11%) were the major compounds of the MPO. The following sequence inhibition effect on S. aureus was observed in treated soups: MPO 0.4% + nisin 100 IU/ml > MPO 0.2% + nisin 100 IU/ml > MPO 0.1% + nisin 100 IU/ml > MPO 0.4% > MPO 0.2% > MPO 0.1% > nisin 100/ml.

Conclusion: The results of the present study demonstrated that antibacterial effects of different concentrations of MPO separately and in combination with were effective in inhibition growth of S. aureus inoculated to the commercial barley soup.

Keywords: Mentha pulegium essential oil; Nisin; Staphylococcus aureus; commercial barley soup

P383 - 415: DETERMINATION OF ANTIMICROBIAL EFFECTS OF NISIN AND MENTHA SPICATA ESSENTIAL OIL AGAINST SALMONELLA TYPHIMURIUM UNDER VARIOUS CONDITIONS

Yasser Shahbazi[1], Nassim Shavisi[2]

1. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Razi University, Kermanshah, Iran
2. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Razi University, Kermanshah, Iran

Background and Aim: Plant essential oils and nisin have been known as antimicrobial agents that could be used to control food-borne pathogenic bacteria such as Salmonella Typhimurium. The aim of this study was to evaluate the antimicrobial efficacies of nisin and Mentha spicata essential oil (EO) both separately and in combination, against S. Typhimurium at different temperatures (4, 9 and 14°C), pH (5, 6 and 7) and NaCl concentrations (0, 1, 2 and 4%).

Methods: The chemical components of EO were analyzed by gas chromatography-mass spectrometry (GC-MS). The minimum inhibitory concentrations (MIC) of nisin and EO were assessed using a broth micro-dilution method. For combinations of the antimicrobials, the Differences in Population assay were used to determinate their effects.

Results: The dominant active components of EO were carvone (78.76%) and limonene (11.50%). The EO MIC value was 80 µl/ml, but nisin did not inhibit the growth of S. Typhimurium. The susceptibility of S. Typhimurium to nisin and EO was found to enhance with increasing incubation temperature, pH and NaCl concentration.

Conclusion: Our findings demonstrate that a combination of nisin and Mentha spicata essential oil might be a potential source of preservative for the control of S. Typhimurium in the food industry.

Keywords: Mentha spicata essential oil; Nisin; Salmonella Typhimurium

P384 - 416: CHEMICAL COMPOSITION AND IN VITRO ANTIBACTERIAL ACTIVITY OF FERULAGO GLAREOSA ESSENTIAL OIL

Yasser Shahbazi[1], Nassim Shavisi[2]

1. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Razi University, Kermanshah, Iran
2. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Razi University, Kermanshah, Iran

Background and Aim: Spices and essential oils usually exhibit different characteristics such as antimicrobial and flavoring effect. The aim of the present study was to investigate chemical composition and in vitro antibacterial activity of Ferulago glareosa essential oil against bacterial food-borne pathogens (Staphylococcus aureus, Bacillus subtilis, Bacillus cereus, Listeria monocytogenes, Salmonella typhimurium and Escherichia coli O157:H7).

Methods: The chemical components of the essential oil were analyzed by gas chromatograph coupled with mass spectrometer detector (GC-MS). The antibacterial activity of the essential oil was assessed using broth micro-dilution and agar disk diffusion methods.

Results: According to results of GC-MS, 37 constituents were identified. The dominant components were α-pinene (22.11%), z-β- ocimene (18.33%), bornyl acetate (11.92%), ɣ-terpinene (14.21%), The Minimum Inhibitory/Bactericidal Concentration (MIC/MBC) values of the essential oil did not differ between gram negative and positive bacteria. S. aureus, B. subtilis, S. typhimurium and E. coli O157:H7 had similar sensitivity to the essential oil, L. monocytogenes and B. cereus showed more sensitivity.

Conclusion: Our results indicate that F. glareosa essential oil has might be a potential rich source of antibacterial components for the control of food-borne bacteria.

Keywords: Ferulago glareosa essential oil; Antibacterial activity; Chemical composition

P385 - 442: INVESTIGATION OF REMOVAL AMOUNT OF HEAVY METALS CADMIUM AND LEAD FROM AQUEOUS SOLUTION BY PSEUDOMONAS AERUGINOSA BACTERIA

Esmaeil Roohbakhsh[1], Mahnaz Karimpour[2], Daryush naghipour [3]

1. School of Health, Guilan University of Medical Sciences, Rasht, Iran
2. School of Health, Guilan University of Medical Sciences, Rasht, Iran
3. School of Health, Guilan University of Medical Sciences, Rasht, Iran

Background and Aim: Pollution of water resources by these heavy metals is one of the global environmental concerns which habeen increased due to activities such as industrialization and urbanization. Heavy metals' Ions are very dangerous for health and environment. Today, using low cost methods for removing metals has attracted attention significantly and searching for such methods are highly recommended due to economic and technical limitations.

Methods:. In order to assess the effect of operational parameters on absorption of Lead and Cadmium and process modeling, five main factors were studied as follows: living and non-living cell mass (mg), amount of Lead and Cadmium (mg/L), process temperature (°C), pH and time of reaction (min). Finally, based on these factors, test were designed in Minitab 15 software.

Results: Maximum efficiency of removing Lead and Cadmium was achieved in following conditions: time duration: 60 hours, pH=7, living mass cell of Pseudomonas aeruginosa= 9 (gr), concentration of Lead and Cadmium 1(mg/L) and 20(mg/L) were 95.13 and 89.8 respectively.

Conclusion:results show that both Pseudomonas aeruginosa bacteria have high ability in removing Lead and Cadmium in aqueous environment. This method is cost effective and environment-friendly

Keywords:biosorption, bioaccumulation, Lead, Cadmium, Pseudomonas Aeruginosa bacteria

P386 - 452: ANTIBIOTIC RESISTANCE AMONG STAPHYLOCOCCUS AUREUS AND ESCHERICHIA COLI ISOLATED FROM TRADITIONAL AND INDUSTRIAL FOOD SAMPLES

Mojtaba Sade[1]

1. - Department of Microbiology, Islamic Azad University, Tehran Medical Branch, Iran

Background and Aim:: Foodborne diseases are one of the serious problems in the world. Every year, more than 100 million people are affected by foodborne and waterborne diseases particularly immunocompromised diseases

Methods:A total of 1625 different food samples including dairy products, meat and pastries were collected randomly from different parts of the west of Tehran. All samples were kept at 4°C. The samples were first cultured according to the standard bacteriological methods and then Staphylococcus aureus and Escherichia coli isolates were identified using standard bacteriological tests. .

Results: During 2007 and 2008, 2.8% and 3% of the food samples were contaminated with S. aureus. Similarly, 3.5% and 6.4% of the food samples were contaminated with E. coli. E. coli isolates were highly resistant to amikacin and cephotaxime and this resistance was increased in 2008. Similarly S. aureus isolates were resistant to ciprofloxacin, cephotaxime, gentamicin, and tetracyclin. There was no significant difference during 2007-2008

Conclusion:: The rate of contamination during 2007 was 2.8% and during 2008 was 3% for S. aureus. This strain was isolated from the food samples. Further studies should be done to determine the changes of bacterial resistance pattern for various food samples. Thus, the baseline for comparison with future prospective studies should be established, enabling the determination

Keywords:: Antibiotic Resistance, Staphylococcus aureus, Escherichia coli, Food

P387 - 490: INVESTIGATION OF FREQUENCY AND VIRULENCE GENES OF TYPICAL AND ATYPICAL ENTEROPATHOGENIC ESCHERICHIA COLI (EPEC) AND SHIGA TOXIN –PRODUCING ESCHERICHIA COLI (STEC) IN BIOLOGICAL SAMPLES.

Mahdie Jafarian[1], Siavosh Salmanzadeh-Ahrab[2], Mohammad-Mehdi Aslan[3], Tahereh Falsafi[4]

1. Department of Biological Sciences, Alzahra University, Tehran, Iran
2. Department of Biological Sciences, Alzahra University, Tehran, Iran
3. Department of Microbiology, Pasteur Institute of Iran, Tehran, Iran
4. Department of Biological Sciences, Alzahra University, Tehran, Iran

Background and Aim: Foodborne diseases are a major public health problem with growing concern.The contamination of food by enteric pathogens such as EPEC and STEC is an important cause of diarrheal disease in worldwide. E.coli has been isolated from food such as vegetables,meat,seafood ,fruit and from milk.EPEC strains are classified as “typical and atypical” according to the presence or absence of bfp-A and eae genes.Typical EPEC a leading cause of infantile diarrhea in developing countries,and atypical EPEC is responsible for sporadic outbreak in developed country.STEC have been implicated as the causative agent in several human diseases including mild nonbloody or sever bloody diarrhea,Hemolytic Uremic Syndrome(HUS) and renal failure.

Methods: In this research One hundred raw beef and forty milk samples collected in Tehran and alborz during November 2017 to May 2018,and were transported to the laboratory. Beef samples homogenized by stomacher in EC broth containing cefexime.Milk samples inrichmented in EC broth containing cefexime.so all samples culture on MacConkey agar medium.Bacterial DNA was extracted by boiling method and PCR was done for eae A,bfp, stx1 and stx2 genes .Biochemical test were done to confirm Ecoli.

Results: Pcr analysis showed that four of these isolates were atypical EPEC positive and six were STEC positive(nine of raw beef & one milk).All positive isolates were confirmed by biochemical tests as E.coli.

Conclusion: This research show that raw beef and milk may be the source of EPEC and STEC infection,and could be as a vehicle for transmission of diarrheagenic E.coli.

Keywords: Enteropathogenic e.coli,Shiga toxin –producing E.coli,Raw beef,Milk,Pcr

P388 - 504: BIOFILM-PRODUCING ABILITY OF STAPHYLOCOCCAL SPP ISOLATED FROM DIFFERENT FOODSTUFFS PRODUCTS

Laleh Hoveida[1], Soodabeh Rostami[2], mehrdad halaji[3], Sina Mobasherizadeh [4]

1. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Falavarjan, Isfahan, Iran
2. Nosocomial Infection Research Center, Isfahan University of Medical Sciences, Isfahan, Iran
3. Department of Microbiology, Clinical Laboratory of ALZAHRA Medical Center, Isfahan, Iran
4. Nosocomial Infection Research Center, Isfahan University of Medical Sciences, Isfahan, Iran

Background and Aim: In recent times, microbial-biofilm contamination has attracted considerable attention from the food industry. Pathogenic microorganisms can attach to food surfaces, grow on them, and form biofilm that caused an increase in the food safety risk. The mechanisms of biofilm formation have become an important issue in the food-processing industry, therefore, the aim of this study is to determine the biofilm formation and profiles of genes involved in biofilm production of staphylococci isolated from various foodstuff products.

Methods: This cross-sectional study was conducted at some grocery stores and confectionaries from September 2015 to October 2016 in different areas of Isfahan, Iran. Staphylococcus spp. were isolated from different foodstuff samples including sweet pastries, cakes and similar baked goods, dairy products such as cheese and yogurt, meat products such as sausages, and hamburgers. Antibiotic susceptibility pattern was determined by the disc diffusion method and determination of presence of icaA/icaD genes was performed by the PCR method.

Results: From a total of 194 different foodstuffs samples, 84 Staphylococcus spp. were isolated. Out of the 84 Staphylococcus isolates, 95.2% (80/84) were positive to the ability of biofilm formation. Overall, 35.7% (30/84) and 26.2% (22/84) of Staphylococcus spp. isolates were positive for icaA and icaD genes, respectively.

Conclusion: The results of the present study indicate that the remarkable rate of biofilm formation with a higher rate of antibiotic resistance still remains a significant risk for the food safety, especially in foodstuffs samples.

Keywords: Biofilm formation, Staphylococcus spp, icaA, icaD

P389 - 522: EVALUATION OF CONTAMINATION OF TRADITIONAL LACTIC CHEESES TO ESCHERICHIA COLI, STAPHYLOCOCCUS AUREUS AND LISTERIA MONOCYTOGENES

Fatemeh Rabinejd[1], Fatemeh Rabinejad[2], Ania Ahani Azari[3], Ahmad Danesh[4]

1. -
2. Gorgan Branch, Islamic Azad University, Gorgan, Iran
3. Department of Microbiology, Gorgan Branch, Islamic Azad University, Gorgan, Iran
4. Department of Medical Sciences, Golestan University of Medical Sciences, Gorgan, Iran

Background and Aim: Lactic cheese is a group of fresh and semi-hard cheeses that are traditionally produced from raw milk in some provinces of the country, including Golestan province. The aim of this study was to determine the prevalence of contamination of traditional lactic cheeses in Gorgan and the suburbs with Escherichia coli, Staphylococcus aureus and Listeria monocytogenes

Methods: In this study, 40 traditional lactic bovine and sheep cheeses and 5 bovine pasteurized lactic cheese samples from dairy stores in Gorgan and the suburbs of Golestan province were evaluated for their contamination with these bacteria.

Results: Based on the results obtained from 20 bovine cheese samples, only 2 samples (10%) and from 20 sheep cheese samples 6 samples (30%) had contamination with E. coli. Contamination with S. aureus was observed in 3 (15%) and 5 (25%) samples of bovine cheese and sheep cheese samples in respect. Contamination with L. monocytogenes was not obser ved in any cheese samples. Industrial pasteurized cheeses did not have contamination with any of the bacteria studied in this research. According to the results, sheep's cheeses were more contaminated with E. coli and S. aureus than bovine cheeses.

Conclusion: The results of this study showed that contamination with food borne pathogenic bacteria is high in traditional cheeses supplied in Gorgan and the suburbs. Therefore, considering the great popularity of these types of cheeses among consumers, it seems necessary to observe sanitary notes and use of pasteurized milk to prepare these cheeses.

Keywords: Escherichia coli, Lactic cheese, Listeria monocytogenes, Staphylococcus aureus

P390 - 529: ASSESSMENT OF THE MICROBIOLOGICAL QUALITY OF HERBAL HAIR COLORS IN YAZD, IRAN

Somayeh Mousavi nodoushan[1], Nahid Ghasemi1[2], Somayeh Mousavi Nodushan2[3], Zahra Tavakoli[4]

1. MS.c in Medical Biochemitry, Shahid Sadoughi University of Medical science, Yazd, Iran
2. Student of PhD in Microbial Toxins, Shahid Sadoughi University of Medical science, Yazd, Iran
3. BS.c in Food Science, Shahid Sadoughi University of Medical science, Yazd, Iran.

Background and Aim: Hair is protective appendages on the body. Use of herbal hair colors are perceived to be safe and without side effects. However, one of the major problems faced by formulators using herbal material in personal care products is the high risk of microbial contamination. This study aimed to investigate the microbiological load in herbal hair colors marketed in Yazd

Methods:total of 32 samples consist of several types of herbal hair colors from Yazd were collected. Total count and the presence of pathogenic microorganism E. coli, Pseudomonas aeruginosa and Staphylococcus aureus were analyzed by standard methods.

Results:the contamination level of herbal hair colors to Escherichia coli (97%), Pseudomonas aeruginosa (78%), Staphylococcus aureus and Total count (56%) were contaminated higher than standard level of Iranian national standards protocols.

Conclusion: Results revealed that the prevalence of microbial contamination is heavily high in herbal hair. Therefore it is important to take precautions during production process in order to prevent infections due to microbial contamination

Keywords: Herbal hair- Escherichia coli- Pseudomonas aeruginosa

P391 - 532: EFFECT OF POLYLYSINE AND CARRAGEENAN COATING ON MICROBIAL PROPERTIES OF RAINBOW TROUT (ONCHORYNCHUS MYKYSS) DURING CHILLED STORAGE AT 4˚C

Maryam Abbasvali[1], Sedigheh Rahimi[2], Hamdollah Moshtaghi[3]

1. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord 88186/34141, Iran
2. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord 88186/34141, Iran
3. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord 88186/34141, Iran

Background and Aim: Extending the shelf life of foods and delaying their spoilage is one of the most important goals in the food industry. The use of coatings and natural, non-chemical and safe preservatives is one of the useful ways to increase the shelf life of food.

Methods: This study was conducted to investigate the effects of ε-polylysine, carrageenan coating and ε-polylysine + carrageenan coating on microbial properties of rainbow trout stored at 4 ± 1℃ for a period of 15 days. All samples were subjected to microbial analysis on the day of treatment and periodically every 3 days until 15 days.

Results: Throughout the storage period, the number of bacteria in the control group was higher than the treatment groups and the lowest microbial count was observed in ε-polylysine + carrageenan coated group. At the end of the storage period in control group, the number of enterobacteriaceae, lactic acid, mesophilic and psychrophilic bacteria increased to 9.03, 6.77, 10.95, 11.17; whereas in ε-polylysine + carrageenan coated group reached to 5.22, 4.55, 7.48, 10.06 log CFU/g, respectively.

Conclusion: In this study, ε-polylysine could effectively prevent the growth and proliferation of bacterial population and showed good potential as a food-grade, novel, safe and effective natural food additive and carrageenan coating also showed good ability to prevent growth of aerobic bacteria. The results of this study showed that the use of ε-polylysine + carrageenan coating was more effective on delaying microbial growth than other treatment. Consequently increased shelf life of trout fillets during 15 days of storage.

Keywords:ε-polylysine, carrageenan, coating, microbial properties, rainbow trout, chilled storage

P392 - 546: EFFECT OF ACTIVE EDIBLE COATING ON MICROBIAL PROPERTIES OF RAINBOW TROUT (ONCHORYNCHUS MYKYSS) DURING CHILLED STORAGE

Maryam Abbasvali[1], Fahimeh Mahmoodi[2], Hamdollah Moshtaghi[3]

1. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord 88186/34141, Iran
2. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord 88186/34141, Iran
3. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord 88186/34141, Iran

Background and Aim: Food safety and shelf life can be improved by using new technologies like modified atmosphere packaging, vacuum packaging, active films and coatings, non-thermal processing, radiation and the use of preservatives to prevent or delay microbial growth.

Methods: In this study, antimicrobial effects of carrageenan coating enriched with olive leaf extract and carrageenan coating alone on microbial properties of rainbow trout fillets stored at 4 ± 1℃ for a period of 15 days were investigated. Microbial analysis such as total bacterial count, psychrophilic bacterial counts, lactic acid bacteria and enterobacteriaceae were determined on days 0, 3, 6, 9, 12 and 15 of storage.

Results: The results showed that, in comparison with control group, carrageenan coating with olive leaf extract and carrageenan coating treatments were significantly ($P<0.05$) more effective in delaying the growth of bacteria during storage time. At the end of the storage period in control group, the number of enterobacteriaceae, lactic acid, mesophilic and psychrophilic bacteria increased to 7.66, 9.02, 8.36, 10.04; whereas in olive leaf extract + carrageenan coated group reached to 6.83, 7.65, 7.36, 8.61 log CFU/g, respectively.

Conclusion: According to the results of this study, olive leaf extract as a natural preservative in combination with carrageenan coatings could increase the shelf life of rainbow trout fillet in the refrigerator and can be replaced with synthetic preservatives.

Keywords:carrageenan active coating, microbial properties, olive leaf extract, rainbow trout

P393 - 549: EVALUATION OF MICROBIAL QUALITY OF SIAHMAZGI CHEESE PRODUCED IN NORTHWESTERN IRAN

Adel Mirza Alizadeh[1], Hedayat Hosseini[2], Samira Beikzadeh[3], Mansoureh Mohammadi[4]

1. PhD Student of Food Safety and Hygiene, Department of Food Technology, Faculty of Nutrition Sciences and Food Technology/National Nutrition and Food Technology Research Institute, Shahid Beheshti University of Medical Sciences, Tehran, Iran
2. Department of Food Science and Technology, Faculty of Nutrition Science, Food Science and Technology/National Nutrition and Food Technology Research Institute, Shahid Beheshti University of Medical Sciences, Tehran, Iran.
3. PhD Student of Food Science and Technology, Department of Food Technology, Faculty of Nutrition Sciences and Food Technology/National Nutrition and Food Technology Research Institute, Shahid Beheshti University of Medical Sciences, Tehran, Iran
4. PhD Student of Food Science and Technology, Department of Food Technology, Faculty of Nutrition Sciences and Food Technology/National Nutrition and Food Technology Research Institute, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: Siahmazgi cheese is an Iranian traditional dairy produced which is producing from cow's milk. This kind of cheese has classified in hard cheeses and it takes 3-4 months to get extremely firm texture at the end of repining period. Commonly, this cheese has some pea-sized holes, with yellowish appearance and fermented taste.

Methods: In this study, 76 samples of Siahmazgi cheese were collected randomly from different regions of Northwestern Iran (especially Zanjan Province between the years of 2017 to 2018). The purpose of this study was to investigate some undesirable microorganisms in cheese including Staphylococcus aureus, Escherichia coli, Salmonella, Coliforms, molds and yeasts.

Results: Statistical analysis was performed using SPSS 25 by ANOVA test based on a significance level of $p<0.05$. The results have shown that out of the total 76 samples of Siahmazgi cheese in terms of Coliforms, Escherichia coli, Staphylococcus aureus, molds and yeasts in cheese were 23 (30.26%), 21 (27.63%), 3 (3.95%) and 23 (30.26%) in samples were not agree with the Iran National Standard Organization (INSO), respectively. In addition, contamination with Salmonella spp. was not observed in all analyzed samples.

Conclusion: Our findings indicated that, the most microbiological (especially in case of Coliforms, Escherichia coli, molds and yeasts) loads of Siahmazgi cheese produced in northwestern of Iran are not agree with the relevant standard, however along with observing the good production conditions such as GMP and GHP, continues supervision, sampling and controlling is required during production of their traditional dairy products from microbial contamination point of view.

Keywords: Siahmazgi Cheese, Traditional Dairy, Microbial Quality, Northwestern Iran

P394 - 557: EFFECT OF E-POLY-LYSINE TO EXTEND THE SHELF LIFE OF READY-TO-EAT TURKEY BREAST

Maryam Abbasvali[1], Neda Vahabi Anaraki[2], Mojtaba Bonyadian[3]

1. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord 88186/34141, Iran
2. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord 88186/34141, Iran
3. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord 88186/34141, Iran

Background and Aim: As regards food recognized as an important carrier of the pathogens in the world and also there are major concerns about the increasing use of chemical preservatives in the food industry, discovering of non-synthetic antimicrobial compounds is one of the interesting topics in the food industries. This study was conducted to investigate the effect of ε-poly-lysine to extend the shelf life of ready-to-eat turkey breast.

Methods:. For this purpose, turkey breast was injected with curing solution and tumbled in two stages. After full cooking, samples were prepared. Treatment samples were immersed in a 1% or 10000 ppm of ε-poly-lysine solution and control samples were immersed in sterile distilled water for one minute. Then all samples were vacuum packed and stored at 8±1◦C (similar to supermarket refrigerator temperature) for 42 days. Microbial properties were determined, with 7 days interval.

Results: Results related to the effectiveness of ε-poly-lysine showed that in control group during 42 days, number (log CFU/g) of mold and yeast, coliform, mesophilic, psychrophilic, anaerobic and lactic acid bacteria increased 3.3, 3.12, 6.79, 5.28, 5.04 and 7.02, respectively. Whereas in samples treated with ε-poly-lysine solution number (log CFU/g) of mold and yeast, coliform, mesophilic, psychrophilic, anaerobic and lactic acid bacteria increased 2.36, 1.26, 5.53, 3.80, 3.31 and 4.14, respectively. Staphylococcus aureus was not found in any of treated and control samples.

Conclusion: The results of this study showed that poly-lysine properly improved the microbiological quality of vacuum cured turkey breast during cold storage and extended its shelf life compared with untreated sample.

Keywords: Vacuum Packaging, Poly-Lysine, Turkey breast, Shelf Life

P395 - 560: DETERMINATION OF MICROBIAL CONTAMINATION IN VEGETABLE CONSUMPTION IN YAZD PROVINCE

Somayeh Mousavi nodoushan[1], Nazgol Hagh Setan2[2], Zahra Tavakoli3[3], Nahid Ghasemi[4]

1. Student of PhD in Microbial Toxins, Shahid Sadoughi University of Medical science, Yazd, Iran
2. BS.c in Food Science, Shahid Sadoughi University of Medical science, Yazd, Iran
3. BS.c in Food Science, Shahid Sadoughi University of Medical science, Yazd, Iran
4. MS.c in Medical Biochemitry, Shahid Sadoughi University of Medical science, Yazd, Iran

Background and Aim: Vegetables are one of the main nutrient baskets today, which is growing due to the growing awareness of its properties. Vegetables are a food category that improves gastrointestinal function and provides the body's essential nutrients and salts, however, can cause problems in the health of the individual and the community if they are not properly sanitized. This study was conducted to determine the amount of microbial contamination in commonly used herbs in Yazd province

Methods: This cross-sectional study was conducted on 53 samples from different area in Yazd city, which were selected random. The samples were tested for fecal contamination, Escherichia coli, using the microbiological tests, which were based on the Iranian national standards.

Results:of 53 samples taken from the province, 78.8% of them were positive for determining the rate of fecal contamination (Escherichia infection)

Conclusion: Due to the growing trend of increasing the consumption of vegetables, especially raw vegetables, more care is needed in the washing process because of the lack of proper sanitation, the emergence of problems for the general health of the community and the outbreak of foodborne diseases

Keywords: Vegetables- E.coli

P396 - 572: EVALUATION OF MICROBIAL CONTAMINATION OF PACKAGED SPICES IN YAZD

Somayeh Mousavi nodoushan[1], Zahra Tavakoli[2], Somayeh Mousavi Nodushan[3], Nahid Ghasemi[4]

1. -
2. BS.c in Food Science, Shahid Sadoughi University of Medical science, Yazd, Iran
3. Student of PhD in Microbial Toxins, Shahid Sadoughi University of Medical science, Yazd, Iran
4. . MS.c in Medical Biochemitry, Shahid Sadoughi University of Medical science, Yazd, Iran.

Background and Aim: Plants or dried plants in powder form alone or mixed are used to taste foods as a spice. Spices are used in a small amount in a wide range of food and food products. Having the desired taste, specific color and aromas, as well as the presence of antimicrobial compounds which may affect the remnants of microorganisms has doubled their importance.The quality of the microbiology of spices depends to a large extent on the area of cultivation, spice processing and storage conditions the aim of this study was to evaluate the microbial contamination of packaged spices in Yazd

Methods:43 samples Such as Turmeric, pepper, Cinnamon, Spice for Shrimp, Fish were collected by experts from the Assistant Food Service in the second six months of the year 1396 and sent to the lab and then were assessed based on reference Iranian organizations (mainly ISIRI) for microbial contamination

Results: The results showed that the contamination level of spices to Escherichia coli and coliform were 23.25% (n= 3) and 55.81% (n= 11), respectively. About 25.58% (n= 8) of total samples were contaminated higher than standard level for molds.

Conclusion:microbial contamination in spices samples were higher than the defined international standard averages for spices

Keywords: Spices- microbial contamination

P397 - 619: AZADIRACHTA INDICA EXTRACT EFFECT AGANIST APPLE BLUE MOLD CAUSED BY PENICILLIUM EXPANSUM

Jalal Gholamnejad[1], Esmaeil Zangoei[2], Jalal Gholamnezhad[3], Eiedi Bazgir[4], Mostafa Darvishnia[5]

1. -
2. Ph.D student of plant pathology, Lorestan University, Lorestan, Iran
3. Assistant Professor of Plant Pathology, Faculty of Agriculture and Natural Resources, Ardakan University, Ardakan, Iran, , Corresponding author: jgholamnezhad@ardakan.ac.ir
4. Assistant Professor of Plant Pathology, Faculty of Agriculture, Lorestan University, Lorestan, Iran
5. Associate Professor of Plant Pathology, Faculty of Agriculture, Lorestan University, Lorestan, Iran

Background and Aim: The objectives of this research was to evaluate the effectiveness of the Neem methanolic and aqueous extracts as an alternative to replace the synthetic fungicide to control blue mold of apple caused by Penicillium expansum. The aim of this study was to investigate the effect of Neem on blue mold apple on blue mold apple invitro and invivo conditions.

Methods: In this research, the paper of aqueous and methanolic extracts of Azadirachta indica were studied to control the apple blue mold caused by P. expansum, in vitro and in vivo. In vitro assays included the use of the paper disk and the extracts mixture with medium tests. Finally, the extracts was used in the 4 ° C storage agonist pathogen-infected apples.

Results: The result of paper disk test showed the 20.66 and 19.79 mm of inhibition zone diameter, for methanolic and aqueous extract, respectively, compared to control (2mm diameter). The result of the mixed extract with media tests showed the aqueous and methanolic extracts of Thyme inhibit with the rate of 56.69 and 45.28 percent of the pathogen were respectively, in comparison with the control. In vivo test, the spot surface, in the treatment of aqueous and alcoholic extracts with a concentration of 6× 1000, reduced 68.12 and 57.18%, respectively, as compared to the control treatment.

Conclusion: Based on the our results, the extract of Neem could control the apple blue mold in viro and in vivo, and it can present as the suitable alternative instead of chemical fungicide.

Keywords: Blue mold, Cold storage, paper disk method, Neem extract

P398 - 620: THE EFFECT OF THYMUS DAENENSIS EXTRACT AGAINST APPLE BLUE MOLD CAUSED BY PENICILLIUM EXPANSUM

Jalal Gholamnejad[1], Esmaeil Zangoei[2], Jalal Gholamnezhad[3], Eiedi Bazgir[4], Mostafa Darvishnia[5]

1. Ph.D student of plant pathology, Lorestan University, Lorestan, Iran
2. Assistant Professor of Plant Pathology, Faculty of Agriculture and Natural Resources, Ardakan University, Ardakan, Iran, , Corresponding author: jgholamnezhad@ardakan.ac.ir
3. Assistant Professor of Plant Pathology, Faculty of Agriculture, Lorestan University, Lorestan, Iran
4. Associate Professor of Plant Pathology, Faculty of Agriculture, Lorestan University, Lorestan, Iran

Background and Aim: Apple blue mold caused by Penicillium expansum. Although synthetic fungicides are effective to protect against fruit losses, their potential effects on human health and the environment are a concern. Plant extracts are one of several non-chemical control alternatives that inspiring great interest due to their availability, non-toxicity and friendliness to the environment. The aim of this study was to investigate the effect of Thyme on blue mold apple invitro and invivo conditions.

Methods: In this research, the effect of aqueous and methanolic extracts of Thymus daenensis were studied to control the apple blue mold caused by P. expansum, in vitro and in vivo. In vitro assays included the use of the paper disk and the extracts mixture with medium tests. Finally, the extracts was used in the 4 ° C storage aganist pathogen-infected apples.

Results: The result of paper disk test showed the 26.65 and 24.79mm of inhibition zone diameter, for methanolic and aqueous extract, respectively, compared to control with 2mm diameter. The result of the mixed extract with media tests showed the aqueous and methanolic extracts of Thyme inhibit with the rate of 62.49 and 70.71 percent of the pathogen were respectively, in comparison with the control. In vivo test, the spot surface, in the treatment of aqueous and methanolic extracts with a concentration of 6× 1000, reduced 84.52 and 71.12%, respectively, as compared to the control treatment.

Conclusion: According to the results of this study, the extract of Thyme had stronge fungicide effect, and it can use as the suitable alternative instead of chemical fungicide.

Keywords: Blue mold, Cold storage, paper disk method, Thyme extract

P399 - 638: EFFECT OF CHITOSAN AND CINAMON ESSENTIAL OIL ON FOOD-BORNE PATHOGEN AND ANTIOXIDANT ACTIVITY IN FROZEN RAINBOW TROUT (ONCORHYNCHUS MYKISS)

Afsaneh Mohajer[1], Tahereh Mohajerfar[2], Parisa Sadighara[3], Ahmad Erfanmanesh[4], Mostafa Mohajerfar[5], payam safaei[6]

1. Department of Environmental Health Engineering, Division in Food Safety and Hygiene, Tehran University of Medical Sciences, Tehran, Iran
2. Academic Center of Education, Culture and Research (ACECR), Tehran, Iran
3. Department of Environmental Health Engineering, Division in Food Safety and Hygiene, Tehran University of Medical Sciences, Tehran, Iran
4. Academic Center of Education, Culture and Research (ACECR), Tehran, Iran
5. Department of Basic Sciences, Faculty of Veterinary Medicine, Semnan University, Semnan, Iran
6. Department of Environmental Health Engineering, Division in Food Safety and Hygiene, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim:food industries use synthetic preservatives to improve the quality and enhance the shelf life of food products during storage. However, the most common industrial strategies for preservation may not always bring the desired protection for curbing corruption. Furthermore, consumer demands for safer foods encourage researchers to find natural and effective preservatives.The purpose of this study is, investigation the antioxidant and antibacterial activity of chitosan in combination with cinnamon essential oil in frozen condition.

Methods:rainbow trouts were combined with 2% chitosan in combination with different concentration of cinnamon essential oils (0.125, 0.25 and 0.5 ml). The samples were kept at -18 ºC. Oxidative stability of samples was assayed by measuring lipid peroxidation level using thiobarbituric acid reactive substances (TBARS) method. The bacterial test was assayed by counting colony forming unit. the evaluation of statistical differences between groups were analyzed using the student's T-test by SPSS software According to the statistical facts, the difference more than 95% ($P \leq 0.05$) was considered significant.

Results:peroxidation level compared to control group and chitosan combination with 0.5 ml cinnamon showed synergistic effect. The antimicrobial activity of chitosan in combination with 0.5 ml cinnamon essential oil was higher than other concentrations and control groups.

Conclusion:chitosan in combination with cinnamon essential oil could considerably increase the oxidative stability and decrease total count of bacteria in frozen fish. These results may suggest that these edible coatings can be used instead of artificial preservatives and non-edible coatings.

Keywords:chitosan, cinnamon essential oil, lipid peroxidation, antibacterial, antioxidant

P400 - 639: DETECTION OF MYCOBACTERIUM AVIUM SUBSP. PARATUBERCULOSIS IN COWS' RAW MILK BY POLYMERASE CHAIN REACTION (PCR) IN SHIRAZ, IRAN

Shirin Safaeian[1], Saeid Hosseinzadeh[2], Seyyed Shahram Shekarforoush[3]

1. School of Veterinary Medicine, Shiraz University
2. Department of Food Hygiene and Public Health, School of Veterinary Medicine, Shiraz University
3. Department of Food Hygiene and Public Health, School of Veterinary Medicine, Shiraz University

Background and Aim: Mycobacterium avium subsp. paratuberculosis (MAP) has been considered as a great concern to the dairy industries and public health for the last decade. The potential role of the bacterium to cause Crohn's disease in human has also remained unresolved. MAP is a known cause of chronic enteritis in animals, including primates, but may be very difficult to detect by conventional culture. The microorganism is mainly excreted in the feces of an infected animal, but it can also be observed in a lower amount in the milk. Hence, dairy products from infected animals are presented as a route of its transmission. Both raw and pasteurized cows' milk is potential vehicles of transmission of MAP to humans.

Methods:DNA extracts of the total of 100 cow's raw milk were prepared using the phenol-chloroform method. IS900 PCR assay using the primers P90, GAA GGG TGT TCG GGG CCG TCG CTT AGG' and P91, GGC GTT GAG GTC GAT CGC CCA CGT GAC' were employed for amplification cycles..

Results: The PCR assay was generated a 413 bp product corresponding to MAP in 15% of the samples.

Conclusion: Despite the low incidence of MAP infection in the dairy products, further studies should be conducted to get more precise information on MAP infection in dairy cow using quick and reliable techniques, especially in areas where animals are maintaining together

Keywords: Crohn's disease, M. avium subsp. paratuberculosis, Raw milk, PCR

P401 - 678: THE ANTIBACTERIAL PROPERTIES OF THE ALLIUM ATROVIOLACEUM (VERCOAZ) PLANT

Behzad Hafeznia[1], Amirali Anvar[2], Shapour Kakoolaki[3]

1. MS Student of Food Biotechnology, Science and Research Branch Islamic Azad University, Tehran, Iran.
2. Assistant Professor, Department of Hygiene, Science and Research Branch Islamic Azad University, Tehran, Iran.
3. Iranian Fisheries Science Research Institute (IFSRI), Agricultural Research and Education Organization, Tehran, Iran.

Background and Aim: After Oncorhynchus mykiss is caught and subsequently dies, complex changes occur within its body due to chemical and microbial activity, so that subsequent to its death bacteria easily reproduce. Therefore, to reduce corruption, the use of chemical and natural preservatives is necessary. The Allium Atroviolaceum (Vercoaz) plant is perennial and native in the Zagros Mountains region and has a high nutritional value. Also, its antitumor effects in the field of medicine has been proven.

Methods: In this study microbiological indices of bacteria (psychrotrophic and coliform) on Oncorhynchus mykiss fillets in suitable temperature conditions (+4 °C) and unsuitable refrigerated conditions (+ 8 °C), in both aqueous and alcoholic extracts, and four time periods (24, 48, 72 and 168 hours) were tested.

Results: The results showed that the lack of growth of psychrotrophic micro-organisms in the treatment samples (in the two extracts mentioned above) was significantly reduced compared to the control samples. Also due to the appropriate transportation, packing in the freezing conditions, as well as the quality of purchased fish, there was no growth in the coliform bacterial in both the treatment and control samples.

Conclusion: The study, which was performed on the results of the two above-mentioned tests, showed that the lack of growth of bacteria reveals the destructive power of the Allium Atroviolaceum (Vercoaz) plant on the micro-organisms and also the effectiveness of this medicinal plant, thus proving the antibacterial properties of the Allium Atroviolaceum (Vercoaz) plant.

Keywords: Allium Atroviolaceum, Vercoaz, Antibacterial, Microbiology, Oncorhynchus mykiss

P402 - 726: SURVEY ON THE MICROBIAL AND QUALITY CHARACTERISTICS OF ORANGE JUICE PROCESSED WITH ULTRASONICATION

Roghieh Ashrafi yourghanloo[1]

1. Department of food science, Technical and vocational university

Background and Aim: Thermal pasteurization is one of the most used methods in the production of orange juice industry, despite that lower the level of microbial population to safety standard, due to the loss of ascorbic acid and the flavonoid compounds, reduces the nutritional value of products.

Methods: This study feasibility of replacing ultrasound thermal pasteurization method, with the aim of preserving the functional properties of orange juice was performed. Oranges after dewatering, at a constant temperature of 35 ° C, under different circumstances sonication (intensity ultrasound: 37 and 80 kHz - for 10, 15 and 20 minutes). The qualitative tests (pH, acidity, total soluble solids , the browning and opacity), microbial (determining the total microbial population count of molds and yeasts and coliforms) together with the analysis of color parameters (L *, a *, b * and ΔE) was performed. In the next step the optimal treatment of the first stage (with a frequency of 37 kHz and a sample treated for 15 minutes) with control heat pasteurized (75-70 degrees Celsius temperature and duration of 5 minutes) and fresh orange juice (control) compared to the above factors. respectively

Results: In the optimal sample ultrasound, the browning and reduced microbial significantly lower the total population of the sample was heated (05/0> p). Colored markers applied on the lack of effect of ultrasound on yellow index (b*), to increase the brightness (L*) and reduce redness (a*), respectively.

Conclusion:. The results showed that microbial production of orange juice with an acceptable level of safety and qualitycharacteristics appropriateispossible.

Keywords: Ultrasound, Orange juice, non-thermal Pasturization

P403 - 729: INVESTIGATING THE EFFECT OF HYDROCOLLOIDS ON SURVIVAL BIFIDOBACTERIUM BIFIDUM IN YOGURT

Roghieh Ashrafi yourghanloo[1]

1. Department of food science, Technical and vocational university

Background and Aim: Among the different foods act as a probiotic carrier, dairy products have special importance. Yoghurt is the most popular fermented milk product in the most parts of the world and commercially produced by inoculation of milk with a mixture of Lactobacillus bulgaricus and Streptococcus thermophilus cultures

Methods: In the current study viability of bifidobacterium bifidum as a probiotic culture have been surveyed in the yoghurts treated with gelatin, corn starch and inulin in the levels of 0.4 and 0.8% (w/w) at 0, 7, 14 and 21 days of storage intervals. In addition, texture, organoleptic and chemical characteristics of probiotic and commercial yoghurts have been comprised. Viable cells were enumerated by plating diluted samples (peptonized water) on solid MRS agar. Cultures were incubated for 72 h at 37 °C to determine bifidobacterium bifidum population

Results: The results showed that the numbers of bifidobacterium bifidum in the yoghurt samples were 8.59 log cfu/gr at the first day of production. These amounts reached to 5.05 log cfu/gr in control sample (without hydrocolloid) and 6.11, 6.19 and 6.05 log cfu/gr in yoghurts contain inulin, gelatin, corn starch after 21 days of storage time respectively. At the end of 21th day, the number of live probiotic cells were higher than those recommended for beneficial effect in the treated samples.

Conclusion: Viability of probiotic bacteria were significantly ($P<0.05$) higher in yoghurts containing 0.8% hydrocolloids.Therefore gelatin can be used successfully in the production of probiotic yoghurt with bifidobacterium bifidum without any advers effect on quality during storage.

Keywords:: Hydrocolloids, bifidobacterium bifidum, Yoghurt, survival

P404 - 745: FREQUENCY AND ANTIBACTERIAL SENSITIVITY OF LISTERIA SPP. AND LISTERIA MONOCYTOGENES ISOLATED FROM FOOD AND ENVIRONMENTAL SAMPLES IN URMIA

Lida Lotfollahi[1], ali mohammadi[2]

1. Urmia, Urmia University of Medical Sciences, faculty of medicine, department of microbiology
2. Urmia, Urmia University of Medical Sciences, faculty of medicine, department of microbiology

Background and Aim: Genus Listeria specially Listeria monocytogenes (L.monocytogenes), as a food-born pathogen, is causative agent of Listeriosis that could be fatal in highrisk people such as immunocompromised person, neonats and elderly.

Methods:in the present study, the frequency of Listeria spp. and L.monocytogenes in 277 food and environmental samples from retail food markets of Urmia city was evaluated . after isolation an identification of strains, antimicrobial susceptibility of isolates was investigated by Kirby – baur method .

Results: out of 277 samples, 10 (3.61 %) were positive for presence of Listeria spp. that confirmed by polymerase chain reaction (PCR) . From these 10 isolates , 3 (1.08 %) identified as L.monocytogenes and molecular confirmation was done by PCR for plc-A gene . The frequency of other species were as follow: L.ivanovii (0.72 %), L.siligerii (0.72 %) and each of welchimeri, grayi and innocua species (0.36 %) . eight of isolates (80%) were resistant to ampicillin and 7 (70%) to penicillin G . resistance to Co-trimoxazole and Gentamicin was not seen among isolates . Beside that, the resistance rate to erythromycin, rifampin & tetracyclin wase 20%, for each antibiotic .

Conclusion:the result of present study indicated the resistance of Listeria species isolated from food against antibacterial agents that are therapeutic choice for Listeriosis . this reveals the prompt need for surveillance program and information system setup about

Keywords: Listeria monocytogenes, Antibiotic susceptibility profile, food and environmental samples

P405 - 746: DETECTION OF ACTA GENE IN LISTERIA MONOCYTOGENES ISOLATED FROM DAIRY PRODUCT

Marzieh Shafiei[1]

1. uiversity azad islamic

Background and Aim: Listeria mono cytogenes is a gram-positive facultative intracellular bacteria. The actA is one of the most important genes in this bacterium, which involves in bacterials movement in the host cell and so in its pathogenesis. The purpose of this study is to evaluate the actA gene in Listeria monocytogenes strains isolated from dairy products

Methods: This cross sectional study was performed on 70 samples of dairy products collected from Tehran and Babolsar, Iran from June to August 1391.The samples were grown onto BHI agar and Mueller agar. A PCR approach was used to detect the presence of the actA gene in the isolated Listeria species . Also , isolated were grown into TSA containing 0.0015% Congo red in order to determine the invasive properties of L.monocytogenes

Results: This study showed contamination of the mIlk, cheese and soft cheese samples with L.monocytogenes (10 cases) , L.innocua(4 cases), L.seeligeri(1 cases). Furthermore, no yogurt and butter samples were contaminated with Listeria. Although all of these isolates contained actA gene in their genome, only 14% of the strain isolated from vegetables were positive for this gene.A total of 10 cases of isolated L.monocytigenes, 100% of the clinical strains, 70% of the strain food and 100% of standard strains purchased from Razi Institute were positive for Congo red phenotype

Conclusion: Detection of actA gene based on PCR can be used as an alternative approach for identification of pathogenic L.monocytogenes in samples without culture method

Keywords: Listeria monocytogenes, actA gene, Congo red phenotype, PCR.

P406 - 750: THE CARVACROL AND P-CYMENE INHIBITORY EFFECTS ON FUNGAL GROWTH AND AFLATOXIN PRODUCTION BY AFLATOXINOGEN STRAINS

Aref Rahimi[1], Mohammad hadi Fakoor[2], Azar Sabokbar[3]

1. Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran. (Student of MSc).
2. Department of Microbiology, Hidaj Branch, Islamic Azad University, Hidaj, Iran. (Faculty member of Islamic Azad University).
3. Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran. (Faculty member of Islamic Azad University).

Background and Aim: The spread of microbial contaminants and the effects of their toxins is one of the problems facing humanity, which has tried to control some of these toxins in the fungal area by natural compounds.

Methods: The antifungal activity of the carvacrol and p-cymene were studied with regard to the inhibition of the growth of Aspergillus flavus PICC-AF39, Aspergillus flavus PICC-AF24. The minimal inhibitory (MIC) and minimal fungicidal (MFC) concentrations of the mentioned compounds were determined. Sub-MIC was selected for the measurement of aflatoxins B concentration.

Results: The results indicated powerful antifungal properties of both compouneds inhibiting growth and aflatoxin production that could be applied to food as preservatives. A significant reduction in aflatoxin production was demonstrated by carvacrol.

Conclusion: The carvacrol and p-cymene could be safely used as preservatives in pharmaceuticals as well as health and food products to protect them against toxigenic fungal infections.

Keywords: Aspergillus flavus, carvacrol, p-cymene, antifungal, Antiaflatoxin

P407 - 757: PURIFICATION OF A PROTEASE FROM AN ORGANIC-SOLVENT TOLERANT ALKALOPHILIC BACILLUS SP.

Shohreh Mohamadi[1], Maryam Mehrabi[2]

1. Department of Biology, Faculty of Sciences, Razi University, Kermanshah, Iran
2. Department of Biology, Faculty of Sciences, Razi University, Kermanshah, Iran

Background and Aim: Microbial proteases are important because they are able to tolerate specific conditions, such as high temperatures, alkaline pH and organic solvents present in various industries

Methods: In this study, Bacillus sp. was isolated from the Dehloran hot springs in Ilam, Iran, and it was grown in Luria–Bertani (LB) medium enriched with cyclohexane and toluene. The desired protease activity was determined from clear zone diameter around the colonies grown in Skim milk agar-plates (SMA) medium. The purification of the protease enzyme was carried out using ammonium sulfate precipitation (85%).The saturated solution was centrifuged at 10,000×g for 10 minutes. The resulting sediments were dissolved in a 50mM Tris-HCl buffer, pH 9 and dialyzed against the same buffer for 24h with three times buffer replacement. The dialysate solution was loaded onto the DEAE-Sepharose column. A salt concentration gradient (NaCl 0-1M) was used to separate proteins attached to the column. Purification efficiency was checked using SDS-PAGE.

Results: Purified enzyme appeared as a single band of molecular weight about 27.5 kDa. One of the prominent features of the purified enzyme is the high activity in a broad range of pH from 4 to 11. Furthermore, the enzyme remained active over a range of temperature from 30 to 55 ◦C. Maximum enzyme activity was observed at 50 °C and pH 10.

Conclusion: Considering its high activity in a broad range of pH and temperature, tolerance and stability in the presence of organic solvent, the purified protease may find potential application in laundry detergents and other industrial processes.

Keywords: Organic solvent, Protease, Bacillus sp., Enzyme activity

P408 - 758: SCREENING AND ISOLATION OF AN ORGANIC-SOLVENT TOLERANT ALKALOPHILIC PROTEASE PRODUCER BACILLUS SP.

Maryam Mehrabi[1], Shohreh Mohamadi[2]

1. Department of Biology, Faculty of Sciences, Razi University, Kermanshah, Iran
2. Department of Biology, Faculty of Sciences, Razi University, Kermanshah, Iran

Background and Aim: Among the microbial enzymes, Bacillus proteases have attracted much attention due to their potential uses in various fields, including the pharmaceutical, food, leather, textile and so on.

Methods: In this study, Bacillus sp. was isolated from the Dehloran hot springs in Ilam, Iran. It was grown in Luria–Bertani (LB) medium enriched with cyclohexane and toluene. After autoclaving, toluene and cyclohexane were added to this medium at a final concentration of 10% and 30%(v/v), respectively. Covered flasks were incubated for 48 hours at 37 °C and shaked at 120 rpm. Repeated cultures were carried out several times in the mentioned environment with the same organic solvents concentration. The desired protease activity was determined from clear zone diameter around the colonies grown onto Skim milk agar-plates (SMA) medium. Then, a strain with high protease activity was selected and inoculated to the liquid medium of the protease production at 10% (v/v) concentration from pre-culture medium and it was incubated for 48 hours at 37 °C and 120 rpm. The isolated strain was identified as Bacillus strain based on the phenotypic characteristics and phylogenetic analysis of the 16S rDNA sequence. For bacterial growth optimization, isolate was incubated at different temperatures, pH and times, and protease activity was assayed.

Results: Result showed that optimal condition for bacterial growth to produce the highest amount of protease was at temperature 37 ° C, pH 9 and 72 hours incubation.

Conclusion: Considering these properties, this Bacillus sp. is a promising protease producer strain that has the potential to be used in laundry detergents and biotechnology applications.

Keywords: Screening, Microorganisms, Organic solvent, Protease, Bacillus sp.

P409 - 773: IDENTIFYCOMMON BACTERIA AND ANTIMICROBIAL SUSCETIBILITY IN ZARANDIEH POPULATION SINCE MARCH TO DECEMBER 2017

Aliakbar Bakhtiari[1], Hamed solimani[2], Marzieh safa[3]

1. Zarandieh health center,Faculty of Medical Saveh,iran
2. Zarandieh health center,Faculty of Medicine Saveh,iran
3. Ziaaian hospital,Tehran University Medical Sciences

Background and Aim:common bacteria and antimicrobial susceptibility in zarandieh populations with diarrhea infectious is one common cause of humman populations causing mortality and morbidity worldwide.this study was perfrmed to identify the common bacteria and thier antimicribial susceptibility in diarrhea patients.

Methods:this study 76 samples of diarrhea patients submitted to the labratory for culture during 24h in Maconky agar and Blood agar and diffrential enviroment,this study performed antibiogram pattern of growth inhibation zone in accordace with the standards was used antibiotic disc company padten Teb.

Results:of 76 colonial bacteria growth this study,29(%38) strains of Ecoli and 7(%9.2)strains of Klebsiella oxytica and 1(%1.3)strains of Shigella and 28(%36.8)strains of pantoea.agglomrans and 2(%2.6)strains of Citrobacter.freundii isolated and 9(%11.8) strains not identified.

Conclusion: The results of antibiotic susceptibility test the bacreia showed that most effective antibiotic(NA,SXT,CP,FM) on gram negative bacteria such as klebsilla and Ecoli and etc were 100 sensitive and resistent to (AMX and GM).

Keywords:diarrhea infections,Microbial causes,Zarandieh

P410 - 801: DETECTION OF ENTEROTOXIGENIC BACILLUS CEREUS ISOLATED FROM MEAT PRODUCTS IN ZANJAN BY PCR

Zahra Deilami Khiabani[1]

1. Zahra Deilami Khiabani

Background and Aim: Most of Bacillus cereus isolates can cause diarrhoeal and emetic types of food poisoning. The diarrhoeal illnesses can be caused by hemolysin BL (HBL), non-hemolytic (NHE) and cytotoxin K. Use of meat products is common nowadays. There is no precise report of B. cereus contamination in Iran, therefore it is important to study in this case.

Methods:100 meat products were collected form stores in Zanjan then the samples were cultured in PEMPA. Following the biochemical tests, the bacterial colonies were identified by PCR. Then B. cereus isolates were checked for NHE complex genes by specific primers using PCR.

Results: Results showed that 30 samples of 100 were contaminated with B. cereus. The NHE complex genes were found in 15 samples.

Conclusion: The results of this study have shown that NHE PCR is a prompt, reliable method for differentiation between non-enterotoxigenic and enterotoxigenic isolates of B. cereus. Enhancing awareness about virulence and prevalence of genes involved in food poisoning would be effective in the prevention of food poisoning.

Keywords: Bacillus cereus, Meat products, NHE complex, PCR

P411 - 820: OPTIMIZATION OF AMYLASE ACTIVITY FROM MONASCUS PURPUREUS

Najme Gord Noshahri[1], Mina Shaban[2], Mostafa Azadmanjiri[3], Maryam Ameri[4], Najme Gord-Noshahri[5]

1. Industrial Microorganism Biotechnology Research Department, Research Institute for Industrial Biotechnology, Academic Center for Education, Culture and Research (ACECR)-Mashhad branch, Mashhad, Iran
2. Industrial Microorganism Biotechnology Research Department, Research Institute for Industrial Biotechnology, Academic Center for Education, Culture and Research (ACECR)-Mashhad branch, Mashhad, Iran
3. Industrial Microorganism Biotechnology Research Department, Research Institute for Industrial Biotechnology, Academic Center for Education, Culture and Research (ACECR)-Mashhad branch, Mashhad, Iran
4. Industrial Microorganism Biotechnology Research Department, Research Institute for Industrial Biotechnology, Academic Center for Education, Culture and Research (ACECR)-Mashhad branch, Mashhad, Iran

Background and Aim: Monascus species are filamentous fungi capable of producing various metabolites including α-Amylase. Which is a endoglucanase catalyzing the internal bonding of α- (1,4) glycosidic in starch to oligosaccharides. Amylase is commercially used in bakery, brewing, corn syrup and alcohol production, detergent and textile industry .the aim of this study was to evaluate the effect of different temperature, PHs and incubation time on the activity of Monascus species amylase.

Methods: The experiments were done at 3 different temperatures(37,50,25 o c), incubation times of 6,37,40 minutes and at pHs 4,7,9 in three replicates. The enzyme activity was evaluated using soluble starch follow by DNS reagent which adsorption measure in 540 nm

Results: The results showed that the fungal amylase has a fairly similar activity at different conditions, doing slightly better at 50 oC, pH of 7 and incubation time of 40 minutes.

Conclusion: It was demonstrated that The enzyme being thermostable and best functional under Neutral condition.

Keywords: Monascus purpureus, Fungal Amylase, Enzymatic activity

P412 - 827: PREVALENCE OF AFLATOXIN BIOSYNTHESIS GENES ACCORDING TO AFLATOXIN LEVELS IN FEEDSTUFF SAMPLES

Nooshin Sohrabi[1], Morteza Taghizadeh[2]

1. Department of Biology, Payame Noor University, Tehran, Iran.
2. Department of Research and development, Razi Vaccine and Serum Research institute, Agricultural Research Education and Extension Organization (AREEO), Karaj, Iran

Background and Aim: Aflatoxins are amongst the major mycotoxins produced by various species of Aspergillus, particularly A. flavus and A. parasiticus. This study aims to study the effect of aflatoxin genes aflPand aflQ on aflatoxigenic species of A. flavus and A. parasiticus in cattle feed.

Methods: To conduct the study, 121 samples of cattle feed were collected and then were isolated and cultured based on macroscopic and microscopic methods. Moreover, PCR technique was also used to undertake a molecular examination of the isolated Aspergillus. To identify the aflatoxigenic species, 10 Aspergillus fungi, containing one or two positive aflatoxin genes were randomly selected and examined under the ultraviolet light. Finally, their aflatoxin content was evaluated based on High Performance Liquid Chromatography.

Results: The results indicate that 55.37% of 121 samples of the cattle feeds contaminated by Aspergillus fungi. Among these isolated samples, 67.16% has aflP and 70.14% has aflQ, and the findings of HPLC also confirms that aflatoxigenic isolates are more common than their non-aflatoxigenic counterparts. Among 10 species of A. flavus and A. parasiticus collected from cattle feeds, wheat bran produced the highest amount of aflatoxin, in which aflatoxin B1 accounted for the highest amount and aflatoxins G1 and G2 accounted for the least amount. It is noteworthy that aflatoxin B1 was produced in all species while aflatoxin G2 was not produced. Aflatoxins B2 and G1 were produced in all species of A. parasiticus and some species of A. flavus.

Conclusion: Controlling cattle feeds contaminated by Aspergillus fungi can secure them against aflatoxin contamination and prevent them from entering the human and animal health cycle.

Keywords: Aflatoxin, Aspergillus flavus, Aspergillus parasiticus, PCR, HPLC, feedstuff.

P413 - 838: STUDY THE PREVALENCE OF HBL AND NHE COMPLEXES IN ISOLATED BACILLUS CEREUS FROM SOME PASTEURIZED MILK AND CHEESE SAMPLES OF IRAN

Zahra Deilami Khiabani[1]

1. Assistant professor, Basic Science faculty, Islamic Azad University, Zanjan Branch, Zanjan,Iran

Background and Aim: Bacillus cereus is human opportunistic pathogen which can cause diarrhoeal and emetic types of food poisoning. The haemolysin BL (HBL), and non-haemolytic enterotoxin (NHE) are three-component toxin proteins which is produced with this bacterium. B. cereus is frequently detected in variety food products including dairy.

Methods: A total of 40 samples of pasteurized full fat milk and cheeses were collected from markets in Iran. The samples were cultured in PEMPA. Following the biochemical tests, the bacterial colonies were identified by PCR. Then B. cereus isolates were checked for NHE and HBL complex genes by specific primers using PCR.

Results: Results showed that 15 samples of 40 were contaminated with B. cereus. The NHE complex genes were found in 5 samples while HBL complex have seen in 3 samples.The results of this study have shown that NHE and HBL complex have seen in approx. 20% of dairy in which are lower than those reported by others

Conclusion:PCR is a reliable method for differentiation between non-enterotoxigenic and enterotoxigenic isolates of B. cereus. Enhancing awareness about virulence and prevalence of genes involved in food poisoning would be effective in the prevention of food poisoning.

Keywords: Bacillus cereus, Dairy, NHE and HBL complex, PCR

P414 - 861: EFFECTS OF CONTINUOUS WAVE LASER RADIATION AGAINST PATHOGENIC BACTERIA ESCHERICHIA COLI O157: H7 IN IRANIAN PROBIOTIC DOOGH

Ali Erafi Beyragh[1], Razzagh Mahmoudi[2], Ata Kabudari[3], Babak Pakbin[4], Ahmad Nasrollahzadeh[5]

1. Afagh Higher Education Institute, Faculty of Agriculture, Department of Food Science and Technology, Urmia, Iran
2. Medical Microbiology Research center, Qazvin University of medical sciences, Qazvin, Iran
3. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Urmia University, Urmia, Iran
4. Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, University of Tehran, Iran.
5. PhD student in food microbilogy. URMIA University.IRAN

Background and Aim: Food contamination draws a lot of attention as one of the major challenges in the food industry. Methods used for reducing these risks are heat, drying, freezing and additives. The non-thermal treatments that can be cited are (PEF) Pulsed Electric Field, (PLT) Pulsed Light and ultraviolet and infrared radiation.

Methods: Strong optical radiation has been used as a protective technique to treat the contamination levels of food through the destruction of microorganisms in the wavelength of 200 to 1000 nm. The homogenized milk with 1.5% fat was pasteurized in 90°C. It was cooled down to 43°C. Then, Streptococcus thermophiles, Lactobacillus delbrueckii subsp bulgaricus, and 2% of salt were added. It was incubated with the starter solution in 42°C and the fermentation was continued until the pH reached over 4.6. Laser with constant wavelength produced by a diode laser with a wavelength of 437 nm and intensity of 50 w/cm2 was radiated to the Iranian probiotic Doogh samples (with Lactobacillus casei, E. coli and control).

Results: The results of the study demonstrated that the survival of the pathogen bacteria during different days of storage had meaningful statistical differences ($p<0.05$). Laser treatment in different times had meaningful statistical differences in pathogen bacteria decrease comparing to the control group ($p<0.05$).

Conclusion: Due to the effects of thermal treatment on the nutritional and organoleptic properties of dairy products such as milk therefore, this method can be used for decontamination and reduction of microbial load in milk.

Keywords:E. coli, Iranian Doogh, Probiotic, Laser Radiation, organoleptic properties

P415 - 868: APPLICATION OF OPTAMER IN THE DETECTION OF AFLATOXIN B1

Saeedeh Shahbazizadeh[1]

1. Food and hygiene science engineer of Guilan University of Medical Sciences

Background and Aim:: In order to detect aflatoxin B1, a fluorescence assay has been developed using the fluorophore labeled optamer and its partial complement (a single-stranded DNA that has been modified as a covalently by the IOWA BLACK T quencher) in this study

Methods: The overall measurement method is simple and fast and has a high sensitivity to aflatoxin B1, which has a great potential to on-site analysis. In the absence of aflatoxin B1, optamamer binds to the cDNA, and fluorophore absorbs the quencher and neutralizes the fluorescence effect. In the presence of Aflatoxin B1, the optamer forms an optamer / aflatoxin B1 complex and results in the release of cDNA that is associated with fluorescence. The fluorescence of optamer, optamer with cDNA and optamer with cDNA and aflatoxin were measured using Trilog f7000 fluorometer.

Results: Using the design expert software, the optimal concentrations of optamer and cDNA were determined to be 10 and 15 nM, respectively. Fluorescence recovery curve versus aflatoxin B1 concentration was linear (r2 = 0.9942). The detection limit of this method with a standard curve of 10-100ppb is 8 / 47ppb. This method was used for potato starch.

Conclusion: This optasensor is suitable to detect aflatoxin B1in foods.

Keywords:optamer, quenching, potato starch, aflatoxin.

Microbial Infection and Cancer

P416 - 43: HELICOBACTER PYLORI INFECTION ASSOCIATION WITH COLON POLYP AND COLORECTAL CANCER

Mohammad Hadi Karbalaie niya[1]

1. Research center of pediatric infectious diseases, Institute of immunology and infectious diseases, Iran University of medical sciences, Tehran, Iran

Background and Aim: Helicobacter pylori (Hp) is an etiology of gastrointestinal problems like gastric cancer. Its role in colorectal cancer is under investigations. Therefore, in this study we proposed the association of Hp infection with colon polyp and colorectal cancer.

Methods: Patients who referred to Gastrointestinal Clinic of Firoozgar Hospital, Tehran, Iran from May 2014 to March 2015, were enrolled in a prospective case control study. Two groups of colorectal cancer (CRC) and colon polyps were compared with a group of healthy individuals. All participants underwent endoscopy, total colonoscopy, PCR test for Hp, Rapid Urease Test (RUT), stomach histological sections, anti- Hp IgG, CagA protein expression, and serum gastrin levels. SPSS v.20.0 used to analysis of variables.

Results:a total of 240 participants, 138 (57.5%) males and 102 (42.5%) females, were divided into three groups of colon polyp (66/240), CRC (58/240), and health control (116/240). Results of PCR for Hp detection in colon samples were negative in all three groups. The association of presence of colorectal cancer and positive RUT in stomach was not significant (p=0.09). There was no significant relationship between positive Hp in the stomach and the site and the type of polyps in colon and anti- Hp IgG, CagA protein expression and serum gastrin levels of three groups (p>0.05).

Conclusion: Our findings revealed that the Hp infection does not show a significant association with CRC and colon polyps

Keywords: Helicobacter pylori; colonic polyps; colorectal neoplasms

P417 - 162: INVESTIGATING EXACERBATING FACTORS HERPES VIRUS INFECTION (HSV1 AND HSV2)

Sina Moradi yeganmahale[1], Mohammad hosein abdoli [2], Mohammad Moain khodatars Dashtmian[3]

1. Student of Educational Sciences, Farhangian University, Rasht, Iran
2. Student of Educational Sciences, Farhangian University, Rasht, Iran
3. MSc Molecular Biology, Babolsar University, Mazandaran,iran

Background and Aim: Herpes simplex is a human pathogenic virus that is divided into two groups (Hsv2 and Hsv1). Most herpes simplex virus is accumulated in the nerve and can remain forever and begin to multiply and stimulate nerve host fibers that cause herpes and infections in various parts of the body. The disease is often transmitted through contact with the virus. Oral and infections. But in this article, the cause of herpes simplex virus infection has been studied due to disease progression worldwide and the effectiveness of the disease in the development of some cancers and other diseases.

Methods: The research method is descriptive-analytical and cross-sectional. In the field method, medical records and questionnaires were prepared in 4 specialized clinics and 6 public health clinics in Guilan province during the first 9 months of 1396 in 194 patients.

Results: Of the 194 suspects, it was roughly 59%. 32% of men and 68% of women, 69% of people with high stress and 18% of menstrual cycles (women), 6% had high blood glucose and immunity less than 7%. 76% of people under 40 are over 40 years of age45% of these people are addicted to cigarette smoking

Conclusion: Women are at greater risk because of their high levels of communication with children and their reproductive system. Stress, nutrition, and physical conditions are the cause of infection, but research on the effect of smoking on this disease is recommended.

Keywords: Herpes Simplex, Infection, Stress, Contact

P418 - 186: PREVALENCE OF HELICOBACTER PYLORI IN PATIENTS WHIT COLORECTAL CANCER

Parisa Abedi elkhichi[1], Hossein dabiri[2], Ehsan Nazemalhosseini Mojarad[3], Sama Reza Soltani[4], Mohammad Javad Nasir[5], Alireza Salimi Chirani[6], Hamid Asadzadeh Aghdaei[7]

1. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran
2. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. Gastroenterology and Liver Disease Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
4. Gastroenterology and Liver Disease Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
5. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran
6. Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran
7. Gastroenterology and Liver Disease Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: Colorectal cancer (CRC) is the growth of cancer cells in the colon or rectum. There are many risk factors associated with colon cancer . one of the risk factors is Microbial infection such as Helicobacter pylori. H.Pylori is one of the most commonly gastrointestinal infections and colonizes the stomach of man and induces severe mucosal inflammation. Recent studies have shown a relation between Helicobacter pylori infection and the risk of colon cancer. However, the results of this study are controversial. The aim of this study was to assess the association between Helicobacter pylori infection and the risk of colon cancer in Iran

Methods:: From 2016 to 2017, biopsy samples were obtained from patients suspected of colorectal cancer .In the next step ,DNA was extracted by Commercial kit .Then for the gene glmM Helicobacter pylori was performed PCR method and finally the data was analyzed.

Results: At total 86 patients that 18 were control and 68 were cancer patients was studied .This study included 32.6% females and 62.8% males (Mean age 56.4 years; age range 21 to 87 years) .Of 86 biopsy specimens all of them were negative for H. pylori ($P < 0.05$).

Conclusion: Although in studies has been suggested role of the H. pylori in CRC but we didn't find any association among H.pylori and Iranian patients.

Keywords: Helicobacter pylori, colorectal cancer

P419 - 221: REPORTING TWO CASES OF STOMACH CARCINOMA WITH HELICOBACTER PYLORI RESISTANT TO CLARITHROMYCIN AND METRONIDAZOLE

Fatemaeh Akbarzadeh[1], Ali Ghorbani Ranjbary[2]

1. 1. Department of Biotechnology, Ferdowsi University of Mashhad, Mashhad, Iran.
2. PhD., biotechnology

Background and Aim: Helicobacter pylori infection is one of the common infections of the digestive tract that leads to gastritis, peptic ulcers, and finally stomach cancer

Methods: This case study deals with two female patients 65 and 59 year old diagnosed with adenocarcinoma of the stomach pylorus with chronic gastritis and helicobacter pylori infection. Both patients were diagnosed with gastric cancer, chronic gastritis, and gastric ulcer 5 and 3 years ago and they were treated with a pharmaceutical mix of Lansoprazole, Amoxicillin, Clarithromycin, and Metronidazole for 2 weeks and 40 days later after they underwent endoscopy they showed gastric ulcer improvement. But after 5 and 3 years, when this study was conducted on the patients referring to the Gastroenterology Ward in hospitals in southern Iran, adenocarcinomas was diagnosed in the pyloric area based the results of endoscopy, CT Scans, and pathological slides, and biopsy tests

Results: Simultaneously, Helicobacter pylori were isolated and cultured and antibiotic resistance testing was performed. Although nuclear P53 levels dropped, it was still traceable. HER2 was also diagnosed through immunohistochemistry. The results of the antibiotic resistance testing indicated that both isolated samples were resistant to metronidazole and clarithromycin.

Conclusion:HER2 was also diagnosed through immunohistochemistry. The results of the antibiotic resistance testing indicated that both isolated samples were resistant to metronidazole and clarithromycin.

Keywords: Stomach carcinoma, Helicobacter Pylori, Antibiotic Resistance, Clarithromycin.

P420 - 404: CORRELATION OF BLOOD MIRNA-221 EXPRESSION WITH DIFFERENT PATHOLOGIC LEVELS OF HELICOBACTER PYLORI INFECTION

Mona Noohi[1], , Mojdeh Hakemi- Vala[2], Ali Hashemi[3], Jamileh Nowroozi[4], Mehrouz Dezfulian[5], Seyed Reza Fatemi[6], Mitra Rafiezadeh[7], Ghazaleh Talebi[8]

1. Department of microbiology , Islamic Azad University Karaj Branch, Iran
2. Department of microbiology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. Department of microbiology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran, Iran
4. Department of microbiology, Islamic Azad University Karaj Branch, Iran
5. Department of microbiology, Islamic Azad University Karaj Branch, Iran
6. Department of Gastroenterology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran, Iran
7. Department of Pathology, Medical School, Shahid Beheshti University of Medical Sciences, Tehran, Iran
8. Department of microbiology, Faculty of basic Sciences,Tehran Science and Research Branch, Islamic Azad University, Tehran, Iran

Background and Aim: Helicobacter pylori (H. pylori), plays a major role in the development of gastric cancer. miRNAs including miRNA-221 are small single stranded non-coding RNA, that their expression level may change in different conditions including H. pylori infection.So, the aim of this study was evaluating the expression variation of miRNA- 221 among endoscopic candidates with or without H. pylori infection.

Methods:50 biopsy samples and 50 blood samples were collected from endoscopic candidates who referred to Taleghani hospital of Tehran during 2016-17. mi-RNA extraction and cDNA synthesis was done based on the manufacturer protocol of Bio Basic and Intron products, respectively. The variation of mi-RNA 221 expression was evaluated by Quantitative Real-time PCR. Statistic analysis was done with SPSS version 17.

Results: The gender of candidates included of 15 males and 35 females and the average age was 18 to 85 Based on the pathologic examination, patients were divided to H. pylori negative and positive infected groups. Also, by Real Time PCR, expression change of miRNA-221 level in H. pylori infected was evaluated and based on the results, the level of miRNA-221 expression changes 2 times more in H. pylori infected Vs. to negative candidates.

Conclusion: Based on the results, it seems that blood miRNA -221 can also serve as a biomarker for the early diagnosis.

Keywords:miRNA, Helicobacter pylori, biopsy, gastric cancer

P421 - 437: MOLECULAR DIAGNOSIS OF MOBILUNCUS CURTISII AND MEGASPHAERA TYPE1 ASSOCIATED WITH BACTERIAL VAGINOSIS IN IRANIAN WOMEN, THE FIRST REPORT

Esmaeil Roohbakhsh[1], Ali Mojtahedi2[2], Nour Amirmozaferi[3]

1. 1.Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. .Associate Professor, Department of Microbiology, Faculty of Medicine, Guilan University of Medical Sciences, Rasht, Iran;alimojtahedi@yahoo.com
3. Department of Microbiology, Faculty of Medicine, Iran University of Medical Sciences, Tehran, Iran

Background and Aim: Bacterial vaginosis (BV) is the most common lower genital tract infection among women in reproductive age. Mobiluncus curtisii and Megasphaera type I are associated with BV; however, our knowledge about their pathogenicity is very limited. This study was performed to elucidate the possible rules these two bacteria play in women with and without bacterial vaginosis with the view of developing molecular criteria for BV diagnosis.

Methods: A total of 211women suspicious of having bacterial vaginosis were examined by PCR and Gram stain for presence of Mobiluncus curtisii and Megasphaera type I. Bacterial vaginosis was tested by four different laboratory methods based on Amsel criteria. These methods included determination of pH, Whiff test, and observation of Clue cells in a direct smear. Results were correlated with those obtained by Polymerase Chain Reaction (PCR) method.

Results: From a total of 211 suspected bacterial vaginosis samples, 66 cases were confirmed by Nugent score (31%). Mobiluncus curtisii was detected by PCR in 18 women with bacterial vaginosis (27.3%) and 2 women without the infection (2.5%). Megasphaera type I was detected by PCR in 7 women with bacterial vaginosis (10.5%) and none in women without BV

Conclusion: It can be concluded that Megasphaera type 1 as well as Mobiluncus curtisii play pathogenic roles in the establishment of bacterial vaginosis. Our results showed a relatively high prevalence of BV in non-pregnant and pregnant women in Guilan province of northern Iran

Keywords: Bacterial vaginosis, Mobiluncus curtisii, Megasphaera type I, PCR

P422 - 438: DETECTION OF HELICOBACTER PYLORI IN THE PATIENTS WITH GASTRIC CANCER BASE ON VARIOUS VIRULENCE GENES USING MULTIPLEX PCR

Mojtaba Sade[1]

1. Department of Microbiology, Islamic Azad University, Tehran Medical Branch, Iran.

Background and Aim: Background: It is estimated that Helicobacter pylori colonizes the stomachs of half the world's population and cagA-positive strains are present in 60–70% of infections in Western countries. Our aim was to determine the prevalence of the cagA/E/T, vacA and hrgA in H. pylori isolates among patients with gastric cancer (GC) in Karaj, Iran.

Methods:: A total of 50 non-repeated gastric biopsies obtained from patients undergoing endoscopy in Shahid Fayazbakhsh endoscopy center. The presence of cagA/E/T, vacA and hrgA genes were determined by multiplex-PCR method.

Results: Of 50 gastric biopsies, 44 (88%) samples were positive for various H. pylori virulence genes. Molecular analysis of these virulence factors showed that th: A total of 50 non-repeated gastric biopsies obtained from patients undergoing endoscopy in Shahid Fayazbakhsh endoscopy center. The presence of cagA/E/T, vacA and hrgA genes were determined by multiplex-PCR method. e frequency of cagA, cagT, cagE, vacA and hrgA were 16 (32

Conclusion:: The presence of different pathogenic genes has considerable effects in causing gastric ulcer, peptic ulcer, and gastric cancer. The effects of other genes, such as hrgA, in tissue damage and inflammation response are markedly important.

Keywords:. pylori, cagA/E/T, vacA and hrgA

P423 - 443: MOLECULAR IDENTIFICATION OF PAPILLOMAVIRUS TYPE 16 AND 18 ISOLATED FROM WOMEN WITH CERVICAL CANCER

Mojtaba Sade[1]

1. Department of Microbiology, Islamic Azad University, Tehran Medical Branch, Iran.

Background and Aim: Women with human papillomavirus (HPV)-associated with cervical and breast cancer have a higher mortality than the general female population. The purpose of this study was to identification HPV-16 and HPV-18 genotypes in patients with cervical cancer or breast cancers by multiplex-PCR

Methods:. In this experimental study, after collecting of samples from malignant cervical cancer, the viral DNA was extracted by SinaClon kit and PCR was done by specific primers for HPV-16 and HPV-18 gene of human papillomavirus in all samples

Results: After the analysis of PCR products by 2% agarose gel electrophoresis. Among 60 patient samples, 19 cases were confirmed to be positive for HPV infection and 41 cases were negative, showing high frequency of HPV in this patient population (about 31.6%). The frequncy of HPV-16 and HPV-18 were 8(1/42%) and 11 (9/57%) cases, respectively

Conclusion: This study showed that PCR by specific primers for HPV-16 and HPV-18 gene of human papilloma virus is a proper and accurate method for detection of this virus and the results confirm the previous reports of correlation between HPV and cancer samples.

Keywords:: Cervix cancer, Human Papilloma Virus, M-PCR.

P424 - 527: STUDY OF SIRT3 EXPRESSION IN PATIENTS SUFFERING FROM GASTRIC CANCER AND HELICOBACTER PYLORI INFECTION SIMULTANEOUSLY.

Leila Montazeri[1]

1. Falavarjan islamic azad university

Background and Aim: Gastric cancer (GC) is one of the most common malignancies with high rates of mortality worldwide. Although incidence of GC is decreasing, it is still a major clinical challenge because of delay in diagnosis, poor prognosis and limited treatment options. Helicobacter Pylori (H.Pylori) is a major cause of peptic ulcer disease and gastric malignancies. Sirt3 may function as an oncogene in different cancers. In this study, we evaluated the expression levels of Sirt3 gene in GC tissue biopsies.

Methods:A total of 44 tissue biopsies of gastric cancer (25 patients with positive test result for H.pylori infection versus 19 ones with negative result) were enrolled in this study. Urease test was used for detection of H.Pylori infection in tissue samples. RNA Extraction of tissue biopsies were performed via RNeasy Mini Kit (QIAGEN-Germany). Expression of Sirt3 was assayed by qRT-PCR using Taq-Man probes and specific primers.

Results: Expression of Sirt3 in H.Pylori positive patients group with gastric cancer significantly increased in comparison with H.pylori negative patients (P value=0.001) There was no significant relation between gender, age and expression of Sirt3 (P value=0.65 and 0.33 respectively).

Conclusion: Sirt3 expression increased in H.Pylori positive tissue samples of gastric cancer and seems a promising biomarker in diagnosis and prognosis of patients suffering from gastric cancer and H.Pylori infection simultaneously.

Keywords: Sirt3, Gastric cancer, Helicobacter Pylori.

P425 - 547: HUMAN PAPILOMA VIRUS STUDY IN PATIENTS WITH BREAST CANCER IN ISFAHAN, 1396

Ahmadreza Shahniani[1], zahra bamzadeh[2], shahin kouhikamali[3]

1. Ph.D Student of Cell Biology and Molecular Microbiology Kazeroun Branch, Islamic Azad University, Kazeroun
2. .Assistant professor of microbiology , Faculty of basic Science, shahrekord Branch, Islamic azad university, shahrekord
3. Master of science, Department of Microbiology.shahrekord Branch, Islamic azad university, shahrekord

Background and Aim:: Viruses such as Human Papiloma viruses have been identified in benign and breast cancerous tissues and have been considered as an etiology of breast cancer, but there is controversial information about the induction of viral breast cancer . The aim of this study was to determine the presence of Human Papiloma virus in patients with pre-existing breast cancer in Isfahan city .

Methods:: In this study 43 cases of breast cancer were investigated to detect the human Papiloma virus DNA with a high risk of malignancy using a PCR molecular method with selective viral primers .

Results:HPV DNA sequences were observed in 8 samples of breast cancer that 2 were reported with a high risk of malignancy.

Conclusion: The association between Human Papiloma virus infection in cancer tissue depends on the many factors , and our results can not confirm the role of HPV in breast cancer.

Keywords: Human Papiloma virus, breast cancer, PCR

P426 - 624: DEMOGRAPHIC DISTRIBUTION OF URINARY TRACT INFECTION AMONG REFERENTS TO A MEDICAL LABORATORY IN KERMANSHAH

Azadeh Foroughi[1], Pouya Pournaghi[2], Shervin Ramezan-Ghannbari[3]

1. Pathobiology and Basic Sciences department, Veterinary School, Razi University, Kermanshah, Iran
2. Department of Biology, Payame Noor University, Tehran, Iran
3. Department of Biology, Azad University, Broujerd branch, Iran

Background and Aim: Escherichia coli is one of the most common causes of urinary tract infection (UTI), which is often caused by uropathogenic E. coli. The prevalence of this infection is 1% and 3-8% in boys and girls, respectively. Around 150 million people worldwide have been diagnosed with UTI which each year, the cost of the treatment is more than 6 billion dollars.

Methods:A total of 180 clinical specimens were collected during a period of 5 months (from February to June, 2015). After diagnostic and differential biochemical tests, 100 samples were diagnosed to be contaminated with E. coli. The antimicrobial susceptibility test was performed using the Disk Diffusion (Kirby-Bauer method) due to CLSI standard.

Results: The average age of the patients was 69.43 years. Of the 100 patient, 74% were women with an average age of 42.77 and 26% of men with an average age of 45.88 years old. The highest rate of urinary tract infection was observed in women aged 70-61 years and the lowest rate was observed in men aged 80-71 years. The lowest age of the patient was 1 year old man and the oldest was a 95 years old women.

Conclusion:: According to the study, women aged 60-70, mostly menopause, were at the most risky group which is necessary to get special attention about health education and prevention of urinary tract infections. In addition, UTI is an important infection that affects people of both genders and under the age of one to 95 years.

Keywords: Urinary tract infection, Antimicrobial susceptibility test

P427 - 671: DETERMINATION OF 16 AND 18 GENOTYPES OF THE HUMAN PAPILLOMAVIRUS (HPV) IN CERVICAL CYTOLOGICAL SAMPLES FROM AHVAZ

Raziyeh Kashisaz[1], Mohamad Roayaei ardkani[2], Seyedeh Elham Rezatofighi[3], Manoochehr Makvandi[4]

1. Department of Biology Faculty of Science Shahid Chamran University of Ahvaz, IRIran
2. Department of Biology Faculty of Science Shahid Chamran University of Ahvaz, IRIran
3. Department of Biology Faculty of Science Shahid Chamran University of Ahvaz, IRIran
4. Department of Virology Ahvaz Jundishapur University of Medical Science, Ahvas, IRIran

Background and Aim:: Human papillomavirus is the main cause of cervical cancer. This cancer is the second most common cancer in women from worldwide especially in developing countries. Evidence of molecular epidemiology showed that the virus is associated with more than 90%of cancer tumore. So that HPV-16 and HPV-18 types include 70% of this .amount this study was prevalence with the aim of determination two high risk genotypes in cervical fluid cytology samples.

Methods: In this study PCR was used to genotype determine. In this study was done on180 samples were collected from 16-72 old married women who referenced to the specialized women –clinics in year 1396. After screening of positive samples specific primers were used to two high risk types determination

Results:: In this study from180 samples HPV was detected in 33 specimens (%18/33).among this only one (%3/03) samples was detected as for the type 18 positive.

Conclusion:: cervical cancer is easily diagnosed and treated at an early stages. But if its diagnosis delayed treatment will difficult and sometimes unsuccessful .Cervical screening has been reduced the incidence of cancer in developed countries. Therefore the effective prevention and treatment there is a need for adequate information about prevalence of HPV in each region.

Keywords:: HPV, PCR, genotype

P428 - 837: THE EFFECT OF HELICOBACTER PYLORI ON THE PATTERN OF METHYLATION OF GENE

Hamed Charkhian[1], Saba Ramez[2]

1. Department of Biotechnology, Urmia branch, Islamic Azad University, Urmia, Iran.
2. Department of Microbiology, Urmia branch, Islamic Azad University, Urmia, Iran.

Background and Aim: Helicobacter pylori affects about half of the world's population and can cause various diseases, including gastric cancer, due to its pathogens. One of the causes of cancer occurrence is epigenetic changes, including increased methylation of genes. In this study, we study the ability of this bacteria in changing the pattern of methylation of promoter gene HS3ST2. HS3ST2 is one of the major enzymes in biosynthesis and the final edition of heparan sulfate.

Methods:H. pylori was prepared from the hospital sources. After preparation, the bacteria were co-cultured for 24, 48 and 72 hours with AGS and MKN-45 cell lines (previously non-methylated) with ratios of 1 cell / 50 HP and 1 cell / 100 HP. Methylation-Specific Quantitative-PCR (MS-qPCR) was performed after extraction and sulfite removal of the genomic DNAs of the cells and the amount of HS3ST2 gene methylation was calculated.

Results:H. pylori was able to significantly increase the amount of methylation of the islands rich in CpG dinucleotides of HS3ST2 promoter gene in AGS cell line from 10 to 33% and in MKN-45 cell line from 4 to 14%. Increasing the methylation of this gene has a direct relationship with the time of adjoining bacteria with the cell and the concentration of the bacteria in the medium.

Conclusion: Probably H. pylori, through its pathogens, disrupts the activity of DNMTs and SAM, resulting in increased DNA methylation of the gastric cells. This causes changes or disruption of the normal activity of the cell and will result in the occurrence of cancer.

Keywords: Helicobacter pylori, HS2ST2, Gastric cancer, DNA methylation, MS-qPCR.

Microbial Metabolites and Cancer Treatment

P429 - 120: CYTOTOXIC EFFECT OF SAPONINS EXTRACTED FROM SPIRULINA PLATENSIS ON THREE CANCER CELL LINES

Mahboobeh Akbarizare[1], Hamideh Ofoghi[2], Mahnas Hadizadeh[3]

1. Iranian Research Organization for Science and Technology (IROST)
2. Iranian Research Organization for Science and Technology (IROST)
3. Iranian Research Organization for Science and Technology (IROST)

Background and Aim: Many researches have emphasized on bioactive compounds extracted from microalgae. Spirulina platensis is an edible, filamentous, photosynthetic microalgae that has 25 kinds of vitamins and minerals and contains many compounds with biotic activity, such as alkaloids, phenolic compounds, terpenoids, saponins, … Saponins are polycyclic aglycones attached to one or more sugar side chains. Saponins mainly presence in plants and there are many studies about these compounds in plants, but there are few studies in S. platensis. This study aimed to estimate total saponin content in S. platensis and effect of this compound on cell viability in 3 cancer cell lines (HepG2, MCF-7, MDA-MB-123).

Methods: Saponins were extracted using mixture of distilled water and n- butanol. Total saponin extracted were then dried and weighed. Cellular viability of HepG2, MCF-7 and MDA-MB-123 were evaluated using MTT assay after 24 h treatment with 0.02-2 mg/ml of saponins extracted from S. platensis.

Results: Total saponin extracted from S. platensis was estimated 28± 0.0005 mg/g. TLC profiles showed four bands for saponins with Rf values of (0.44, 0.48, 0.50,0.55) with UV treatment 230 nm. IC50 values in HepG2, MCF-7, MDA-MB-123 cells obtained in 0.35 mg/ml, 0.4 mg/ml, 0.22 mg/ml respectively.

Conclusion: This finding showed that saponins extracted from spirulina could be introduced as an anticancer agent.

Keywords: Saponin- Spirulina platensis- Anticancer

P430 - 130: STUDY THE ANTI-CANCER EFFECT OF BACTERIOCINS ISOLATED FROM LACTOBACILLUS-RHAMNOSUS ON CANCER CELL LINE AND ITS TOXICITY EFFECT ON NORMAL CELLS BY THE TRYPAN BLUE

Meysam Khodayari[1], Reza Talebi[2], Hamdollah Sharifi[3]

1. Department of Microbiology, Urmia branch, Islamic Azad University, Urmia, Iran.
2. Department of Microbiology, Urmia branch, Islamic Azad University, Urmia, Iran.
3. Department of Pharmacology, Faculty of Pharmacy, Urmia University of Medical Sciences, Urmia, Iran.

Background and Aim: Bladder cancer is the second most common genital-urinary tract cancers in adults. On the other hand, the emergence of resistant tumor cells to chemotherapy medicines has required the discovery of new therapies. Bacteriocins are novel anti-cancer agents. In this study, we examine the anti-cancer activity of "Bacteriocins lactobacillus-rhamnosus" on the bladder cancer cells.

Methods: We inoculated 2 × 10^4 cell/ml of cancer cell line 5637 and normal HUVEC cell in 96-well plate and after 24 hours incubation, at 25, 50, 100, 200, 400 and 800 ppm concentrations Bacteriocins lactobacillus-rhamnosus was treated for 24 hours. The effect of Bacteriocins was measured by "cell mortality" tests. In cell mortality test, we used trypan blue solution and reverse microscope were used.

Results: Bacteriocins inhibit the cancer cell 5637 growth and cause its death. Increasing the concentration of Bacteriocins is directly related to the increase in the death of cancer cells so that at the concentration of 800 ppm, the death of 71.43% of cancer cells is seen. But in normal cells, low toxicity is observed.

Conclusion: Because of the changes in the surface of the cancer cell membrane relative to the normal cell, Bacteriocins can be easily linked to the cancer cell, and cause its death through induction of apoptosis. Therefore, Bacteriocins lactobacillus-rhamnosus can be used as an additional medicine and supplemental therapy for bladder cancer.

Keywords: Bladder Cancer, Bacteriocins, lactobacillus-rhamnosus, Cell mortality.

P431 - 571: SCREENING HEMOLYTIC ACTIVITY OF LUMINESCENT VIBRIOS WITH FURTHER HEMOLYSIN EXTRACTION AND MOLECULAR WEIGHT DETERMINATION

Shokufeh Ghasemian[1], Mansour Mashreghi[2]

1. M.Sc. Student of Microbiology, Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
2. Professor, Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran

Background and Aim: Many pathogenic and non-pathogenic bacteria secrete various extracellular proteins. Among these proteins, hemolysin is an exotoxin which lyses erythrocyte membranes and exerts various roles in the infection process. In many cases, the pore-forming activity of hemolysin is not restricted to erythrocytes, but extends to a wide range of other cell types open up its potential medical applications. The aim of this study was to investigate the hemolytic activity of luminescent Vibrio strains and hemolysin characterization of selected strain.

Methods: Hemolysin-producing Vibrio strains were screened by culturing them on blood agar medium. Then the most active Vibrio strains enabled to create highest diameter of greenish zone was selected and designated as Vibrio harveyi HFB18. In addition, the 96 well plate hemolysin assay was performed to select the strain with highest hemolysin production. The V. harveyi HFB18 hemolysin was extracted by ammonium Sulphate precipitation and Zymography method. Finally, SDS-PAGE method was used to measure the molecular weight of HFB18 hemolysin.

Results:V. harveyi HFB18 showed highest hemolytic activity among 4 Vibrio strains that were investigated. The V. harveyi HFB18 hemolysin was extracted successfully and its lysis properties were confirmed. SDS-PAGE method showed that this bacterium is able to produce hemolysin with molecular weight of 52 kDa

Conclusion: Successful isolation and purification of hemolysin from a non-pathogenic bacterium is advantageous and its characterization could reveal novel properties that may be used in biomedicine studies.

Keywords: Vibrio harveyi, hemolysin, non-pathogenic, luminescence

P432 - 700: STRUCTURAL AND FUNCTIONAL DESIGN AND EVALUATION OF NEW IMMUNOTOXIN STRUCTURES AFFECTING LIVER CANCER IN QUASI-PHYSIOLOGICAL CONDITIONS

Leyli Mir[1]

1. Zabol University of Medical Sciences, Zabol, Iran

Background and Aim: Introduction:Liver cancer is the fifth most common cancer in the world and the second leading cause of death due to cancer in men,Treatments such as surgery, radiation therapy,chemotherapy and liver transplantation are commonly treated.The side effects of these therapies and their inefficiencies have led to the development of strategies for the targeted treatment of cancer cells based on their molecular variations,such as the antigen of cell surface called immunotoxin.

Methods: Detection of specific antigens on the surface of cancer cells and the components that make up these types of drugs and their assembly is a major step in designing these types of drugs,Which was based on computational science related to liver cancer.The results of this research.

Results: Results Has led to the detection of 18 antigenic expressions at the level of liver cancer cells with the highest and most specific expression associated with ANO7,CACNA1A and AFP antigens, In terms of expression, ANO7was selected as the best antigen.Among the protein molecules that can be attached to this antigen,KLK2was selected as the most effective ligand.The assimilation of Pseudomonas aeruginosus toxin-derived and selective ligand by linker (GGGGGG) resulted in the creation of five recombinant structures of varying quality and structure,One of the structures showed the desirable quality of structural and functional stability after being placed in real-world conditions.

Conclusion: The results of this research led to the introduction ANO7 antigen as an appropriate choice In the goals of effective immunotoxin drugs against liver cancer,which should be laboratory tests.

Keywords: Immunotoxin,Toxin,Ligand,Antigen, ANO7 and KLK2

P433 - 738: IDENTIFICATION AND EXTRACTION OF ANTICANCEROUS ENZYMES FROM E.COLI AND A NEW METHOD TO STUDY ITS ACTIVITY

Melika Farzin[1]

1. medicine faculty shahid beheshti university of medical sciences

Background and Aim:L-asparaginase is the most promising anti-tumour enzyme that reduces the level of L-asparagine (an important nutrient for cancer cells) resulting in cancer cell starvation which leads to the cell death. There are many sources of asparaginase but bacterial source i.e. E.coli and Erwinia spp is mostly use as a therapeutic agent against leukaemia.

Methods: In this study screening of different bacteria was done by rapid plate assay for asparaginase producing capability then intracellular and extracellular Asparaginase were extracted from its potent producer i.e. E.coli which was isolated from sewage water. The activity of enzyme was determined by using new procedure i.e. rapid activity analysis on agar plate and in tubes.

Results: Our results shows that an intracellular asparaginase enzyme was found to be more active against asparagines as compare to the extracellular enzyme. This enzyme isn't only the requirement of therapy for tumour cells but also it is use in food industry so in upcoming years the demand for asparaginase will get increase and our new method for intracellular enzyme extraction and activity analysis method (quantitative and qualitative method) will gain its importance for being easy, less expensive, using less volume of enzymatic extracts.

Conclusion: Our aim was the screening, production, extraction of LAsparaginase from E.coli and to develop a new and rapid procedure to analyze activity of the Asparaginase rather than using Nesslerization technique. we have found that Pseudomonas spp , E.coli and Staph spp were the asparaginase producers we have selected E.coli to be use in production and extraction steps.

Keywords: Asparaginase (ASNase), Acute lymphoblastic leukaemia(ALL), Chronic lymphoblastic leukaemia (CLL), Asparagine (Asn), Blood cancer,Therapies

Microbial Metabolites and Diseases

P434 - 26: APPROPRIATE CIRCADIAN DARKNESS MAY HELP RECOVERY OF SEPTIC SHOCK PRODUCED BY BACTERIAL LIPOPOLYSACCHARIDE

Mojtaba Hedayati ch[1], Shadi musavi[2], Rouhollah Gazor[3], Zahra Atrkarroushan[4], Razieh habibipour[5], Hamid morovati[6], Ebrahim Mirzajani[7]

1. Cellular and molecular research center, Faculty of medicine (Department of Microbiology), Guilan University of Medical Sciences, Rasht, , IRAN.
2. Department of Microbiology , Faculty of medicine, Guilan University of Medical Sciences, Rasht, Guilan, IRAN
3. Cellular and molecular research center, Faculty of medicine (Department of Anatmoy), Guilan University of Medical Sciences, Rasht, IRAN
4. Guilan University of Medical Sciences, Rasht, IRAN
5. Cellular and molecular research center (Department of Biochemistry), Faculty of medicine, Guilan University of Medical Sciences, Rasht, IRAN
6. Cellular and molecular research center (Department of Biochemistry), Faculty of medicine, Guilan University of Medical Sciences, Rasht, IRAN
7. Cellular and molecular research center (Department of Biochemistry), Faculty of medicine, Guilan University of Medical Sciences, Rasht, IRAN

Background and Aim: Sepsis is an important killing form of bacterial infection in burned patients. They may suffered Pseudomonas aeroginusa colonization in their lesions and toxicate with its lipopolysaccharide (LPS) systematically which result in cell stress and activation of unfolded protein response (UPR) in different tissues like liver. In another hand circadian condition capability to modified endogenous hormones like melatonin confirmed previously.

Methods:P. aeroginusa bacteria were isolated from the burned hospitalized patients. After bacterial identification, their LPS purified by specific LPS extraction Kit and administrated to LPS treated study group between fifty six male C57BL6 mice which kept in 2 and 6 hours in light and dark. Serum of animals in study groups' check for the level of melatonin and simultaneously liver of animals in study groups' removed after surgery and their RNA extracted to investigate by RT-PCR for activation of specific UPR mRNA X-Box Binding Protein-1 (XBP-1) gene.

Results: Mice which kept 6 hours in dark show the most elevated serum level of melatonin and present significant unspliced pattern in xbp-1 mRNA gene.

Conclusion: Our data revealed clearly preparing appropriate circadian darkness result in natural secretion of melatonin and decreased level of xbp-1 mRNA splicing.

Keywords: Pseudomonas aeroginusa, Burned patients, LPS, UPR, XBP-1, Melatonin.

P435 - 27: EVALUATION ONE MOLECULAR EFFECT OF NEISSERIA GONORRHOEAE LIPOOLIGOSACHARIDE TOXICITY IN MICE SPLEEN, BASED ON ACTIVATION OF UNFOLDED PROTEIN RESPONSE THROUGH INOSITOL REQUIRING ENZYME-1A

Mojtaba Hedayati ch[1], Atabak Nagheli[2], Rahele Sheikhy[3], Zahra Atrkarroushan[4]

1. Cellular and molecular research center, Faculty of medicine (Department of Microbiology), Guilan University of Medical Sciences, Rasht, , IRAN
2. Cellular and molecular research center, Faculty of medicine (Department of Microbiology), Guilan University of Medical Sciences, Rasht, , IRAN
3. Department of Microbiology, Guilan University of Medical Sciences (GUMS), Rasht, Guilan, IRAN
4. Guilan University of Medical Sciences (GUMS), Rasht, Guilan, IRAN

Background and Aim: It is confirmed that long term exposure to bacterial endotoxins, Lipopolysacharide (LPS) or lipooligosacharide (LOS), are one of the key factors result in multi¬-organ failure along with sepsis and septic shock. Despite wide studies on Neisseriameningitidis endotoxin (LOS), no remarkable study has been conducted due to Neisseria gonorrhoeae endotoxin (LOS). The unfolded protein response (UPR) is a cytoprotective response in the endoplasmic reticulum (ER) that promotes cell repair and sustain surveillance by reducing the load of unfolded/missfolded proteins and restores homeostasis following stress condition on ER, which induce innate immune signaling in response to invading microorganisms. Neisseria gonorrhoeae LOS, is a pathogen- associatedmolecular pattern (PAMP) in which, activates ER stress signal transduction through UPR. Among Three UPR stress sensors, Inositol requiring enzyme-1α (IRE-1α) conducts the most conservative signaling. pathway.

Methods:N. gonorrhoeae lipooligosacharide was extracted using specific extraction kit. Intraperitoneally (IP) injected C57BL/6 male mice were ethically sacrificed and their spleen removed after 2, 8 and 24 hours after treatment.Considering aseptic-RNase free condition, Extracted RNA from removed spleen was applied for. cDNA synthesis After Reverse Transcriptase Polymerase Chain Reaction (RT-PCR), the unfolded protein response pathway through IRE-1 stress sensor activation was evaluated via agarose gel electrophoretic pattern.

Results: Treatment of mice with LOS and LPS (3 mg/kg) result in activation of UPR through IRE-1 pathway in order to spliced/unspliced X-box binding protein-1 (XBP-1) mRNA gene.

Conclusion: This study can drop a knowledge and alternative pathway through N.gonorrhoeae pathogenicity mechanism, therapeutic pathway, and a future glance in counteracting with sepsis and septic shock.

Keywords: Neisseria gonorrhoeae, lipopolysacharide (LPS), lipooligosacharide (LOS), unfolded protein response (UPR), inositol requiring enzyme-1 (IRE-1), X-box Binding Protein-1 (XBP-1)

P436 - 61: STUDY OF EPSTEIN-BARR VIRUS (EBV) IN CHILDREN UNDER 5 YEARS SUSPECTED TO INFECTIOUS MONONUCLEOUS

Pezhman Sharifi[1], Woria Babahajian[2]

1. Liver and Digestive Research Center, Kurdistan University of Medical Sciences, Sanandaj, Iran
2. Blood transfusion Research Center, High institute for Research and Education in Transfusion Medicine, Tehran, Iran

Background and Aim: Epstein-Barr virus of the herpes virus family and subfamily of Gamaherpes Virinea. Infection with this virus is common throughout the world, in developing countries, more than 90% of children up to the age of 6 months, to become infected. This virus is a major cause of infectious mononucleosis disease, with symptoms such as headache, malaise, fatigue and sore throat occur.

Methods:60 children with symptoms of infectious Mononucleous, blood were collected And serum was separated after 15 minutes of centrifugation. Then tested for EBV IgM, by closed ELISA system Alegria company, was laid. To verify that their positive, Monotest (Rapid method) and CBC Diff for the presence and amount of large lymphocytes, which was known as Atypical lymphocytes carried out.

Results: In 10 cases (16.67%) boys and 8 patients (13.34%) were female and total 18 patients (30%) were positive for IgM test. Monotest was positive in all cases Peripheral blood smear these patients, atypical lymphocytes was observed, while their value on average was about 3.2. Positive test, no significant relationship with gender

Conclusion: As we can see, all these tests, each, confirmatory tests are good for each other and And monotest and observe atypical lymphocytes Can help in positive cases EBV IgM antibody and suspected infectious Mononucleous.

Keywords:EBV, children, Infectious Mononucleous

P437 - 107: FIRST REPORT OF MICROCYSTIN PRODUCING BY TWO TERRESTRIAL CYANOBACTERIA OF THE GENERA FISCHERELLA SP. F29 AND NOSTOC SP. N27 FROM IRAN

Nooshin Rajabpour[1], Bahareh Nowruzi[2], Mryam Ghobeh[3]

1. Department of Biology, School of Basic Science, Science and Research Branch, Islamic Azad University, Tehran, Iran.
2. Department of Biology, School of Basic Science, Science and Research Branch, Islamic Azad University, Tehran, Iran.
3. Department of Biology, School of Basic Science, Science and Research Branch, Islamic Azad University, Tehran, Iran.

Background and Aim: Cyanobacteria produce an unparalleled variety of toxins that can cause severe health problems or even death in humans and wild or domestic animals. The most frequently reported cyanobacterial toxin is hepatotoxin microcystin. Microcystin is predominantly produced by different genera of freshwater cyanobacteria, including Microcystis, Planktothrix and Anabaena, although it has also been detected in terrestrial strains of the genera.

Methods: As there have been no reports of toxicity from terrestrial cyanobacteria of Iran, we decided to conduct a preliminary study of the molecular toxicology in order to identify the possible toxic cyanobacteria strains. In this study, we detected the presence of mcyG in twenty five cyanobacteria strains collected from fifty different agricultural areas in Kermanshah province by means of PCR.

Results: The results of molecular toxicology and phylogenetic analysis the genes responsible for the production of secondary metabolites showed the occurrence of only two microcystin producers.

Conclusion: This is the first report of cyanotoxin-producing strain in Iran.

Keywords: Cyanobacteria microcystin molecular toxicology

P438 - 156: COMPARATIVE STUDY OF PROTEINASE ACTIVITY IN CANDIDA ISOLATES

Mohsen Ilkhani zadeh Ghomi[1], Zahra Nourmohamadi [2], Mahdi Razaghi-Abyaneh [3], Zahra Jahanshiri [4]

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 Mycology, Pasteur Institute of Iran, Tehran 13164, Iran
4. Department of Mycology, Pasteur Institute of Iran, Tehran 13164, Iran

Background and Aim: Proteinases play pivotal roles in Candida albicans infectionsand they are necessary to colonize and invade host tissues.This study aims to characterize proteinase activities of the 30 clinicalCandidaalbicans and non-albicans isolates.

Methods: Proteinase activity of Candida isolates was evaluated by their ability to secrete aspartyl proteinase (SAP) on a solid medium. All of the Candida isolates were cultured on bovine serum albumin (BSA) agar medium and the plates were incubated at 37° C.The diameter of the colonies and the colonies plus precipitation zone (Pz) was evaluated after 3-8 days. Each isolate was tested in triplicate, and the enzyme activity value was taken as the average of the three measurements.C.albicans ATCC 10231 strain was used as positive control.The phospholipase activity was calculated according to Price et al. All the Candida isolates were grouped according to the Pz value as following: Pz = 1, no phospholipase activity; 0.64 >Pz< 1, moderate phospholipase activity (+); Pz<0.64 high phospholipase activity (++). By this classification, a high Pz value indicates low enzymatic activity.

Results: All of Candida isolates were proteinase positive. Twenty one isolates (70 %) represented strong proteinase activity and 9 isolates (30 %) had moderate activity.

Conclusion: Taken together, identification of proteinase activity of clinical isolates of Candida may be helpful to use suitable antifungal drugs and prevent increased drug resistance and nosocomial infections.

Keywords: Candida albicans, Proteinase activity, Clinical isolates, Candida non-albicans

P439 - 203: DETECTION OF BIOFILM DEVELOPMENT IN CLINICAL ENTEROCOCCUS FAECIUM AND ENTEROCOCCUS FAECALIS ISOLATES FROM KASHAN

Niloofar Sabzi[1], Ali Nazari Alam[2], Rezvan Moniri[3], Malihe Solouki[4]

1. Department of Microbiology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran
2. Department of Microbiology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran
3. Department of Microbiology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran
4. Department of Microbiology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran

Background and Aim: Enterococcus faecium and Enterococcus faecalis are the most common Enterococci species, which are the most important cause of human enterococcal infections. The role of bacterial biofilms in repeated infections and antimicrobial resistance has huge significance for public health. The objective was to detection of biofilm development in clinical Enterococcus faecium and Enterococcus faecalis isolates from Kashan

Methods:A total of 48 isolates of Enterococci were collected from patients. Enterococcus species were identified using gram staining, grow in 6.5% NaCl and bile, hydrolyze esculin and others conventional microbiological methods. Quantitative determination of biofilm production was performed by using a modified Microtiter plate method.

Results: Among the Enterococci species strains 36 (75%) isolates were found to be strong and 11 (22.92%) isolates 0% were found to be moderate and 1 (2.08%) isolates were found weakly adherent.

Conclusion: The study demonstrates a high propensity among the isolates of Enterococcus faecium and Enterococcus faecalis to form biofilm which this is production biofilm can increase increases virulence of this bacterium.

Keywords: Enterococcus faecium, Enterococcus faecalis, Biofilm formation, Method.

P440 - 225: STUDY PREVALENCE OF AGR IN STAPHYLOCOCCUS AUREUS

Shekoofeh varmaziar[1], Abotaleb Nikpour[2]

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

Background and Aim: This bacterium is one of the main causes of hospital and community-acquired infections worldwide, leading to diseases including skin and soft tissue infections, necrotic pneumonia, endocarditis, septicemia , osteomyelitis, and food poisoning (due to production of enterotoxin). Infections caused by S. aureus are due to various factors like toxins and the creation of biofilms with quorum sensing (QS). The accessory gene regulator (agr) gene, as the regulator of biofilm production and isolation, is an effective factor for pathogen and bacteria resistance. The present study was carried out with the aim to determine the agr gene content among S. aureus isolates. This research is the first special study of coagulase gene polymorphism among isolates of S. aureus isolated from patients in Iran

Methods: In this study, 90 isolates of S. aureus were identified and confirmed by phenotypic method and their DNA was extracted using lysostaphin enzyme. Then, the agr gene was analyzed by multiplex polymerase chain reaction (Multiplex PCR) method

Results: The results of PCR and electrophoresis of S. aureus isolates indicated the agr I, agr II, agr III, and agr IV gene levels as 43.33%, 92.03%, 43.33%, and 16.08%, respectively

Conclusion: In many human diseases caused by S. aureus, the agr system is responsible for controlling and coordinating the production of virulence factors, exotoxin secretion, and hemolysins. Taking into account the significance of agr gene in regulating expression of cell surface proteins, exotoxin secretion, hemolysins, and virulence factors, examining its rate in each area is inevitable in order to prevent and treat this bacterium

Keywords:S. aureus, Biofilm, Multiplex PCR, agr, Electrophoresis

P441 - 349: MOLECULAR ANALYSIS OF INFLUENZA VIRUS A/H1N1 NON-STRUCTURAL GENE ISOLATED FROM IRANIAN PATIENTS WITH SEVERE SYMPTOMS

Zahra Asadollahi[1], Farida Behzadian[2], Sina Moeini[3], Samaneh Kohestani[4]

1. Student, Master of Molecular Biotechnology, Department of Molecular Biotechnology, Sciences and Biotechnology Institute, Malek-e-Ashtar University, Tehran, Iran
2. phd of virology, Department of Molecular Biotechnology, Sciences and Biotechnology Institute, Malek-e-Ashtar University, Tehran, Iran
3. Master of Molecular Biotechnology, Department of Molecular Biotechnology, Sciences and Biotechnology Institute, Malek-e-Ashtar University, Tehran, Iran
4. Student, Master of Molecular Biotechnology, Department of Molecular Biotechnology, Sciences and Biotechnology Institute, Malek-e-Ashtar university, Tehran, Iran

Background and Aim: Influenza A viruses are responsible for annual epidemics and occasional pandemics. The eighth segment of the viral genome coded for non-structural (NS) proteins is one of the known virulence determinants of virus. In this study we investigate the characterization and variability of the NS gene recovered from high pathogen H1N1 influenza viruses isolated from Iranian patients.

Methods: Nasopharyngeal swabs collected from outpatients with clinical symptoms were subjected for influenza detection and subtyping using real-time PCR. Positive specimens with high viral load underwent virus amplification on cell culture. The NS segments were amplified and sequenced from four 2015 samples from patients with severe symptoms and eight 2017 samples randomly selected. Genetic characterization, phylogenetic and protein modeling analysis carried on the obtained data with those of other full-length sequences from other geographic regions available in GenBank using MEGA7,ModWeb,Modfold softwares.

Results: Phylogenetic analysis on the NS gene of A/H1N1 isolates revealed that the Iranian strains were close to strains of A/Egypt/42/2014, A/Saudi Arabia/22/2015 and A/Ankara/WRAIR1425T/2009. The molecular analysis of these sequences also identified 5 mutations. Three-dimensional structure of Iranian NS proteins compared with those from reference genes available in GeneBank showed no significant deviation in functional domain.

Conclusion: The high similarity of Iranian NS gene with those from Middle-eastern countries, may indicate that they all derived from the same origin. None of the observed mutations implied the severity of symptoms so molecular analysis of other alleles is needed to explain the high pathogenic feature of those isolates.

Keywords: Influenza A(H1N1), NS,Phylogenetic

P442 - 393: THE EFFECT OF UV MUTAGENESIS TO PRODUCE MORE CLAVULANIC ACID BY FACTORS SUCH AS THE PRODUCTION OF ENZYMES, THE CONSUMPTION OF CARBON AND NITROGEN, AND ENZYMES AND SUGARS. STREPTOMYCES CLAVULIGERUS

AMIR HOSSIEN ArabVand[1], , Javad Hamed[2], Ramamehr Aria manufacturing company[3], Razieh Nazar[4]

1. Department of Microbiology, School of Biology, Qom Branch, Islamic Azad University-Group Masters Microbiology.
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
3. Providing finance and purchasing equipment and devices,Qom - Iran
4. Department of Microbiology, School of Biology, Qom Branch, Islamic Azad University-Group Masters Microbiology.

Background and Aim: In this research, a method of mutagenicity with ultraviolet radiation was used to increase the ability of clavulanic acid production by S. clavuligerus. To the results, 16 strains were eliminated and only 6 strains were identified as the highest total production activity clavulanic acid was selected, this strain again in the fermentation culture and HPLC Method for the production of antibiotics than the strain DSMZ 738 was determined and then in the second round of mutagenesis to increase the production capability of the strain in the process of mutagenesis Ultraviolet radiation was used and after culture in a liquid medium, clavulanic acid production was measured by HPLC and results obtained were comparable to that of 738 DSMZ. To find out the relationship between the production of clavulanic acid with factors such as the production of enzymes, carbon and nitrogen and enzyme and sugar sources, standard one-way yields and six mutated strains were calculated.

Methods:HPLC

Results: The results show that mutagenesis has been responsible for the expression of some of the decomposing genes of the decomposition and inhibition of some of the genes.

Conclusion: There is a link between the production of clavulanic acid with factors such as the production of enzymes, the consumption of carbon and nitrogen, and enzymes and sugars, a standard one-way yield, and six mutated strains.

Keywords:actinomycetes, antibiotics, clavulanic acid, mutagenesis, Streptomyces clavuligerus

P443 - 630: ANALYSIS OF QUORUM SENSING RELATED GENES IN PSEUDOMONAS AEUROGINOSA ISOLATES FROM CYSTIC FIBROSIS PATIENTS

Farahnoosh Doustdar[1], Farshad Farnaghi[2], Mona Ghazi[3], Saeedeh Khaleghnejad[4]

1. Shahid Beheshti Uni of Med Sci
2. Shahid Beheshti Uni of Med Sci
3. Shahid Beheshti Uni of Med Sci
4. Shahid Beheshti Uni of Med Sci

Background and Aim: Chronic Pseudomonas aeruginosa infections cause significant morbidity in patients with cystic fibrosis (CF). The pathogenesis of these infections is multifactorial and the production of many virulence factors is regulated by quorum sensing (QS), a cell-to-cell communication mechanism. QS regulates the production of pathogenic virulence factors and biofilm formation in P. aeruginosa. The four genes lasR, lasI, rhlR and rhlI were found to regulate this QS system. To elucidate the dynamics of P. aeruginosa QS systems during chronic infection of the CF lung, we have investigated QS Genes in isolates obtained from CF patients.

Methods: Fourty three P. aeruginosa clinical isolates were collected from 6 months to twelve years old CF patients. QS Genes including lasR, lasI, rhlR and rhlI were amplified by polymerase chain reaction (PCR), and PCR results subsequently underwent sequencing.

Results: All of 43 clinical isolates harbored all of quorum sensing related genes including lasR, lasI, rhlR and rhlI genes. Sequence analyses of these isolates showed that 41.66 and 33.33 percent of isolates had point mutations in lasR and lasI genes respectively.

Conclusion: These results emphasize the importance of QS genes in establishment and virulence of P. aeruginosa isolates in cystic fibrosis.

Keywords:pseudomonas aeruginosa, virulence factors, Quorum sensing, cystic fibrosis (CF).

P444 - 634: PREVALENCE OF THE CLOSTRIDIUM DIFFICILE TOXINS IN TEHRAN HOSPITALS

Fatemeh Savaheli moghadam[1], Ashraf Mohabati Mobarez[2], Sepideh Khodaparast[3]

1. Departement of Bacteriology ,Faculty of Medical Sciences ,Tarbiat Modares University ,Tehran ,IRAN
2. Departement of Bacteriology,,Faculty of Medical Sciences,Tarbiat Modares University,Tehran,Iran
3. Departement of Bacteriology,,Faculty of Medical Sciences,Tarbiat Modares University, Tehran.Iran

Background and Aim: Introduction and Objective: Clostridium difficile (C. difficile) is an important nosocomial pathogen in hospitals and causes antibiotic-associated diarrhea and pseudomembranous colitis. The main virulence factors of C. difficile include the toxin A (TcdA), toxin B (TcdB) and binary toxin (CDT), produced by some isolates of C. difficile. The role of CDT during infection has not been well understood, but it has been elucidated that CDT enhances virulence conferred by toxin A and B in animal models.

Methods: Materials and Methods: A total of 580 stool samples were collected from patient with suspected to C. difficile infection (CDI). C. difficile was identified by culture onto enriched media and in anaerobic conditions. (PCR) was performed for detection of toxin A, toxin B, Cdta and Cdtb .

Results: Results: A total of 60 (10 % of stool cultures) C. difficile were isolated from patients suspected to CDI. Of them, 7.3% (n=3) were positive for binary toxin, 87.7% (n=36) were positive for toxins A and B (A+B+), 7.3% (n=3) were positive for toxin (A-B+), 4.8% (n=2) for A+B- and 32% (n=19) were non-toxigenic C. difficile.

Conclusion: Conclusion: Our data showed that existence of toxigenic (A+B+) C. difficile was high in the patients with long-term hospitalization, old age and use of previous antimicrobial drugs. Prevalence of binary toxin was relatively low and was found mostly in those patients with severe illness. Its production enhances virulence of toxin A&B.

Keywords: Clostridium difficile infection, TcdA, TcdB, CDT

P445 - 704: EVALUATION OF HERPES SIMPLEX VIRUS I&II IN SUSCEPTIBLE PSEUDOMONAS AERUGINOSA KERATITS BY PCR MOLECULAR METHOD

Milad Zarini[1], Mohammad Hassan Shahhosseiny[2], Jamileh Nowroozi[3]

1. Department of Biotechnology, Islamic Azad University, Tehran North Branch, Tehran/ Iran
2. Department of Microbiology – Shahr-e-Qods Branch – Islamic Azad University –Tehran / Iran --Iranian Gene Fanavar Institute (IGF), Tehran/Iran
3. Department of Microbiology, Islamic Azad University, Tehran North Branch, Tehran/ Iran

Background and Aim: Herpes simplex virus (HSV) causes a wide range of diseases in humans. The main idea in this study is to evaluate the presence of HSV I&II in clinical susceptible pseudomonas keratitis. To investigate the presence of HSV virus in susceptible pseudomonas aeruginosa keratitis by PCR molecular method

Methods:70 samples of suspected Pseudomonas keratitis were collected from the eye by a specialist physician from Labafinejad Hospital. DNA extraction from samples was done by boiling\DNG plus method. The PCR test was optimized and specificity and limit of detection (LOD) were performed on samples.

Results: Amplicon with the size of 454bp observed in 1.5% agarose gel electrophoresis. Out of 70 samples, 5 cases (7%) were positive for HSV. Primers were banded just with HSV DNA in specificity test, that indicating high specificity. The LOD was indicated 50 copy/reaction

Conclusion: Certainly, some of the detected pseudomonads keratitis is clinically related to the presence of HSV, which is further investigated. In addition, the PCR molecular method is a fast, precise, high-precision method for detecting factors.

Keywords: Herpes Simplex Virus, keratitis, PCR, Pseudomonas aeruginosa

P446 - 764: PREVALENCE OF MYCOPLASMA HOMINIS AND UREAPLASMA UREALYTICUM INFECTIONS IN PATIENTS REFERRED TO SHAHID MOTAHARI HOSPITAL IN URMIA BY PCR

Azam Mokhtari[1], Peiman Mokhtarian[2], Mohammadreza Mahzounieh[3], Azizollah Ebrahimi Kahrizsangi[4]

1. Department of Pathobiology, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
2. Department of Pathobiology, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
3. Department of Pathobiology, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
4. Department of Pathobiology, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran

Background and Aim: Mycoplasma is a genus of bacteria that lack a cell wall around its cell membrane and it is believed to be involved in pelvic inflammatory diseases. Mycoplasma species are the smallest bacterial cells discovered up to now. The aim of present study was to investigation the prevalence of Mycoplasma hominis and Ureaplasma urealyticum infections in patients referred to Shahid Motahari hospital in Urmia by PCR method.

Methods:PCR was performed using 70 urine samples collected. Also 70 urine samples from healthy people were studied as control group. Genomic DNA was extracted from the blood samples by using a DNA extraction kit.

Results: Based on the results obtained, there was no significant difference between the presence of Mycoplasma hominis and Ureaplasma urealyticum in the case and control groups. In fact we did not have any positive samples.

Conclusion: The results of this study demonstrated there weren't any evidence of Mycoplasma hominis and Ureaplasma urealyticum urine infection in shahid Motahari hospital in Urmia

Keywords: Mycoplasma hominis, Ureaplasma urealyticum, PCR, Urmia

P447 - 821: VIRTUAL MODELING OF INHIBITING THE HELICOBACTER PYLORI ACID RESISTANCE SYSTEM

zahra tootiaei[1], Shadab Jabbarzadeh[2], zeinab majidzadehmoghadam[3]

1. Malek Ashtar University of Technology.
2. Malek Ashtar University of Technology.
3. Malek Ashtar University of Technology.

Background and Aim: One of the most important pathogens in the digestive system is Helicobacter pylori. The catalytic activity of urease enzyme is dependent on nickel. One of the key subunits of urease, which causes the transfer of nickel to an enzyme active site, is UreG. The aim of this study was to investigate the pharmacodynamics properties of compounds on inhibiting UreG proteins and proton pump

Methods: Twenty same combinations of the composition with the 1,3-caffeoylquinic acid plant composition were investigated. the most effective plant compounds have been identified. With the help of the PubChem database, the structure of the compounds was obtained and the ligands were designed with Chemsketch software. The UreG protein crystallographic file and proton pump were obtained by PDB protein database (4HI0, 3ux41) and SPDBV software optimized its energy level. Protein-ligand docking configuration was defined with AutoDock4 software and the algorithm was created with Cygwin software, and finally, the analysis of the information obtained from the files which were reported.

Results: The binding energy between this ligand and the substrate 4HI0, would be -7.75Kcal/mol, and this parameter for the interconnection of this compound with the 3UX41 substrate would be -5.99Kcal/mol. The best result which was obtained in this study belongs to the interaction of this ligand with the desired substrates.

Conclusion:the plant was introduced as an effective herb in the treatment of Helicobacter pylori infection. For this purpose, extraction of this plant extract and molecular and laboratory dynamical studies can be expanded and completed

Keywords: Helicobacter pylori pharmacodynamics UreG

P448 - 878: PRODUCTION AND FAST PARTIAL PURIFICATION OF STAPHYLOCOCCUS AUREUS SUPER ANTIGEN C

Ramezan Ali Ataee[1], Gholam Hosien Alishiri[2], Ardeshir Hesampoor Mahalati[3], Mohammad reza Ataie kachoee[4]

1. Department of Medical Microbiology, Faculty of Medicine, Baqiyatallah University of Medical Sciences, Tehran, Iran
2. Department of Rheumatology, Faculty of Medicine,and Hospital Research Development Committee, Baqiyatallah University of Medical Sciences, Tehran, IR Iran
3. Department of Biology Azad University Tehran Markaz IR Iran
4. Department of Biology Azad University Tehran Markaz IR Iran

Background and Aim: Up to now, different methods have been described for the production and purification of bacterial toxins in native forms. In all these ways, Time consumption, high expensive equipment, high degree of specialty and costs were crucial. The purpose of this study was to provide rapid and inexpensive producer to semi- purifying the bacterial toxins.

Methods:in this study, a standardize strain of S aureus with high level production of super antigen C was used. Mass production was lead to decanter precipitation and then centrifugation. The supernatant was subjected to sequential ultrafiltration 100, 50 30 1nd 10 Kda. The output was SDS- PAGE and confirmatory blotting.

Results: The results revealed that, remaining 24- hour cultivation of mass production in decanter within 48 hours causes the participate of bacterial cells and proteins. The results of sequential ultrafiltration showed that the super antigen C 'is under ultra-filter 30KDa and were concentrated by ultra-filter 10KDa.

Conclusion: Staphylococcal super antigen C is perhaps best recognized as the causative agents of food intoxications, although its role in other diseases such as inflammatory disorders is now being actively investigated. Clarification new hypothesis of this regards, it requires a native form of the toxins. The method used in this study would probably help to achieve these goals.

Keywords: Production, purification, Staphylococcus aureus, super antigen C and ultrafiltration

Microbial vaccines

P449 - 38: CHITOSAN-BASED NANOVACCINE CANDIDATE AGAINST ESCHERICHIA COLI O157:H7

Jaleh Khanifar[1], Reza Haji Hosseini[2], Rohoallah Kazemi[3], Mahdi Fasihi Ramandi[4], Jafar Amani[5], Ali Hatef Salmanian[6]

1. Department of Biology, Faculty of Basic Sciences Tehran Shargh Payaam Noor University, Biochemistry Research Center.
2. Department of Biology, Faculty of Basic Sciences Tehran Shargh Payaam Noor University, Biochemistry Research Center.
3. Green Gene Company, Tehran, Iran
4. Molecular Biology Research Center, Systems Biology and Poisonings Institute, Baqiyatallah University of Medical Sciences, Tehran, Iran.
5. Applied Microbiology Research Center, Systems Biology and Poisonings Institute, Baqiyatallah University of Medical Sciences, Tehran, Iran.
6. Department of agriculcheral Biotechnology. National Institute of Genetic Engineering and Biotechnology (NIGEB), Tehran, Iran

Background and Aim:E. coli O157:H7 is an important entric phathogen in human causing diarrhea, which may be complicated by hemolytic uremic syndrome (HUS). This research aimed at nanovaccination with recombinant protein composed of EspA, Intimin and Tir as important virulence factors expressed by EHEC (Enterhemorrhagic Escherichia coli).

Methods:A chimeric trivalent recombinant protein EIT (EspA,Intimin,Tir) . In present study the rEIT antigen was nanoparticled with chitosan to produce a protective EHEC nanovaccine candidate. Mice were immunized with this antigen and level of immunization IgG and IgA were verified in mice after expression and purification by ELISA. In challenging tests different groups of immunized mice were infected orally with E. coli O157:H7.

Results:this nanovaccine candidate induced strong humoral and mucosal immune responses and protected the mice from live challenge with EHEC. After pre incubation of EHEC with antisera the lowest E. coli counts adhering to monolayer Caco-2 cells were in binding inhibition assay. In a challenging study with different groups of immunized mice by feeding EHEC, a reduction in number of colonies was observed in all the immunized groups for over two week.

Conclusion:present candidate, reduced signs and symptoms of EHEC infections with efficiency and can be a new strategy for increasing immunity against E. coli O157:H7 and suggests the use of combined (oral –injectable) vaccination routes in orther to achieve a higher humoral and mucosal immunogenicity.

Keywords:EHEC, Chitosan, Nanovaccine, rEIT

P450 - 39: IMMUNIZATION WITH NANOPARTICLED CHITOSAN CONTAINING OF RECOMBINANT EIT AND STX2B ANTIGENS AGAINST E. COLI O157:H7 IN J

aleh Khanifar[1], Reza Haji Hosseini[2], Rohoallah Kazemi[3], Mahdi Fasihi Ramandi[4], Jafar Amani[5], Ali Hatef Salmanian[6]

1. Department of Biology, Faculty of Basic Sciences Tehran Shargh Payaam Noor University, Biochemistry Research Center.
2. Department of Biology, Faculty of Basic Sciences Tehran Shargh Payaam Noor University, Biochemistry Research Center.
3. Green Gene Company, Tehran, Iran
4. Molecular Biology Research Center, Systems Biology and Poisonings Institute, Baqiyatallah University of Medical Sciences, Tehran, Iran.
5. Applied Microbiology Research Center, Systems Biology and Poisonings Institute, Baqiyatallah University of Medical Sciences, Tehran, Iran.
6. Department of agriculcheral Biotechnology. National Institute of Genetic Engineering and Biotechnology (NIGEB), Tehran, Iran

Background and Aim: E. coli O157:H7 is an infectious zoonotic pathogen causing human hemolytic uremic syndrome (HUS) with renal failure that can be deadly dangerous. Here two important virulence nanoparticulate recombinant proteins with chitosan, (the rEIT (ESPA, Intimin, Tir) and rStx2B the nontoxic sticky part of Shiga toxin2 B subunit monomers were mixed together and used as nanovaccine candidate.

Methods: Synthetic pET28-genes with eit and stx2B were transformed into E. coli BL21 (DE3) separately for Expression of rEIT and rStx2B recombinant proteins. These antigens were purified and confirmed with Western blotting. Female- five- weeks old BALB/c mice immunized. The specific Immune responses were measured by ELISA. In challenging tests different groups of immunized mice were infected orally with E.coli O157:H7.

Results: Higher titers of serum and feces anti rEIT and rStx2B IgG , IgA were achieved after the last immunization proses in all of the groups.. The reduction in the number of colonies was observed for all the immunized groups for over two weeks. After preincubation of EHEC with antisera the lowest E. coli counts adhering to monolayer Caco-2 cells were in binding inhibition assay. All the vaccinated groups were challenged with lethal dose of Stx2. More than 66% of immunized mice with these vaccines were survived and protected against toxi .

Conclusion: The results showed these recombinant nanovaccine candidates induced strong humoral and mucosal immune responses and greatly reduced signs and symptoms of E.coli O157:H7 infections.

Keywords:E. coli O157:H7, EIT, Stx2B, Nanovaccine, immunization

P451 - 101: CHARACHTRIZATION OF ASAIA SP. ISOLATED FROM MALARIA VECTORS IN SOUTHWEST OF IRAN

Hamzeh Alipour[1], Masoomeh Bagheri [2], Majid Asgari[3], Abasali Raz[4], Marziae Shahriari-Namadi[5]

1. Research Center for Health Sciences, Institute of health, Shiraz University of Medical Sciences, Shiraz,Iran
2. Departmant of medical Entomology, School of Health, Shiraz University of Medical Sciences, Shiraz,Iran
3. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran, Tehran, Iran
4. Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran, Tehran, Iran
5. Departmant of medical Entomology, School of Health, Shiraz University of Medical Sciences, Shiraz,Iran

Background and Aim:different strategies have been suggested by scientists to control the malaria disease. Paratransgenesis is one of the solutions for vector control. In this strategy, symbiont microorganisms are used for disrupting the parasite life cycle or vector fitness. Asaia is a bacterium from acid acetic alpha proteobacterium which stably associated with some mosquito species like several Anopheles. Asaia has some specific characteristics that make it as a potent candidate for paratransgenesis to control malaria such as: cultivation in cell-free media, colonization in different parts of the vector body (gut, salivary glands, reproductive organs, etc.), easy transformation and vertical and horizontal transmission to larvae

Methods: Different larval smples of Anopheles were collected from Fars province of Iran. Samples were transfered to Insectary of school of health. Bacteria were isolated from larval and adult midguts and cultured in specefic media of Asaia. Morphological and biochemical analysis were performed on each sample. Molecular confirmation was performed by 16s rRNA PCR with genus specific primers.

Results: Based on the specific culture situations and molecular test, we isolated Asaia bacteria from An. Stephensi, An.fluvitilis and An.D,thali. the samples collected from kazeron and nour-abad districts in summer2016

Conclusion: Asaia has some basic characteristics such as: no pathogenicity for human, simple genetic manipulating, vertical and horizontal transmission, cultur on non-expensive media. Therefore, Asaia can be considered as a very potent agent for developing a robust paratransgenesis tool to control malaria based on vector control.

Keywords: Asaia, Malaria, paratransgenesis, Anopheles, 16s rRNA

P452 - 102: THE EFFECT OF BCG ON IRON METABOLISM IN THE EARLY NEONATAL PERIOD: A CONTROLLED TRIAL IN IRANIAN NEONATES.

Seyed ehsan Asadi[1], raha latifi[2], elahe mohtasham[3]

1. phd in Nursing, Esfahan Medical University, Esfahan, Iran.
2. msc in Nursing, ahwaz Medical University, ahwaz, Iran.
3. Midwifery Student OF shahrekord University ,shahrekord .Iran

Background and Aim: Bacillus Calmette-Guerin (BCG) vaccination has been reported to protect neonates from non-tuberculous pathogens, but no biological mechanism to explain such effects is known. We hypothesised that BCG produces broad-spectrum anti-microbial protection via a hepcidin-mediated hypoferraemia, limiting iron availability for pathogens.

Methods: To test this we conducted a trial in 250 iranian neonates comparing iron status in the first 5-days of life after allocation to: (1) All routine vaccinations at birth (BCG/Oral Polio Vaccine (OPV)/Hepatitis B Vaccine (HBV)); (2) BCG delayed until after the study period (at day 5); and (3) All routine vaccinations delayed until after the study period.

Results: Vaccine regime at birth did not significantly impact on any measured parameter of iron metabolism.

Conclusion: However, the ability to detect an effect of BCG on iron metabolism may have been limited by short follow-up time and high activation of the inflammatory-iron axis in the study population.

Keywords:BCG; Hepcidin; Heterologous effects; ISRCTN93854442; Iron; Neonate

P453 - 133: IMMUNOGENICITY STUDY OF RECOMBINANT AUTOLYSIN OF STAPHYLOCOCCUS IN BALB/C MICE

Mandana Bagherzadeh mogaddam[1], Setareh Haghighat [2], Mehdi Mahdavi [3]

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. 2- Recombinant Vaccine Research Center, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: Staphylococcal infections are common in the entire world. In this respect, autolysin protein as one of the adhesion molecule of bacteria plays an important role for binding bacteria to the host cells and cell division. Herein, the role of autolysin protein was evaluated as a vaccine candidate against all of Staphylococcus strains.

Methods: Recombinant autolysin protein was produced and evaluated by SDS-page and western blot. Balb/c mice were injected subcutaneously with 20 µg of r-autolysin formulated in Montanide ISA-266 and Alum adjuvants three times with two week intervals with proper control group. Two weeks after the last immunization, sera were collected; total and specific isotype antibodies were evaluated by ELISA. IFN-γ and IL-4 assessed with commercial ELISA kits. Experimental mice were challenged with a sub-lethal dose of staphylococcus strains and following that, the number of bacteria from kidneys, liver and spleen were determined. Survival rate was recorded for 30 days.

Results: Significant increase of antibody with high level of IgG1 and IgG2a isotypes was demonstrated in vaccinated mice versus the control groups ($P < 0.005$). IFN-γ and IL-4 cytokines did not showed any significant differences in all of the experimental vaccine groups versus each other. The bacterial load in the internal organs from immunized mice was 1000 times less than control groups. Finally the life span of immunized mice after bacterial challenge was extended versus control mice.

Conclusion: These results may indicate the capacity of autolysin as candidate vaccine to control the staphylococcus infections.

Keywords: Autolysin;Staphylococcus; Microbial vaccine.

P454 - 161: B CELL EPITOPE-BASED VACCINE CANDIDATE AGAINST BACTEROIDES FRAGILIS BY IMMUNOINFORMATICS APPROACH

Shirin Dashtbin[1], Ramin Abiri[2], Amirhooshang Alvandi[3]

1. Students Research Committee, Kermanshah University of Medical Sciences, Kermanshah, Iran
2. School of Medicine, Kermanshah University of Medical Sciences, Kermanshah, Iran
3. School of Medicine, Kermanshah University of Medical Sciences, Kermanshah, Iran

Background and Aim: Bacteroides fragilis is one of the most abundant anaerobes found in humans and cause intra-abdominal infection, sepsis, soft tissue abscess and bacteraemia. The traditional approach to design a vaccine is a long process that involves the attenuation of the pathogen through sub-culturing followed by its administration. The administration of whole pathogen raises several safety issues and toxicity owing to the unwanted biomaterial. Thus, peptide can also serve as a vaccine candidate, as well as can be used for designing immunotherapeutic. It has been shown in the past that a small peptide or antigenic regions can also activate different arms of the immune system. The conventional approach for designing vaccine against a particular disease involves stimulation of the immune system using the whole pathogen responsible for disease.

Methods: First, vaccine targets were selected according to standard characteristic. Then B-cell epitope of canditate peptide were predicted using well-known online bioinformatics server (IEDB, Bcepred, Ellipro, DiscoTope) and then were selected and compared based on the highest score and the highest repetition.

Results: In this study, we designed a new structural model containing two putative antigenic determinants of SusC/RagA family TonB-linked outer membrane protein and membrane protein insertase YidC fused together by hydrophobic linkers.

Conclusion: The fusion peptide construct may be used as epitope-based vaccine for development of Bacteroides fragilis vaccine candidates.

Keywords: Immunoinformatics; in silico; epitope based vaccine; Bacteroides fragilis

P455 - 229: APPLICATION OF MINITAB SOFTWARE ON THE OPTIMIZATION OF INACTIVATION CONDITIONS OF RABIES VIRUS USED IN VET RABIES VACCINE BY BETA-PROPIOLACTONE

Zohre Eftekhari[1], Ali Khodaeipour[2], Arsalan Afrasiabi[3], Hamed Shakouri[4]

1. Quality Control Department ,Research & Production Complex, Pasteur Institute of Iran
2. Microbiology Master of Science ,Islamic Azad University, North Tehran Branch
3. Microbiology Master of Science ,Islamic Azad University, North Tehran Branch
4. Islamic Azad University, Science and Research Branch, Tehran

Background and Aim: Veterinary rabies vaccine which is routinely produced contains tissue culture-adapted rabies Pasteur Virus strain propagated on BHK-21 cells. Various methods can be used for inactivating the rabies virus, such as treatment with β propiolactone , acetylethyenemine or ultraviolet irradiation.

Methods: In present study, Pasteur Virus strain grown was treated with BPL based on Mini Tab program by design of excremental and used Two Level Factorial Design and Central Composite Design method in 3 factors and 3 levels which in final design twenty base runs, sixty totals run with final blocks: 1 carried out. Each sample titrated after various intervals and tested for the viral infectivity in BSR cells and in vivo inactivity test carried out on mice.

Results: Based on in vivo and in vitro obtained results, absolute loss of infectivity of the virus treated with 1:3000, 1:4000 and1:5000 final concentrations of BPL were evident at the end of the 72 h in 21◦C and 4◦C.In each samples at the end of the 72 hr and 120 hr in 4°C and 21°C did not any infectivity of the virus. Complete loss of infectivity of the virus treated with 1:3000, 1:4000 of BPL was evident at the end of the 48 hours hr in 4°C and 21°C.

Conclusion: The aim of this study was to evaluate the effects of temperature, time of exposure and concentrations of BPL on the infectivity of the rabies virus, in order to achieve the ideal conditions for inactivation of the virus, harvested from the cell cultures.

Keywords: Optimization , BPL , Variables

P456 - 232: NEW GENERATION OF ADJUVANTS IN VACCINE DELIVERY

Zohreh Fasihi[1], Iraj khodadadi[2], Fatemeh Nazemi[3], Freshteh Mehri[4]

1. Food and drug laboratory, Hamedan university of medical sciense, Hamedan, Iran
2. Department of biochemistry and nutrition, school of medicine,Hamedan university of medical sciense, Hamedan, Iran
3. Food and drug laboratory, Hamedan university of medical sciense, Hamedan, Iran
4. Food and drug laboratory, Hamedan university of medical sciense, Hamedan, Iran

Background and Aim: The vaccines with pure recombinant and synthetic antigens are poorly immunogenic and thus cannot induce an strong protective immune response. Threfore, to bused up these response, a safe and improved adjuvant is essential.

Methods: In this article, we reviewed the adjuvants used in the development of vaccines, from the aspect of immune respons, especially in the last 10 years.

Results: Adjuvants in human vaccine formulations should be biocompatible, biodegradable, biologically inert and capable to induce of immune responses. New adjuvants as an alternative for alum has been studied specially in last decade. In this review we discuss the role of appropriate adjuvants and their role as ‘delivery systems’ in human vaccines. Some strategies such as use of emulsion, liposomes and micro/nano particle as second generation adjuvants on alum are interested. Although these adjuvants are more potent than alum, associated toxicity issues (spacially in combination with a vaccine) and regulatory concerns stoped their use in human vaccines.

Conclusion: It is not yet clear which formulation(emolsione, liposome, nano/micro particle) has the ‘best’ technologies in the long term for vaccine delivery, but these vaccines are more potent immunogenic and thus can induce an appropriate protective immune response. However, new infectious diseases and new drug-resistant microbial infections warrant development of safe and improved new adjuvants.

Keywords: Vaccine, adjuvant, immune response

P457 - 298: IDENTIFICATION OF NOVEL VACCINE CANDIDATES AGAINST SHIGELLA SPP. THROUGH REVERSE VACCINOLOGY METHODS

Abolfazl Hajialibeighi[1], Seyed Latif Mousavi Gargari[2]

1. M.Sc student of microbial biotechnology, Faculty of Basic Science, Department of Biology, Shahed University
2. Professor, Faculty of Basic Sciences, Department of Biology, Shahed University

Background and Aim: Shigella is among the most important four health-threatening diarrheal diseases in the world. Diarrhea causes by Shigella occurs annually about 165 million around the world and especially in developing countries. Currently, there is no licensed vaccine against Shigella. Current strategies for developing vaccine against Shigella, Such as cellular, hybrid or subunit vaccines have been ineffective. Reverse vaccinology is a new method that explore proteome for novel vaccine candidates. Based on this method the aim of this study is in silico identification of new vaccine candidates against Shigella.

Methods: Sequences of extracellular and outer membrane proteins of Shigella (S.flexneri 2a, S.flexneri 5, S.dysenteriae sd197, S.boydii sb227, S.sonnei 53G) were obtained (from Uniprot, Vaxign, and PSORTb). Protein similarity to host-cell, antigenicity and solubility, then were determined (using Vaxijen, PROSO II, and BLASTp). Then high-score proteins were selected and characterized (ProtParam, TMHMM, SignalP and VFDB). Also protein sequences conservation were studied in multiple sequence alignment (BLAST, Clustal and T-Coffee). Finally secondary and tertiary structure of the best proteins were predicted (I-Tasser and Gor IV).

Results: Among 550 proteins as potential vaccine candidates, 10 proteins showed highest scores and therefore were selected for experimental Studies.

Conclusion: The results indicate that all 10 selected proteins could be used as vaccine candidates. In addition more specialized analysis can be carried out on these proteins such as epitope mapping, truncation, chimerization, combination and optimization for in vitro studies. The results support that reverse vaccinology is a new and appropriate method for discovering new effective antigens.

Keywords: Shigella, Shigellosis, Diarrhea, Reverse Vaccinology, Bioinformatics.

P458 - 316: POLYTOPE VACCINE DESIGN AGAINST STREPTOCOCCUS PNEUMONIAE AND INFLUENZA VIRUS: AN IN SILICO APPROACH

Sahar Sadeghi[1], Fatemeh Zahedipour[2], Mojgan Bandehpour[3]

1. School of Advanced Technologies in Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran
2. Cellular and molecular Biology Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. Cellular and molecular Biology Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Background and Aim: Based on limitations about current vaccines for respiratory pathogens: Streptococcus pneumoniae and Influenza virus, more effective, conserved, cost-affordable and population-specific vaccination approaches are needed.

Methods: Several virulence proteins were chosen from Influenza virus and pneumococcus based on their function and role during infection. Their amino acid sequences were retrieved from UniProtKB database, then were exploited to epitope prediction. For prediction of linear B-cell epitopes Kolaskar and Tongaonkar antigenicity method in IEDB server was applied. T-cell epitopes were determined among MHC I and II binding predicted peptides with higher scores for selected mice MHC alleles. Chosen epitopes were linked together with proper linkers. SOLpro was used to determine solubility of constructs upon overexpression in E. coli. Their antigenicity and allergenicity was estimated by ANTIGENpro and AlgPred predictors. Secondary structures were predicted with PSIPRED program. Tertiary structures prediction was done by Swiss-model and Phyer2 servers. Cluspro2.0, the protein-protein docking web server, was applied for study of the interactions between epitopes and MHC molecules.

Results: Based on various bioinformatics servers it is shown that the polypeptide constructs have ideal features to be cloned and expressed in a proper E. coli host and then used as a vaccine in animal experiments. Designed polytopes are immunogenic antigens and are not allergens; and are soluble upon overexpression. Results from Cluspro2.0 server, demonstrated the high binding affinity (docking scores) between epitopes and MHC molecules.

Conclusion: By help of immunoinformatics tools, we have designed two polytope constructs which can be used together as bivalent intranasal vaccine against two mentioned serious pathogens.

Keywords: Streptococcus pneumoniae, Influenza virus, Vaccine, Immunoinformatics

P459 - 354: OPRL CLONING OF PSEUDOMONAS AERUGINOSA IN ESCHERICHIA COLI BL21 AFTER BIOINFORMATICS VERIFICATION AS A CANDIDATE FOR VACCINE.

Omid Shirmohammadi[1], Mohammad Hadi Fakoor[2]

1. Department of Microbiology, Hidaj Branch, Islamic Azad University,Hidaj, Iran.(Student of MSc microbiology)
2. Department of Microbiology, Hidaj Branch, Islamic Azad University, Hidaj, Iran. (faculty member of Islamic Azad University).

Background and Aim: Pseudomonas aeruginosa is a Gram-negative bacterium that is considered to be one of the most important bacterial pathogens responsible for serious opportunistic infections among cystic fibrosis (CF) and immunocompromized patients. Perhaps, choosing the right vaccine can solve the problem. So, we suggest other membrane protein L (OprL).

Methods: Primer design, PCR (Polymerase Chain Reaction) and cloning for oprL in the plasmid pET 28a done after bioinformatics studies. Then, its transfer to Escherichia coli BL21 was performed. Finally, it was approved by universal primer PCR and enzymatic digestion methods.

Results: The bioinformatics studies shown protein conservation. Also, it was strong antigenic and immunogenic properties for OprL by IEDB Analysis and vaxijen software respectively. In the laboratory experiments, the oprL was cloned in Escherichia coli BL21. Finally, the approval tests were positive.

Conclusion: This protein is suitable for evaluating animal experiments.

Keywords: Vaccine, Pseudomonas aeruginosa, Clonning, oprL

P460 - 418: IDENTIFICATION OF NOVEL OUTER MEMBRANE PROTEINS OF SALMONELLA TYPHI AS VACCINE CANDIDATE BY REVERSE VACCINOLOGY APPROACH

Ehsan Esmailnia[1], Ehsan Esmailnia kamangar[2], Seyed Latif Mousavi[3]

1. Department of Cell Biology, Faculty of Basic Sciences, Shahed University, Tehran, Iran
2. Department of Cell Biology, Faculty of Basic Sciences, Shahed University, Tehran, Iran

Background and Aim: Salmonella enterica serovar Typhi (S. Typhi) cause enteric fever, which is very common in the developing world. The recent emergence of antimicrobial resistant isolates of S. Typhi makes typhoid fever, a global public health risk. Vaccination is an important strategy to control new isolates of S. Typhi and to interrupt transmission during outbreaks. Outer Membrane Proteins (OMPs) of S. Typhi are potent immunogens, which could serve as vaccine candidates. Reverse vaccinology as a revolutionary genome-based approaches, can be used to identify novel vaccine candidates. In this study a collection of bioinformatic tools based on the principle of reverse vaccinology were employed to identify novel OMPs as potential vaccine candidates for future vaccine development.

Methods: In silico prediction of vaccine candidates among 7 complete genomes of S. Typhi including subcellular localization, human protein homology, antigenicity, solubility, transmembrane helices, BLASTp and virulence factors were performed. Proteins failing to comply with the set parameters were filtered at each step.

Results: Among all OMPs of S. Typhi analyzed in this study, outer membrane fimbrial user protein (tsaC), Vi polysaccharide export protein (vexA) and outer membrane usher protein (steB) were identified as potential candidates qualifying all the set criteria.

Conclusion: These predicted vaccine antigen candidates can be used in a basis for development of different vaccine types such as subunit protein vaccines and epitope peptide vaccines against S. Typhi.

Keywords:enteric fever, Salmonella Typhi, vaccine, vaccine candidate, reverse vaccinology, outer membrane proteins

P461 - 446: DETECTION AND SEQUENCE EVALUATION OF UPAH GENE AMONG UROPATHOGENIC ESCHERICHIA COLI ISOLATED FROM URINARY TRACT INFECTIONS AS A NEW VACCINE CANDIDATE

Saba Azimi[1], Mohammad Reza Asadi Karam[2], Saeid Bouzari[3], Mehri Habibi[4]

1. Department of Cell and Molecular Biology, Maragheh university, East Azerbaijan, 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. E. mail: m_habibi1362@yahoo.com

Background and Aim: Urinary tract infections (UTIs) caused by Uropathogenic Escherichia coli (UPEC) are among the most common infections worldwide. Increasing rate of antibiotic resistance among the isolates will make treatment of these infections ever more complicated and costly. Therefore, there is a need for an efficacious vaccine against UTI. UPEC has several types of autotransporter proteins such as upaH that play important roles in pathogenesis. In this study, we investigated the presence of upaH gene in UPEC collected from patients with UTI.

Methods:A total of 100 UPEC isolates were collected from hospitalized patients in Tehran, Iran. Bacterial identification was performed by biochemical tests. PCR amplification of upaH gene was performed by specific primers. The PCR products of 10 isolates were purified from the agarose gel and were subjected to sequencing. Then, the sequences of these genes were compared with the genes deposited in GenBank and Expasy.

Results: The upaH gene was amplified in 89% of the UPEC isolates tested. Comparison of the upaH sequences from our UPEC isolates with sequences of upaH gene in the GenBank showed significant homology (>98%) that indicated the conserved nature of this gene among the UPEC isolates.

Conclusion: Our results in agreement with other studies confirmed the conservation of upaH gene among UPEC isolates. Thus, upaH gene could be an ideal vaccine candidate for prevention of UTI caused by UPEC. Expression of recombinant UpaH protein and evaluation of the immune responses against this vaccine candidate in vivo and in vitro is under study.

Keywords: Urinary tract infection, UPEC, Vaccine candidate, UpaH

P462 - 503: ASSESSMENT OF FREQUENCY AND NUCLEOTIDE SEQUENCE OF IRON RECEPTOR PMI0842 IN PROTEUS MIRABILIS COLLECTED FROM URINARY TRACT INFECTIONS CASES IN TEHRAN, IRAN

Behnam Kavehei[1], Mehri Habibi[2], Mohammad Reza Asadi Karam[3]

1. Department of Biochemistry, Pharmaceutical Sciences 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. E. mail: m_asadi12@yahoo.com.

Background and Aim: Proteus mirabilis strains are among the most important causes of Urinary tract infections (UTI) especially in complicated UTIs. Increasing rate of antibiotic resistance will complicate future treatment of UTIs, making the development of a vaccine more urgent. There is no study about the evaluation of some iron adsorption systems of Proteus mirabilis as vaccine candidates. Thus, in this study we evaluated the presence and nucleotide sequence of iron receptor PMI0842 in Proteus mirabilis collected from UTIs cases in Tehran, Iran.

Methods: Totally, 120 Proteus mirabilis isolates were collected from UTI patients in Tehran, Iran. Bacterial identification was performed by biochemical tests. Polymerase Chain Reaction (PCR) was applied to amplify the PMI0842 gene in the isolates. Then, the amplified PCR products of 15 isolates were purified from the agarose gel and were subjected to sequencing by designed primers. After sequencing, the sequences of these genes were compared with the genes deposited in GenBank and Expasy.

Results: The PMI0842 gene was present in 80% of the Proteus mirabilis isolates tested. According to the results of Blast in NCBI, comparison of the nucleotide sequence of these sequenced genes with sequences deposited in Gen banks showed high similarity between these sequences.

Conclusion: Our findings confirmed for the first time the conservation of PMI0842 gene among the Proteus mirabilis isolated from UTI patients. Thus, PMI0842 gene could be an ideal vaccine candidate against UTIs caused by Proteus mirabilis. Evaluation of efficacy of this iron adsorption receptor in vivo and in vitro is under study.

Keywords: Urinary tract infection, Proteus mirabilis, Iron receptors, PMI0842

P463 - 650: ISOLATION AND CHARACTERIZATION OF OUTER MEMBRANE VESICLES (OMVS) FROM BORDETELLA PERTUSSIS TOHAMA STRAIN

Mohammad Sekhavati[1], Ashraf Mohabati Mobarez[2], Seyed davar Siadat[3], Mojtaba Nofeli[4], Seyed Reza Banihashemi[5], Keyvan Tadayon[6], Rainak Ghaderi[7], Seyed Hosain Razaz[8], Ava Behrouzi[9], Maryam Taghdiri[10]

1. Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
2. Department of Microbilogy, Tarbiat modares university, Faculty of Medical sciences
3. Department of Microbilogy,Pasteur Institute of Iran, Tehran, Iran
4. Human Bacterial Vaccine Department, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
5. Department of Immunology, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
6. Department of Veterinary Aerobic Bacteria Vaccines, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
7. Department of Veterinary Aerobic Bacteria Vaccines, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
8. Department of Veterinary Aerobic Bacteria Vaccines, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
9. Department of Microbilogy,Pasteur Institute of Iran, Tehran, Iran
10. Department of Immunology, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran

Background and Aim: Despite huge vaccination against pertussis, it is a global health problem because of low efficacy of aP (acellular vaccine) that substituted with reactogenic wP (whole cell vaccine). So a third generation of pertussis vaccine with good safety and potency is needed. Outer membrane vesicles (OMVs) of Bordetella pertussis contain several immunogens and they are good candidate for vaccine production. The main target of this study is to extract and characterization of OMVs from B. pertussis

Methods: Firstly the OMVs isolated by sequential ultracentrifugation. After negative phosphotungstate potassium staining the shape and size of extracted OMVs analysed by electron microscopy studies. Protein content measured by Bradford method and protein profiles studied by SDS-PAGE assay.

Results: The Size ranging of obtained OMVs was between 40 to 200nm. The protein content of the OMVs was 150 µg/ml and the protein profiles of extracted OMVs studied by SDS-PAGE indicated that there is several proteins in the OMVs.

Conclusion: Sveral resurgences of pertussis reported in several countries that shifted to aP from wP. Because of the side-effects associated with wP and low efficacy of aP, it is crucial to design a potent and safe vaccine against pertussis. OMVs of B.pertussis contains main immunogens and can induce Th1, Th2, Th17 as similar as wP. So the OMVs are good vaccine candidate for pertussis. The results showed that obtained OMVs were spherical nanoparticles and contain several proteins and can be used as acellular vaccine after further inestigation.

Keywords: Bordetella pertussis, Outer membrane vesicle, acellular vaccine, whole cell vaccine

P464 - 693: ISOLATION AND IDENTIFICATION OF BRUCELLA ABORTUS BIOVAR 3 IN A DAIRY CATTLE HERD VACCINATED WITH BRUCELLA ABORTUS RB51 VACCINE IN IRAN

Saeed Alamian [1], Maryam Dadar [2], Ali mohammad Behrozikhah [3], Gamal Wareth[4]

1. Razi Vaccine and Serum Research Institute (RVSRI); Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran.
2. Razi Vaccine and Serum Research Institute (RVSRI); Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran.
3. Razi Vaccine and Serum Research Institute (RVSRI); Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran.
4. Friedrich-Loeffler-Institut, Institute of Bacterial Infections and Zoonoses, 07743 Jena, Germany

Background and Aim: Bovine brucellosis is a widespread zoonosis with critical effects on animal and public health. The disease is prevalent nationwide and the rate of infection is dramatically increasing. Eradication of brucellosis in Iran is a big challenge. Surveillance and control programs facing challenge in Iran and complete eradication of the disease is seemed to be impossible.

Methods: The aim of the current study was to identify brucellosis among dairy Holstein cattle herd showed cases of abortion and seropositive reactions after vaccination with B. abortus RB51.

Results: Twenty cows have been aborted and 30 non-pregnant cows gave seropositive reactions. Sixteen B. abortus biovar 3 isolates were recovered from fetal organs and fetal placenta. Source of infection is not determined and most likely is the uncontrolled introduction of the agent via persons, infected animals, semen and vectors.

Conclusion: In endemic countries serodiagnosis of brucellosis alone is not sufficient and has to be accompanied with isolation and molecular diagnosis.

Keywords: Bovine brucellosis; B. abortus RB51; Abortion ; B. abortus biovar 3

Microbiomes

P465 - 30: STUDY OF CCR5-59353C/T POLYMORPHISM IN THE IRANIAN PATIENTS WITH CHRONIC HBV INFECTION

Farahnaz Bineshian[1], Zohreh Sharifi[2], Farahnaz Bineshian*[3], Sajjad Jalali [4]

1. -
2. Blood Transfusion Research Center, High Institute for Research and Education in Transfusion Medicine, Tehran,Iran
3. Department of Parasitology & Mycology, Faculty of Medicine, Semnan University of Medical Sciences, Semnan, Iran
4. Blood Transfusion Research Center, High Institute for Research and Education in Transfusion Medicine, Tehran,Iran

Background and Aim:CCR5 is identified as one of the most important chemokine receptors which have a major role in the creation of chemotaxis and mobilization of immunocompetent cells and moving them to the liver for thorough cleaning of the virus. CCR5-59353 (C/T) is an important promoter polymorphism of chemokine receptor 5 gene. In some studies showed that there is a relationship between CCR5-59353 (C/T) polymorphism with clearance or persistence of HBV infection. The aim of this study was to evaluate polymorphism CCR5-59353 (C / T in Iranian patients with chronic HBV infection.

Methods:A total of 200 blood samples including 100 healthy controls and 100 HBs Ag positive patients were randomly selected. Samples were tested for HBs Ag by ELISA and HBV-DNA by PCR method. Genomic DNA was extracted from blood buffy coat using the salting out method. CCR5-59353 (C/T) polymorphism was genotyped by allele specific amplification (ASA) PCR. Chi-square test was used for statistical analysis.

Results: Five percent of control samples and Twelve percent of patient samples had CC mutant genotype. Nevertheless, there was no significant difference in genotypes frequency of CCR5-59353 between the two groups (P=0.1).

Conclusion: It seems that CCR5-59353 polymorphism is not associated with chronic HBV infection outcome in Iranian population. However, frequency of CC genotype was higher in the patient group (12%) than control group (5%).

Keywords:polymorphism; CCR5-59353C/T; Chronic HBV; Infection

P466 - 94: THE MICROBIOTA OF FEMALE REPRODUCTIVE TRACT AND ITS RELATION TO FERTILITY AND ASSISTED REPRODUCTIVE TECHNOLOGY

Zahra Golestani[1], Esmaeil Ebrahimie[2]

1. B.Sc. in Cellular & Molecular Biology, Cellular & Molecular Biology Department, Higher Education Center of Estahban
2. Department of Crop Production & Plant Breeding, College of Agriculture, Shiraz University, Shiraz, Iran

Background and Aim: The vaginal microbiome is an important site of bacterial women that has continuum with microbial communities in cervical canal, uterus, fallopian tubes and peritoneal fluid. The human vaginal microbiota seem to play a key role in preventing a number of urogenital diseases, such as bacterial vaginosis, yeast infections, sexually transmitted infections, urinary tract infections , HIV infection and infectious infertility.

Methods: In the past researcher analysis vaginal microbiome in culture- base method but this method have many problem such as: we cannot see all bacterial in Culture medium and.... So nowadays researcher useed 16S rRNA gene amplicon sequencing(bioinformatic method). In this method we can have a metaanalysis on all data that gained from sequencing. We have different plateform and software do analysis microbiome data with them such as QIIME or Snowman and...

Results: Here ‘we characterized the vaginal microbiota with bioinformatic method and used QIIME and CLC software. In this study we identify some bacterial that plays key role in infertility and also and bacteria that if their concentration decreases ‘increase the risk of Preterm birth.

Conclusion: There is a need for further exploration of the vaginal microbiota, and how the microbiota members or profile interplays with fertility or assisted reproductive technologies.

Keywords:female, infertility, microbiota, vagina

P467 - 525: FREQUENCY AND RISK OF ATOPOBIUM VAGINAE IN PRETERM DELIVERY

Sedigheh Livani[1], Sepideh Bakhshandeh Nosrat[2], Asieh Sadat Bani-Aghil[3], Ezzat-allah Ghaemi[4]

1. Laboratory Sciences Research Center, Golestan University of Medical Sciences, Gorgan, Iran
2. Department of gynaecology and obstetrics, School of Medicine, Golestan University of Medical Sciences, Gorgan, Iran
3. Department of Midwifery, School of Nursing and Midwifery, Golestan University of Medical Sciences, Gorgan, Iran
4. - Department of Microbiology, School of Medicine, Golestan University of Medical Sciences, Gorgan, Iran

Background and Aim: Preterm is defined as babies born alive before 37 weeks of pregnancy are completed. It is still increasing in most countries. There is growing evidence that the vaginal microbiome influences risk for preterm birth. The aim of this study was to estimate the frequency and relationship between vaginal presence of Atopobium vaginae and the risk of preterm delivery.

Methods:A case-control study was designed. 100 pregnant women with term delivery (the control group) and 100 pregnant women with preterm delivery (as the case group) were attended in this study. Vaginal secretion was taken from vagina by dacron swab. DNA extraction and PCR with specific oligonucleotides were done. Statistical analysis X2 were performed

Results: The frequency of Atopobium in term and preterm delivery group was 7.5% and 7%, respectively. Pvalue was not significant (Pvalue=0.8).

Conclusion: The risk of preterm delivery is not associated with vaginal presence of Atopobium vaginae in women with preterm delivery.

Keywords: Atopobium, Preterm delivery, Pregnancy

P468 - 823: COMPARED PROTEIN PROFILES OF THE OUTER MEMBRANE VESICLES (OMV) AND OUTER MEMBRANE PROTEINS (OMP) STANDARD STRAINS OF AKKERMANSIA MUCINIPHILA

Arefeh Shahriary[1], seyed davar siadat[2], farzam vaziri [3]

1. olom tahghighat
2. pastur iInstitute
3. pastur iInstitute

Background and Aim: The gastrointestinal tract containing 10 to 100 trillion bacteria and other microorganisms. Gastrointestinal microbiota play an important role in human health, the permeability of the intestinal barrier, the distribution of fat mass, and energy homeostasis. Change in patterns of gut microbiota, increases permeability of the intestinal barrier, and increases the plasma LPS that leads to metabolic syndrome disease including obesity. A.muciniphila is a gram-negative anaerobic bacteria and gang of from 3-5% of intestinal microbial community. This bacteria is considered as a positive health index of individuals The aim of this study, was compared protein profiles of the outer membrane vesicles (omv) and outer membrane proteins (omp) standard strains of Akkermansia muciniphila

Methods: In this method first of all we cultured lyophilize of standard strains of Akkermansia muciniphila then after enrichment we can extract Omv and Omp ; To study physicochemical properties, scanning electron microscope ,nano drop , LAL, pyrogenic test were done . Finally we assayed proteins with SDS page method

Results:it is observed that the sampels non pyrogenic,the range size of omv in SEM is from 36 to 153 nm , the band range of omv is from 245 to 75 kd and omp is from 180 to 100 kd

Conclusion: Finally because of significance of A.muciniphila as a remarkeabl common member of the human gut microbiota and its beneficial influence in curing diseases, the diagnosis of protein profile A.muciniphila can be help full in Immunology and Molecular studies.

Keywords: Akkermansia muciniphila,omv ,omp

Molecular Diagnosis and Typing

P469 - 10: ECOR PHYLOTYPING AND DETERMINATION OF VIRULENCE GENES IN ESCHERICHIA COLI ISOLATES FROM PATHOLOGICAL CONDITIONS OF BROILER CHICKENS IN POULTRY SLAUGHTERHOUSES OF SOUTHEAST OF IRAN.

Akbar Asadi[1], navid asadi[2], yousef karami[3]

1. faculty of university of azad shahrbabak iran
2. veterinary student of bahonar university kerman iran
3. veterinary student of bahonar university kerman iran

Background and Aim:A number of virulence are considered important in the pathogenicity of these diseases. The APEC isolates are also assigned to different phylogenetic groups. The aims of the present study were phylogenetic typing and detection of virulence genes in Escherichia coli isolates from colibacillosis and cellulitis cases of broiler chicken in poultry slaughterhouses of Shahrbabak region, Kerman, Iran

Methods:A total number of eighty three E. coli isolates were taken from broiler chickens with colibacillosis and thirty four isolates were taken from carcasses with cellulitis in the industrial slaughter houses. E. coli isolates were confirmed biochemically

Results: The confirmed E. coli isolates were subjected to PCR assays to determine phylogenetic groups and the presence of pap C, sfa/focDE, iucD, afaIB-C, hlyA, fimH and crl virulence genes. Colibacillosis E. coli isolates belonged to A (54.21%), B1 (7.22 %), B2 (6.02 %) and D (32.53 %) phylogroups. Whereas, the E. coli isolates from cellulitis cases belonged to three main phylogroups A (55.88%), B1 (5.88%) and D (38.23%). Statistical analysis showed a specific association between the presence of crl virulence gene and phylogroups of A and D ($P < 0.05$) in colibacillosis isolates. According to the results

Conclusion:E. coli isolates from colibacillosis and cellulitis broilers could be assigned to various mainly A, phylogenetic groups

Keywords: Escherichia coli, Phylogenetic group, Celluitis, Collibacillosis, Virulence genes, Broiler chicken

P470 - 42: IL-28B POLYMORPHISM IN HCV PATIENTS OF TEHRAN FIROOZGAR HOSPITAL

Mohammad Hadi Karbalaie niya[1]

1. Research center of pediatric infectious diseases, Institute of immunology and infectious diseases, Iran University of medical sciences, Tehran, Iran

Background and Aim: Nowadays, the immune response to hepatitis C (HCV) treatment has become a crucial issue mostly due to the interleukin 28B (IL-28B) polymorphism effects in chronic HCV patients. The aim of this study was to detect the polymorphism of IL-28B gene (rs12979860) in HCV genotype 1 patients treated with pegylated Interferon and Ribavirin

Methods: Samples categorized based on the presence of sustained virologic response (SVR and no-SVR). Variables including age, gender, serum alanine aminotransferase (ALT) and aspartate aminotransferase (AST) levels of the two groups were investigated based on different IL-28B genotypes.

Results: Analysis by the variables of age and gender showed a mean age ± SD of 42.1±14.0 and gender variability of 44 females (38.2%) and 71 males (61.8%). Adding up these results, the analysis of ALT levels revealed that there was between 293 and 14 mg/ml; AST levels ranged between 217 and 17 mg/ml; the viral load (HCV RNA) ranged between 7,822,000 and 50 IU/ml; the prevalence of CC, CT and TT genotypes were 90.9%, 54% and 25.0%.

Conclusion:IL-28B polymorphism has an effective impact on the therapeutic response to ribavirin and peginterferon combination therapy in chronic HCV patients infected by different genotypes. This polymorphism is crucial in natural clearance

Keywords: Chronic HCV infection, Sustained virologic response, Interleukin 28B polymorphism

P471 - 44: RESISTANT ASSOCIATED VARIANTS (RAVS) INVESTIGATION IN THE NAÏVE HCV PATIENT CANDIDATE FOR DAA THERAPY

Mohammad Hadi Karbalaie niya[1]

1. Research center of pediatric infectious diseases, Institute of immunology and infectious diseases, Iran University of medical sciences, Tehran, Iran

Background and Aim: Viral hepatitis C is an important global health problem that affects about 2.2% of humans. Strategies on the control of this hepatotropic virus focused on chemotherapy and surveillance of emerging HCV drug resistant mutants, respectively. HCV genotype 1 response to therapy is one of major interests. The aim of this research was to study the prevalence of resistant associated variants (RAVs) in the naïve HCV patient candidate for direct acting antiviral (DAA) therapy.

Methods:A total of 70 HCV confirmed patients which referred to hospitals affiliated to Iran University of Medial Sciences, Tehran, Iran from May 2014 to March 2015 were enrolled in this cross sectional study. After RNA extraction, RFLP-RT-Nested-PCR was performed for HCV genotyping, then some genotypes 1 and 3 strains were used for further amplification of NS5B gene S282T mutation site and purified products were sequenced. Bioinformatics software was used for analysis of sequences

Results: From a total of 70 HCV patients, 54 were male (mean age (y)±SD 35.1±8.2) and 16 were female (mean age (y)±SD 43.4±10.1); 26 isolates from 1a, 1b and 3a showed that there were no S282T resistant mutants. Moreover, 2 (4.8%) had a synonymous point mutation (C to T). Statistical analysis didn't found any significant correlation between age, sex and genotype variables.

Conclusion: Finally, it can be concluded that there were no resistant mutants in our HCV genotypes 1 and 3 infected patients and broader scale of studies are required in this area using larger specimens, genotype groups and stages of treatment.

Keywords:resistant associated variants (RAVs), Hepatitis C virus (HCV), direct acting antiviral

P472 - 45: IDIOPATHIC PULMONARY FIBROSIS INVESTIGATION FOR VIRAL INFECTION

Mohammad Hadi Karbalaie niya[1]

1. Research center of pediatric infectious diseases, Institute of immunology and infectious diseases, Iran University of medical sciences, Tehran, Iran

Background and Aim: Idiopathic pulmonary fibrosis (IPF) is a progressive lung disease, which can be lethal with chronic complications. Viral infections may be associated with IPF and other fibrotic lung diseases. In the present study, we investigate for the first time in Iran the related viral etiology of IPF in order to detect three respiratory viruses; human adenovirus, enterovirus and bocavirus

Methods: In this cross-sectional study which was supported by Iran University of Medical Sciences, Tehran, Iran. The diagnostic criteria for IPF were based on internationally accepted clinical and imaging criteria in accordance with the 2011 IPF guidelines. 30 nasopharyngeal (NP) swabs or bronchoalveolar lavage (BAL) samples were obtained from the lung of IPF patients that were diagnosed by a sophisticated practitioner from April 2015 to February 2016. Real-time (RT) polymerase chain reaction (PCR) method was performed to detect the three viruses. Fluorescence dye of a labeled probe recorded the results in order to create positive and negative controls. SPSS version 20 software was used to calculate basic descriptive and frequency features.

Results: Of 30 specimens, 13 (43.4%) were male and 17 (56.6%) were female with the total mean age ± standard deviation 68.2 ± 12.0. RT-PCR assay results illustrated there was no infection of human adenovirus, enterovirus, and bocavirus detected in these samples. Significant results between IPF incidence and variables were not significant ($p > 0.05$).

Conclusion: The causes of IPF in Iranian patients need more research although, based on the results of this study, there was no association between human adenovirus, enterovirus, bocavirus, and IPF.

Keywords: Human bocavirus, Real-time PCR, Idiopathic pulmonary fibrosis, Human adenovirus, Human enterovirus

P473 - 64: DETECTION OF TICK-BORNE RELAPSING FEVER BORRELIAE IN TICK DNA SAMPLES BY USING PCR

Faezeh Houman sadr[1], Mohammad Soleimani[2]

1. Tasnim Biotechnology Research Center (TBRC), 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: Tick-Borne Relapsing Fever (TBRF) caused by Borreliae spp. has been reported in many parts of the world, including North and South America, Africa, Asia, and Europe.as In this study, a PCR assay based on glpQ gene was used to detect TBRF Borreliae DNA in ticks collected from endemic regions in Iran.

Methods: Sixty Ornithodoros. tholozani ticks were collected from endemic areas of Iran during 2017. Then the samples were subjected to DNA extraction. A pair primer targeting glpQ gene was used to amplify a 200 bp conserved fragment.

Results: Agarose gel electrophoresis analysis showed the amplification of a 200 bp fragment in 13 extracted DNA. The rest of the specimens were not positive in this experiment. Positive and negative control samples showed the expected results and thus the accuracy of the test.

Conclusion:A significant amount of O. tholozani ticks in endemic areas of Iran are contaminated with TBRF Borreliae. The glpQ-PCR is a precise and reliable tool for evaluating ticks contamination in molecular epidemiological studies.

Keywords: Borreliae- Tick- TBRF - LAMP - GlpQ

P474 - 68: COMPARISON OF GENOMIC POLYMORPHISM OF ENTEROCOCCUS FAECALIS ISOLATED FROM CLINICAL SAMPLES USING ERIC-PCR AND BOX-PCR METHODS

Fateme Ahmadi[1], Elham Siasi[2], Kumars Amini[3]

1. Department of Microbiology, Faculty of Basic Sciences, Islamic Azad University, Tehran North Branch, Tehran, Iran
2. Department of Microbiology, Faculty of Basic Sciences, Islamic Azad University, Tehran North Branch, Tehran, Iran
3. Department of Microbiology, Faculty of Basic Sciences, Saveh Branch, Islamic Azad University, Saveh, Iran.

Background and Aim: Enterococci are gram positive and catalase-negative cocci. The most common Enterococci involved in human infection is Enterococcus faecalis, which consists of 85-90% of cases. Several molecular methods are used for bacterial genotyping. Various methods have been used for the typing of these bacteria, including polymerase chain reaction based on Repetitive-Element PCR (rep-PCR) and BOX-PCR.

Methods: In the cross-sectional study, 60 clinical isolates of E. faecalis were obtained from patients with urinary tract infection referred to Shariati Hospital from a 6-month period. After confirming of E. faecalis strains using standard biochemical and microbiological methods, genomic DNA was extracted using a DNA extraction kit (Fermentas, UK). Then genomic polymorphism was performed using ERIC-PCR and BOX-PCR. Finally, using the NTsys software, the phylogeny tree was mapped.

Results:phylogenetic tree showed that all strains had 25 distinct clusters at a level of similarity of 58%. The highest number of strains was found in ERIC-PCR in the fifteenth group, the nineteen isolates and in the BOX-PCR group in the seventeenth and eighteenth groups, six isolates. The power of BOX-PCR and ERIC-PCR differentiation was 0.95% and 85%, respectively.

Conclusion: In the present study, E. faecalis strains have different BOX patterns that indicate the genetic diversity of E. faecalis strains, and probably these strains have a different origin that is spinning between animals and humans.

Keywords: Enterococcus faecalis, BOX-PCR, ERIC-PCR

P475 - 77: IDENTIFICATION OF MYCOPLASMA MURIS ISOLATED FROM VAGINAL SAMPLES OF NIH MICE

Mohammad Reza Zinatizadeh[1], Fatemeh Abedini[2], Mostafa Jafarpour[3], Zahra Masoumalinejad[4]

1. Department of Genetics, Faculty of Science, Tonekabon Branch, Islamic Azad University, Mazandaran, Iran
2. Department of Animal Breeding, Razi Vaccine and Serum Research Institute, Karaj, Iran
3. Department of Microbiology, Faculty of Science, Tonekabon Branch, Islamic Azad University, Mazandaran, Iran
4. Department of Microbiology, Sirjan Branch, Islamic Azad University, Sirjan, Iran

Background and Aim: Mycoplasma muris (M.M) is a small pathogenic bacterium that lives in the female mouse genital tract. Mycoplasma muris may have harmful effects on the reproductive health of female. This research was performed to optimize the detection of M. muris in NIH mice in the Department of Animal Breeding, Razi Vaccine and Research Institute, Iran.

Methods: In this cross-sectional study, 29 vaginal samples of NIH mice were selected through simple random sampling. For detection of the mycoplasma, the vaginal tissue removal of samples was done. First, samples were crushed using mortar and pestle with PBS 1ml, then were cultured in the PPLO broth and incubated at 37°C for 24h, they were passed through 0.45 µm pore-size filters and inoculated into specific PPLO broth and agar media for 3-4 weeks. In the next section, the PCR test was used with primers of 16S rRNA gene of M. muris.

Results: From 29 tested samples, 17.24% samples were positive for M. muris by PCR method, while 35.93% cultures showed positive. The phylogenetic analysis indicated a new strain of M. muris. The results of culture and PCR methods displayed the contamination in NIH mice.

Conclusion: Therefore, more researches are needed regarding the presence of mycoplasma for treatment and clinical signs.

Keywords: Mycoplasma, PCR, New strain, 16S rRNA sequences, NIH Mice

P476 - 110: PREVALENCE OF RESISTANCE TO FLUOROQUINOLONES ESCHERCHIA COLI QNR GENES ISOLATED FROM PATIENTS ADMITTED TO JAHROM´S HOSPITALS BY PHENOTYPIC AND MOLECULAR METHODS, 2016-2017

Abdolreza Sotoodeh[1], Manoochehr shabani[2], kavous solhjoo[3]

1. Zonooses Research Center, Jahrom University of Medical Sciences, Jahrom, Iran
2. Zonooses Research Center, Jahrom University of Medical Sciences, Jahrom, Iran
3. Zonooses Research Center, Jahrom University of Medical Sciences, Jahrom, Iran

Background and Aim: Quinolones are considered as antibiotics which play a key role in the treatment of ureteral, digestive, respiratory infections and septicemia and gonorrhoea as well. Excessive use of these antibiotics has raised resistance through these antibiotics; because of the presence of quinolones-resistance genes which are carried by plasmids. The present study was done to determine the frequency of quinolones-resistance in quinolones-producing Escherichia coli bacteria, using phenotypic and molecular methods.

Methods: The number of 446 Escherichia coli samples were gathered from patients referrer to Jahrom health centres from spring 2016 to autumn 2017 and were surveyed by MR, VP, SIM, TSI, Urease and citrate diagnostic methods. To specify the phenotypic antibiotic resistance pattern, disc diffusion method was used and positive samples, after DNA extraction, were assayed by the molecular method to identify the quinolones genes in positive samples

Results: Disk diffusion results showed that the maximum resistance frequency belonged to Cefotaxim 184(41%), respectively. In addition, the least resistance was seen in Meropenem 0%. PCR results of quinolones-resistance genes indicated, 12 (%2.7) samples for qnrA and 9(2%) samples for qnrB and 10(2.2%) samples were positive for qnr S genes. Among all samples, 8 samples had two genes simultaneously, there were 3 (0.7%) samples with qnrA & B, 3(0.7%) samples with qnrA&S and 2(0.4%) samples with qnrB&S simultaneously.

Conclusion: The results of the present study show the frequency of quinolones-resistance genes in Escherichia coli bacteria. According to raising of the prevalence of quinolones-resistance Escherichia coli bacteria, the sensitive antibiogram before any therapy is suggested.

Keywords: Quinolones-antibiotic resistance, Escherichia coli, qnrA ،qnrB, qnrS

P477 - 123: DETECTION OF STREPTOCOCCUS AGALACTIAE SURFACE PROTEIN ANTIGEN GENES ISOLATED FROM URINARY TRACT INFECTION IN TEACHING HOSPITALS OF ISFAHAN BY MULTIPLEX PCR.

Saba Jalalifar[1], Bahram Nasr Esfahani[2], Seyed Asghar Havaei[3]

1. Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, IR Iran.
2. Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, IR Iran.
3. Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, IR Iran.

Background and Aim: Streptococcus agalactiae is one of the uropathogens responsible for urinary tract infections (UTI) in children, pregnant women and elderly people with chronic underlying diseases. Surface protein antigens of Group B Streptococci (GBS) is important for understanding of the epidemiology of infection and designing vaccine components. The aim of this study was to evaluate the surface proteins of GBS isolates obtained from patients with UTIs referred to teaching hospitals of Isfahan, Iran.

Methods: In this cross-sectional study, a total of 100 GBS strains were isolated from urine specimens of patients with UTIs referred to teaching hospitals of Isfahan, Iran. Bacterial isolates were identified by conventional microbiological methods; including Gram staining, catalase, oxidase, CAMP, and confirmed by genotyping method (the presence of the dlts gene). All GBS isolates were screened for the presence of five surface protein of alpha family , namely, Alpha-C, Rib, Epsilon, Alp2/3, Alp4 by Multiplex PCR. Positive control was confirmed by direct sequencing of the PCR products of positive GBS isolate.

Results: One hundred isolates were identified as GBS. The distribution of surface protein antigen genes was as follows: rib (40%), alpha-c (22%), alp2/3 (18%) and epsilon (15%), although no alp4 gene was detected in the isolates. Five GBS isolates did not harbor any of the genes from the alpha family .

Conclusion: Although the distribution of surface protein of GBS strains will be useful in epidemiological studies and design of vaccines but further genetic research on a larger number of GBS isolates is necessary for epidemiological investigation and vaccine development.

Keywords: Surface protein, Multiplex PCR, Group B Streptococci, Urinary tract infection

P478 - 142: HIGH INCIDENCE OF TOXIN AND BIOFILM GENES AMONG METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS STRAINS

Mitra Motallebi[1], Mohammad Emaneini[2], Fereshteh Jabalameli[3]

1. Infectious Diseases Research Center, Kashan University of Medical Sciences, Kashan, Iran.
2. Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran
3. Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: Methicillin-resistant S. aureus (MRSA) is one of the predominant bacteria that causes wound infections in burn patients. MRSA produces several virulence factors such as adhesin and biofilm, hemolysins, enterotoxins, and exfoliative toxins. Staphylococcal cassette chromosome mec (SCCmec) typing method used to study MRSA molecular epidemiology. Therefore, the aim of this study was to determine frequencies of genes encoding virulence and SCCmec types in a MRSA collection that obtained from the burn patients.

Methods:S. aureus isolates were obtained from wound infection of burn patients. Isolates were identified to species level using standard biochemical methods. The mecA gene was targeted by PCR in order to identify isolate as MRSA. PCR assay was performed to determine of SCCmec types, biofilm and virulence genes.

Results: Of 165 S. aureus isolates, 69% isolates were MRSA. SCCmec typing of these isolates produced three different SCCmec types. 53% isolates were identified as type IIIA, 17% as type V and 2% as type I. The prevalence of genes encoding virulence factors in MRSA isolates were hla (61%), hlb (44%), sea (23%) and seb (2%). The sec, eta, tst, pvl, genes were not detected in any of the MRSA isolates in this study. The most prevalent genes encoding biofilm was eno, found in 61.1% of isolates, followed by fib and icaA found in 48.1% and 38.8% of the isolates, respectively.

Conclusion: The results of this study are indicating the high prevalence of MRSA and virulence factors among S. aureus isolated from burn wound infection.

Keywords:MRSA, SCCmec ,Biofilm, Toxin genes, Burn

P479 - 143: PREVALENCE OF THE 4 GENES ENCODING FIMBRIAE IN UROPATHOGENIC ESCHERICHIA COLI CLINICAL ISOLATES AND STATISTICAL ANALYSIS OF RELATIONSHIP BETWEEN THE ABUNDANCE OF THIS VIRULENCE FACTORS AND PHYLOGENETIC GROUPS

Mahsa Mirzarazi Dehaghi[1], Seyedeh Elham Rezatofighi[2]

1. 1- shahid Beheshti University of medical science, Tehran , Iran, school of Advanced technologies in medicine
2. Shahid Chamran University, Biology Department, science Faculty

Background and Aim: Escherichia coli is one of the microorganisms most frequently involved in urinary tract infections (UTIs); E. coli strains generally fall into one of four phylogenetic groups A, B1, B2, and D and that virulent extra strains belong mainly to group B2 and, to a lesser extent, to group D. Uropathogenic E.coli (UPEC) show different virulence factors too.

Methods:138 UPECs clinical isolates were investigated , In addition 30 E.coli as a control were collected from feces of healthy humans. On the one hand multiplex PCR assays were performed for investigating 4 genes encoding fimbriae and on the other hand PCR assays were performed for investigating Phylogenetic Groups distribution. finally statistical analysis was used to compare the occurrence of virulence markers in cases and controls. Results were considered as statistically significant at $P < 0.05$.

Results: From 138 (UPEC), 1(12%), 76(55%), 29 (21%) and 17 (12%) strains were related to B1, B2, D and A phylogenetic groups respectively and 86 (62.3%), 20 (14.4%), 1 (0.7%) and 17 (12.3%) isolates presented fimH, sfa/focDE, focG and sfaS genes respectively. Prevalence of the fimH gene in isolates were statistically more than those belonging to Flora groups ($P \leq 0.001$).

Conclusion: Although in some studies, more virulence were observed in the B2 phylogenetic group and indicating that most isolates of virulence factors belong to the group B2 But in the current study, fimH as a virulence factor was found to be statistically significant correlated to phylogenetic groups and these factors ($p < 0.05$)

Keywords: Escherichia coli, phylogenetic groups, virulence factors

P480 - 173: ISOLATION AND MOLECULAR IDENTIFICATION OF BIOFILM PRODUCING PSEUDOMONAS AERUGINOSA BACTERIA FROM LIQUID STORAGE OF CONTACT LENS AND COSMETIC IN JAHROM PROVINCE

Manoochehr Shabani[1], farzan modarresi[2], Fatemeh taghizadeh[3]

1. Zoonoses Research center, Jahrom University of Medical Sciences,jahrom, Iran
2. Research center for non.Communicable diseases , Jahrom University of Medical Sciences, Jahrom, Iran
3. Research center for social Determinants of Health, Jahrom University of Medical Sciences,jahrom, Iran

Background and Aim: Psuodomonas aeruginosa is known as the most prevalent agent of keratitis associated with contact lenses and the common organism cultured in eye trauma associated with non-contact lenses which leads to keratitis. The present study was done aiming isolation and molecular identification of Psuodomonas aeruginosa bacteria producing biofilm from preservation liquids of medical and cosmetic contact lenses in Jahrom city.

Methods: The numbers of 324 samples were collected from preservation liquid of medical and cosmetic contact lenses from medical centers and students dormitories of Jahrom city during March to October of 2017. Psuodomonasbacteria were isolated and identified using phenotypic and molecular methods. Phenotypically, Disk Diffusion technique was carried out to determine the antibiotic resistant pattern and after DNA extraction, PCR technique was used to survey the biofilm production genes (PSLA).

Results: Out of 324 samples, 28 samples were infected by Psudomonas. The maximum antibiotic resistant was observed in Nalidicsic Acid antibiotic (86%) and the maximum sensitivity was seen in Meropenem antibiotic (98%). Molecular results showed that 8 samples had PSLA genes.

Conclusion: Our results clearly revealed the presence of biofilm producing Psuodomonasbacteria in the preservation solutions of contact lenses. Hygiene observation regarding the use and preservation of these lenses could be helpful in prevention of infection.

Keywords: Psuodomonas, biofilm, cosmetic and medical contact lenses

P481 - 175: PREVALENCE OF PAPA, FIMH, MALX AND ISS GENES IN ESCHERICHIA COLI ISOLATES FROM PATIENTS WITH COMMUNITY-ACQUIRED UTIS

Zahra Naziri[1], Abdollah Derakhshandeh[2], Mohammad Motamedifar[3], Arash Soltani Borchaloee[4], Nafiseh Karimi[5], Azar Ghaedi[6], Jamil Ataei[7], Negar Azimzade[8]

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. Department of Bacteriology and Virology, Shiraz University of Medical Science, Shiraz, Iran
4. Department of Pathobiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
5. Department of Pathobiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
6. Department of Pathobiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
7. Department of Pathobiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
8. Department of Pathobiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran

Background and Aim: Uropathogenic Escherichia coli (UPEC) are responsible for ~80-90% of community-acquired urinary tract infections (UTIs). These strains possess a variety of virulence factors that allow their transition from the gastrointestinal tract to the urinary tract and enable them to adhere and colonize the uroepithelium and causing UTIs. Therefore, the aim of this study was to investigate the prevalence of some virulence factors of E. coli isolates from patients with community-acquired UTIs.

Methods:A total of 78 urinary E. coli were isolated from unrelated case of community-acquired UTIs patients referred to laboratory of Shahid Faghihi hospital in Shiraz, Iran. The isolates were confirmed as E. coli by the conventional biochemical tests. Bacterial DNA was extracted using the boiling method. Virulence factors were detected by amplifying the increased serum survival (iss), maltose phosphotransferase system (malX), Type 1 fimbiral adhesion (fimH) and pyelonephritis-associated pili (papA) genes by PCR.

Results: The prevalence of fimH, papA, malX and iss genes in 78 urinary E. coli isolates were 73.1%, 34.6%, 26.9% and 23.1%, respectively. The most prevalent gene was fimH and by lesser extent papA gene.

Conclusion:UPEC strains do not produce the same set of virulence factors. Fimbrial adhesions are the most frequent virulence genes in UPEC, which promote colonization, invasion, and replication of E. coli within uroepithelium. Identification of virulence genes, which role in adhesion of UPEC to uroepithelial cells can be useful for development of targeted therapy for prevention of UTIs.

Keywords: Uropathogenic E. coli, Community-Acquired UTIs, Virulence Factors, Adhesin, PCR

P482 - 178: MOLECULAR DIAGNOSIS OF HELICOBACTER PYLORI IN SEMEN OF INFERTILE MEN

Mostafa Khoshbin[1], Mohammad hassan shahhosseiny[2], Mansoureh Paknejadi[3]

1. Department of Microbiology – shahre-e-Qods Branch – Islamic Azad University –Tehran / Iran
2. 1.Department of Microbiology – shahre-e-Qods Branch – Islamic Azad University –Tehran / Iran 2.Iranian Gene Fanavar Institute (IGF), Tehran/Iran
3. Department of Microbiology – shahre-e-Qods Branch – Islamic Azad University –Tehran / Iran

Background and Aim: Bacterial infections of the genital system are common causes of infertility. One of the most important causes of male infertility is seminal and genital tract infections. In the meantime, a wide range of bacteria, in varying degrees, contribute to infertility in men. Helicobacter pylori may be involve in infertility. This bacterium is widespread and about half the world's population is infected with this bacterium, so timely diagnosis can be effective in treatment and prevention. Background and aim: Determination of the role of H. pylori in seminal semen of infertile men by PCR.

Methods:100 samples of semen collected from Saram hospital and DNA Extracted from these specimens using Boiling/DNG_PLUS method. Optimized PCR test was performed on samples. PCR test evaluated from the respect sensitivity and specificity.

Results: In this study, amplicon with the size of 294 bp, observed with agarose electrophoresis. In the specificity test, primers created only a band for Helicobacter pylori DNA. Of the 100 samples tested, only 10 samples (10%) were positive for amplification.

Conclusion: According to the results of this study, Helicobacter pylori may be one of the bacterial agents that can be considered for male infertility, of course requires further studies. While PCR is suitable, quick and sensitive molecular technique for detection of Helicobacter pylori in infertile men.

Keywords: Helicobacter pylori, PCR, , infertile men

P483 - 179: DETECTION OF SOME ADHESIVE GENES IN ESCHERICHIA COLI ISOLATES FROM PATIENTS WITH URINARY TRACT INFECTIONS IN MASHHAD BY MULTIPLEX PCR

Mahnaz Najafi[1], Mehrnaz Rad[2], gholamreza Hashemitabar[3]

1. Master of Science in Microbiology.
2. DVM, Ph.D. Associated professor, Department of pathobiology.School of Veternaty Medicin Ferdowsi University of Mashhad
3. DVM, Ph.D professor, Department of pathobiology.School of Veternaty Medicin Ferdowsi University of Mashhad

Background and Aim: Urinary tract infection is the most common hospital infection that caused by colonization of uropathogenic E. coli in host mucosal epithelium and (infected)host tissue. Three virulence genes of this organism (adhesines) pap, sfa, afa are responsible for pathogenicity and adherence to epithelial cell. This study aimed to determine the prevalence of virulence genes in E. coli strains isolated from urine samples in Mashhad. The results of this study can determine information about the study area.

Methods: In this study were collected 70 isolates of E. coli from outpatients with urinary tract infection and 45 hospitalized patients with Ute IN Ghaem hospital. Biochemical and standard microbiological techniques were used to identify the E.coli. . DNA extraction from samples was performed using the boiling method followed by gene Multiplex PCR method.

Results: The prevalence of adhesines genes in hospitalized patients sample sfa 24.6% afa 21.5% pap 21.5%and in Outpatients samples are sfa 52.8% afa15.7% pap67.1%.

Conclusion: The present study showed that the pap virulence genes are highly prevalent in outpatient's samples and sfa genes are highly prevalent in hospitalized patients samples. The prevalent of sfa and pap is equal .

Keywords: Uropathogenic, Escherichia coli, urinary tract infection, adhesine gene, polymerase chain reaction.

P484 - 190: DIAGNOSTIC OF VBNC BACTERIA IN SYNOVIAL FLUID OF RHEUMATOID ARTHRITIS PATIENTS

Seyyed reza Hashemi miyan abad[1], Ramezan ali Ataee[2], Gholam Hossein Alishiri[3], Mahdi ghorbanali zadegan[4]

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
3. Department of Rheumatology, Faculty of medicine, Baqiyatallah University of Medical Sciences, Tehran, Iran
4. Department of Microbiology, Faculty of medicine, Baqiyatallah University of Medical Sciences, Tehran, Iran

Background and Aim: In recent years, the Viable but Non- Culturable (VBNC) of bacteria has created a global problem. Because of they are able to retrieve their metabolic activities and duration of the infectious disease without detectable. The aim of this study was set up diagnostic procedure of VBNC bacteria.

Methods: In this study, a molecular based PCR method for recognition of VBNC was designed. Then, 50 synovial fluid samples which were stored in -80 ° C were evaluated. The bacteria genome extraction will be the first step, and identification of the presence of the bacterial genome by using the Universal primer (16srRNA) performed. Then, sequencing on amplicons was carried out and the results were analyzed. In the next step, the Nested PCR performed and to confirm the presence of the specific gene multiplication was determined. The sequencing of PCR products and BLAST alignment analysis were done.

Results: The results revealed that, Of the 50 synovial fluid samples which were negative in bacteriological culture, 19 samples were positive in PCR base on 16srRNA gene. And Nested PCR had clarified of the 10 for Staphylococcus aureus strains as VBNC.

Conclusion: However, all samples were negative for bacterial growth, the manifestation of Staphylococcus aureus was determined by nested PCR in the synovial fluid patients with rheumatoid arthritis. It may be illustrated the presence of the VBNC bacteria. .

Keywords:VBNC, Diagnostic, Molecular Method, Rheumatoid arthritis and synovial fluid

P485 - 194: ISOLATION OF PORCINE BOCAVIRUS FROM NASOPHARYNGEAL SWAB OF A CHILD WITH ACUTE RESPIRATORY TRACT INFECTION IN NORTHEASTERN IRAN

Saghar Safamanesh[1], Amir Azimian[2], Kiarash Ghazvini[3], Saeid Amel Jamehdar[4], Masoud Youssefi[5]

1. Department of Pathobiology and Laboratory Sciences, faculty of medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
2. Department of Pathobiology and Laboratory Sciences, faculty of medicine, North Khorasan University of Medical Sciences, Bojnurd, Iran.
3. Department of Microbiology and Virology, faculty of medicine, Mashhad University of Medical Sciences, Mashhad, Iran.
4. Antimicrobial Resistance Research Center, Mashhad University of Medical Science, Mashhad, Iran.
5. Department of Microbiology and Virology, faculty of medicine, Mashhad University of Medical Sciences, Mashhad, Iran.

Background and Aim: Porcine bocavirus (PBoV) is a newly identified parvovirus that is classified within the family Parvoviridae, subfamily Parvovirinae and genus Bocavirus. Based on our knowledge, as yet the importance of this virus has been discussed in veterinary science and there have been no reports of virus isolation from humans. Here we report the first identification of PBoV in a boy with respiratory tract infection symptoms in the northeastern IRAN.

Methods:DNA was extracted and analyzed for Bocavirus by PCR using the common pair primer targeting a region of NP1 gene. For determination of Bocavirus type we detected and sequenced 800 bp region of VP1, 2 genes.

Results: Porcine Boca virus was isolated from a nasopharyngeal swab of a 3-year-old boy admitted to Imam Reza Hospital, Bojnurd, Iran. In physical examination, he had a rhinorrhea, cough, low-grade fever and wheezing, typical manifestation of a viral acute respiratory tract infection.

Conclusion: Bocaviruses have been recognized in humans, canines, cattle, cats, gorillas and seal. Porcine bocavirus (PBoV). In our country because of the prohibition of pork consumption based on Islamic rules, human-pig contact is not likely through swine raising or pig breeding process. It should be noted that our patient had rural residence background. Due to this, it is probable that virus excretion in the feces or urine and other secretions of the wild hogs infected the child through a Fecal-oral pathway. To summarize, our observations provide evidence of transmission of the porcine virus to humans, though still more studies are needed to establish this finding.

Keywords: Porcine, Bocavirus, PCR

P486 - 205: PREVALENCE OF PAPC GENE IN UROPATHOGENIC E.COLI ISOLATES FROM URINARY TRACT INFECTIONS IN RASHT AND THEIR ANTIBIOTIC RESISTANCE PATTERN

Zahra Askari[1], Seyedeh Tooba Shafighi[2]

1. Student of MSc in Microbiology, Faculty of Basic science, Rasht branch, Islamic Azad University, Rasht, Iran
2. Assistant Professor, Faculty of Basic science, Rasht branch, Islamic Azad University, Rasht, Iran

Background and Aim: Escherichia coli (E. coli) is the most common cause of urinary tract infections (UTIs) in many developing countries. Fimbriae, including P-fimbriae, are one of the factors involved in the virulence of this bacterium that plays an important role in the pathogenesis of uropathogenic E.coli (UPEC). The aim of the present study was to investigate the frequency of papC virulence gene in E.coli isolated from urinary tract infections in Rasht.

Methods: In this study, a total of 76 clinical gram-negative isolates were collected from patients with UTI in some Rasht hospitals. The isolates were examined using different biochemical tests. Antibiotic resistance pattern of isolates was also evaluated by disc diffusion method. Genomic DNA of isolates was extracted using TIAGEN kit and presence of papC virulence gene was determined by specific primers using PCR method and sequenced for confirmation.

Results: Of the 76 isolates examined, 50 isolates were confirmed as E. coli. The results of the antibiogram test showed that most isolates were resistant to cefazolin (74%) and ceftazidime (64%) and were sensitive to gentamicin (68%) and chloramphenicol and kanamycin (52%). The results of investigating the frequency of papC gene in E. coli isolates showed that 45 isolates (90%) of the 50 isolates had the above gene.

Conclusion: These results confirm the essential role of papC gene in the pathogenesis of uropathogenic E. coli strains (UPEC).

Keywords: Escherichia coli, papC, urinary tract infection

P487 - 207: INVESTIGATION OF SFA/FOC GENE IN UROPATHOGENIC E.COLI ISOLATES FROM URINARY TRACT INFECTIONS IN RASHT

Zahra Askari[1], Seyedeh Tooba Shafighi[2]

1. Student of MSc in Microbiology, Faculty of Basic science, Rasht branch, Islamic Azad University, Rasht, Iran
2. Assistant Professor, Faculty of Basic science, Rasht branch, Islamic Azad University, Rasht, Iran

Background and Aim: Urinary Tract Infection(UTI) following respiratory system infection is the most common bacterial infections in human. Escherichia coli (E. coli) is the most isolated bacteria in UTIs. The sfa/foc gene codes S and 1C fimbria in this bacterium and is consisted as virulence factors in E.coli. The aim of this study was to determine the frequency of sfa/foc virulence gene in uropathogenic E. coli isolates in some hospitals in Rasht.

Methods: In the present study 76 persons with clinical symptoms and suspected to urinary tract infection were sampled. Urine of the patients were collected from October 2017 to January 2018 and were cultured. The isolated bacteria were identified using biochemical tests. Genomic DNA of E. coli isolates was extracted using TIANGEN kit and the presence of sfa/foc virulence gene was determined by specific primers using PCR method and sequenced to determine whether they are confirmed as E. coli isolates.

Results: Out of 76 samples examined, 50 isolates were confirmed as E. coli. The results of this study showed that 14 (28%) out of 50 E.coli isolates had sfa/foc gene.

Conclusion: The results of this study showed that the most isolated bacteria were E.coli and sfa/foc gene has a fundamental role in pathogenesis of uropathogenic E. coli (UPEC).

Keywords: Uropathogenic, Escherichia coli, sfa/foc, Rasht

P488 - 223: PREVALENCE OF EBP B AND EBP C GENES IN ENTEROCOCCUS FAECALIS PRODUCING BIOFILM ISOLATED FROM MEAT

Parisa Maleki[1], Elahe Tajbakhsh[2], Ebrahim Rahimi[3]

1. Department of Microbiology, Faculty of Basic Sciences, Shahrekord Branch, Islamic Azad University, Shahrekord, Iran
2. Department of Microbiology, Faculty of Basic Sciences, Shahrekord Branch, Islamic Azad University, Shahrekord, Iran
3. Department of Food Hygiene, Faculty of Veterinary Medicine, Shahrekord Branch, Islamic Azad University, Shahrekord, Iran

Background and Aim: Enterococcus faecalis is apathogenic bacteria, Some strains have the ability to produce biofilms. The aim of this study was to determine the frequency of ebp B and ebp C genes in Enterococcus faecalis isolates producing biofilm isolated from meat in Shahrekord.

Methods: In this study, 80 meat samples were examined by biochemical and molecular methods to presence of Enterococcus faecalis. Evaluation of biofilm formation was assessed using micro titer plate test. The polymerase chain reaction (PCR) with using specific primers were used to detection of ebp B and ebp C genes

Results: Among 80 meat samples, E. faecalis detected in 31 samples. Biofilm formation detected in 25 (80.64%) isolates. After PCR ebp B and ebp C genes detected in 10 isolates (32.25%) and 0 isolate (0%).

Conclusion: There is not relationship between ebp B and ebp C genes and biofilm formation in E. faecalis isolates.

Keywords: Biofilm, Enterococcus faecalis, Meat, ebp C gene, ebp C.

P489 - 241: PSEUDOMONAS AERUGINOSA VIRULENCE MARKERS

Shahrbanou Izadi Pour Jahromi[1], Jalal Mardaneh[2], Asghar Sharifi[3]

1. Cellular and Molecular Research Center, Yasuj University of Medical Sciences, Yasuj, Iran.
2. Department of Microbiology, School of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran.
3. Cellular and Molecular Research Center, Yasuj University of Medical Sciences, Yasuj, Iran.

Background and Aim: Pseudomonas aeruginosa is a gram negative, bacillary shape, non-spore forming, ubiquitous opportunistic bacterium present in many various environmental settings in different geographical regions, and it can be isolated from diverse living sources, such as humans, animals, and plants. The goals of the current multicenter research were to assess virulence factors genes among the P.aeruginosa clinical isolates.

Methods: Pseudomonas aeruginosa isolates were recovered from inpatients. Bacterial identification was done by standard diagnostic tests, and species was confirmed by detection of exoA gene by PCR technique. Virulence markers were detected by PCR.

Results: Among surveyed isolates, plcH+, lasB+ genotype (100% isolates) were the most common virulence genes patterns. Thirty-nine (48.75%) out of 80 P.aeruginosa isolates showed algD+, plcH+, lasB+, IMP+genotype. The blaIMP resistance gene was detected in all MHT positive and MDR isolates. Another interesting finding in our study was the more frequent occurrence of algD+, MDR, MHT+ and blaIMP+ strains among the Pseudomonas aeruginosa isolates from Yasuj compared with those from Shiraz.

Conclusion: Emergence of multi-drug resistant P. aeruginosa, especially to carbapenems and aminoglycosides, and the high prevalence of virulence traits in our study could be regarded as an alarming situation.

Keywords: Virulence Markers, Pseudomonas aeruginosa, Hospital.

P490 - 257: ENHANCMENT OF CD22 EXPRESSION PROFILE IN ESCHERICHIA COLI ROSSETA (DE3) BY EXPOSURE TO EXTREMELY LOW FREQUENCY MAGNETIC FIELDS

Behnaz Rashidieh[1]

1. Department of Microbiology, Faculty of Advanced Sciences & Technology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, Iran

Background and Aim: Over the last two decades, application of bacterial host cells, especially Escherichia coli (E. coli), for heterologous expression of proteins have gained much attention, mainly due to their ease of genetic manipulation, rapid growth and low cost media. Alongside, many studies have reported the significant biological effects of non-thermal extremely low frequency magnetic field (ELF-MF) produced by an alternating current (AC) on bacteria, proposing the possibility of improving expression profile of proteins by further applying magnetic fields in these host cells.

Methods: In present work, the expression profile of cluster of differentiation-22 (CD22) as a eukaryotic membrane protein in E. Coli Rosetta (DE3) was examined in the presence of ELF-MF. Different concentrations of isopropyl-b-D-thiogalactopyranoside (IPTG) (0.25, 0.5, 0.75 and 1 M) were applied as inducer and expression was carried out completely in the presence of ELF-MF. Depending on the extend of applied IPTG, an electromagnetic fields (EMFs) with an strength equal to 55 mT and the frequency range of 2.5-2.8 Hz

Results:a significant enhancement in protein expression levels. Nevertheless, EMFs with intensities rather than 55 mT resulted a significant decrease in protein expression levels when the IPTG concentrations were equal to 1 M or 1.25 M. In conclusion, current study, demonstrated that exposing E.coli to ELF-MF within a specific narrow frequency window can bring about significant enhancement in protein expression.

Conclusion:exposure to non-thermal ELF-MF within a specific narrow frequency window can significantly improve heterologous expression of CD22 as a Eukaryotic membrane protein in E. coli.

Keywords:CD22, ELF-MF, expression, Escherichia coli

P491 - 262: ANTIBIOTIC RESISTANCE GENES CODING OF EFFLUX PUMP (ADEA AND ADES GENES) IN ACINETOBACTER BAUMANNII ISOLATED FROM PATIENTS BY MOLECULAR METHODS

Mohammad Niakan[1], Batool Basatian[2], Zahra soltani Kermanshahi[3]

1. Shahed University.Medicine Faculty.Microbiology Department
2. MSc in Microbiology. Shahed University.Medicine Faculty.
3. MSc in Microbiology. Azad islamic University.Science Faculty.

Background and Aim: Background and objective: One of the important mechanisms of resistance in this bacterium is multidrug efflux pumps, playing an essential role in development of resistance in this bacteria. The aim of this study has been investigating the frequency of adeA and adeS genes of adeABC efflux pump in Acinetobacter baumannii clinical isolates.

Methods: Materials and methods: 60 Acinetobacter baumannii isolates were collected from different hospitals in Tehran, and detected using standard biochemical tests. Eventually, they were confirmed by detecting blaOXA-51-like gene using PCR method. The pattern of antibiotic sensitivity was determined by agar disk diffusion method according to CLSI instructions. adeA and adeS genes of adeABC efflux pump were detected in the isolates using PCR method.

Results: Results: the frequency of resistance to antibiotics in Acinetobacter baumannii isolates was as follows: piperacillin 100%, ceftazidime 98%, amikacin 96.66%, tetracycline 92%, ampicillin-sulbactam 65%, meropenem 63.33%, ciprofloxacin 60%, imipenem 50%, and gentamicin 48.33%. The frequency of presence of adeA and adeS genes in the Acinetobacter baumannii isolates was 80% and 81.66%, respectively.

Conclusion: Conclusion: the high frequency of adeABC efflux pump genes as well as multidrug resistance across all of the studied Acinetobacter baumannii isolates suggests the fact that adeABC efflux pump is one of the mechanisms for development of drug resistance among these isolates to antibiotics.

Keywords: Keywords: Acinetobacter baumannii, adeABC efflux pump, drug resistance.

P492 - 273: STUDY PHYLOGENETIC GROUPS OF PATHOGENIC E.COLI STRAINS ISOLATED FROM PATIENTS IN IMAM REZA HOSPITAL, KERMANSHAH

Arezoo Asadi[1]

1. 3Department of Microbiology, Faculty of Medicine, Iran University of Medical Sciences, Tehran, Iran

Background and Aim: Escherichia coli strains have been assigned to four main groups – A, B1, B2 and D. Group A and B1 are generally associated with commensals, Strains from phylogenetic group B2 and D are generally more virulent, but also less resistant and contain resistance encoding integrons to a lesser extent than strains from groups A and B1. The aim of this study is to determine the prevalence rate of each phylogenetic group of E. coli strains obtained from urinary tract infections.

Methods:96 clinical samples have collected from the patients referring to Imam Reza hospital in Kermanshah, Iran. The samples were cultured on MacConkey agar medium and subsequently various biochemical tests were performed to confirm the isolates. DNA extraction of E. coli isolates was done by boiling method. To classify the E. coli strains, specific primers for the chuA and yjaA genes and the TSPE4.C2 were applied for the PCR test.

Results: Of all samples collected from patients, a total of 98 isolates were identified as E. coli by conventional biochemical methods. The PCR method showed that the most common phylogroup was group B1 (33 isolate; 33.37%), followed by groups B2 (24 isolate, 25%), D (22 isolate,22.91%) and group A(17 isolate, 17.7%).

Conclusion:: Our study revealed the frequency distribution of phylogenetic groups in different strains of E.coli in our study has been as B1>B2>D>A. Further studies in addition to controlling the infections caused by E.coli contribute to the reduction of MDR strains.

Keywords:E.coli , PCR ,chuA, yjaA

P493 - 282: PLASMID-MEDIATED QUINOLONE RESISTANCE GENES IN ESBL PRODUCING KLEBSIELLA PNEUMONIAE ISOLATED FROM URINARY TRACT INFECTIONS IN TEHRAN HOSPITALS

Zahra Khodabandelo[1], prof. Fereshteh Shahcheraghi[2]

1. pasteur institute of Iran
2. pasteur institute of Iran

Background and Aim: Recent studies have shown that the increasing prevalence of plasmid-mediated quinolone resistance (PMQR) in Klebsiella pneumoniae isolates, worldwide. The aim of this study was to investigate the prevalence of PMQR and blaCTX-M genes determinants among the K. pneumoniae isolates in patients with urinary tract infection (UTI) and their clonal relatedness in Tehran, Iran.

Methods:A total of 70 K. pneumoniae isolates were recovered from urine samples. Antimicrobial susceptibility testing and minimum inhibitory concentrations (MICs) were determined. Also, ESBLs production was screened. The presence of qnrA, qnrB, qnrS and blaCTX-M genes were determined by PCR. Conjugation experiments and PCR-based replicon typing was used to identify plasmid replicons. Also, the clonal relatedness of isolates was evaluated by random amplified polymorphic DNA (RAPD) typing.

Results: The resistance rate to antibiotics especially fluoroquinolones among the isolates was high. 75.7% (53/70) of isolates were ESBLs positive. The rate of qnrB, qnrS and blaCTX-M genes were 62.9% (44/70), 64.3% (45/70) and 77.1% (54/70), respectively. All isolates were negative for qnrA gene. Analysis of the plasmid profiles showed that there was no relationship between the plasmids and antibiotic resistance. In conjugation experiments, 5 of 8 tested isolates had conjugative plasmids. IncL/M was the most common replicon type (94.1%). Also, RAPD-PCR results showed a high heterogeneity.

Conclusion: This study showed a high heterogeneity and frequency of PMQR genes among the isolates. The spread of plasmids carrying resistance genes would be resulted in fulminant antimicrobial resistance and treatment failure which are severe concerns recently.

Keywords: Klebsiella pneumoniae, PMQR, Plasmid replicon typing, RAPD-PCR

P494 - 319: MOLECULAR ANALYSIS OF PSEUDOMONAS AERUGINOSA ISOLATED FROM CLINICAL, ENVIRONMENTAL AND COCKROACH SOURCES BY ERIC-PCR

Hadi Hossainpour[1], Omid Zarei[2], Leili shokoohizadeh[3], Mohammad Yousef Alikhani[4]

1. Student Research Committee, Hamadan University of Medical Sciences, Hamadan, Iran
2. Student Research Committee, Hamadan University of Medical Sciences, Hamadan, Iran
3. Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran
4. Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran

Background and Aim: The objective of this study was to investigate the antibiotic susceptibility, virulence factors and clonal relationship among P. aeruginosa isolated from environmental sources, hospitalized patients and the surfaces of cockroaches in ICUs of four hospitals in Hamadan, west of Iran.

Methods:A total of 237, 286 and 156 bacterial isolates were collected from clinical, environmental and cockroaches, respectively from May to September, 2017. The antimicrobial susceptibility determined using the disk diffusion method. The virulence factors; exotoxins A, S and U were detected by PCR. The genetic linkage of P. aeruginosa isolates were analyzed by Enterobacterial Repetitive Intergenic Consensus (ERIC) - PCR

Results: According to our findings, 58 (24.4%), 46 (16%) and 5 (3.25) P. aeruginosa was isolated from clinical, environmental and cockroaches samples, respectively. The MDR phenotypes were detected in 18 (45%) and 15 (37.5%) of Clinical and environmental strains. The environmental isolates harbored more exotoxin A and exoenzyme S than clinical isolates. A genetic diversity was established among P. aeruginosa isolates, which 14 different ERIC fingerprints were detected. The clonal relationship was detected among clinical, environmental and isolates from cockroaches

Conclusion: Our results indicated to the importance identification and controlling the potential sources of P. aeruginosa infections in hospitals

Keywords: Pseudomonas aeruginosa; ERIC-PCR, Clinical, environmental, Cockroaches

P495 - 341: MOLECULAR DETECTION OF YELLOW FEVER AND RIFT VALLEY FEVER VIRUS USING MULTIPLEX PCR

Afshin Samimi nemati[1], Mehdi Zeinoddini[2], Mohamad Javad Dehghan Esmatabadi[3], Fateme Sheikhi[4]

1. Malek Ashtar University of Technology
2. Malek Ashtar University of Technology
3. Malek Ashtar University of Technology
4. Malek Ashtar University of Technology

Background and Aim: Yellow fever (YFV) and Rift valley fever virus (RFV) are RNA virus belonging to the family of flaviviridae and bunyaviridae, respectively. The gold standard for detection of these viruses is cell culture that is time-consuming, laborious, and costly and need expert support (biosafety level 3) for the diagnosis process. For this reason, molecular detection with synthetic construct is an alternative and smart choice for detection of these viruses.

Methods: In this study, we used a synthetic vector, containing M Segment for RFV and polyprotein gene for YFV. After designing specific primers, a multiplex PCR reaction was performed and the reaction products were analyzed by 2% agarose gel electrophoresis stained with ethidium bromide.

Results: The gel electrophoresis evaluation for the multiplex PCR reaction products analysis showed clear dual band in the regions of 130 bp and 197 bp confirming M Segment & polyprotein gene, respectively. The sensitivity of this method was about 100 ng of plasmid.

Conclusion: Multiplex PCR assay is very simple and sensitive for detection of infectious agents. In conclusion, this multiplex PCR method can be used as a simple diagnostic test for identification of RFV and YFV.

Keywords: Rift valley virus, Yellow fever virus, Detection, Multiplex PCR, Infection.

P496 - 342: SIMPLE DETECTION OF YERSINIA AND FRANCISELLA USING POLYMERASE CHAIN REACTION (PCR)

Nafiseh Pourmahdi[1], Mehdi Zeinoddini[2], Mohamad Javad Dehghan Esmatabadi[3], Fatemeh Sheikhi[4]

1. Malek Ashtar University of Technology
2. Malek Ashtar University of Technology
3. Malek Ashtar University of Technology
4. Malek Ashtar University of Technology

Background and Aim: Yersinia and Francisella are pathogens, known as a serious threat for public health. So, they are classifying as a biological agent category by Centers for Disease Control and Prevention (CDC). Laboratories (biosafety level 3) are required for working with these bacteria, but they are not easily available and also immunological and culture-based detection methods are complicated, so expanding molecular detection methods are valuable. Y. pestis causes plague and F. tularensis lead to tularemia. Due to lack of standard strain of these bacteria, designing a gene structure to use as positive control sample in detection tests is important.

Methods: In this research, we used a synthetic construct, containing a conserved gene of each bacterium. Target region for Francisella is fopA and for Yesinia is caf1(F1 capsule antigen). After that, the construct inserted in PUC57 and transformed into E.coli DH5α. After an overnight culture, plasmids extracted and used for Monopelex PCR. Results was analyzed in 2% agarose gel.

Results: We expect to see a 148bp band for Francisella and a 176 bp band for Yersinia. The results showed that amplification from each region was successful and expected bands were observed in electrophoresis.

Conclusion: Due to lack of standard microbial strain for some bacteria, we can clone conserved regions of their genome into other bacteria and use them as positive control samples for other detection tests.

Keywords: Francisella, Yesinia, PCR, Detection, Positive Control Sample

P497 - 344: DETECTION OF TETRACYCLINE AND FLUOROQUINOLONES RESISTANCE AMONG CAMPYLOBACTERS ISOLATED FROM DIARRHEA PATIENTS IN MARKAZI PROVINCE - 2015

Elnaz Abbasi[1], Ehsanollah Ghaznavihaznavi-Rad [2]

1. Department of Microbiology & Immunology, Faculty of Medicine, Arak University of Medical Sciences,Arak, Iran
2. Molecular and Medicine Research Center, 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.In recent years, tetracycline and fluoroquinolones resistance have emerged among many pathogenic and nonpathogenic species of bacteria .In Iran, limited studies have been determined antibiotic resistance of these bacteria,therefore, this study aimed to determine the frequency of tetracycline and fluoroquinolones resistance and to investigate genotypic determinant of tet(O) and gyrA 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 tetracycline and fluoroquinolones were assessed using disk diffusion method. In addition,tet(O) and gyrA genes contributing to tetracycline and fluoroquinolones resistance in campylobacter were also investigated

Results: Out of 108 dysenteric stool specimens, 28 (26%) campylobacter were isolated of which 26 (24%) were C. jejuni and 2 (1.8%) were C. coli. Phenotypic tetracycline and fluoroquinolones resistance prevalence in C. jejuni was obtained as 19 (73%),16 (61.5%) and in C. coli as 2 (7.1%) of all 2 types of resistance respectively.Frequency of,tet(O) tetracycline and gyrA fluoroquinolones resistance gene was found as 17 (65.3%),14 (53.8%) and 1(50%),1(50%) in C. jejuni and C. coli, respectively

Conclusion: This study showed tetracycline and fluoroquinolones resistance in campylobacter isolates. This is very useful data for empirical therapy and demanding comprehensive study with more samples size to be accomplished.

Keywords: Campylobacter, tetracycline, fluoroquinolones, Drug Resistance, Bacterial, Iran

P498 - 355: COMPARISON OF PCR AND CULTURE METHODS TO DETECT LISTERIA MONOCYTOGENES IN VAGINAL SPECIMENS

Zahra Sadeghi[1], Soude Hatefi1[2], Mohammad Ahanjan[3]

1. . Department of Medical Microbiology and Virology, Faculty of Medicine, Mazandaran Univercity of Medical Siences, Sari, Iran,
2. .Dpattment of Micribiology, Faculty of Biological Science, Islamic Azad Univercity, Damghan Branch, Damghan, Iran,
3. . Member of Pediatric Infectious Diseas Research Center, Mazandaran Univercity of Medical Siences, Sari, Iran

Background and Aim: Listeria monocytogenes is a facultative-anaerobic Gram-positive bacilli and causes infections such as meningoencephalitis, septicemia and abortion in humans, especially pregnant women. One of the basic problems with this organism is its determine the prevalence and comparison of culture and PCR methods in diagnosis of this organism in vaginal samples.

Methods: In this study, 126 vaginal samples were collected from patients hospitalized in hospitals of Sari (North of Iran) based on demographic characteristics including age, education, occupation, history of abortion, stillbirth and preterm labor, type of delivery and contraceptive method. Samples were cultured in Blood agar medium. The bacterial genome was also extracted from vaginal specimens and used in the PCR method using ActA gene amplification.

Results: Listeria monocytogenes were detected in 42 (33.3%) samples by PCR method and from 4 (3.1%) samples using culture method. The prevalence of this bacterium in this study was 39%.

Conclusion: The results indicate that PCR is a faster, more sensitive and accurate method for diagnosis of listeria monocytogenes in vaginal samples compared with the culture method. Also, using a standard and reliable method, such as PCR, is essential for rapid detection of this bacterium.

Keywords: Listeria monocytogenes, culture, PCR, laboratory diagnosis.

P499 - 378: A RELIABLE COMBINATION METHOD TO IDENTIFICATION AND TYPING OF EPIDEMIC AND ENDEMIC CLONES AMONG CLINICAL ISOLATES OF ACINETOBACTER BAUMANNII

Arezoo Piran[1], Farzad Badmasti[2], Fereshteh Shahcheraghi[3]

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 Bacteriology, Microbiology Research Center, Pasteur Institute of Iran, Tehran, Iran

Background and Aim: The Gram-negative coccobacillus Acinetobacter baumannii as an important nosocomial pathogen has emerged a global health concern in recent years. Resistance to a broad range of antimicrobial agents (MDR), the tendency for epidemic spread and long-term persistence in the hospital setting make A. baumannii as a common yet difficult-to-treat pathogen. Three epidemic lineages are responsible for the majority of A.baumannii infections in clinical settings worldwide. Few reports have been published the epidemiology of nosocomial A.baumannii infection in Iran. The aim of this project is to investigate the molecular epidemiology of the A. baumannii isolates

Methods: In this study, we applied three easier, faster, and cost-effective methods including PCR-based open reading frames (ORFs) typing, sequence typing of blaOXA-51-like and MLST method to rapid typing of A. baumannii strains

Results: Taken together in the present study the results of ORFs typing, PCRsequencing of blaOXA-51-like genes and MLST sequence typing revealed there was a high prevalence (62%, 35/57) of ST2 as international and successful clone which detected among clinical isolates of multi-drug resistant A.baumannii with ORF pattern B and blaOXA-66 gene. Only 7% (4/57) of MDR isolates belonged to ST1 with ORF pattern A and blaOXA-69 gene. Interestingly, we detected singleton ST513 (32%, 18/57) that encoded blaOXA-90 and showed the ORF pattern H as previously isolated in Middle East.

Conclusion: The using both of the PCR-based typing of seven ORFs and determination of allele number of blaOXA-51-like, could be effectively applied to rapid typing of A.baumannii strains without performing of MLST or PFGE.

Keywords: Multi-drug resistant A. baumannii blaOXA-51-like allele Open reading frame

P500 - 387: ISOLATION AND SUDY OF DRUG-RESISTANT GENE (EFFLUX PUMP) IN PSEUDOMONAS AERUGINOSA ISOLATED FROM CLINICAL SAMPLES AND MILK FOOD BY MPCR AND DETERMINE ANTIBIOTIC SUSCEPTIBILITY PATTERN

Narges Olya[1], mohamadreza barzegar[2], kumarss amini[3]

1. Department of Microbiology, Faculty of Basic Sciences, farahan Branch, Islamic Azad University, , I.R.Iran
2. Department of Microbiology, Faculty of Basic Sciences, qom Branch, Islamic Azad University, qom, I.R.Iran
3. Department of Microbiology, Faculty of Basic Sciences, Saveh Branch, Islamic Azad University, Saveh, I.R.Iran

Background and Aim: Pseudomonas aeruginosa is an important cause of nosocomial infections in burn patients, one of the most important types of bacteria resistant to antibiotics and therefore aeruginosa infection is difficult to treat. Efflux pumps mex key role in the development of multiple resistance to other antimicrobial drugs. OprM-MexAB pump capable of a range of antimicrobial compounds without any similarity between the structure and function will leak out of the cell. This study aimed to investigate prevalence of isolated genes of efflux pumps mex and the Determination of antibiotic resistance on ceftriaxone,clavonic acid,gentamicin and amikacin was performed.

Methods: Initially 30 samples of P. aeruginosa isolated from clinical specimen's burn wounds Tehran hospitals and 30 food samples of milk, after approval by the diagnostic tests Vaftraqy, were studied. Finally, for every 60 samples, isolated, Multiplex PCR was performed to detect target genes to be considered as the gold standard in the sense that its results are more reliable

Results: According to the results obtained using the PCR gene efflux pumps has been mex 100% and The highest resistance to antibiotic ceftriaxone was observed in comparison with amicassin.

Conclusion: Mentioned results correspond with the results of other studies and Due to the presence of 100% of the genes of the pump of Influx in both clinical specimens and infected milk of Pseudomonas aeruginosa and due to the chromosomal nature of these genes, they can be used as markers for the identification of Pseudomonas aeruginosa by molecular methods.

Keywords: Psudomonas aeroginosa, Multiplex PCR, Drug resistans

P501 - 390: DETECTION OF MIXED STRAIN INFECTIONS OF MYCOBACTERIUM TUBERCULOSIS IN RESOURCE-LIMITED SETTINGS

Mansour Kargarpour Kamakoli[1], Sharareh Khanipour[2], Morteza Masoumi [3], Hasan Ghajavand[4], Ghazaleh Farmanfarmaei [5], Abolfazl Fateh [6], Seyed Davar Siadat [7], Farzam Vaziri [8]

1. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran 2-Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
2. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran 2-Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
3. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran 2-Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
4. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran. 2-Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
5. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran. 2-Microbiology Research Center (MRC), 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. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran. 2-Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
8. 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: One of the main topics about tuberculosis (TB) is mixed (polyclonal) infections. MIRU-VNTR is the best and most widely accepted method for detecting polyclonal infections in TB. Many studies have shown that polyclonal infections in TB is well detected in the sputum samples by the MIRU-VNTR method. Despite the limitations of using sputum samples in many laboratories, setting up MIRU-VNTR directly on smear slide can be useful. The aim of the present study was to investigate the ability to diagnose mixed infections on the smear slide by MIRU-VNTR.

Methods: Of 14 clinical specimens, Ziehl–Neelsen-stained microscopic slides were prepared. The PCR on smear slide, their clinical specimens and their respective cultures was performed to amplify a standard set of 24 MIRU-VNTR loci.

Results: According to 24 loci MIRU-VNTR analysis, the rate of polyclonal infections in the smear slides was 42.85%. On the other hand, the rate of the polyclonal infections in their respective clinical specimens was 8/14 (57.1%). Intriguingly, in their corresponding cultures 7.14% (1/14) mixed infection was observed.

Conclusion: Smear slides are a safe system for transmitting clinical specimens between the reference and environmental labs. In countries with high rate of mixed infections and limited resources, the diagnosis of mixed infections can be so crucial because of its significant effect on TB treatment. We have clearly shown that performing MIRU-VNTR directly on smear slides can detect mixed infections conveniently.

Keywords: Tuberculosis; MIRU-VNTR; Smear slide; Polyclonal infections; Resource-limited setting

P502 - 400: ASSOCIATION OF INDUCIBLE NITRIC OXIDE SYNTHASE (INOS) GENE POLYMORPHISMS WITH SUSCEPTIBILITY TO VISCERAL LEISHMANIASIS IN THE IRANIAN POPULATION

Akram Pourkazem[1], Naghili behrooz[2], Haiaty Sanya[3], Bazmani Ahad[4], Panah Fathemeh[5], mohammad saleh al e molana[6], Hajilooi Mehrdad[7], Farzin azar Abbas[8], Mohamadi vahed Fereshteh[9]

1. Higher education Institute of Rab-Rashid, Tabriz, Iran
2. Infectious and Tropical Diseases Research Center, Tabriz University of medical Sciences, Tabriz, Iran
3. Student Research Committee, Tabriz University of medical Sciences, Tabriz, Iran
4. Infectious and Tropical Diseases Research Center, Tabriz University of medical Sciences, Tabriz, Iran
5. Student Research Committee, Tabriz University of medical Sciences, Tabriz, Iran
6. Infectious and Tropical Diseases Research Center, Tabriz University of medical Sciences, Tabriz, Iran
7. Department of Immunology, Hamadan University of Medical Sciences, Hamadan, Iran
8. Infectious and Tropical Diseases Research Center, Tabriz University of medical Sciences, Tabriz, Iran
9. Department of medicine, Tabriz branch, Islamic Azad University, Tabriz, Iran

Background and Aim: Leishmaniasis affects about 12 millions of people worldwide and is the main public health problem in some areas of Iran, including East Azarbaijan province. Cell mediated immunity is critical for protection against leishmaniasis. Indeed, studies show that the induction and maintenance of Th1 immune response is necessary for effective clearance of Leishmania parasites. Th1 cells induce iNOS that is responsible for killing Leishmania parasites. According to the important role of cellular immunity against VL, this study was directed to determine the frequency of -954G/C genotypes in iNOS gene.
Methods:284 individuals participated to evaluate the frequency of -954G/C genotypes in this study. The study included 93 individuals as VL diagnosed patients, 86 individuals as seropositive healthy controls, and 105 individuals as seronegative healthy controls. iNOS genotyping was carried out using an Amplification Refractory Mutation System-PCR (ARMS-PCR) and gel electrophoresis.
Results: Molecular analysis revealed an increased frequency of mutant homozygote genotype (C/C) in the case group (4, 4.3%) compared to the seronegative control group (1, 1.0%). Also the frequency of the wild homozygote genotype (G/G) in the seronegative control group (88, 83.8%) was higher than that in the case group (56, 60.2%). A significantly increased risk of leishmaniasis was found in the iNOS genotype [odd ratio (OR) 1.24, 95% confidence interval (CI) 2.0-7.2, p value < 0.001]. Distribution of genotypes were in consistent with Hardy-Weinberg equilibrium.
Conclusion: These results suggest that iNOS gene polymorphism can be considered as a genetic susceptibility factor for increased risk of Leishmaniasis.

Keywords: Visceral Leishmaniasis, -954G/C iNOS, genetic polymorphism

P503 - 401: EVALUATING THE RELATIONSHIP BETWEEN SERUM IMMUNOGLOBULIN G (IGG) AND A (IGA) ANTI-CAGA ANTIBODY AND THE CAGA GENE IN PATIENTS WITH DYSPEPSIA

Ali Baradaran[1], Hashem Fakhre-Yaseri[2], Ali Baradaran-Moghaddam[3]

1. Gastroenterology, Research Center for Gastroenterology and Liver Diseases, Firoozgar Hospital, Iran University of Medical Sciences, Tehran, Iran
2. Department of Microbiology, School of Medicine, Iran University of Medical Sciences, Tehran, Iran

Background and Aim: The cytotoxin-associated gene (cag) pathogenicity island is reported to be a major virulence factor of Helicobacter pylori infection. It is previously reported that the cagA-positive strains are more virulent, so it can be postulated that the cagA-positive gastritis will be more severe and the serum immunoglobulin G (IgG) and A (IgA) anti- CagA antibody titer will be higher. The aim of this study was to compare the relationship between IgG and IgA anti-CagA antibody and the cagA gene expression in patients with dyspepsia

Methods: Serum samples obtained from 130 dyspeptic patients with positive H. pylori in histological and Geimsa staining were tested for serum IgG and IgA anti-CagA antibody using the enzyme-linked immunosorbent Assay. The expression of the cagA gene was determined using PCR on the biopsy samples, taken via endoscopy.

Results: The sensitivity of IgG anti-CagA antibody in identifying patients with a proven infection with the cagA-positive strains was 97.67%, and the negative likelihood ratios was 0.06. There was not significant correlation between serum IgA anti-CagA and the expression of the cagA gene among the dyspeptic patients

Conclusion: The IgG antibody titer was significantly higher in patients with the cagA-positive H. pylori strain. However, in daily practice, the level of the IgG antibody titer cannot predict whether or not an individual carries a cagA-positive H. pylori strain, because there is a major overlap in the IgG antibody titer between the cagA-positive and cagA-negative patients

Keywords:cagA, IgG anti-CagA,Dyspepsia

P504 - 402: DILEMMA OF DIRECT MIRU-VNTR GENOTYPING OF CLINICAL SAMPLES OF TUBERCULOSIS

Ghazaleh Farmanfarmaei[1], Mansour Kargarpour Kamakoli [2], Shima Hadifar [3], Sharareh Khanipour[4], Abolfazl Fateh [5], Seyed Davar Siadat [6], Farzam Vaziri [7]

1. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran. 2-Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
2. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran 2-Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
3. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran 2-Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
4. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran. 2-Microbiology Research Center (MRC), Pasteur Institute of Iran, Tehran, Iran
5. 1-Department of Mycobacteriology and Pulmonary Research, Pasteur Institute of Iran, Tehran, Iran. 2-Microbiology Research Center (MRC), 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. 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: Twenty-four loci mycobacterial interspersed repetitive unit-variable number tandem repeat analysis (MIRU-VNTR) is extensively used for genotyping and detection of polyclonal infections in tuberculosis (TB). The aim of the present study was to compare the accuracy of direct and indirect MIRU-VNTR genotyping and detection of polyclonal infections between old and fresh clinical samples.

Methods: Two series of TB samples were collected for retrospective and prospective comparison. After genomic DNA extraction from clinical samples and their respective cultures, 24 loci MIRU-VNTR was performed.

Results: In the 14 old samples, no mixed infections were observed, in clinical samples and their respective cultures. In nine fresh samples, 44.4% of mixed infection was observed in the clinical samples, but no mixed infections were observed in their respective cultures. Surprisingly, in the old samples, 92.86% of samples (13/14) had an allelic change between clinical samples and their respective cultures. On the other hand, in fresh samples, only one sample (1/9) had an allelic change between clinical samples and their respective cultures.

Conclusion: We concluded that 24 loci MIRU-VNTR undoubtedly has a high reliability in direct genotyping of clinical samples, especially in the prospective studies. However, selecting starting material, such as clinical specimen or respective culture can be controversial in the retrospective studies. Regarding polyclonal infections the prospective studies gives us a better view to detect these infections, especially in clinical specimen.

Keywords: Tuberculosis; MIRU-VNTR; retrospective studies; prospective studies

P505 - 410: MOLECULAR IDENTIFICATION OF WHIB7 EXPRESSION IN DRUG RESISTANT MYCOBACTERIUM TUBERCULOSIS

Fahimeh Morteza[1], Dr.Saeed Zaker Bostan Abad[2], Dr.Sarvenaz Falsafi[3]

1. Islamic Azad University , Science and Research Branch
2. Islamic Azad University, Parand Branch
3. Islamic Azad University , Medical Sciences Branch

Background and Aim: One third of the world's population are infected by Mycobacterium tuberculosis.This bacteria has a family of genes called WhiBs ,Their function is to induce the infectionand establishment of bacteria whitin the cells.In this study ,the expression of WhiB7 were discussed which leads to antibiotic resistance and produces MDR species.

Methods: For this study 25 MDR and 25 sensetive species of Mycobacterium tuberculosis were collected then cultured on Lowenstein Jensen Medium(L.J) ,contains Rifampin , Izoniaizd , Ethambutol.Afterwards,by Real Time PCR the expression of WhiB7 were compared among resistant and sensitive species ,and then compared with the standard species called H37Rv.

Results: Results of antibiogram showed all MDR species are resistant ,at least, to two out of three drugs that were used in L.J Medium .Although the results of Real Time PCR indicated that WhiB7 expressed more in resistant species than sensitive ones,the results of statistical analysis ,done by Rest and MWGA6 indicated that WhiB7 has shown no difference in expression among resistant and sensitive species,while both were down regulated in comparison to H37Rv.

Conclusion: According to genesis of new resistant species of Mycobacterium tuberculosis ,we can feel the need of new identification methods to prevent the emergence of new resistant strains.The main purpose of this study was to research the effect of WhiB7 expression in drug resistance .

Keywords: Real Time PCR, Mycobacterium Tuberculosis ,WhiB7 Gene,MDR TB(Multi Drug Resitant TB)

P506 - 428: DETERMIND VIRULENCE FACTORAND ANTIBIOTICS RESISTANCE AMONG CLINICAL ISOLATES OF UROPATHOGENIC E.COLI IN NORTHEAST OF IRAN

Mahdis Ghavidel[1], tahereh golamhosseini moghaddam[2], kimia nourian[3], kiarash ghazvini[4]

1. 1. Microbiology and Virology Research Centre, Mashhad University of Medical Sciences, Mashhad, Iran. Department of Microbiology and virology, Mashhad University of Medical Sciences, Mashhad, Iran
2. school of veterinary medicine, shiraz , Iran.
3. DVM, graduate student of school of veterinary medicine, Ferdowsi university of Mashhad, Mashhad, Iran.
4. 1. Microbiology and Virology Research Centre, Mashhad University of Medical Sciences, Mashhad, Iran. 2. Department of Microbiology and virology, 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 and determine antibiotics resistance among clinical isolates in northeast of Iran.

Methods:three hundred Escherichia coli isolates obtained from patients with urinary tract infection (UTI) referred to the Ghaem and Emam Reza Hospital different section, 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), type1fimbriae (fimH gene), aerobactin (aer gene). The antibiotic susceptibility tests were done by the disk diffusion method. Different antibiotics were used such as B lactam, Aminoglycosides, Cephlosporine, Quinolone, Flurquinolone, Carbapenem and Trimethoprim-sulfamethoxazole.

Results: The PCR results identified the fimH gene in (78.4%), aer in (70.5%), sfa gene in (13.6%) and the pap gene in (8.2%) of the isolates. The rate of antibiotic resistance of the strains is as follows: 64.7% resistant to cephalosporins, 34% to trimethoprim-sulfamethoxazole, 30.9% to fluoroquinolones, 15.2% to aminoglycosides, 13.2% to beta lactams 7.8% to quinolones and 4.4%. to carpabenems.

Conclusion:in these study fimH and aer were found more than 50% UPEC strain isolated from patients that two gene have important role in pathogenesis. Major isolates have fimH as adhesion factor for colonization. More isolates resistance to cephalosporins cause of inappropriate administration

Keywords:UTI, E.coli, virulence factors, Multiplex PCR, Antibiotics resistance

P507 - 435: TNFA GENE POLYMORPHISMS IN PEDIATRICS WITH AUTOIMMUNE HEPATITIS IN CHILDREN'S MEDICAL CENTER

Sarvenaz Falsafi[1], Mohammad Karim Rahimi[2], Shadi Halimi[3], Nima Rezaei[4]

1. Department of microbiology Islamic Azad University-Tehran Medical Branch-Tehran-Iran
2. Department of microbiology Islamic Azad university-Tehran Medical Branch-Tehran-Iran
3. Islamic Azad university-Tehran Medical Branch-Tehran-Iran
4. Children's Medical Center, Tehran University of Medical Sciences, Iran

Background and Aim: Autoimmune hepatitis(AIH) is an inflammatory disease with unknown etiologies, whereas genetic and environmental factors seem to play roles in presence of disease. Tumor necrosis factor(TNF)-α seems to have an essential role in activating autoreactive effector cells and advancing the immune reaction, while their production could be affected by single nucleotide polymorphisms of the genes encoding these cytokines.

Methods: This observational investigation that was performed as a case-control survey, performed on 57 pediatric patients with ALH. TNFA typing was performed by polymerase chain reaction with sequence-specific primers (PCR-SSP) assay.

Results: In this study it was seen that TNFA AA and GG genotypes at position 238 were significantly overrepresented in the patient group compared to the controls (17.5% in AIH patients vs. 0.7% in controls, and 79% in AIH patients vs.57.7% in controls, respectively). Significant higher frequency of TNFA GA genotype at position 308 was also detected in AIH patient group(47.4% in patients vs 28.5% in controls).

Conclusion: Totally according to the obtained result in this study, it may be concluded that TNFA single nucleotide polymorphisms are shown to have significant differences between AIH patients and healthy controls. These data could bring new insights in pathophysiology of disease, which could be translated into clinical practice if repeated in other studies.

Keywords: Autoimmune hepatitis, Single nucleotide polymorphism, Tumor necrosis factor(TNFA)

P508 - 479: ISOLATION, MOLECULAR IDENTIFICATION AND GENOMIC DNA FINGERPRINTING OF MYCOBACTERIUM STRAINS FROM TUBERCULIN POSITIVE CATTLE IN KERMAN PROVINCE

Mahfam Sadri[1], Naheed Mojgani[2], Nader Mosavari[3], Seyed Abolhasan Shahzade Fazeli[4]

1. Departmenr of Microbial Biotechlogy, Faculty of Basic Sciencces and Advanced Technologies in Biology, University of Science and Culture, Tehran, Iran
2. Department of Biotechnology, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization, Karaj, Iran
3. Bovine Tuberculosis Reference Laboratory, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization, Karaj, Iran
4. Departmenr of Microbial Biotechlogy, Faculty of Basic Sciencces and Advanced Technologies in Biology, University of Science and Culture, Tehran, Iran

Background and Aim:M.bovis is an important member of MTBC causing BT(bovine tuberculosis) in cattle and humans. This study aimed to We isolate and identify M.bovis strains from tuberculin positive cattle of Kerman province.

Methods: Twenty five lymph nodes samples from BT suspected cattle from the Kerman province sent to Tuberculin reference Laboratory at Razi institute were analyzed. The isolates were initially decontaminated and cultivated on Lowenstein Jensen media with pyruvate and glycerin. Genomic DNA was isolated from pure colonies and subjected to 16srRNA and IS6110 primers for identification at Genus and Species level of the MTBC. The RFLP method determined the genomic pattern of M.bovis strains.

Results: According to the obtained results, 10 samples appeared culture positive and were acid fast. Amplification of the genomic DNA by PCR-16srRNA and PCR-IS6110 showed that all the isolates belonged to the genus Mycobacterium and MTBC species. Based on RFLP typing and DNA hybridization results using the mentioned probes the M.bovis strains were determined and their DNA finger prints compared with the prevailing strains in the country. The strains specific to Kerman province were highlighted.

Conclusion: The results confirms the presence of M.bovis infected cattle in Kerman province and indicates the possibility of the transfer to humans.

Keywords: Mycobacterium bovis, RFLP typing, PCR-16srRNA, PCR-IS6110, PGRS and DR probes

P509 - 540: ISOLATION AND IDENTIFICATION OF MYCOBACTERIUM FROM RAW MILK AND TRADITIONAL CHEESE SAMPLES COLLECTED FROM DAIRY STORES IN KARAJ, IRAN

Tahereh Tafreshi[1], Naheed Mojgani[2], Nader Mosavari[3], Shaghayegh Nasr[4]

1. Department of Microbial Biotechnology, Faculty of Basic Sciences and Advanced Technologies in Biology,University of Science and Culture,Tehran,Iran
2. Department of Biotechnology, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization, Karaj, Iran
3. Bovine Tuberculosis Reference Laboratory, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization, Karaj, Iran
4. Department of Microbial Biotechnology, Faculty of Basic Sciences and Advanced Technologies in Biology,University of Science and Culture,Tehran,Iran

Background and Aim: Milk and its products are one of the nutritious food that is necessary for human body. However, consumption of unpasteurized dairy products can be a source of concern for the transmission of pathogens. Among these pathogens, Mycobacterium is a significant contaminant present in milk that can be lead to tuberculosis disease in human. The aim of present study was to isolate and identify Mycobacterium species in unpasteurized cow milk and cheese samples collected from Karaj city in Iran.

Methods: Forty raw milk and traditional cheese samples collected from dairies in Karaj city were transported to Tuberculin department, Razi Institute. All samples were decontaminated by NaOH (1N) and cultured on Lowenstein-Jensen and Herrold's egg medium, at 37ºC for at least 8 weeks. DNA was extracted from pure colonies by the method of Van Solingen. The extracted DNA was subjected to 16SrRNA genus-specific primer pairs in a PCR reaction. The samples showing a bond of approximately 543bp were considered Mycobacterium positive. All positive samples are further being analyzed for identifying the Mycobacterium species.

Results: Among the forty collected samples, 7 milk and 2 cheese samples appeared Mycobacterium positive by PCR method using 16SrRNA primers. However, by culture method only 2 milk and 2 cheese samples appeared positive.

Conclusion: Dairy products might be a source of Mycobacterium contamination, especially unpasteurized dairy products. Additionally, 16S rRNA PCR method is a suitable method for rapid and reliable detection of Mycobacterium.

Keywords: Mycobacterium, dairy products, 16S rRNA, PCR

P510 - 545: THE FREQUENCY OF REVERSE TRANSCRIPTASE'S (RT) GENES IN ESCHERICHIA COLI ISOLATED OF URINARY TRACT INFECTIONS

Fatemeh Jokar[1], Dr.Ali Nazemi[2]

1. Department of genetic,Tonekabon branch,Islamic azad university,Tonekabon,Iran
2. Department of genetic,Tonekabon branch,Islamic azad university,Tonekabon,Iran

Background and Aim: The variable genome of Escherichia coli has caused the size of genome, MsDNAs, the Retrones, and the Reverse Transcriptase enzyme gene to vary in different strains of this bacterium. These genes called orphan genes that their function and origin is yet unknown. This study's purpose is to determine the relative frequency of Reverse transcriptase in E. coli isolated from urinary tract infections.

Methods: In this study 200 samples of urinary tract infections were collected from Tehran, Rasht, Tonekabon and Sari. DNA extraction from the specimens was performed using Boiling method and commercial kits (ROCHE). After designing and synthesizing specific primers, the gene was multiplied by PCR and its frequency was determined by SPSS software

Results: After performing statistical steps, out of 200 specimens, 27 samples had RT gene, and 31 were male (16%) and 169 were female (84%). Analysis by SPSS software showed that there is a significant difference between sexes about the presence or absence of the gene with 95% probability and 5% statistical level.

Conclusion: The presence or absence of RT can not be a reason for the pathogenicity of the E. coli. Analysis by SPSS software also showed that there is no significant difference between age groups regarding the presence or absence of the gene

Keywords:orphan genes: - Escherichia coli - RT

P511 - 561: THE NUCLEOTIDE ANALYSIS OF REVERSE TRANSCRIPTASE (RT) ENZYME GENE IN ESCHERICHIA COLI ISOLATED OF URINARY TRACT INFECTIONS

Shabnam Pourmohammadian[1], Dr.Ali Nazemi[2]

1. Department of microbiology,Tonekabon branch,Islamic azad university,Tonekabon,Iran
2. Department of genetic,Tonekabon branch,Islamic azad university,Tonekabon,Iran

Background and Aim: Parts of the Escherichia Coli's genome caused urinary tract infections, include MsDNAs, the retrons, and the Reverse Transcriptase enzyme gene,and are referred as Orphan genes, Lacking origin, and performance in different strains of this bacterium. Retrons play a role in production of RT(Reverse transcriptase) enzymes.the RT was generally an eukaryotic enzyme,but it has also been observed in bacteria. The research's purpose is the nucleotide analysis of Reverse Transcriptase in Escherichia isolated from urinary tract infections

Methods: In this study 200 samples of urinary tract infections were collected from Tehran, Rasht, Tonekabon and Sari. After DNA extraction by using Boiling method and commercial kits (ROCHE), designing and synthesizing specific primers, The presence of RT gene was investigated by PCR, electrophoresis and sequencing

Results: The results of PCR and Melting Curve Analysis (HRM) indicated that primers designed in this study could identify the full specificity of the RT gene and confirm its presence in E. coli.out of 200 specimens, 27 samples had RT gene

Conclusion: Identification, Nucleotide Analysis and sequencing of the orphan genes that are part of the non-homologous genes are necessary to compare with other sequences and to understand the origin and functions of these genes. Considerable results are selective pressure on the gene encoding the RT enzyme in E. coli. We found that the sequence of this gene was not different in terms of nucleotide analysis in different strains, and was retained in all bacteria.

Keywords: Escherichia coli - RT - orphan genes

P512 - 586: MOLECULAR CHARACTERIZATION OF CLINICAL AND ENVIRONMENTAL PSEUDOMONAS AERUGINOSA ISOLATED IN A BURN CENTER

Pezhman Karami[1]

1. Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran

Background and Aim: Pseudomonas aeruginosa is one of the major agents of nosocomial infections in burn centers.Therefore, The aim of this study was to characterize molecularly Pseudomonas aeruginosa isolates collected from environmental and burn patients.

Methods:A total of 58 clinical and 20 environmental strains of the P. aeruginosa were collected from Beasat hospital of Hamadan, west of Iran, and identified via API 20NE. The antimicrobial resistance was tested by disk diffusion method as recommended by CLSI. Biofilm formation was quantified by the microtiter plate test. Pulsed Field Gel Electrophoresis (PFGE) was used to evaluate the genomic features of the isolated strains.

Results: We found that 94.8% of clinical and 80% environmental isolates were capable of forming biofilm. The rate of MDR in clinical and environmental isolates was 51.7% and 40%, respectively. There was a significant correlation between multiple drug resistance and biofilm formation capability ($p < 0.05$). PFGE typing showed 11 different clusters with two major clusters A with 30 (38.5%) and B with 14 (17.9%) members, containing up to 56.4% of all isolates. There was no relationship between biofilm formation ability and antibiotic resistance patterns with Pulsed-Field Gel Electrophoresis (PFGE) clusters.

Conclusion: In this study, we demonstrated that clonal spread of environmental P. aeruginosa isolates is related to that of clinical isolates, being both associated with a high prevalence of the antibiotic resistance and biofilm formation ability. This study highlighted the prevention programs need to be implemented in the hospital environment to limit the transfer of P. aeruginosa in this burn units.

Keywords: Psedumonas.aeruginosa, MDR, biofilm formation, antibiotic resistance, PFGE

P513 - 595: THE PREVALENCE OF RESPIRATORY VIRUSES IN IRANIAN CHILDREN WITH ASTHMA

Farhad Babaei[1], nasimkondori[2], seyed hamid reza mortazavi[3]

1. kermanshah university of medical sciences
2. kermanshah university of medical sciences
3. kermanshah university of medical sciences

Background and Aim: Our aim in this study, was evaluation of the viral infections prevalence in the children with asthma in 2016 to 2017. Viral infections induce NF-kB activation and inflammatory pathways that led to produce cytokines, chemokines, inflammatory proteins, and finally reduce lung volume and function disorder Asthma is a chronic inflammatory of the lung airways that about 300 million people suffering from the disease worldwide.

Methods: Materials and Methods: One hundred throat swab sample were collected from children with asthma. RNA extraction and cDNA synthesis were done for frequency determination of parainfluenza viruses, rhino virus, influenza and respiratory syncytial virus (RSV) using Real Time PCR.

Results:41 positive cases were detected including 21 cases of rhinovirus (51.22%), 10 cases of parainfluenza (24.39%), 7 cases of respiratory syncytial virus (17.07%) and 3 cases of influenza virus (7.32%). However, there was no significant statistical relationship between the frequency of viruses with the age and gender of patients

Conclusion: The most important cause of asthma in this study was rhinovirus. Parainfluenza was most commonly reported in children after rhino virus. The lowest prevalence is related to RSV and influenza virus. The two viruses also showed the least seasonal outbreaks in the studies

Keywords: Asthma, Respiratory viruses, Inflammation

P514 - 596: DIAGNOSIS OF CRYPTOSPORIDIUM IN BRONCHOALVEOLAR LAVAGE SPECIMENS OF IMMUNOCOMPROMISED PATIENTS BY TWO METHODS, ARAK CITY, IRAN

Zahra Eslamirad[1], Ali Arash Anoushirvani [2], Mojtaba Didehdar[3], Reza Hajihossein[4]

1. Department of Parasitology and Mycology, Arak University of Medical Sciences, Arak, Iran
2. Department of Internal Medicine, Arak University of Medical Sciences, Arak, Iran
3. Department of Parasitology and Mycology, Arak University of Medical Sciences, Arak, Iran
4. Department of Parasitology and Mycology, Arak University of Medical Sciences, Arak, Iran

Background and Aim: The various protozoa can be spread to lung and create complications, but the most prominent protozoa that are common in immunodeficient patient include opportunistic parasites such as Toxoplasma, Acanthamoeba, Microsporidia and Cryptosporidium. Considering that in recent years, unusual cases of respiratory infections such as Cryptosporidium have increased in people with immunodeficiency, the need for attention to this type of contamination in people at risk is necessary.

Methods: This cross-sectional study was performed on immunocompromised patients including AIDS and cancer patients, recipient transplantation, patients treated with immunosuppressive drugs, undergoing chemotherapy and radiotherapy. After confirming the disease by specialists and obtaining informed consent from patients, a sample of pulmonary secretions was prepared through a bronchoalveolar lavage (BAL) by a specialist. Each sample was examined by direct method (observation of Ziehl Neelson stained BAL smear) and molecular (PCR method).

Results: Of the 55 samples, the cryptosporidiosis was confirmed in 9 samples by staining and 4 samples by molecular methods. In other words, PCR method can only detect about half the cases of cryptosporidiosis.

Conclusion: Therefore, staining is a suitable method for detecting cryptosporidium in BAL samples.

Keywords:BAL sample, Cryptosporidium, Immunocompromised patient, Lung, PCR

P515 - 711: GENOTYPING OF MYCOPLASMA AGALACTIAE ISOLATED FROM SHEEP IN ARDABIL AND GOLESTAN PROVINCES OF IRAN COUNTRY

Khatereh Kabiri[1], Keyvan Tadayon[2], Seiyed Ali Pourbakhsh[3], Jamile Norouzi[4]

1. Department of Microbiology, North Tehran Branch, Islamic Azad University, Tehran, Iran.
2. Department of Veterinary Aerobic Bacteria Razi Institute Karaj
3. Mycoplasma reference laboratory, Razi vaccine and serum research institute, Karaj, Iran
4. Department of Microbiology, North Tehran Branch, Islamic Azad University, Tehran, Iran.

Background and Aim: Currently, Multilocus 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. Mycoplasma agalactiae is the etiologic agent of contagious agalactia of sheep and goats, a disease involving acute mastitis, arthritis, keratoconjunctivitis, and abortion when first introduced in a susceptible population. The aim of this study was molecular typing of M.agalactiae isolates was done throughout MLST the most reliable typing method, which is based on DNA sequencing.

Methods: The MLST typing system targeting 5 house keeping genes of dnaA ,gltX ,gyrB ,metS and tufA with few modifications was performed on strains. The amplification products were sequenced to guaranty accuracy of sizing and nucleotide structure of unit repeats. The Sequence Type (ST) and the corresponding clonal complex of the strains was determined by consulting the MLST database.

Results: One categorically different sequence types (ST) identified in this study with one new allele found at gyrB gene has not been reported before.

Conclusion: Detection of one ST type among two isolates from different geographical locations reflects a low level of diversity in the M.agalactiae population. We have a belief that still a lot needs to be done at the national level so that the epidemiology of M.agalactiae in Iran is fully acknowledged

Keywords:housekeeping genes, agalactia, Mycoplasma agalactiae, allele, MLST database

P516 - 715: UTILIZATION OF MLST GENOTYPING IN PHYLOGENIC STUDY OF MYCOPLASMA AGALACTIAE IN SEMANAN

Khatereh Kabiri[1], Keyvan Tadayon[2], Seiyed Ali Pourbakhsh[3], Jamile Norouzi[4]

1. Department of Microbiology, North Tehran Branch, Islamic Azad University, Tehran, Iran.
2. Department of Veterinary Aerobic Bacteria Razi Institute Karaj
3. Mycoplasma reference laboratory, Razi vaccine and serum research institute, Karaj, Iran
4. Department of Microbiology, North Tehran Branch, Islamic Azad University, Tehran, Iran.

Background and Aim: In Asia, Mycoplasma agalactiae, the causative agent of agalactia is still a serious threat to Small ruminants farming with significant economic losses. Various methods have been provided for typing of M.agalactiae Such as VNTR, RFLP, PFGE and DGGE. MLST analysis is currently the standard globally accepted genotyping system for M. agalactiae. This study investigates the molecular epidemiology and genetic diversity of M.agalactiae isolates obtained from Semanan in 2017 by MLST.

Methods: Genomic material was prepared from freshly cultured strains through a simplified boiling protocol. UvrC -PCR was used to authenticate identity of strains as M.agalactiae. Amplification protocols proposed by the MLST database were used, including primers which have been selected from the set of primers presented under the titles of amplifications and sequences. The five house keeping genes was amplified and sequences, and submitted in MLST and Genbank database.

Results:MLST analysis of the isolates showed the homology of all isolates to alleles previously reported. moreover, our results suggest the genetic diversity of the isolates.

Conclusion: Since the MLST results showed relatively high diversity, this method can be used as powerful tool for further epidemiological investigations and population biology studies of M.agalactiae isolates.

Keywords: Genbank, Agalactia, Mycoplasma agalactiae, Semanan

P517 - 717: PREGNANCY- RELATED LISTERIOSIS: FREQUENCY AND GENOTYPIC CHARACTERISTICS OF L. MONOCYTOGENES FROM HUMAN SPECIMENS, KERMAN-IRAN

Zahra Zahirnia[1], Shahla Mansouri[2], Fereshteh Saffari[3]

1. Department of Microbiology and Virology, Kerman University of Medical Sciences, Kerman, Iran
2. Department of Microbiology and Virology, Kerman University of Medical Sciences, Kerman, Iran
3. Department of Microbiology and Virology, Kerman University of Medical Sciences, Kerman, Iran

Background and Aim: Listeria monocytogenes is a foodborne pathogen that can pose serious complications during pregnancy and neonatal infection. This study aimed to determine the frequency of L.monocytogenes infection, prevalent serotypes and virulence genes among pregnant women and those experiencing miscarriages in Kerman, Iran.

Methods: This study was performed on 200 women who were referred to Afzalipour Hospital that ranged from 18 to 42 years old. 124 vaginal swab specimens were for aborted women and 76 cases for pregnant. Vaginal swab specimens were placed in two enrichment transport (TSB and yeast extract with and without antibiotics). Tubes containing antibiotic were placed in the refrigerator, but another tubes used for DNA extraction. inl B, prf A , act A and genotyping were studied by PCR method. The enriched specimens were cultured on Blood agar and Palcam agar. The isolates were confirmed by specific phenotypic tests.

Results: Out of 200 vaginal swabs, 4.5% and 29.5% of specimens were positive for L. monocytogenes infection as identified by culture and molecular methods, respectively. The majority of isolates from positive cultures (89%) of pregnant women resulted in stillbirth, death and blindness. The most prevalent virulence determinants were inl B, prf A, act A and hly (table1&2). The majority of isolates were non-typable. A history of miscarriage and gestational age are known to be significantly associated with the presence of infection.

Conclusion: This study emphasizes the importance of initial screening for L. monocytogenes in pregnant women in Iran. Increasing the awareness of pregnant women could be effective in reducing pregnancy-related listeriosis.

Keywords: Listeria monocytogenes, miscarriage, pregnancy-related listeriosis, vaginal swab

P518 - 734: SPECIFIC AND ACCURATE IDENTIFICATION OF MYCOBACTERIUM TUBERCULOSIS IN CLINICAL SAMPLES BY PCR-ELISA TECHNIQUE

Reihaneh Ramezani[1]

1. Department of Biomedical Sciences, Women Research Center, Alzahra University, Tehran, Iran

Background and Aim:: Precise and timely diagnosis of tuberculosis is one of the important issues in the treatment management of this disease. Because of the slow growth of mycobacterium tuberculosis in the culture medium and the serious barriers of conventional methods such as microscopic testing, the urgent need for quick, sensitive and precise techniques to detect mycobacterium tuberculosis is felt. In this study, the aim was to detect M. tuberculosis, in specimens isolated from TB patients using PCR-ELISA with high sensitivity and specificity.

Methods:: Using TUF7 and TUF4 specific primers, a 760 nucleotide fragment of the tuf gene from Mycobacterium tuberculosis was amplified by PCR. DIG-labeled amplicons were hybridized with a specific biotinylated oligonucleotide probe in solution phase and subsequently transferred to streptoavidin coated plates. The captured DNA were colorimetrically detected by the addition of anti-digoxigenin antibody HRP conjugate and 2,2-azino-di-(3-ethylbenzthiazolinsulfonate) substrate.

Results: The results indicated a high sensitivity of PCR-ELISA for TB diagnosis. By employing this system, we could detect M. tuberculosis DNA as much as 20 pg in concentration and no interference was encountered in the amplification and detection of Mycobacterium tuberculosis in the presence of non-target DNA.

Conclusion: The PCR-ELISA system offers several advantages in terms of sensitivity, rapidity and simplicity for detection M. tuberculosis in clinical specimens. Since there is a lot of problems in detecting a rapid and accurate TB disease, launching such a technique in laboratories can solve many of the leading problems in diagnosing and treating the disease.

Keywords: Mycobacterium Tuberculosis, PCR-ELISA, tuf

P519 - 778: INVESTIGATING THE FREQUENCY OF BLAZ GENE AND MECA GENE IN STAPHYLOCOCCUS AUREUS ISOLATED FROM CLINICAL SAMPLES IN GORGAN

Yasaman Rahnama [1], Ailar Jamalli[2], Teena Dadgar[3]

1. MS.c - Department of biology, Gorgan Branch, Islamic Azad Univercity, Gorgan, Iran
2. Professor - Department of Microbiology, School of Medicine, Golestan Univercity of Medical Sciences, Gorgan, Iran
3. Professor - Department of Biology, Gorgan Branch, Islamic Azad Univercity, Gorgan, Iran

Background and Aim: Staphylococcus aureus is a most common of the main cause of nosocomial infections.Treatment of Staphylococcus aureusinfections has become more complicated with emergence of a methicillin-resistant Staphylococcus aureus (MRSA) strain. The purpose of this study was to investigate the frequency of blaZ (β-lactamase resistance gene) and mecA (methicillin resistance gene) in Staph.aureus isolated from clinical samples by using PCR method in Gorgan.

Methods: In this study, within 6 months, 1395-1396, 59 Staph.aureus strains that were collected from clinical samples of medical centers in GORGAN.Antibiotic resistant and β-lactamase production were investigated by phenotypic methods .After the revival of the strains in Monitol Salt Agar , plasmid DNA was extracted by using Phenol Chloroform.Then the frequebcy of β-lactamase gene (blaZ) and methicillin resistant gene (mecA) was determined with specific primers by using PCR method.

Results:PCR analysis showed that the most frequency gene was blaZ (100%) and followed by mecA (45/8%) and the isolates that had mecA, were positive blaZ together. Oxacillin resistant strains (5%) and Cefoxitin resistant strains (3%) had mecA.The Staph strains (79/4%) had blaZ and β-lactamase.

Conclusion: It is recommended to limit the antibiotic uses without prescription or in unnecessary cases in order to decrease rate of microbial resistance to antibiotics.

Keywords: staphylococcus aureus, blaZ gene, mecA gene, PCR, Gorgan.

P520 - 794: PREVALENCE OF CAGA GENE AND RELATION WITH DIFFERENT CLINICAL FORMS OF HELICOBACTER PYLORI INFECTIONS IN ISOLATED STRAINS OF AHVAZ-SOUTHWEST OF IRAN

Amirarsalan Serajian[1], Mansour Amin[2], Ali Akbar Shayesteh[3], Maryam Labibzadeh[4]

1. Department of microbiology, Faculty of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
2. Department of microbiology, Faculty of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
3. Research center for infectious diseases of digestive system [Alimentary tract research center], Ahvaz Jundishapur University of Medical Sciences, Iran
4. Clinical Laboratory dept.Infertility Research and Treatment Center of Jahade-daneshgahi Khuzestan

Background and Aim: Helicobacter pylori is a gram negative and curved bacterium that infects more than 50% of the Humans. This organism is involved in gastric diseases, including chronic inflammation and ulcers, as well as malignancies.One of the most important virulence factor of helicobacter pylori is the cagA gene.The prevalence of this gene in Iran is about 70%, while in the Western countries it is 60-70% and in the eastern countries is more than 95%.Various studies have shown that the presence of cagA gene in Helicobacter pylori strains increases the risk of gastric ulcer, gastric cancer and MALT lymphoma.

Methods:A gastric biopsy specimen was taken from 244 gastric patients and cultivated on a Colombia agar plate containing various antibiotics and incubated for 3 to 5 days under Microaerophilic conditions at 37 ° C.The biochemical tests, were applied to identify the grown strains as H. pylori. Following DNA extraction, polymerase chain reaction were done to find ureC and cagA genes.

Results:93 strains of H. pylori were identified . 69 strains had cagA gene(74% prevalence).The correlation between the clinical forms of the disease and the cagA gene was analyzed by statistical tests. No significant correlation was found between the clinical forms of the disease and the cagA gene.

Conclusion: The reported prevalence of cagA gene in the present study is similar to the some studies conducted in different parts of the world And is difference in other cases. This discrepancy is due to the difference in the type of gastric disorders and the sample size.

Keywords:cagA-PCR-Helicobacter pylori

P521 - 830: MOLECULAR CHARACTERIZATION OF THE CHICKEN ANAEMIA VIRUSES ISOLATED FROM BROILER FARMS OF EAST AZERBAIJAN, IRAN

Masoud Ezami razliqi[1], Dr.raheleh majdani[2]

1. Student
2. Professor

Background and Aim: Infectious anemia of poultry as one of the immunosuppressive viral diseases is associated with high mortality and economic losses worldwide. The causative agent of the disease, CAV (Chicken Anemia Virus), is a non-enveloped, icosahedral virus with a negative-sense, single-stranded circular DNA genome. In the present study, molecular analysis of CAV circulating isolates from East-Azerbaijan, Iran was done.

Methods:100 Liver samples from broilers were collected. DNA extraction of the samples were done and then, amplification of the VP1 gene was carried out. PCR products were purified and finally, the purified products were subjected to restriction fragment length polymorphism (RFLP) using XbaI and AluI endonuclease enzymes digestion.

Results:VP1 gene were amplified in 38 of 100 obtained samples successfully. Viral isolates were classified to 10 different groups using AluI while digestion with XbaI were grouped the virus isolates in seven distinct clusters.

Conclusion: Results of the current study suggests high rate of genetic variation among virus circulating isolates of CAV in poultry farms of East Azerbaijan of Iran.

Keywords:CAV-anemia-Vp1

Oral Microbiology

P522 - 226: EVALUATION OF ANTIMICROBIAL SUSCEPTIBILITY OATTERN STREPTOCOCCUS MUTANS ISOLATED FROM DENTAL PLAQUES TO CHLORHEXIDINE, NANOSIL AND COMMON ANTIBIOTICS

Salim Shahabi[1], Abotaleb Nikpour[2]

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

Background and Aim: Streptococcus mutans is one of the most important leading cause of dental diseases worldwide and is considered as one of the main causative agent of dental caries. Increasing resistance of oral pathogens to conventional antibacterial agents has resulted to find alternative therapies to overcome resistance development problems. The aim of this study was to examine susceptibility of Streptococcus mutans isolates to some antibiotics, chlorhexidine and nanosil

Methods: The study subjects comprised of caries active individual volunteers attending the outpatient department of different dental college hospitals of Kerman. The saliva sample of 2-5 ml was collected from each individual in sterile capped bottles and were immediately transported to the laboratory and processed for the screening of S. mutans. The specific selective media, Blood agar and Tryptone yeast cysteine media agar were used for the screening and isolation of Streptococcus mutans and incubated anaerobically at 37˚C for 48 hrs. Colonies of mutans streptococci were examined under a dissecting microscope and identified by their distinctive colony morphology and biochemical tests .Mutacin production of all isolates were investigated.The isolates were tested for susceptibility to some antibiotics (penicillin, gentamycin, vancomycin, cephalotin), chlorhexidine and nanosil mouthwashes by disc diffusion method

Results: The results showed that the majority of mutacin and non mutacin-producing isolates were more sensitive to the nanosil than antibiotics and chlorhexidine

Conclusion: More extensive research on the use of mouthwashes containing silver nanoparticles is suggested

Keywords: Streptococcus mutans, Antibiotic, Chlorhexidine, Nanosil

P523 - 263: THE ANTIMICROBIAL AND CLINICAL EFFECTS OF OZONIZED WATER, CHLORHEXIDINE, AMOXICILLIN -METRONIDAZOLE, ON PORPHYROMONAS GINGIVALIS

Mohammad Niakan[1], Zahra sarabadani[2], Zahra soltani Kermanshahi[3], Hasan Semyari[4]

1. Shahed University.Medicine Faculty.Microbiology Department
2. DDS . Shahed University.Detistry Faculty.
3. MSc in Microbiology. Azad islamic University.Science Faculty.
4. Associated professore . Dentistry surgery

Background and Aim: Background: Recently ozone as a disinfectant effective in the treatment of periodontal disease has been suggested, this study investigated the in vitro antimicrobial activity Ozonized water, chlorhexidine, amoxicillin, metronidazole and amoxicillin-metronidazole combination on the bacterium Porphyromonas gingivalis (Pg).

Methods: Material and Methods: In Vitro study, double-blind by different concentration from ozone- water, chlorhexidine, amoxicillin, metronidazole injection, suspension of metronidazole and amoxicillin-metronidazole combination with 7 times in the presence of bacteria in a test tube Pg and its antimicrobial effect by the method of MIC using turbidity and MBC and count the number of colonies were determined. Statistical analysis was performed with two way ANOVA and LSD methods.

Results: Results: the MIC of ozone- water, chlorhexidine, amoxicillin, metronidazole injection, suspension of metronidazole and amoxicillin-metronidazole combination of respectively 7.0, 3, 190, 310, 12 500 and 10 micro grams per ml. and MBC respectively 1, 7, 390, 310, 2500 and 10 micro grams per ml, respectively, MIC and MBC were obtained ozone- water, chlorhexidine and amoxicillin-metronidazole combination with significant differences ($P \leq 0.05$) .

Conclusion: Conclusion: ozone- water strong antimicrobial effect than chlorhexidine, amoxicillin, metronidazole and amoxicillin-metronidazole combination on the bacterium Porphyromonas gingivalis can be used in the treatment of periodontal disease.

Keywords: Keywords Porphyromonas gingivalis, Ozone water, Chlorhexidine, Amoxicillin- Metronidazole

P524 - 289: PREVALENCE AND RISK FACTORS OF ENTAMOEBA GINGIVALIS AND TRICHOMONAS TENAX IN PATIENTS WITH PERIODONTITIS IN LORESTAN PROVINCE, IRAN

Setare Azade[1], Setare Azadeh[2], Hossein Mahmoudvand[3], Azadeh Sepahvand[4], Zahra Mehri[5], Nahid Derikvand[6]

1. -
2. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
4. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
5. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
6. Department of Periodontics, School of Dentistry, Lorestan University of Medical Sciences, Khorramabad, Iran.

Background and Aim: Periodontitis is well-known as a severe gum infection that harms the soft tissue and destroys the bone that supports the teeth. This investigation was aimed to evaluate the prevalence of Entamoeba gingivalis and Trichomonas tenax in periodontitis patients from Lorestan province, Western, Iran.

Methods:A total of 42 periodontitis patients were included in this study. Saliva and gingival crevicular fluid were collected and transferred to parasitology laboratory for microscopic examinations. A questionnaire was provided for some demographic and risk factors such as age, genus, smoking habits, brushing, etc.

Results: The obtained findings revealed that E. gingivalis was present in the samples from 4 periodontitis patients (9.5%), while 5 (12.5%) patients were positive for T. tenax. The results also showed that genus (male), smoking habits, and brushing were significantly related to the prevalence of these parasites.

Conclusion: Here, we found that the remarkable prevalence of oral cavity in patients with periodontitis; indicating that these parasites are able to be involved in the gum diseases such as periodontitis. However, additional studies using standardized experimental designs of epidemiologic studies are required.

Keywords: Prevalence; Entamoeba gingivalis; Trichomonas tenax; periodontitis

P525 - 291: PREVALENCE AND ASSOCIATED RISK FACTORS OF ORAL CAVITY PROTOZOA (ENTAMOEBA GINGIVALIS & TRICHOMONAS TENAX) IN THE PATIENTS WITH DENTAL CAVITY CARIES IN LORESTAN PROVINCE, IRAN

Zahra Mehri[1], Massumeh Behzadian[2], Akram Sepahvand[3], Setareh Azadeh[4], Hossein Mahmoudvand[5]

1. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
4. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
5. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran

Background and Aim: Tooth decay (dental cavity caries) is one of the major issues in the field of oral health around the world, which affects 60 to 90% of school children and often adults. This investigation was aimed to evaluate the prevalence of Entamoeba gingivalis and Trichomonas tenax in patients with dental cavity caries from Lorestan province, Western, Iran.

Methods:A total of 68 patients with dental cavity caries were included in this study. Saliva and the rotten cavities of the tooth were collected and transferred to parasitology laboratory for microscopic examinations. A questionnaire was provided for some demographic and risk factors such as age, genus, smoking habits, brushing, etc.

Results: The results exhibited that E. gingivalis was present in the samples from 6 periodontitis patients (8.8%), while 7 (10.3%) patients were positive for T. tenax. The results also showed that genus (male), use of mouthwash, and teeth brushing were significantly associated to the prevalence of these parasites.

Conclusion: The obtained findings demonstrated the considerable prevalence of oral cavity in patients with dental cavity caries; indicating that these parasites have capacity to be involved in the dental cavity caries. However, further studies using standardized experimental designs of epidemiologic investigations are mandatory.

Keywords: Prevalence; Entamoeba gingivalis; Trichomonas tenax; dental cavity caries

P526 - 817: THE EFFECT OF SILICON DIOXIDE AND ZEOLITE-ZINC NANOPARTICLES AGAINST STREPTOCOCCUS MUTANS BIOFILMS

Zahra Hosseinali hakim gheshlaghi[1], hadi piri doghahe[2], alireza jafari[3], mohsen arzanlou[4], vida Hosseinali hakim gheshlaghi[5]

1. Department of Microbiology, School of Medicine, Ardabil University of Medical Sciences, Ardabil, Iran
2. Department of Microbiology, School of Medicine, Ardabil University of Medical Sciences, Ardabil, Iran
3. Inflammatory Lung Disease Research Center, Department of Internal Medicine, Razi Hospital, School of Medicine, Guilan University of Medical Sciences, Rasht, Iran
4. Department of Microbiology, School of Medicine, Ardabil University of Medical Sciences, Ardabil, Iran
5. Department of Microbiology, School of Science, Islamic Azad University of Ardabil, Ardabil, Iran

Background and Aim: Streptococcus mutans are able to form biofilms on the surface of oral cavity. The pathogenicity of Streptococcus mutans is related to the production and tolerance of acid. Silicone and zeolite nanoparticles(NPs), due to porous structure, high levels of absorption and antimicrobial properties in the oral cavity, reduce the spread of biofilms at the surface of the teeth.

Methods: Standard strain of Streptococcus mutans, Silicon dioxide and zeolite-zinc NPs from the Tehran University of Medical Sciences Research Center were prepared. NPs with 2 mg / ml concentration diluted into Tryptic Soy Broth and Todd hewiett broth by the addition of bacteria and incubation for 24 hours, 5% CO2at 37 °C. The minimal inhibitory concentration (MIC) was studied based on the opacity and lack of it.To determine MBC , Transfer 10 µL of the last well with opacity to Blood Agar culture and incubation for 24 hours, CO2 and 37 ° C, and MBC were studies based on colony formation.

Results:MIC for Streptococcus mutans in NPs of silicon dioxide with CO2 and without CO2 were 2 mg / ml and 1 mgr/ml, respectively. Minimum Bactericidal Concentration) MBC(was 4 mg/ml and 2mgr/ml. MIC for Streptococcus mutans in zeolite-zinc NPs under conditions of CO2 and without CO2 were 32 mg/ml and 8mg/ml, respectively, and MBC was 64 mg/ml and 8 mg/ml, respectively.

Conclusion: The study showed that silicon dioxide and zeolite-zinc NPs are an effective inhibitor against the formation of biofilms and dental plaque from Streptococcus mutans.

Keywords:nanoparticles, silicon dioxide, zeolite, biofilm, Streptococcus mutans, dental plaque

P527 - 834: QUORUM SENSING INHIBITION POTENTIAL OF RUBUS ULMIFOLIUS BLOSSOM EXTRACT IN VITRO AGROBACTERIUM TUMEFACIENS NTL/PZLR4

Elham Pishgar[1], Mohammd Kargar[2]

1. M.Sc., Department of Microbiology, Islamic Azad University, Jahrom, Iran.
2. Associate Professor, Department of Microbiology, Islamic Azad University, Jahrom, Iran

Background and Aim: Many bacteria specially Staphylococcus aureus utilize quorum sensing mechanism in order to coordinate their vital functions such as survival, motility, production of biofilm, pathogenicity factors, etc. wereas signaling system Quorum sensing has a role in controlling disease factor, destruction by herbal plant is a good goal for anti Quorum sensing therapy, without using antibiotics. In this study interfering effects of distinguished plant extract, Rubus Ulmifolius Blossom on bacterial quorum sensing of Agrobacterium tumefaciens NTL/PZLR4 was evaluated.

Methods: Staphylococcus aureus was isolated from patients with dental implant infection. Rubus Ulmifolius Blossom plant specie were collected from the surrounding agricultural areas of JahromCity. The collected plants were extracted using three organic solvents, 96% ethanol. The anti-quorum sensing and anti biofim bioassays were then performed to depletion of violacein and find out their microtiter plate property respectively. Results: Based on the results, Rubus Ulmifolius Blossom extract possess meaningful anti-QS activity and anti biofilm.

Results: Based on the results, Rubus Ulmifolius Blossom extract possess meaningful anti-QS activity and anti biofilm.

Conclusion: Due to decrease in the production level of violacein by NTL/PZLR4 as a result of the anti-quorum sensing activity of Rubus Ulmifolius Blossom extract, and als the destraction of the power of producting the biofilm of Staphylococcus aureus application of the extract can be considered as an appropriate approach for controlling bacterial pathogens without developing resistance.

Keywords: Rubus Ulmifolius Blossom, Staphylococcus aureus, Inhibition, Quorum sensing, Agrobacterium tumefaciens NTL/PZLR4

Pharmaceutical Microbiology

P528 - 29: ANTI-CANDIDA ACTIVITIES OF SEEDS HYDROALCOHLIC EXTRACT OF RUMEX OBTUSIFOLIUS

Hossein Nazari [1], Farahnaz Bineshian[2], Neda Bakhshandeh[3], Mahbubeh Gholami[4], Jamshid Mehrzad[5]

1. Department of Biochemistry, Faculty of Medicine, Seman University of Medical Sciences, Semnan, Iran.
2. Department of Parasitology & 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. Department of Biochemistry, Faculty of Medicine, Seman University of Medical Sciences, Semnan, Iran.
5. Department of Biochemistry, Faculty of basic and research Science, Azad University, Neyshabur Branch, Neyshabur, Iran

Background and Aim: Nowadays, the uses of herbal medicines have increased in the prevention and treatment of diseases in the world, especially Iran. The development of resistance in some Candida species and side effects of chemical drugs consumption new resources especially medicinal plants is very important. The purpose of this study was to investigate of anti-Candida activities of hydroalcohlic extract from seeds of Rumex obtusifolius.

Methods: The Rumex obtusifolius seeds were extracted using Ethyl acetate: methanol: distilled water (6:3:1) by Soxhelet system. The antifungal activity was examined. The extract was screened against 40 isolated pathogenic Candida species such as C. albicans, C. glabrata by agar well diffusion method.

Results: The minimum inhibitory concentration values at 24 and 48 hours were 100-150 µg/µL for C. albicans 150 µg/µL for C. glabrata.

Conclusion: The seed of Rumex obtusifolius has strong anticandidial antioxidant activities. This seems may be correlated to the presence of high levels of phenolic compounds, particularly pyrogallol.

Keywords: Rumex obtusifolius; Candida; Hydro alcoholic extract; Seed

P529 - 36: INVESTIGATION OF BACITRACIN FUNGICIDAL EFFECTS PRODUCED BY BACILLUS SP. ISOLATED FROM SOIL OF FOREST PARKS IN TEHRAN

Ali Sayyah Varg[1], Farzaneh Hosseini[2], Mina Abotorabi[3]

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

Background and Aim: Bacitracins, ribosomally synthesized antimicrobial peptides, display potential applications in agriculture, medicine and industry. The aim of this study was optimization and partial characterization of a bacteriocin substance from a soil bacterium taxonomically affiliated as Bacillus sp .

Methods: In this study eleven forest soil samples were collected from different regions of Tehran and for separating of Bacillus sp . After biochemical and molecular identifications, cellular metabolites of strains were extracted by centrifugation. Peptone yeast beef medium (PYB in g/L: 10 g peptone, 5g yeast extract and 3g beef extract) was used as a bacitracin core production medium. The fungicidal activity of Bacitracin against standard strains of Aspergillus fumigatus, Aspergillus flavus and Aspergillus niger was investigated by means of Disk diffusion, Well diffusion, MIC and MFC methods.

Results: The results showed that, 10 strains were collected from 11 strains of soil, belonged to Bacillus subtilis. The Minimum Inhibitory Concentration (MIC) of ethyl acetate extract against A. fumigates and A. niger , were 25.0 µg ml-1, and 12.5 µg ml-1, respectively. There are significant differences between the amount of fungal growth inhibition in the Disk diffusion, Well diffusion, MIC and MFC methods compared to the control group .

Conclusion: It can be concluded that Bacillus subtilis might be a promising candidate for new pharmaceutical agents.

Keywords: Bacillus subtilis, Bacitracin, Aspergilus, Fungicidal effect

P530 - 111: COMPARISON OF ERME GENE EXPRESSION IN SACCHAROPOLYSPORA ERYTHRAEA WILD TYPE AND OVERPRODUCTION MUTANTS

Hossein Rassi[1], Parasto Fagihnasiri[2], Jalil Vand Yousefi[3]

1. Department of Microbiology, Faculty of Sciences, Islamic Azad University , Karaj, Iran
2. Department of Microbiology, Faculty of Sciences, Islamic Azad University , Karaj, Iran
3. Department of Microbiology, Faculty of Sciences, Islamic Azad University , Karaj, Iran

Background and Aim: Erythromycin is the most potent and clinically important member in macrolide antibiotic produced by Saccharopolyspora erythraea. It is a potent 14-membered antibiotic active against pathogenic Gram-positive bacteria. Resistance methylase gene, ermE confers resistance to MLS antibiotics by N6-dimethylation of 23s rRNA at a single site. Ethyl methanesulfonate (EMS) mutagenesis and selection of overproduction mutant, is the most important and convenient method in enhancement of antibiotic production.

Methods: In the present study, Saccharopolyspora erythraea was mutagenized using EMS and selection by tylosin resistance mutant to improve yield of erythromycin. In other sides, ermE expression analyzed by Real Time PCR in high producer mutant and wild strains.

Results: When EMS used at 4% (w/v) concentration, high producer mutant isolated after 30 minutes of exposure to the mutagen. In total, from 120 colonies of high producer mutant in primary screening, 25 colonies in fermentation environments also showed an overproduction. The expression of ermE gene in five mutant strains from 25 strains that enhanced more than the wild strain. Finally, the RHEMS438 mutant with an average of 2.18 mg / ml antibiotic selected with an increase of production about 3 times that of the wild strain.

Conclusion: It was concluded that the expression of ermE gene in high producer mutant increased compared with the wild strain and the ermE expression rate was about 6 times greater than that of the wild strain.

Keywords: Saccharopolyspora erythraea, Erythromycin, ermE expression

P531 - 118: EVALUATION OF THE SYNERGISTIC EFFECTS OF THE ALCOHOLIC EXTRACT OF STACHYS BYZANTINA IN COMPARISON WITH GENTAMYCIN, ERYTHROMYCIN AND PENICILLIN ANTIBIOTICS

Roya Safarkar[1], Seyyedeh Masumeh Mirnurollahi[2], Reza bonabi[3], Alireza massiha[4]

1. Department of biology, Faculty of Science, Ardabil Branch, Islamic Azad University, Ardabil, I.R.Iran
2. Department of Microbiology, Islamic Azad University, Varamin-Pishva Branch,Iran
3. Department of Medicine, Faculty of Medicine, Ardabil Branch, Islamic Azad University, Ardabil, Iran
4. Department of Biotechnology, Islamic Azad University, Lahijan Branch, Lahijan, Iran

Background and Aim: Due to the increasing of microbial resistance strains to antibiotic, identify and introduce the antimicrobial substances with plant origin are important. Plants of Lamiaceae family with antimicrobial property are used for the treatment of infectious diseases.

Methods: This experimental study was conducted to investigate the synergistic effects of the alcoholic extract of Stachys byzantina on standard strains and in comparison with three antibiotics Gentamycin, Erythromycin and Penicillin. Phytochemical experiments were also carried out.

Results: The results of this study showed that the alcoholic extract of the Stachys byzantina only has an antagonistic effect on penicillin antibiotic activity against Staphylococcus epidermidis.And does not affect on the performance of gentamicin against Staphylococcus aureus, but it increases the sensitivity of Pseudomonas aeruginosa to penicillin, gentamicin and erythromycin.Phytochemical results revealed that the presence of alkaloid, carbohydrate, tannin, terpenoid, steroid, saponin and flavonoid.

Conclusion: It seems that the extract of Stachys byzantina has an inhibitory effect, both alone and in combination with other antimicrobial agents and improves the performance of some of antibiotics.

Keywords: Alcoholic extract, Stachys byzantina, synergistic effect, Phytochemical compound, antimicrobial activity

P532 - 181: ISOLATION OF SCLEROGLUCAN ORIGINATED FROM SCLEROTINIA SCLEROTIORUM AND INVESTIGATION OF ITS BIOLOGICAL PROPERTIES

Mahboobeh Heidari[1], Sattar tahmasebi enferadi[2], Saeideh rajaii[3]

1. Department of Energy and Environmental Biotechnology, School of Industrial and Environmental Biotechnology, National Institute of Genetic Engineering and Biotechnology
2. Department of Energy and Environmental Biotechnology, School of Industrial and Environmental Biotechnology, National Institute of Genetic Engineering and Biotechnology
3. Department of Energy and Environmental Biotechnology, School of Industrial and Environmental Biotechnology, National Institute of Genetic Engineering and Biotechnology

Background and Aim: Scleroglucan –the polymer of glucose with (β 1-3) glycoside bonds and (β 1-6) branches- is produced by the pathogenic fungus, Sclerotinia sclerotiorum. Considering chemical properties of scleroglucan, it has different applications in various industries such as petroleum, cosmetics, food and drug.

Methods: In order to study immunomodulatory function of scleroglucan, it was isolated from S. sclerotiorum and its antibacterial and antioxidant properties was evaluated using disk diffusion agar, 2,2-Diphenyl-1-picryl-hydrazyl (DPPH) free radical scavenging test and Reactive Oxygen Species (ROS) assay. The structure of extracted scleroglucan was confirmed by Fourier Transform InfraRed (FTIR) spectroscopy and High Performance Liquid Chromatography (HPLC).

Results: Under in vitro condition, no antibacterial activity was observed for extracted scleroglucan against Escherichia coli and Staphylococcus aureus. No toxic effect was detected on the normal healthy fibroblasts using cell viability (MTT=3-[4,5-dimethylthiazol-2-yl]-2,5 diphenyl tetrazolium bromide) test. DPPH experiment indicated that the antioxidant property of scleroglucan is up to 23 percent. ROS test showed that the florescent intensity in 1000 ug.ml-1 concentration of extract decreased significantly.

Conclusion:MTT assay proved that scleroglucan has no cytotoxic effect on normal fibroblasts. Antioxidant tests (DPPH and ROS) showed that scleroglucan could be a antioxidant agent against free radicals but in the disk diffusion agar no direct antibactrial effect was shown.

Keywords: antibacterial, antioxidant effect, Isolation, scleroglucan, sclerotinia sclerotiorum

P533 - 265: SYNTHESIS, PREPARATION, CHARACTRIZATION AND ANTIBACTERIAL PROPERTIES OF AG/PLA NANOFIBER

Mohammad Hassan Moshafi[1], Mehdi Ranjbar[2]

1. Department of Pharmaceutics, Faculty of Pharmacy, Kerman University of Medical Sciences, Kerman, Iran.
2. Pharmaceutics Research Center, Institute of Neuropharmacology, Kerman University of Medical Sciences, Kerman, Iran

Background and Aim: In the past two decades, the field of nanotechnology has grown exponentially since its birth and has made an immense impact on physical, chemical, earth and biological sciences [1–5]. There has been an immense extension of nanomaterial applications and uses as a result of basic and applied research from scientists all over the world. One such class of nanomaterials are the metal oxide (MeO) and metal sulfides (MeS) nanoparticles (NPs), ranging in size from 1 to 100 nm and available in different shapes and sizes.

Methods: Ag/PLA Nanofiber synthesized by nanoemulsion assistance with electrospinning method. 50 mg of AgNO3 and 200mg polylactic acid were precursors to getting started. In a typical and the creative method at the first stoichiometric amount of Tween 80, 60 as surfactant phase and Span 20, 40 as cosurfactant phase (1:1) were dissolved in 20ml deionized water under vigorous stirring for 2 h using a magnetic stirrer at room temperature. After formation of Ag nanoemulsions, we loaded this nanoemulsion on PLA Nanofiber

Results: To prepare 100 ccs of the medium, weigh the Hinton broth 2.1 grams, and in another 500 ml, it dissolves and dissolves. Then we make microbial leachate from the tested microorganisms and compare with the half McFarland their turbidity, to the extent that they are half McFarland. Then, with a micropipette of 2.5 microns from the lagoon, remove the bacteria on the plates, and finally place the plates in the incubator for 24 hours, and the next day the results are read.

Conclusion:we found that 32% of nanoparticles prevents

Keywords: Nanostructures, Ag/PLA Nanofiber, Antibacterial Properties, Gram Positive and Negative Bacteria.

P534 - 266: SYNTHESIS, PREPARATION, CHARACTRIZATION AND ANTIBACTERIAL EFFECT OF AG NPS LOADED ON CHITOSAN/PLA NANOFIBER

Mohammad Hassan Moshafi[1], Mehdi Ranjbar[2]

1. Department of Pharmaceutics, Faculty of Pharmacy, Kerman University of Medical Sciences, Kerman, Iran.
2. Pharmaceutics Research Center, Institute of Neuropharmacology, Kerman University of Medical Sciences, Kerman, Iran

Background and Aim: In the past two decades, the field of nanotechnology has grown exponentially since its birth and has made an immense impact on physical, chemical, earth and biological sciences [1–5]. There has been an immense extension of nanomaterial applications and uses as a result of basic and applied research from scientists all over the world. One such class of nanomaterials are the metal oxide (MeO) and metal sulfides (MeS) nanoparticles (NPs), ranging in size from 1 to 100 nm and available in different shapes and sizes

Methods: Ag nanoparticles loaded on Chitosan/PLA Nanofiber synthesized by nanoemulsion assistance with electrospinning method. 50 mg of AgNO3, 100mg polylactic acid, and 100 mg chitosan were precursors to getting started. In a typical and the creative method at the first stoichiometric amount of Tween 80 as surfactant phase and Span 20 as cosurfactant phase (1:1) were dissolved in 20ml deionized water under vigorous stirring for 2 h using a magnetic stirrer at room temperature. After formation of Ag nanoemulsions, we loaded this nanoemulsion on Chitosan/PLA Nanofiber

Results: In this research, nanoparticles were first made in different sizes and stabilizing concentrations, and then microbiological culture media were prepared using (Minimum Inhibitory Concentration) MIC and several gram-negative bacteria were examined for several nanostructures. To prepare 100 ccs of the medium, weigh the Hinton broth 2.1 grams, and in another 500 ml, it dissolves and dissolves.

Conclusion:we found that 16% of nanoparticles prevents the growth of bacteria in the control

Keywords: Nanostructures, Chitosan/PLA Nanofiber, Antibacterial Properties, Gram Positive and Negative Bacteria.

P535 - 277: EVALUATION OF THE ANTIMICROBIAL EFFECT OF THE ALCOHOLIC EXTRACT OF FLOWER, LEAVES BEFORE AND DURING FLOWERING OF CLERODENDRUM BUNGEI ON THE CLINICAL ISOLATES OF KLEBSIELLA SPP. , PSEUDOMONAS SPP. AND SHIGELLA SPP.

Zahra Azmoudeh kasmaei[1], Seyedeh Tooba Shafighi[2], Somayeh Ataei-e jaliseh[3]

1. Master of Science in Microbiology, Faculty of Basic science, Rasht branch, Islamic Azad University, Rasht, Iran
2. Assistant Professor, Faculty of Basic science, Rasht branch, Islamic Azad University, Rasht, Iran
3. Assistant Professor, Faculty of Basic science, Rasht branch, Islamic Azad University, Rasht, Iran

Background and Aim: The use of herbs for treatment of diseases has increased in recent years. Clerodendrum spp. is a plant of the Verbenaceae family. The aim of the present study was to investigate the antibacterial properties of alcoholic extract of Guilan native Clerodendrum bungei.

Methods: Clinical isolates of Klebsiella spp., Pseudomonas spp. and Shigella spp. were collected from patients referred to Social welfare polyclinic in Rasht. After performing confirmatory diagnostic tests, alcoholic extracts of different parts of Clerodendrum bungei (leaves before and during flowering, flower) were prepared by maceration method and the antimicrobial activity of the extracts was evaluated using disk diffusion and broth dilution methods on 6 isolates of Klebsiella spp., Pseudomonas spp. and Shigella spp.

Results: The results of the disc diffusion showed that the alcoholic extract of the leaves before flowering was more effective on Pseudomonas spp. than other bacteria. The MIC values of the different alcoholic extracts of Clerodendrum bungei on all isolates were 8.06 to 500 mg/ml. The MBC values of the different extracts of Clerodendrum bungei on isolates were 500 mg/ml, except for shigella spp., which was 250 mg/ml.

Conclusion: It is concluded from the present study that Clerodendrum bungei possesses antibacterial properties.

Keywords: Clerodendrum bungei, broth dilution, disk diffusion, klebsiella, pseudomonas, shigella

P536 - 302: CHEMICAL COMPOSITION AND ANTI-DERMATOPHYTE ACTIVITY OF CUMINUM CYMINUM ESSENTIAL OILS

Rezvan Heidary tabar[1], Mohaddese Mahboubi[2], Elahe Mahdizadeh[3]

1. Department of microbiology, Research center of Barij, Kashan, IRan
2. Department of microbiology, Research center of Barij, Kashan, IRan
3. Department of microbiology, Research center of Barij, Kashan, IRan

Background and Aim: Dermatophytes are responsible for serious superficial skin infections in human. Development of novel antifungal drugs instead of chemical agents to control such pathogens is important. Cumin species is widely used in folklore medicine for treatment of infectious disease as antiseptic or disinfectant. The aim of this study was to evaluate the chemical composition and anti-fungal effect of Cuminum Cyminum essential oils from two different geographical area of Iran.

Methods: Essential oils of C. Cyminum were obtained by hydrodistillation and analyzed by GC and GC-MS. Anti-dermatophyte activities against five strains of dermatophytes including Trichophyton mentagrophytes, T. rubrum, T. schoenleinii, Microsporum canis and M. gypseum were evaluated by food poisoning technique, and micro broth dilution assay.

Results:51 different compounds were identified in the oil with major components of Cuminaldehyde (22.2-31.6%), p-Cymene (6.6-8.8%) and β-Pinene (1.4-7.7%). The essential oils exhibit considerable antifungal capacity dose-dependently against all tested dermatophytes with MIC values ranging from 0.03±0.0 to 0.12±0.0 µl/mL, and MFC value amount 0.04±0.017 to 0.33±0.14 µl/ml. The mycelium inhibitory effects showed 150 and 250 ppm of essential oils inhibited 6-45% and 23-78% of dermatophytes mycelium growth, respectively.

Conclusion: For the first time, in this article we provide the evidence that essential oil of C. Cyminum have anti- dermatophyte properties. Our finding suggest that this essential oil can be considerate as alternative natural antifungal agent for more investigations.

Keywords:anti-dermatophyte, food poisoning technique,micro broth dilution assay, Cuminum Cyminum

P537 - 352: ANTIFUNGAL ACTIVITY OF ROSEMARY OIL EXTRACT AGAINST AND ITS EFFECT ON THE AFL.1 GENE EXPRESSION IN THE ASPERGILLUS FLAVUS BY RT-PCR

Mojtaba Mohammadi[1], Seyed Jamal Hashemi [2], Sasan Rezaei[3], Mansoor Bayat[4], Shiva Golkaram[5]

1. ph.D Thesis Mycology, Department of Microbiology, Faculty of Sciences, Islamic Azad Universihy, Zanjan, Iran.
2. Department of Medical Mycology, Faculty of Public Health, Tehran University of Medical Sciences, Tehran, Iran.
3. Department of Medical Mycology, Faculty of Public Health, Tehran University of Medical Sciences, Tehran, Iran.
4. Department of Microbiology, Faculty of Veterinary, Science and Reasearch Branch, Islamic Azad Universihy, Tehran, Iran
5. Department of Microbiology, Faculty of Sciences, Islamic Azad Universihy, Zanjan, Iran.

Background and Aim: Investigating about the extract of Rosemary in various groups of fungi and this extract's minimum 1effective deterrence density on types of fungi and also the survey of this extract in expressing the AFL.1 gene in Aspergillus flavus is the main target of this research. Rosemary is a very important medicinal herb. Although its antimicrobial effect is fully considered, but its effect on toxin-causing and pathogenic funguses is not studied very much. Therefore, considering the limitation of antifungal drugs, chemical effects, and drug resistance of them, it seems the access of reaching an effective herbal medicine really matters.

Methods: First of all we cultivate Fungi in sabouraud dextrose agar and Mycocell agar perimeter and then we put Rosemary impregnated paper disks on the surface of perimeter to determine the anti-fungal effect with disk difussion method and creation of inhibition zone then with the help of 10 standard sterile tubes we dilute Rosemary extract in the perimeter of sabouraud dextrose broth to gain this extract's effective concentration and finally Rosemary's effect on expressing the AFL.1 gene was examined.

Results: Achieved results indicate that the extract of Rosemary on various types of fungi has an inhibitory effect. The average diagonal of bright anti growth haloes are about 16-18 mm. Therefore the average MIC is 4 to 6 mg per literl and the results of RT.PCR confirm this inhibitory effect on expressing the AFL.1 gene which produces Aflatoxin in molecular level.

Conclusion: The extract of Rosemary can have a considerable inhibitory effect on expressing the AFL.R gene and production of Aspergillus flavus.

Keywords: Rosemary, Asperjillus flavus, AFL.1 gene, Real Time-PCR.

P538 - 413: ANTIMICROBIAL EFFECT OF AQUEOUS AND HYDROALCOHOLIC EXTRACTS OF PLANTAGO PSYLLIUM AGAINST EXPERIMENTAL INFECTION OF HELICOBACTER PYLORI IN FEMALE RAT.

Shima Keshavarzi[1], Masood Sepehrimanesh[2]

1. 1. Department of Microbiology, Fars Sciences and Research branch, Islamic Azad University, Fars, Iran 2. Department of Microbiology, Shiraz Branch, Islamic Azad University, Shiraz, Iran
2. PhD of Biochemistry, Assistant Professor of Guilan University of Medical Science

Background and Aim:pharmaceutical microbiology

Methods: Fifty female rat of Sprague Dawley race were divided into five groups of equal numbers. One group served as a negative control group and the other as a positive control group. After isolating and culture, Helicobacter infection was examined by hospital samples. Except of the negative control group, the remaining groups received 0.5 ml of solution containing 2×107 cfu/ml Helicobacter pylori .Groups 2 and 3 were treated with aqueous and hydro-alcohol extracts of 100mg/kg concentration respectively. They received 300 mg of extract per kg of body weight. The group 4 with a solution of 50 mg amoxicillin concentrations was treated, which receiving 50 mg of antibiotics for per 1 kg of body weight daily. Positive and negative control group were not treated.

Results:: All groups except the positive control group, were negative for antigen in stool, which indicates the effectiveness of the treatment. Experiments suggested that extracts does not affect the process of disease recovery which is because of the small size of the samples. Statistical analysis showed that blood samples have not significant difference in terms of factors affecting liver and kidney.

Conclusion: The extract of the P.psyllium can be used as a selective treatment for Helicobacter pylori infection.

Keywords:plantago Psyllium, Helicobacter pylori, amoxicillin, gastric cancer.

P539 - 458: ANTIMYCOTIC EFFECT OF MENTHOL ON EXPRESSION OF SAP1-ENCODING GENE IN CANDIDA ALBICANS

Shahrzad Shayegan[1], Alireza Khodavandi[2]

1. Department of Biology, Gachsaran Branch, Islamic Azad University, Gachsaran, Iran
2. Department of Biology, Gachsaran Branch, Islamic Azad University, Gachsaran, Iran,

Background and Aim: Using of biological compounds such as menthol could be one of the most frequently ways to alleviate antifungal resistance phenomenon. Hence, in this study, we endeavored to investigate the effect of menthol on the morphology switching in Candida albicans due to expression of SAP1 gene.

Methods: The relative minimum growth inhibitory concentrations were determined by broth microdilution according to the CLSI M27A3 standard protocol with slight modification for all isolates with both menthol and fluconazole. Eventually, the expression level of one of the effective genes in hyphae production of Candida albicans was measured using Real Time RT- PCR.

Results:MICs for fluconazole were reported in all isolates that ranged from 1 to 64 µg/ml, while the menthol content of this ranged from 0.8 to 25 µg/ml, and all isolates showed a ratio of sensitivity. The result of the analysis of the expression of SAP1 gene involved in hyphae production for two concentrations of fluconazole equals 2MIC and MIC showed 1.85 and 1.86-fold reduction, respectively ($P \leq 0.05$) while, for menthol was decreased ranged from 2.02 to 1.85-fold, respectively in 2 MIC and MIC concentrations ($P \leq 0.01$).

Conclusion: The results of this study showed that the secretion of aspartyl proteinase enzyme in the presence of hyphae could be effective in pathogenicity and deterioration of host tissues and is reduced in the presence of menthol compound. In addition, the Real Time RT-PCR analysis of SAP1 gene suggested the probable molecular targets of methanol in Candida albicans.

Keywords: Candida albicans, menthol, antifungal effects, SAP1

P540 - 495: LETHAL EFFECTS OF VARIOUS EXTRACTS OF NIGELLA SATIVA SEED ON PROTOSCOLECES OF ECHINOCOCCUS GRANULOSUS

Saghar Modaresi[1], Elnaz Kianmehr[2], Fatemeh Akbarpour[3], Zahra Chegeni[4], Hossein Mahmoudvand[5], Behrouz Ezatpour[6]

1. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
4. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
5. Razi Herbal Medicines Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran (dmahmodvand@gmail.com).
6. Razi Herbal Medicines Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran (bezatpour@gmail.com).

Background and Aim: Nowadays, a large number of scolicidal agents are available for inactivation of hydatid cyst protoscolices during surgery, but most of them are associated with adverse side effects such as sclerosing cholangitis and liver necrosis. The present study was aimed to evaluate scolicidal effects of various extracts of Nigella sativa seeds against protoscoleces of hydatid cyst in an in vitro model.

Methods: Protoscoleces were aseptically aspirated from naturally infected livers of sheep and goats. Various concentrations of the different extracts of N. sativa (5 to 50 mg/ml) were used for 5 to 60 min. Viability of protoscoleces was confirmed by 0.1% eosin staining.

Results: The findings exhibited that methanolic extract at the concentration of 50 mg/ml after 10 min of incubation, and aqueous extract at the concentration of 50 mg/ml after 30 min of incubation can kill 100% of protoscoleces. In addition, all of experiments revealed dose-dependent and also time-dependent scolicidal effect of various extracts of N. sativa on the protoscoleces of hydatid cyst.

Conclusion: The results of the present study demonstrated that N. sativa may be a natural source for the production of new scolicidal agent for use in hydatid cyst surgery. However, further studies will be required to evaluate scolicidal effects of N. sativa in the in vivo model.

Keywords: Hydatid cyst, Echinococcus granulosus, Nigella sativa

P541 - 497: LEISHMANICIDAL EFFECTS OF BIOGENIC SELENIUM NANOPARTICLES AGAINST SENSITIVE AND GLUCAN-TIME-RESISTANT LEISHMANIA TROPICA STRAINS

Elnaz Kianmehr[1], Zahra Chegeni[2], Saghar Modarresi[3], Fatemeh Akbarpour[4], Hossein Mahmoudvand[5]

1. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
4. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
5. Razi Herbal Medicines Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran (dmahmodvand@gmail.com).

Background and Aim: Leishmaniasis is one of the most important public health problems in tropical and sub-tropical countries. In this study, we evaluated the antileishmanial activity of biogenic selenium nanoparticles (Se NPs) alone and in combination with MA against sensitive and glucantime- resistant L. tropica on in vitro model.

Methods: The Se NPs were synthesized by employing the Bacillus sp. MSh-1. The antileishmanial effects of Se NPs alone and in combination with MA on promastigote and amastigote stages of sensitive and glucantime-resistant L. tropica strains have been investigated using a colorimetric MTT assay and in a macrophage model. In addition hemolytic activity in type O+ human red blood cells and infectivity rate of the promastigotes before and after treatment with the Se NPs was evaluated.

Results: In the promastigote stage, various concentrations of Se NPs significantly inhibited ($P<0.05$) the growth of promastigotes of both strains in a dose-dependent manner. Similarly, Se NPs especially in combination with MA significantly reduced the mean number of amastigotes of both strains in each macrophage. Se NPs showed no hemolytic effect on human RBCs at low concentrations. Moreover, infection rate of macrophages by promastigotes significantly ($P<0.05$) was reduced when promastigotes pre-treated with Se NPs.

Conclusion: The findings of this study suggest a first step in the search of Se NPs as a new antileishmanial agent. Further experiments are needed to investigate antileishmanial effects of biogenic Se NPs on L. tropica using a clinical setting.

Keywords: Cutaneous leishmaniasis, Selenium nanoparticles, Promastigote, Amastigote, Glucantime resistant

P542 - 499: IN VITRO SCOLICIDAL EFFECT OF BERBERIS VULGARIS EXTRACT AND BERBERINE ECHINOCOCCUS GRANULOSUS PROTOSCOLECES

Zahra Chegeni[1], Saghar Modarresi[2], Fatemeh Akbarpour[3], Elnaz Kianmehr[4], Hossein Mahmoudvand[5]

1. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
4. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
5. Razi Herbal Medicines Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran (dmahmodvand@gmail.com).

Background and Aim: Hydatid cyst, a zoonotic parasitic infection caused by the larvae form of dog tapeworm Echinococcus granulosus and considered as a main economic and public health concern in the world. This study aimed to investigate the in vitro scolicidal effect of methanolic extract of Berberis vulgaris L. roots and its main compound, berberine against protoscoleces of hydatid cysts.

Methods: For this purpose, protoscoleces were aseptically aspirated from sheep livers having hydatid cysts. Various concentrations of the methanolic extract (0.25- 2 mg/ml) and berberine (0.062- 0.5 mg/ml) were used for 5 to 30 min. Viability of protoscoleces was confirmed by eosin exclusive test.

Results: In the present study, all of the various concentrations of the B. vulgaris methanolic extract (0.25, 0.5, 1 and 2 mg/ml) and berberine (0.062, 0.125, 0.25 and 0.5 mg/ml) revealed significant ($P<0.05$) scolicidal effects against protoscoleces of E. granulosus in a dose-dependent manner. Both berberine and methanolic extract exhibited 100% inhibition against protoscoleces of E. granulosus at the concentra- tion of 2.0 and 0.5 mg/ml after 10 min incubation respectively.

Conclusion: According to the results, both B. vulgaris methanolic extract and berberine alone demonstrated high scolicidal activities against protoscoleces of hydatid cysts in low concentration and short exposure time on in vitro model. However, in vivo efficacy of B. vulgaris and berberine also requires to be evaluated using an animal model with hydatid infection.

Keywords: Hydatid cyst, European barberry, Scolicidal, Echinococcus granu- losus

P543 - 582: PHOTOCHEMICAL EFFECTS OF ECHIUM AMOENUM EXTRACT AGAINST STREPTOCOCCUS MUTANS

Jaber Ghorbani[1]

1. Department of Microbiology, School of medicine, Tehran university of medical science, Tehran, Iran

Background and Aim: Increasing the resistance of oral pathogens such as Streptococcus mutans to antibiotics has prompted the incentive to use alternative methods including photodynamic therapy. However, few studies have attempted to develop the antimicrobial activity of a novel, natural-derived photosensitizer. The aim of this study was to investigate the in-vitro photochemical effects of echium amoenum extract against Streptococcus mutans suspension and its comparison with chlorhexidine di-gluconate (CHX).

Methods: In this experimental study, suspension of Streptococcus mutans was treated in four separate groups: 1) echium amoenum extract (50 µM) 2) CHX (2%) 3) echium amoenum extract (50 µM) + light irradiation using diode laser with a wavelength of 450 nm 4) diode laser radiation; using micro broth dilution test. Data were analyzed by one way ANOVA and Tukey HSD tests ($p<0.05$).

Results: Regarding the Minimum Inhibitory Concentration (MIC), echium amoenum Extract showed a significant decrease of MIC in the presence of laser light compared with the absence of laser light. The minimum inhibitory concentration of CHX was significantly lower than that of the echium amoenum extract.

Conclusion: These preliminary in vitro findings imply that echium amoenum derivatives can be studied in more investigations as a novel photosensitizer.

Keywords: Photodynamic therapy, Streptococcus mutans, antimicrobial Photodynamic therapy, photosensitizer

P544 - 662: ANTIMICROBIAL POTENTIAL OF TIO2 NANOPARTICLES AGAINST MDR PSEUDOMONAS AERUGINOSA

SADiDi SADiDi[1], roya sadidi[2], Hatef Ajoodanifar[3], Saeid Amel Jamehdar[4]

1. Department of Microbiology, Islamic Azad University, Damghan Branch, Damghan, Iran
2. Department of Microbiology, Islamic Azad University, Damghan Branch, Damghan, Iran
3. Antimicrobial Resistance Research Center, Mashhad University of Medical Sciences, Mashhad, Iran

Background and Aim: Infections caused by multi-drug resistant (MDR) strains Pseudomonas aeruginosa are becoming extremely difficult to treat with conventional antibiotics, leading to a sharp rise in clinical complications. Along with the increase in the prevalence of resistant strains due to the abuse of antibacterial agents, there is an urgent need for a new class of antibacterial agents with an entirely different structure and mode of action. In recent years, various nanoparticles have been reported to display good biological activities. In the present study, the efficacy of TiO2 nanoparticles as an antibacterial agent against MDR P. aeruginosa was explored.

Methods: Ten clinical MDR isolates of P. aeruginosa were obtained from Imam Reza Hospital, Mashhad. Antimicrobial susceptibility of all the P. aeruginosa isolates was performed according to the CLSI guidelines (CLSI, 2017). The optical property of TiO2 nanoparticles was studied by ultraviolet-visible (UV-vis) spectroscopy.

Results: As mentioned before , bacterial strains identification was performed through Phenotyping and Genotyping. In identification step , 35 bacterial smaples with highest nanoparticle production were identified . Microbial strains identification As mentioned before , bacterial strains identification was performed through Phenotyping and Genotyping. In identification step , 10 bacterial smaples with highest nanoparticle production were identified .

Conclusion: Obtained results from TEM confirmed the presence of Tio2 nanoparticles in microorganisms' supernatant culture . Silver nanoparticles existed in culture as bacillus and dispersed which their sizes were from 20 to 400 nm .

Keywords: Titanium oxide , S.aerjinosa bacterium , bedsore , antibiotic

P545 - 669: ANTIFUNGAL ACTIVITY OF ROSEMARY OIL EXTRACT AGAINST AND ITS EFFECT ON THE AFL.1 GENE EXPRESSION IN THE ASPERGILLUS FLAVUS BY RT-PCR

Mojtaba Mohammadi[1], Seyed Jamal Hashemi [2], Sasan Rezaei[3], Mansoor Bayat[4], Shiva Golkaram[5]

1. Department of Microbiology, Faculty of Sciences, Islamic Azad Universihy, Zanjan, Iran.
2. Department of Medical Mycology, Faculty of Public Health, Tehran University of Medical Sciences, Tehran, Iran.
3. Department of Medical Mycology, Faculty of Public Health, Tehran University of Medical Sciences, Tehran, Iran.
4. Department of Microbiology, Faculty of Veterinary, Science and Reasearch Branch, Islamic Azad Universihy, Tehran, Iran
5. Department of Microbiology, Faculty of Sciences, Islamic Azad Universihy, Zanjan, Iran.

Background and Aim: Rosemary is a very important medicinal herb. Although its antimicrobial effect is fully considered, but its effect on toxin-causing and pathogenic funguses is not studied very much. Therefore, considering the limitation of antifungal drugs, chemical effects, and drug resistance of them, it seems the access of reaching an effective herbal medicine really matters. Since the Aflatoxin is concerned in various food, livestock, pharmaceutical, and medical industries, this research illustrates the mchanism of growth containment by this fungus.

Methods: First of all we cultivate in sabouraud dextrose agar and mycosel agar perimeter and then we put Rosemary impregnated paper disks on the surface of perimeter to determine the anti-fungal effect with disk difussion method and creation of inhibition zone then with the help of 10 standard sterile tubes we dilute Rosemary extract in the perimeter of sabouraud dextrose broth to gain this extract's effective concentration and finally Rosemary's effect on expressing the AFL.1 gene was examined and eventually statistical analysis was done by the new version of "SPSS" software.

Results: Achieved results indicate that the extract of Rosemary on various types of fungi has an inhibitory effect that its effect is depended on its effective concentration so that with the increase of this extract's density, the fungal colony will be weaker and inhibited and the results of RT.PCR confirm this inhibitory effect on expressing the AFL.1 gene which produces Aflatoxin in molecular level

Conclusion: The extract of Rosemary can have a considerable inhibitory effect on expressing the AFL.R gene and production of Aspergillus flavus

Keywords: Rosemary, Asperjillus flavus, AFL.1 gene, Real Time-PCR.

P546 - 741: PREVALENCE OF ANTI- HELICOBACTER PYLORI ANTIBODIES IN PATIENTS WITH MULTIPLE SCLEROSIS IN TABRIZ

Aytak Farhangazar[1], Mehdi Ghiami rad[2]

1. Department of biochemistry- faculty of since-Islamic Azad University Ahar branch- Ahar- Iran
2. Department of microbiology- faculty of since-Islamic Azad University Ahar branch- Ahar- Iran

Background and Aim:: Multiple sclerosis (MS) is chronic autoimmune disease that disables central nervous system (CNS) system. Pathogenesis involves a complex interaction between genetic and environmental factors. Helicobacter pylori is the main cause of chronic gastritis and a major risk factor for gastric cancer. In recent years the infection with H. pylori also is recognized as a protective against MS in human. The aim of this study was to determine the prevalence of IgG and IgM anti- H. pylori antibodies in patients with Multiple sclerosis and determine association between the H.pylori infection and prevalence and severity of MS in Tabriz.

Methods: In this cross-sectional study 100 serum samples of MS patients were collected randomly. ELISA kite was used to detect the presence of specific IgG and IgM antibodies against H.pylori in the serum samples. Expanded Disability Status Scale (EDSS) was used to evaluate the MS patients.

Results: No significant difference was observed in seropositivity among ages and between genders. A statistically significant difference was seen in EDSS value between seropositive and seronegative patients ($P \leq O.O5$).

Conclusion: The result indicated that , MS patient with Helicobacter pylori infection showed lower neurologic complication, which can demonstrate a protective role of Helicobacter pylori infection in the MS development.

Keywords: Multiple sclerosis - Helicobacter pylori - Antibodies- Tabriz

P547 - 776: ETHANOL EXTRACT MECHANISM OF RUMEX ALVEOLATUS ON CANDIDA ALBICANS

Nasim Ghayour[1], Nasim Ghayour and mahboobeh madani [2]

1. -
2. Department of Microbiology , falavarjan Branch,Islamic Azad university Isfahan, Iran

Background and Aim: Candida albicans is an opportunistic pathogenic yeast that is a common member of the human gut flora. Rumex alveolatus is traditionally used for the treatment of pain and inflammation The aim of this research was the study of the ethanol extract mechanism of R. alveolatus on Candida albicans.

Methods: In the present study, the mechanism of anticandidial activity of R. alveolatus toward Amphotricin B was investigated by flame-photometry, outoanalyzer and HPLC.

Results: Our results showed significant anticandidia effect of R. alveolatus. Ethanolic extract of R. alveolatus causes release of Na^+,K^+, glucose and aminoacids from candida albicans similar to Amphotricin B.

Conclusion: Our study encourage examination of the efficacy of R. alveollatus against candida spp.

Keywords: Rumex alveolatus, Candida albicans, HPLC, flame-photometry, outoanalyzer.

P548 - 803: ANTIFUNGAL PROPERTIES OF CLOVE ETHANOLIC EXTRACT ON ASPERGILLUS NIGER

Zohreh Gholizadeh Siahmazgi[1], Mirsasan Mirpour[2], Hamideh Asayeshtalab[3], Masoud Yaghmoorian khojini[4], Maryam Ramtin[5]

1. Varna ppm , Biotechnology company, Rasht , Iran
2. Microbiology Department, Islamic Azad University Lahijan Branch, Iran
3. Varna ppm , Biotechnology company, Rasht , Iran
4. Varna ppm , Biotechnology company, Rasht , Iran
5. Microbiology Department, Islamic Azad University Tehran Shomal ,Iran

Background and Aim: Fungi of A. niger is widespread and contaminates the environment. This fungi is considered as an important mycose-causing agents in hospitals. In this study, the antifungal effect of clove ethanolic extract on A. niger was evaluated.

Methods: The clove ethanolic extract were prepared and its antifungal activity was evaluated against A. niger with pourplate method (100, 50, 25, 12.5, 6.25 mg/ml extract in medium)

Results: The Results indicated that clove extract prevents the grow of A. niger and MFC was 25 mg/ml.

Conclusion: The study confirm antifungal activity of clove ethanolic extract and suggest that clove extract can be use as a antifungal drug.

Keywords: Clove, Antifungal , A. niger

Zonosis and Veterinary Microbiology

P549 - 5: ISOLATION AND IDENTIFICATION OF PATHOGENIC BACTERIA OF RAINBOW TROUT FISH IN KERMAN PROVINCE.

Laleh Yazdanpanah[1]

1. Iranian fishery science research institute, Kerman agricultural and natural resources research and education center, Kerman, P.O. Box :7617913739, Agricultural Research, Education and Extension, Organization (AREEO), Tehran, Iran

Background and Aim: Aquaculture industry is very important to produce nearly one-third of the world's seafood supplies. One of the biggest problems in this industry is infectious bacterial disease, which effect livelihoods of communities causing heavy financial that production loses and a subsequent decrease in food availability

Methods:. pathogenic bacteria from 120 samples belonging to 10 rainbow trout populations from different localities of kerman province were isolated

Results: Cold-water fish have mostly gram-negative bacteria in their biota. Commonly appearing bacteria genera are Acinetobacter sp, Aeromonas hydrophila . Gram-positive organisms such as Bacillus, Micrococcus, and Corynebacterium can also be found in rainbow trout.

Conclusion: The results of the study open up the opportunity to perform further investigations which could determine the possible role of temprature in fish pathogens.

Keywords:pathogenic bacteria, rainbow trout, kerman Province.

P550 - 18: A SEROLOGICAL SURVEY ON COXIELLA BURNETII IN PREGNANT WOMEN WHO WERE HISTORICAL ABORTION IN KHORRAMABAD, WESTERN IRAN

Eiman Azizyari ghobadi[1], Soheila Akbari Torkemani[2], Fariba Hadi Panah[3]

1. Department of Pathobiology,Faculty of Veterinary Science, Lorestan University,Khorramabad,Iran.
2. Associate Professer, Department of Obstetrics and Gynecology,Faculty of Medicine,Lorestan University of Medical Science,Khorramabad,Iran
3. Asali hospital,Lorestan University of Medical Science,Khorramabad,Iran.

Background and Aim:Q fever is zoonotic disease caused by Coxiella burnetii , this bacteria is gram negative obligate intracellular. This disease have different clinical symptoms such as spontaneous abortion, premature birth, intrauterine growth retardation, oligoamonios and abnormal pregnancy in pregnant women. The aim of this study was to investigate the seroprevalence infection of C.burnetii in pregnant women who were historical abortion in Khorramabad (western Iran).

Methods:A total of 184 samples were collected randomly from pregnant women who reffered to clinical laboratory and center health in Khorramabad in 2017. Were exmined using indirect ELISA assay kit for the detection of C.burnetii phase II human antibodies in their serum sample.

Results: The total 184 serum samples from pregnant women, 39 sample was historical abortion that 19 sample(48/7%) was positive and 15 sample(38/5%) was negative and 5 sample(12/8%) was suspected.there is not statistically significant(pv=0/820).

Conclusion: According to result of this study, high prevalence of Q fever in pregnant woman who had historical abortion is necessary in due to the complexity of symptoms this disease in pregnant women,.For preventation and cure of unwanted side effects of this disease, pregnant women should pay more attention to this disease.

Keywords: Serological, Coxiella burnetii, Women Pregnant, Abortion.

P551 - 54: STUDY OF BACTERIAL CONTAMINATION IN GALLBLADDER OF SHEEP SLAUGHTERED IN SHIRAZ ABATTOIR

Mohammad Tabatabaie[1], Arash Soltani Borchaloee[2]

1. Department of Pathobiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
2. Department of Pathobiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran

Background and Aim: Generally gallbladder is a sterile organ, but pathogenic microorganisms can reside transiently or permanently in the gallbladder. The aim of this study was to isolate and characterize the bacterial contamination present in bile and gallbladder of sheep slaughtered in slaughter house in Shiraz, Fars province.

Methods: From April to May 2018 from 26 samples were taken by syringe from gallbladder at the slaughter house for isolation and identification of bacterial contamination. All samples were transferred to the laboratory of microbiology, faculty of veterinary medicine, Shiraz University, in cold condition in about 2 hr. in laboratory bile samples inoculated on Blood and MacConkey agar plates and incubated at 37°C for 24-48hr. then from colonies were grown prepared smear and gram stained. Then according to morphological and biochemical traits bacterial isolates characterized.

Results: From 26 bile samples 8 samples did not growth (30.81%). But in 18 samples after morphological and biochemical evaluation different bacteria were isolated. According to our finding percentage of bacteria in bile cultures were Staphylococcus spp. 19.23%, Salmonella spp. 15.38%, Escherichia coli 11.53%, Neisseria 11.53%, Micrococcus 3.8%, Seratia 3.8%, Yersinia 3.8%.

Conclusion: According to different studies factors such as fasciolosis, hepatitis and Cholelithiasis can cause chronic inflammation of the gallbladder. In my opinion these situations can act as a predisposing factor for entrance of some bacteria into the gallbladder.but it is not likely to become clinically significant.

Keywords: Gallbladder, Bacterial, Slaughterhouse, Shiraz

P552 - 67: AMPLIFICATION AND CLONING OF A OUTER MEMBRANE PROTEIN (OMPL37) OF LEPTOSPIRA INTERROGANS SEROVAR CANICOLA, SERJOE HARDJO, GRIPPOTYPHOSA

Elaheh Rezaei[1], Pejvak Khaki[2], Soheila Moradi Bidhendi[3], MojtabaNoofeli[4]

1. Department of Microbiology, Razi Vaccine and Serum Research Institute, Agricultural Research , Education and Extension Organization (AREEO), Tehran, IR Iran
2. Department of Microbiology, Razi Vaccine and Serum Research Institute, Agricultural Research , Education and Extension Organization (AREEO), Tehran, IR Iran
3. Department of Microbiology, Razi Vaccine and Serum Research Institute, Agricultural Research , Education and Extension Organization (AREEO), Tehran, IR Iran
4. Department of Microbiology, Razi Vaccine and Serum Research Institute, Agricultural Research , Education and Extension Organization (AREEO), Tehran, IR Iran

Background and Aim: Leptospirosis is the most widespread zoonotic disease in the world, mainly in countries with humid subtropical or tropical climates. Outer membrane protein OmpL37 is an immunogenic protein which is present only in pathogenic serovars expressed during infection and it is conserved among different Leptospira serovars. In order to evaluate genetic conservation of the ompL37 gene, we cloned and sequenced this gene from Leptospira interrogans serovar Canicola, Serjoe hardjo, Grippotyphosa.

Methods: Following the DNA extraction from the serovar, the ompL37 gene was amplified and cloned into pTZ57R/T vector and transformed into the competent E. coli (DH5α). Recombinant clones were confirmed by colony PCR and DNA sequencing. The related sequences were then analyzed and compared with the sequences in the Genbank database

Results:PCR amplification of the ompL37 gene resulted in a 996 bp PCR product. The PCR based on the ompL37 gene detected all the pathogenic reference serovars of the tested Leptospira spp. In our study nucleotide sequencing results showed that the ompL37 has high identity between 84% and 99.5%. Vaccinal serovar Canicola(RTCC2805) exhibited 99.2% sequence identity with field serovars Canicola(RTCC2824,RTCC2836). There were 98.5% identity between vaccinal and field serovars of Grippotyphosa and 99.5% identity between vaccinal and field serovars of Serjoe hardjo

Conclusion: According to the results of this study and other researches, ompL37 gene was highly conserved among various pathogenic Leptospira serovars and can be cloned, expressed and used to develop an effective recombinant vaccine against leptospirosis. OmpL37 recombinant protein can also be used in an ELISA kit for the serodiagnosis of leptospirosis

Keywords: Cloning, Leptospira, Outer membrane proteins, ompL37 gene

P553 - 70: THE ROLE OF THE AEROMONAS HYDROPHILA IN THE SAFETY OF FISHERY PRODUCTS

Laleh Yazdanpanah[1], Laleh Yazdanpanah goharrizi[2], Mohammad sheikhasadi[3]

1. Iranian fishery science research institute, Kerman agricultural and natural resources research and education center, AREEO, Kerman, 7617913739, Iran
2. Iranian fishery science research institute, Kerman agricultural and natural resources research and education center, AREEO, Kerman, 7617913739, Iran

Background and Aim: Aeromonas hydrophila is causes disease in fish. This bacteria is found in water, water habitants, domestic animals and foods (fish, shellfish, poultry, and raw meat). Fish infected with Aeromonas hydrophila may have many different clinical signs. Organs commonly affected with this disease are include: skin, gills, kidneys, liver, spleen, pancreas, and skeletal muscle. Aeromonas hydrophila infection of fish is a zoonotic disease and can be spread from animals to man.

Methods: The medium used for the isolation of A. hydrophila is TSA. Microscopic tests were done by staining Gram by observing the color and shape of bacteria was done. Biochemical test involved motile test, indol test, O/F test, and H2S test. Isolation of A. hydrophila was conducted on 30 samples of fish that were taken that showed pathologic conditions including hemorrhagic septicemia and tail or fin rot.

Results: The results of the identification of the bacterial isolate showed negative staining Gram, motile, form rod, and biochemical test results are fermentative, positive oxides, positive glucose and negative indol.

Conclusion: The bacterium Aeromonas hydrophila is one of the dangerous disease-causing bacteria in freshwater fish farming. Aeromonas hydrophila is a bacteria that can grow in the waters temperature of 20-30°C. Aeromonas hydrophila is pathogens because it only can cause disease in fish populations that are weak or as secondary infections when fish are infected with other diseases.

Keywords: Aeromonas Hydrophila, Safety, Fishery products

P554 - 78: MOLECULAR DETECTION OF TOXOPLASMA GONDII FROM LIVESTOCK IN KASHAN

Sima Rasti[1], Nader Marandi[2]

1. Department of Parasitology and Mycology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran
2. Department of Parasitology and Mycology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran

Background and Aim: Toxoplasmosis is one of the most common zoonotic diseases, which cause abortion in human and animals. Consumption of undercooked meat is one of the main routes of the infection. The present study was conducted to detect T. gondii infection by molecular method in livestock samples in Kashan, Iran.

Methods: This Cross-Sectional study was carried out on livestock slaughtered in Kashan in different seasons. A total of 180 heart samples from sheep and goats were investigated. After DNA extraction, Polymerase Chain Reaction method (PCR) was carried out using tox4 and tox5 primers. By observation of a 529 bp band, PCR was assigned as positive. Data such as sex, season, and molecular results were recorded in SPSS ver 16 and analyzed by chi-square and Fisher test.

Results: The T. gondii DNA was detected in 24 out of 180 animals (13.3%) by PCR. The highest and lowest infection rates were 24.4% and 2.2% in the autumn and winter respectively (P=0.001). Also, there was no significant difference between male and female (P=0.619).

Conclusion: The rate of infection with T. gondii in livestock was relatively high. Since the sheep and goats are the most important meat sources of Iranian people, health education in order to consumption of cooked meats could be considered for control and prevention of infection.

Keywords: Toxoplasma gondii, PCR, Livestock, Kashan

P555 - 79: COMPARISON PREVALENCE OF TOXOPLASMA GONDII IN KIDNEY TRANSPLANTATION REGIMES

Sima Rasti[1], Alireza Soliemani[2], Malihe Hasanzadeh[3]

1. Department of Parasitology and Mycology, School of Medicine, Kashan University of Medical Science, Kashan, Iran.
2. Department of Internal Medicine (Nephrology), Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran.
3. Department of Parasitology and Mycology, School of Medicine, Kashan University of Medical Science, Kashan, Iran.

Background and Aim: Toxoplasmosis is one of the common worldwide parasitic zoonosis, caused by the protozoan parasite Toxoplasma gondii. This disease in solid organ transplantation is uncommon but causes serious morbidity and mortality. The aim of this study was to determine the prevalence of T. gondii IgG and IgM in kidney transplant patients receiving three regimes Sirolimus (SSR), Cyclosporine A (SCA) and Tacrolimus (TAC) in Kashan.

Methods: In this historical cohort study, fifty serum samples were collected from kidney transplant recipient in Beheshti hospital of Kashan during 2014-2015. Enzyme-linked immunosorbent assay (ELISA) was used for detection of T.gondii-IgG and T.gondii-IgM antibodies. Toxoplasma IgG and IgM were negative in all of patients before kidney transplantation. The patients received three drugs regimes including Sirolimus, Cyclosporine A and Tacrolimus plus Micophenlate Mofetil (MMF) and Glucocorticoid (GCC) and followed for mean six years (1-15yrs). SPSS and X2 and Fisher exact tests were used for statistical analysis.

Results:T.gondii-IgG antibody was detected in 34.8% of patients receiving SSR+MMF+(GCC), 68.2% of patients receiving SCA+MMF+(GCC) and 60% TAC+MMF+(GCC), respectively (P=0.09). T.gondii-IgM antibody was negative in three groups.

Conclusion: According to the results of this study, prevalence of T. gondii was lower in patients receiving Sirolimus plus MMF and GCC compared to other regimes. Therefore applying of Sirolimus regime is better than other medications for toxoplasmosis in kidney recipients.

Keywords: Toxoplasma gondii, Kidney Transplantation, Sirolimus, Cyclosporine A, Tacrolimus

P556 - 104: THE EVALUATION OF IMMUNITY OF INACTIVATED RAZI BLACKLEG VACCINE BY AN INDIRECT ELISA AND COMPARISON OF THE METHOD WITH CHALLENGE TEST.

Ali Haghroosta[1], Reza Pilehchian langroudi [2], Lida Abdolmohammadi khiav [3], Mona Hasanzadeh [4]

1. Department of Anaerobic Bacterial Vaccines Production, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization(AREEO), Karaj, Iran.
2. Department of Anaerobic Bacterial Vaccines Production, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization(AREEO), Karaj, Iran.
3. Department of Anaerobic Bacterial Vaccines Production, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization(AREEO), Karaj, Iran.
4. Department of Anaerobic Bacterial Vaccines Production, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization(AREEO), Karaj, Iran.

Background and Aim: Blackleg is an acute infectious disease caused by Clostridium chauvoei and is characterized by inflammation of muscles, severe toxemia. The main purpose of this study was the evaluation of immunity of blackleg vaccine by using an indirect ELISA system and comparison of the method with challenge.

Methods: In this case, after preparation of whole cell antigens of Clostridium chauvoei, positive and negative sera were prepared by injection of rabbits, the blood samples were collected on 0, 15, 28 days after first vaccination and on 15, 45, 90, 180, 270, 360 days after second vaccination. An indirect ELISA test was carried out for detection of antibodies against Clostridium chauvoei and then the results were compared with the challenge assay in which animals were inoculated with Clostridium chauvoei.

Results: The results showed the rabbit ELISA titers remained up to on 270 days after second vaccination had a cut off titer 305.6 Unit/ml (100% protection), whereas on 360 days showed considerable decrease in rabbit ELISA titers. This experiment was confirmed by the challenge assay on guinea pigs. It was showed that correction coefficient ($r=0.74$) was significant between an ELISA titers and challenge assay and also there was a significant variation by t-test ($t=1.376$, $P<0.05$) between two groups of vaccinated (test) and unvaccinated animals(control).

Conclusion: It could be concluded that the ELISA is a proper test for evaluation of immune status of rabbit and has a significant correlation with challenge test and also ELISA method can use as an alternative for challenge test.

Keywords: Clostridium chauvoei, Blackleg, Vaccine, ELISA, Challenge.

P557 - 153: ALTERATION IN GST ACTIVITY IN LIVER, KIDNEY AND SPLEEN TISSUE OF IMMUNIZATION RAINBOW TROUT (ONCORHYNCHUS MYKISS) AGAINST ICHTHYOPHTHIRIUS MULTIFILIIS

Marzieh Heidarieh[1]

1. Nuclear Agriculture Research School, Nuclear Science and Technology Research Institute, Karaj, Iran.

Background and Aim: Ichthyophthirius multifiliis is a large ciliated protozoan parasite with distribution of throughout the world. Vaccination against I. multifiliis can be considered as the option ways to chemotherapy in fish. Because of not handling fish stocks, non-stressful method and less time consuming; oral administration can be considered as a good candidate. To improve the effectiveness of oral vaccination, development of an efficient delivery method is of major importance. The aim of present study was to clarify the effects of nanoparticles system for protection of the irradiated trophonts on glutathione S-transferase (GST) as oxidative stress biomarker in liver, kidney and spleen tissues of immunized rainbow trout against I. multifiliis.

Methods:A total of 150 parasite free rainbow trout were randomly assigned to 5 groups in triplicate, 30 fish per each aquarium. Group 1 served as healthy control. Group 2 was administered with gamma-irradiation trophonts. A group 3 was administered with alginate nanoparticles. A group 4 was administered with encapsulated gamma-irradiatied trophonts with alginate nanoparticles. A group 5 was non-immunized but infected with 10000 live trophonts. After sampling, GST activity in the tissues was assayed by using commercially available kits.

Results:GST activity in the liver, kidney and spleen tissues of rainbow trout treated with encapsulated gamma-irradiatied trophonts with alginate nanoparticles was significantly higher than the other groups.

Conclusion: Therefore, these results suggest that alginate nanoparticles could be more useful for development of gamma irradiated trophonts as radiovaccine

Keywords:glutathione S-transferase (GST), Alginate nanoparticles, Gamma irradiated I. multifiliis trophonts

P558 - 164: SURVEY OF HYDATID CYST SURGERIES IN PATIENTS REFERRED TO SHAHID BEHESHTI HOSPITAL OF KASHAN DURING 2012-2017

Sima Rasti[1], Tayebeh Taghipour niasar[2], Tahereh Khamehchian[3]

1. Department of Parasitology and Mycology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran
2. Department of Parasitology and Mycology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran
3. Department of Pathology, Faculty of Medicine, Kashan University of Medical Sciences, Kashan, Iran

Background and Aim: Hydatidosis is one of the most important zoonotic parasitic diseases in humans and animals caused by the larva stage of Echinococcus granulosus. This disease has been reported to be endemic in various parts of Iran .This study was conducted to investigate the demographic and clinical findings of hydatid cyst surgeries in Kashan, central of Iran.

Methods: In this descriptive study, data of hydatid cyst surgeries performed in Shahid Beheshti hospital of Kashan during the 5-year period from 2012-2017 were collected. Patients' data were age, gender, location of the cyst. The data were analyzed using SPSS and Chi-square test.

Results: Out of 81suspected hydatid cyst surgeries, 76 cases (93.8%) were positive and 5(6.2%) negative. The rate of hydatid cyst among female and male was 42(55.3%) and 34(44.7%) (p=0.86). The mean age of the patients was 40.5±17.23 years. Also, the highest and the lowest percentages of the disease were observed in the age group 20-39 (48.7%) and 60-80 (11.8%), respectively (p=0.001). The highest prevalence of the hydatid cyst was in the Lung 34.2%, followed by Liver 31.6%, gall bladder 3.9%, spleen 2.6%, and gall bladder +spleen +liver 5.3%.

Conclusion: Due to the high prevalence of Hydatidosis in this region, and high costs of diagnosis and treatment of disease, increasing people awareness, eliminating stray dogs are recommended to reduce the disease

Keywords: Hydatid Cyst, Echinococcus granulusos, Surgery

P559 - 180: SEARCHING FOR MYCOBACTERIUM AVIUM SUBSPECIES PARATUBERCULOSIS FROM BREAST MILK OF TWO CROHN'S DISEASE PATIENTS AND THEIR INFANTS BY NESTED-PCR: CASE REPORT

Saba Faeli[1], Farshad Hashemian[2], Setareh Haghighat[3], Naser Ebrahimi-Dariani[4], Farhad Moosakhani[5], Minoo Partovi Nasr[6]

1. Department of Clinical Pharmacy, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, Iran
2. Department of Clinical Pharmacy, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, Iran
3. Department of Microbiology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, Iran.
4. Department of Gastroenterology, Digestive Disease Research Center, Imam Khomeini Hospital, Tehran University of Medical Sciences, Tehran, Iran
5. Department of Microbiology, Faculty of Veterinary Medicine, Islamic Azad University, Karaj branch, Karaj, Iran
6. Tehran_karaj highway, Pajoohesh Blvd, Tehran province, NIGEB

Background and Aim: Crohn's disease (CD) is one major types of Inflammatory bowel disease (IBD), a chronic inflammatory condition which affects millions of people around the world. However the cause of the disease is still unknown, a number of theories regarding the aetiology of Crohn's disease have been proposed. The two leading theories are the infectious and autoimmune theories. Considering the isolation of Mycobacterium avium subspecies paratuberculosis (MAP) from intestinal tissue, blood, stool and milk samples of Crohn's disease patients and reports that have presented about its transmission from pasteurized milk and meat to human, it's thought to be one of the factors causing Crohn's disease is MAP. The purpose of this study was to identify the MAP from the breast milk of Crohn's disease patients and its transmission probability from mother to infant.

Methods:9 breast milk samples (2 mothers with CD and 7 healthy controls) and 9 fecal specimens of their infants were obtained. DNA extraction was performed from the samples. In order to identify contaminated samples, specific primers IS900 gene was amplified with Nested-PCR assay. Finally PCR products were electrophoresed on 1.5% agarose gel.

Results: From 18 examined samples of milk and feces, none of the specimens was found positive and infected with MAP on the basis of Nested-PCR analysis.

Conclusion: Despite the fact that our identification method was accurate, we did not identify the MAP in the samples of milk and stool. But controversy over the relationship between MAP and CD and other autoimmune diseases is still ongoing.

Keywords: Mycobacterium avium subsp. paratuberculosis, Inflammatory bowel disease, Crohn's disease, IS900 Nested PCR, Milk, Autoimmune disease.

P560 - 209: DETECTION OF NOVEL PICORNAVIRUS IN BROILER FLOCKS ,IRAN, 2018 : THE FIRST REPORT

Arash Ghalyanchilangeroudi[1], Masoumeh Jabbarifakhr[2], Mohammad Hossein Falah[3], Fatemeh Sadat Mousavi[4], Zahra Ziafati[5], Leila Aghaeean[6], Reyhaneh Khezrdoust[7], Amir Modiri[8], Hussein Rezaee[9], Pouria Chaboki[10]

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 Research and Production of Poultry Viral Vaccine, Razi Vaccine and Serum Research Institute, 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
7. Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
8. Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
9. Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
10. Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran

Background and Aim: Runting-stunting syndrome (RSS) in broiler chickens is an enteric disease that causes significant economic losses to poultry producers worldwide due to elevated feed conversion ratios, decreased body weight during growth, and excessive culling.Recent analyses of the enteric viromes in turkeys and chickens have revealed complex viral communities comprised of multiple viral families.

Methods: We got 50 cecal samples from broiler flocks with RSS and after RNA extraction, we run RT-PCR for detection and amplification of the variable gene of picornaviruses. After sequencing, we draw phylogenetic tree based on the results.

Results: The results confirmed the new picornavirus have been detected in the samples and 90 percent of samples are positive for the picornavirus.

Conclusion: This is the first report on identification of Sicinivirus in commercial layer chickens with a severe clinical disease in Iran, however, further studies are needed to evaluate the pathogenic potential of this picornavirus in chickens.

Keywords: Picornavirus, Iran, Chicken

P561 - 216: GENOMIC DETECTION OF CHLAMYDOPHILA ABORTUS IN SHEEP VAGINAL SWAB SAMPLES WITH ABORTION HISTORY IN LORESTAN PROVINCE USING NESTED-PCR METHOD

Homa Shamshiri[1], Jaydari Amin[2], Neamat Shams[3], Dalirannea Ali[4], BeiranvandMeasomeh[5]

1. . Master of science in bacteriology, Faculty of veterinary medicine, Lorestan University, Khorammabad, Iran.
2. . Assistant Professor, Department of microbiology, Faculty of veterinary medicine, Lorestan University, Khorammabad, Iran.
3. Assistant Professor, Department of microbiology, Faculty of veterinary medicine, Lorestan University, Khorammabad, Iran.
4. . Head , Department of veterinary medicine, Lorestan province, Khorammabad, Iran
5. Master of science in bacteriology, Faculty of veterinary medicine, Lorestan University, Khorammabad, Iran.

Background and Aim: Chlamydophila abortus is one of the most important infectious agents, causing abortion in ruminants. C.abortus is responsible for ovine enzootic abortion in sheep and goats, but is less commonly in cattle. Chlamydial abortion typically occurs in the last 2-3 weeks of pregnancy with the appearance of stillborn lambs and inflamed placentas. In Lorestan Province due to lack of sufficient information about Chlamydia aborttions because of the mountainous region sheep breeding is very important and considering to economic losses of abortion finding out the factors is very important.

Methods: In this cross – sectional study (from October 2017 – May 2018), 210 sheep vaginal swab sample were collected of aborted sheep in Lorestan Province. Samples were tested for the presence of Chlamydophila abortus by Nested PCR method related to 16srRNA gene.

Results: In this study, 19 samples (9.04%) were found to be positive for the presence of Chlamydophila abortus.

Conclusion: It can be concluded from this study that Chlamydophila abortus is one of infectious agents abortion in Lorestan Province and we have to do more studies and vaccination program can be used as a preventive method.

Keywords: Chlamydophila abortus, Nested – PCR, sheep vaginal swab, Lorestan province

P562 - 231: GENOMIC DETECTION OF MYCOPLASMA AGALACTIAE IN SHEEP VAGINAL SWAB SAMPLES WITH ABORTION HISTORY IN LORESTAN PROVINCE BY PCR

Masoumeh Bairanvand[1], Nemat Shams[2], Amin Jaydari[3], Homa Shamshiri[4]

1. 1MSc of Bacteriology, Department of Pathobiology, Faculty of Veterinary Medicine, Lorestan University, Khorramabad, Iran.
2. 2Assistant Professor, Department of Pathobiology, Faculty of Veterinary Medicine, Lorestan University, Khorramabad, Iran.
3. 2Assistant Professor, Department of Pathobiology, Faculty of Veterinary Medicine, Lorestan University, Khorramabad, Iran.
4. MSc of Bacteriology, Department of Pathobiology, Faculty of Veterinary Medicine, Lorestan University, Khorramabad, Iran.

Background and Aim: Contagious agalactiae caused by mycoplasma agalactiae is known as one of the most common infection diseases of sheep and goats in most parts of the world and Iran. The disease affects sheep and goat dairy herds due to abortion in pregnant ewes and medical expenses. Due to limited information about the rate of mycoplasma agalactiae aborted sheep in Iran, this study was conducted with the aim of genomic detection of mycoplasma agalactiae in vaginal secretion of sheep aborted in Lorestan province using polymerase chain reaction (PCR).

Methods: This cross- sectional study carried on 150 vaginal swab specimens of aborted sheep from October to March 2017. Mycoplasma genus was detected using specific primers in the 16sRNA gene region and 163bp band formation in received sample. Then, all positive samples were evaluated using specific primers in the surface lipoprotein region by forming a band of 375bp to detect the mycoplasma agalactiae species.

Results: Of the 150 vaginal swab specimens obtained from aborted sheep, 4 samples (2/6%) were positive for Mycoplasma. All of the positive samples were identified the mycoplasma agalactiae.

Conclusion: The results of the study showed that mycoplasma agalactiae cannot be considered as an important factor in abortion of sheep in Lorestan province and further studies are needed to determine the contribution of other causes of abortion in the study area.

Keywords: Mycoplasma agalactiae, abortion, vaginal swab

P563 - 243: THE EFFECT OF PROBIOTICS CELL FREE SUPERNATANT ON GROWTH AND VIABILITY OF IRANIAN ISOLATE OF PAENIBACILLUS LARVAE, THE ETIOLOGICAL AGENT OF AMERICA FOULBROOD DISEASE

Ramsina Betesho babrud[1], Rouha Kasra Kermanshahi[2], Farahnaz Motamedi Sede[3], Seyedeh Zahra Mousavinejad[4]

1. PhD candidate; Depatment of Microbiology, Faculty of Biological Sciences, Alzahra University, Vanak, Tehran, Iran; rbetesho@alzahra.ac.ir, Tel: +98218805812, Postal Code: 199383973
2. 3 Full Professor of Microbiology; Depatment of Microbiology, Faculty of Biological Sciences, Alzahra University, Vanak, Tehran, Iran; rouha.kasra@gmail.com, Tel: +989131150779, Postal Code: 1993893973
3. Associate Professor; Research School of Radiation Application, Nuclear Science and Technology Research Institute; fmotamedi@nrcam.org, Tel: +982612708717
4. Associate Professor; Depatment of Biotechnology, Faculty of Biological Sciences, Alzahra University, Vanak, Tehran, Iran; zahramoosavinejad@yahoo.com, Tel:+982188058912, Postal Code: 1993893973

Background and Aim: American Foulbrood (AFB) caused by Paenibacillus larvae is the most devastating bacterial disease in honey bee (Apia mellifera) larvae. The aim of the present work was to study the effect of cell free supernatant of probiotics on the growth and viability of an Iranian strain, P.larvaeKB10.

Methods: The strain was isolated from a comb with signs of AFB and identified on the basis of culture, biochemical characteristics and partial 16srRNA sequencing. Antibacterial effect of Lactobacilli strains was determined by drop plate method using cell free supernatant(CFS) of overnight cultured Lactobacilli in MRS broth. The minimal inhibitory(MIC) and bactericidal(MBC) concentrations were studied by microplate technique. The effect of CFS on viability of the isolate was investigated in 2 to 6 hour of exposure.

Results:P.larvaeKB10 was identified on the basis of colony morphology on CSA and MYPGP media, long gram-positive bacilli appeared single or arranged chains in gram staining. Catalase negative, gelatinase and Methyl Red positive, unable to use starch and unable to grow in Nutrient broth colonies were selected for molecular identification. The alignment of partial 16srRNA of P.larvaeKB10, with database revealed 97% identity with P.larvae subspecies larvae and 98% identity with P.larvae subspecies pulvifacience. The most antibacterial effect was observed in L.reuteriATCC23272. The MIC and MBC of the CFS were 1/1 v/v CFS/MRS. Viability test of 1.5×108 cfu/ml P.larvaeKB10 revealed that two hours of exposure with CFS in MIC concentration was enough to completely eliminate the pathogen.

Conclusion: The obtained results indicate bactericidal effect of L.reuteriATCC23272 CFS on P.larvaeKB10 growth and viability.

Keywords:beekeeping; American Foulbrood disease; probiotics; cell free supernatant; antimicrobial activity

P564 - 267: REEMERGENCE OF VELOGENIC NEWCASTLE VIRUS GENOTYPE 7D (7L) IN GILAN PROVINCE 2018

Reyhaneh Khezrdoust[1], Arash Ghalyanchi Langeroudi[2], seyed ali ghafouri[3], kambiz Ebrahimi [4], Leila Aghaiyan[5], Zahra ziafatikafi [6], amir modirihamadan[7], fatemeh sadat mousavi[8]

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. Iranian veterinary Organization, Tehran, IRAN
4. Sepidmakyan Co, Rasht , 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.
7. Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran.
8. Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran.

Background and Aim: Newcastle Disease Virus (NDV) is a single-stranded RNA virus of the Paramyxoviridae family that causes a contagious bird disease affecting many domestic and wild avian species. It is a zoonotic disease, and it‘s one of the major economically important poultry diseases distributed worldwide. This virus can survive for several weeks in warm environments such as in manure or between bird feathers. Newcastle disease virus strains are endemic in poultry in Iran and are witnessed annually in Iran. The different genotypes of NDV have been reported in our country.

Methods: Viral RNA extraction was performed from brain and trachea samples of 4 broiler flocks which were sent from Gilan province of Iran to our laboratory. The 203 bp region of the F gene was amplified using a pair of specific primers. The reaction products were analyzed by electropho-resis. The RT-PCR products were sequenced in the forward and reverse direction.

Results:bioinformatics and phylogenetic analysis were performed for sequencing result. Analyzed results indicated 7D (7L) genotype for the flocks which have previously been reported in the country. This genotype has existed in Gilan province and had disappeared for a period and now witnessed as a reemerged genotype.

Conclusion: The epidemiological data(pattern) were provided for the first time in 2018 from Gilan province, as one of the country's poultry production centers. These data can present epidemiological data(pattern) for circulation rate of this virus; however, This study suggests the Evaluation of Whole Genome Sequencing for NDV.

Keywords: Newcastle, Genotype 7D, Iran

P565 - 362: EVALUATION OF NEUTRALIZING ANTIBODY ON VACCINATED CHICKEN BY GAMMA IRRADIATED AVIAN INFLUENZA VACCINE SUBTYPE H9N2

Saba Mesbah[1], Farahnaz Motamedi-Sadeh[2], Omid Madadgar[3], Iraj Khalili[4], Parvin Shawrang[5], Mehdi Behgar[6]

1. Faculty of veterinary medicine, university of Tehran, Tehran, Iran
2. Nuclear Agriculture Research School -Nuclear science and technology Research Institute of Iran, Karaj, Iran
3. Department of Microbiology and Immunology, Faculty of veterinary medicine, university of Tehran, Tehran, Iran
4. Quality control department, Razi vaccine and serum research institute, Karaj, Iran
5. Nuclear Agriculture Research School -Nuclear science and technology Research Institute of Iran, Karaj, Iran
6. Nuclear Agriculture Research School -Nuclear science and technology Research Institute of Iran, Karaj, Iran

Background and Aim:: Avian influenza A subtype H9N2 virus belongs to Orthomyxoviridae family and causes low-pathogenic disease. H9N2 subtype was first reported to have infected turkeys in the United States in 1966 and has been enzootic in Eurasia. In Iran, the H9N2 virus was first isolated from broiler chickens in 1998 in Ghazvin Province and it is the most prevalent subtype of influenza virus in poultry industry in Iran at the present time causing serious economic losses in the poultry industry. The hemagglutinin (HA) antigen is the most important viral glycoprotein for attachment and fusion in virus replication cycle and is highly immunogenic.

Methods: Avian Influenza virus (AIV) subtype H9N2 was multiplied on embryonated SPF chicken eggs of 9–11 days. AIV was irradiated by a Nordian model 220 gamma cell instrument at a dose rate of 2.07 Gy/s and activity of 8677 Ci to damage influenza virus genomic RNA to inactivate virus infectivity with 30 kGy gamma radiation. The neutralizing antibody response by hemagglutination inhibition (HI) method was evaluated on vaccinated broiler chickens in three vaccine concentrations (1, 10-1, and 10-2).

Results: The result of antibody titers was analyzed by Anova one-way method. The result of antibody titration by HI method was shown inhibition of erythrocyte agglutination by an antigen-antibody reaction was increase significantly for two vaccinated groups (1 and 10 -1 vaccine concentrations) against negative control group ($P<0.05$).

Conclusion: The neutralizing antibody titration was increased after on vaccination broiler chicken by gamma irradiated Avian Influenza vaccine subtype H9N2.

Keywords: Avian Influenza , Gamma Irradiation, Hemagglutinin Antigen, Inactivation, Hemagglutination Inhibition test, Broiler Chicken

P566 - 363: EFFECTS OF GAMMA IRRADIATED AVIAN INFLUENZA VACCINE SUBTYPE H9N2 ON VACCINATED CHICKEN'S SPLENIC CELL PROLIFERATION

Saba Mesbah[1], Farahnaz Motamedi-Sadeh[2], Omid Madadgar[3], Iraj Khalili[4], Parvin Shawrang[5], Mehdi Behgar[6]

1. Faculty of veterinary medicine, university of Tehran, Tehran, Iran
2. Nuclear Agriculture Research School -Nuclear science and technology Research Institute of Iran, Karaj, Iran
3. Department of Microbiology and Immunology, Faculty of veterinary medicine, university of Tehran, Tehran, Iran
4. Quality control department, Razi vaccine and serum research institute, Karaj, Iran
5. Nuclear Agriculture Research School -Nuclear science and technology Research Institute of Iran, Karaj, Iran
6. Nuclear Agriculture Research School -Nuclear science and technology Research Institute of Iran, Karaj, Iran

Background and Aim: Influenza is one of the most important diseases in the poultry industry. It has adverse economic effects on the poultry industry as well as public health. In the middle of July 1998, this virus caused a kind of unknown illness in poultry around Tehran and Qazvin. It was then isolated and identified under the Type A/chicken / Iran / 259/1998 H9N2 in Razi vaccine and serum research institute of Iran and Tehran Veterinary School. Unfortunately, the disease has spread rapidly in the country, and despite the special plans, the disease has been endemic and has caused extensive damage to the country's poultry industry.

Methods: Avian Influenza virus (AIV) subtype H9N2 was multiplied on embryonated SPF chicken eggs of 9–11 days. AIV was irradiated by a Nordian model 220 gamma cell instrument at a dose rate of 2.07 Gy/s and activity of 8677 Ci to damage influenza virus genomic RNA to inactivate virus infectivity with 30 kGy gamma radiation. The spleeny T lymphocyte proliferation was evaluated on vaccinated broiler chickens by three vaccine concentrations (1, 10-1, and 10-2) and injection method according to the MTT test.

Results: The result of stimulation index was analysis by Anova one-way method. The result of MTT test was shown proliferation of spleeny T lymphocyte was increase significantly for two vaccinated groups (1 and 10 -1 vaccine concentrations) against negative control group ($P<0.05$).

Conclusion: The gamma irradiated Avian Influenza subtype H9N2 antigen stimulated the increasing effects on proliferation of chicken's spleeny T lymphocyte.

Keywords: Avian Influenza Virus, Gamma Irradiation, Inactivation, Splenic Lymphocyte, MTT test

P567 - 447: DETERMINATION OF ANTIBIOTIC RESISTANCE 1 PATTERN AND VIRULENCE GENES IN 2 ESCHERICHIA COLI ISOLATED FROM BOVINE WITH MASTITIS IN SOUTHWEST OF IRAN

Masoud Marashifard[1], Seyed Sajjad Khoramrooz[2], Zahra Karimi Aliabad[3], Asghar Sharifi[4], Mohsen Naghmachi[5]

1. Student Research Committee, Yasuj University of Medical Sciences, Yasuj, Iran
2. Cellular and Molecular Research Center, Yasuj University of Medical Sciences, Yasuj, Iran
3. Department of Basic Sciences, Islamic Azad University, Yasooj Branch, Yasooj, Iran
4. Cellular and Molecular Research Center, Yasuj University of Medical Sciences, Yasuj, Iran
5. Cellular and Molecular Research Center, Yasuj University of Medical Sciences, Yasuj, Iran

Background and Aim: The aims of the present study were to investigate the prevalence of some virulence genes and also determine the antimicrobial resistance pattern of E. coli isolated from bovine with subclinical mastitis. The milk of 502 cows was collected from 8 dairy herd in the southwest of Iran.

Methods: Conventional biochemical tests were used for identification of E. coli at the species level. Antimicrobial susceptibility patterns of E. coli isolates were determined by Disc Agar Diffusion method and Polymerase Chain Reaction (PCR) was used for detection of seven virulence genes including f17A, afaE-8, afaD-8, eaeA, cnf1, cnf2, and iucD. Seventy (13.94%) isolates of E. coli were identified in 502 milk samples.

Results: The highest rate of resistance was observed against tetracycline (18.6%), while none of the isolates were resistant to streptomycin. Eight (11.5%) out of 70 E. coli isolates carried at least one of the virulence genes. The afaD-8 was the most prevalent gene detected in 5 (7.1%) isolates. The afaE-8, iucD, and eaeA detected in 3, 3 and 2 isolates respectively

Conclusion: Low prevalence of virulence factors may be indicating that most of the E. coli isolates originated from the commensal flora of cows and enter to the udders via environment contamination with feces.

Keywords: Mastitis, E. coli, antibiogram, virulence genes

P568 - 449: USING THE MULTIPLEX-PCR METHOD FOR DETECTION FOUR VENEREAL BACTERIA (TAYLORELLA EQUIGENITALIS ‘KLEBSIELLA PNEUMONIAE ‘PSEUDOMONAS AERUGINOSA AND STREPTOCOCCUS ZOOEPIDEMICUS) FROM THE MARE’S CLITORAL SAMPLES

Rasoul Imanian Njaf Abadi[1], Ali Kadivar[2], Najme Davoodian[3], Mohammad Reza Mahzoonie[4]

1. Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
2. Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
3. Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
4. Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran

Background and Aim: Sexually transmitted diseases are one of the major problems in reproductive management of horses. These diseases cause large economic losses to horse and horse breeding. The aim of this study was to design a multiplex-PCR method in order to detect four bacterial sexually transmitted diseases (Tylerella echinogenitalis, Klebsiella numonia, pseudomonas aerogenosa and Streptococcus zoepidemicus).

Methods: For this study, we sampled from the Clitoris of 106 horses using sterile swab. The primer design was based on the specific genes of each bacterium and was designed to be eligible for multiplex PCR. DNA extraction from each sample was performed using a special extraction kit. Pure sample from each bacterium were used as positive control and the PCR reaction conditions continued until favorable results were obtained in multiplex conditions on positive control samples.

Results: Regarding the accuracy of the positive control and PCR conditions, all samples were free from the sexually transmitted factors and no bacteria were isolated.

Conclusion: Multiplex-PCR responses to identify the four bacterial sexually transmitted factors can be designed and performed, although the samples taken in this study were free of bacteria.

Keywords: Taylorella equigenitalis, Klebsiella pneumonia, pseudomonas aeruginosa, Streptococcus zooepidemicus, multiplex-PCR

P569 - 453: USING THE MULTIPLEX-PCR METHOD FOR DISCOVERY FOUR VENEREAL BACTERIA (TAYLORELLA EQUIGENITALIS ‘KLEBSIELLA PNEUMONIAE ‘PSEUDOMONAS AERUGINOSA AND STREPTOCOCCUS ZOOEPIDEMICUS) FROM THE MARE’S CLITORAL SAMPLES

Rasoul Imanian Njaf Abadi[1], Ali Kadivar[2], Najme Davoodian[3], Mohammad Reza Mahzoonie[4]

1. 1Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
2. 1Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
3. 1Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
4. 1Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran

Background and Aim: Sexually transmitted diseases are among the major problems in reproductive management of horses. These diseases cause large economic losses to horse breeding farms. The aim of this study was to design a multiplex-PCR method in order to detect four bacterial sexually transmitted diseases (Tylerella echinogenitalis, Klebsiella numonia, pseudomonas aerogenosa and Streptococcus zoepidemicus) from the mare’s clitoral samples.

Methods: For this study, we sampled from the Clitoris of 106 horses using sterile swab. The primer design was based on the specific genes of each bacterium and was designed to be eligible for multiplex PCR. DNA extraction from each sample was performed using a special extraction kit. Pure sample from each bacterium were used as positive control and the PCR reaction conditions continued until favorable results were obtained in multiplex conditions on positive control samples. In order to ensure the correctness of the PCR reaction, using Universal primer on all samples, a PCR reaction was performed and the samples were sent to Rena Biotechnology Company for sequencing.

Results: Using universal primer and sequencing of samples, genera were isolated from Porphyromonadaceae, Campylobacteraceae, Bacteroidaceae, Clostridiaceae and others.

Conclusion: In order to confirm the validity of Multiplex-PCR, the use of Universal Primer and sequencing is appropriate.

Keywords: Taylorella equigenitalis, Klebsiella pneumonia, pseudomonas aeruginosa, Streptococcus zooepidemicus, multiplex-PCR

P570 - 454: CLONING AND EXPRESSION OF RECOMBINANT LIPL32 ANTIGEN FROM LEPTOSPIRA INTERROGANS IN PROKARYOTIC SYSTEM.

Nina Bakhshandeh[1], Majid tebianian[2], Pejvak khaki[3], Majid Esmaelizad[4], Sara Saadatmand[5]

1. Department of Biology,Science and Research Branch,Islamic Azad university,Tehran,Iran
2. Razi Vaccine & Serum Research Institute,karaj,iran
3. Razi Vaccine & Serum Research Institute,karaj,iran
4. Razi Vaccine & Serum Research Institute,karaj,iran
5. Department of Biology,Science and Research Branch,Islamic Azad university,Tehran,Iran

Background and Aim: Leptospirosis,caused by infection with pathogenic leptospira species is recognized as the most widespread zoonosis with a global distribution. Lipl32 is an immunogenic outer membrance protein found in pathogenic Leptospira species. The protein expressed by lipl32 gene may be used in diagnostic method and also can be a good candidate for recombinant vaccine against leptospirosis. The aim of this study was Cloning and expression of recombinant LipL32 antigen from Leptospira interrogans in prokaryotic system

Methods: LipL32 was clonned in E. coli strain BL21 using pET32 + plasmid as a vector and induced with 25 µM IPTG at 22 °C for 16 hours. The bacterial pellet was obtained by centrifugation (5,000 rpm). The resuspended cells were disrupted by sonication. The cell lysate was centrifuged at 15,000 rpm at 4 °C for 20 min. Samples were solubilized in sample buffer plus mercaptoenthaol , Proteins were separated on 10% sodium dodecyl sulfate (SDS) and followed by Coomassie Brilliant Blue staining

Results: The protein was successfully expressed in E.coli BL21 and purified. SDS-PAGE results showed that the full-length 38kD protein was induced by 25 µM IPTG

Conclusion: Leptospirosis is considered as a reemerging infectious disease, not only for the increase in its incidence during the past recent years but also for the increased severity of the illness. The cloned gene could be further used for expression of recombinant protein for serodiagnosis and leading candidate vaccine antigens of leptospirosis. .

Keywords:lipl32 ,recombinant protein , leptosoirosis

P571 - 456: EPIDEMIOLOGICAL STATUS OF HUMAN CCHF IN DIFFERENT REGION OF IRAN FROM 1999 TO 2017

Nona Moradpour[1], Simin Nayebi moghaddam[2], Hassan Mashhadi[3]

1. ph.D of parasitology, Faculty of Science, Islamic Azad University of Mashhad,Iran
2. Department of Biology, Faculty of Science, Islamic Azad University of Mashhad,Iran
3. Department of Biology, Faculty of Science, Islamic Azad University of Mashhad,Iran

Background and Aim: Crimean-Congo Hemorrhagic Fever (CCHF) is a tick-borne virus with the risk of death. Considering the high prevalence of this disease in Iran, a study was conducted to evaluate a epidemiological status of human CCHF during 1999 to 2017.

Methods: This study was in form of retrospective cross-sectional and the data includes demographic characteristics such as age, occupation, residence, nationality.

Results: Of 1,340 CCHF patients, 90.82% had Iranian nationality and 9.17% had other nationalities. The most contaminated occupation group were Ranchers and farmers with (21.34%) and the majority of the patients (65%) were urban. The age range was 20-39 and the highest prevalence rate of contamination was observed for 20 – 29 age groups. The highest affected patients (77.81%) were infected in the first half of the year. The most rate of infection was observed in provinces of Sistan & Baluchistan, Khorasan Razavi and Fars, respectively. In 89% of cases, there is a gap of 0-1 days between the diagnosis of the disease and the preparation of the first patient sample.

Conclusion: Considering the fact that CCHF is a work-related illness and there is no specific antiviral therapy available thus far, necessity of training to better understand the disease, the way of the disease transmission and controlling methods as well as prevention is inevitable. Awareness campaigns regarding the risk factors and control measures can aid in reducing the spread of this disease to a greater extent, particularly in urban area.

Keywords: Epidemiology, CCHF, Iran

P572 - 468: PREVALENCE OF BRUCELLOSIS IN MILK AND BLOOD OF MARES OF YAZD PROVINCE IN 1396

Ladan Reisimotlagh[1]

1. School of Public Health, Shahid Sadoughi University of Medical Sciences, Yazd, Iran

Background and Aim: Brucellosis or brucellosis is one of the most well known and most important zoonoses in the world and especially in Iran. The consumption of milk and livestock products is one of the main ways of transmitting disease to humans. Horse milk is a rare and expensive product with higher nutrients than cow's milk. Due to the consumption of horse milk in infants and adolescents in Yazd, there is no information about the prevalence of brucellosis among animals, including mares of this city. The aim of this study was to determine the prevalence of brucellosis using serological methods and polymerase chain reaction in marijuana and marijuana in Yazd.

Methods: In this study, 82 blood samples and 82 milk samples from the marijuana of Yazd clubs were collected in a sequential sampling. Serologic methods of Rose Bengal and ring testing were used. DNA was extracted directly from milk and blood samples. PCR test was performed using the primers ISP1 and ISP2 to detect Brucella genus using Ba-SP, Bm-SP and IS7 primers for detection of abortus and National Teniss species.

Results: Based on serological tests no positive cases were found. By performing PCR to detect Brucella genus, 3 samples from milk samples were positive. All three positive specimens were identified as Brucella abortus.

Conclusion: According to the findings of the study, the consumption of raw horses can cause a serious risk to the health of the community, thus revealing the need for health measures and information on horseradish milk.

Keywords: Brucella,Raw milk , Blood, Horse, PCR

P573 - 477: THE INFORMATION SOURCES OF STUDENTS NON-MEDICAL UNIVERSITIES IN KERMANSHAH PROVINCE, IRAN ABOUT SALMONELLOSIS

Amir Amiri paryan[1], Amir Amiri paryan[2]

1. Department of basic Science and Pathobiology, microbiology section, Faculty of Veterinary Medicine, Razi University,Kermanshah,Iran
2. Veterinary Student, Pathobiology & Basic Sciences, Faculty of Veterinary Medicine, Razi University, Kermanshah, 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. The aim of this study was evaluate the knowledge in Non-Medical Students Kermanshah province of Iran about Salmonellosis.

Methods: This cross-sectional prospective questionnaire survey was carried out in Non-Medical students Kermanshah province of Iran and Knowledge about Salmonellosis was evaluated. 300 students in grades BSc, Mas, PhD and DVM were included.x2 & oneway ANOVA tests and P value<0.05 were applied for statistical analysis.

Results: The majority of study population (%72) mentioned television as their main source of information, while only less percentage (%28) obtained information from newspapers, journals and others. A significant correlation between field of study and source type of information were observed (P<0.05).

Conclusion: Our result indicated educate about the risk factors that lead to Brucellosis infection was important. Because, according to our findings health education against Salmonellosis is necessary. Moreover, modification of the red lines existed in strategist sights and the media, especially in RA&TV, will reduce the risk of Salmonellosis with improving Knowledge, revision and improvement of SI should be a priority for all institutions and universities especially in study area.

Keywords:: Information sources, Students Non-Medical, Salmonellosis

P574 - 483: STUDYING THE KNOWLEDGE OF NON-MEDICAL STUDENTS IN KERMANSHAH PROVINCE ABOUT VETERINARIANS' PERSPECTIVES ON THE PREDICTION OF THE CRIMEAN-CONGO HEMORRHAGIC FEVER (CCHF) AS A NECESSITY IN BIOSAFETY

Mona Mohammad zaheri[1], Mehrdad Pouyanmehr[2], Mona Mohamadzaheri[3]

1. -
2. Assistant Professor of Immunology, Department of Basic Sciences and Pathobiology, Faculty of Veterinary Medicine, Razi University, Iran
3. Veterinary student,pathobiology & basic sciences, faculty of veterinary medicine,razi university,kermanshah,iran

Background and Aim: Crimean Congo Hemorrhagic Fever (CCHF) is an acute febrile and bleeding disease that is transmitted through bites or contact with blood, secretions or carcasses. The CCHF in humans causes a severe illness with about 30% mortality rate and the prevalence of the hospital is very high. The purpose of this study was to assess the knowledge of non-medical students in Kermanshah province about the role of veterinarians in Predicting CCHF as a biosafety necessity in community.

Methods: In a descriptive research, a questionnaire about CCHF prediction was distributed among a statistical population of university students and non-medical higher education institutions of Kermanshah province in 3 groups of different educational levels (bachelor, master or doctorate and doctorate) with the total number of students 300 people (150 people: female, 150 male: male). The collected data was analyzed by SPSS Statistics version 20.0.

Results: The results of this study on the question of veterinarian role in predicting CCHF, relative to students, undergraduate, postgraduate or doctorate and doctorate were 33. 39, 42.34 and 18.33 percent respectively. Also, the level of awareness of male and female students about other sexually transmitted infections (such as prevention, infection control, etc.) was 33. 29% and 67.70%.

Conclusion:CCHF is an animal-borne viral disease. The transmission of virus-infections by its various causes is due to poor health and traditional animal husbandry. Along with lack of knowledge of community members is important in vulnerable groups. The role of veterinarians and the Ministry of Health in controlling the disease is very important.

Keywords: Crimean-Congo (CCHF), biosafety, veterinarians

P575 - 487: STUDYING THE KNOWLEDGE OF NON-MEDICAL STUDENTS IN KERMANSHAH PROVINCE ABOUT VETERINARIANS' PERSPECTIVES ON THE PREDICTION OF THE SALMONELLOSIS (TYPHOID) DISEASE AS A NECESSITY IN BIOSAFETY

Mona Mohammad zaheri[1], Mehrdad Pouyanmehr[2], Mona Mohamadzaheri[3]

1. -
2. Assistant Professor of Immunology, Department of Basic Sciences and Pathobiology, Faculty of Veterinary Medicine, Razi University, Iran
3. Veterinary student,pathobiology & basic sciences, faculty of veterinary medicine,razi university,kermanshah,iran

Background and Aim: Salmonellosis is an important zoonotic disease. Animal-derived foods, especially meat and eggs are important sources of Salmonella typhimurium and typhoid bacteria that causes gastroenteritis (typhoid fever) in humans and other mammals and also significant increases in various health-economic damages. The purpose of this study was to investigate the knowledge of non-medical students in Kermanshah province as an example of the non-medical scientific community in Iran regarding Salmonella disease.

Methods: In a descriptive research, a questionnaire about Salmonellosis (Typhoid) Disease prediction was distributed among a statistical population of university students and non-medical higher education institutions of Kermanshah province in 3 groups of different educational levels (bachelor, master or doctorate and doctorate) with the total number of students 300 people (150 people: female, 150 male: male). The collected data was analyzed by SPSS Statistics version 20.0.

Results: The results of this study on the question of veterinarian role in predicting Salmonellosis as a necessity of biosecurity in the community, relative to students, undergraduate, postgraduate or doctorate and doctorate were 33. 39, 42.34 and 18.33 percent respectively. Also, the level of awareness of male and female students about other sexually transmitted infections (such as prevention, infection control, etc.) was 33. 29% and 67.70%.

Conclusion: Salmonellosis is a common human and animal-borne viral disease. The transmission of virus-infections by its various causes is due to poor health and bioenvironmental problems. Along with lack of knowledge and Awareness of community members is especially important in vulnerable groups. The role of veterinarians and the Ministry of Health in controlling the disease is very important

Keywords: Salmonellosis, biosafety, veterinarians

P576 - 492: SEROPREVALENCE OF TOXOPLASMA GONDII INFECTION AMONG CHILDBEARING AGE WOMEN IN KERMAN CITY, SOUTHEASTERN IRAN

Fatemeh Akbarpour[1], Hossein Mahmoudvand[2], Zahra Chegeni[3], Saghar Modarresi[4], Elnaz kianmehr[5], Amir Tavakoli Kareshk[6]

1. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
2. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
3. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
4. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
5. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran
6. Cutaneous Leishmaniasis Research Center, Mashhad University of Medical Sciences, Mashhad, Iran (atk9388@gmail.com).

Background and Aim: Toxoplasma gondii is a ubiquitous obligatory intracellular coccidian protozoan organism found throughout the world that infects a wide range of warm-blooded animals and approximately one-third of the world's human population. The present investigation aims to determine the prevalence of IgM and IgG anti-T. gondii antibodies and the associated risk factors among childbearing age women referring to counseling centers before marriage in Kerman city, southeast of Iran.

Methods: Totally, 300 serum samples were collected from women referred to Central Laboratory for Marriage Consultation in Kerman city were screened for IgG and IgM anti-T. gondii antibodies by enzyme linked immunosorbent assay (ELISA).

Results: Out of the 300 serum samples, 38 (12.6 %) tested seropositive for anti-T. gondii antibodies; 31 (10.3 %) samples tested seropositive for only IgG antibody, 1 (0.33 %) tested seropositive for both IgM and IgG and 6 (2.0 %) were positive for IgM antibody alone. Statistical analyses also indicated that seroprevalence of anti-T. gondii antibodies increased with age ($p < 0.05$). Moreover, some risk factors such as, living in rural regions, contact with cats, raw/half-cooked meat consumption, and agricultural activities were significantly ($p < 0.05$) related to T. gondii seropositivity.

Conclusion: The findings revealed that more than three-quarters of the childbearing age women studied in the present investigation are susceptible to infection during pregnancy. Thus, by adopting correct and improved practices we can improve their living conditions, and prevent infection and awareness and con- trol of pathogens associated with disease is recommended.

Keywords: Toxoplasmosis; IgG antibody; IgM antibody; ELISA

P577 - 494: STUDY OF THE KNOWLEDGE OF STUDENTS RELATED TO BIOLOGICAL SCIENCES IN UNIVERSITIES AND FACULTY OF KERMANSHAH PROVINCE ABOUT THE EFFECTS OF GENETICALLY MODIFIED SUBSTANCES ON ECOSYSTEM AND HEALTH

Mehrdad Pooyanmehr[1], Ghazal Keyvanfard[2]

1. Assistant Professor of Immunology,Department of Basic Sciences and Pathobiology,Faculty of Veterinary Medicine,Razi University,Kermanshah,Iran
2. Veterinary Student,Pathobiology and Basic Sciences,Faculty of Veterinary Medicine,Razi University,Kermanshah,Iran

Background and Aim: Creatures or biological materials that part of their DNA Change through genetic engineering , they are called transgenic. The purpose is to create a new trait in living organisms such as resistance to chemical agents, diseases or specific environmental conditions, reduce corruption or produce various products. Although these knowledgeable products can benefit from high yields and resistance to pests, they can cause many problems for human health, livestock, poultry, aquatic animals and ecosystems, for years to come

Methods: In a study, a questionnaire among 300 female and male students (total number of female students 90 and male 210) in Universities and FACULTY of Kermanshah into 4 groups: undergraduate, postgraduate, doctoral and PHD done gathered information was given on the awareness of the potential problems and the unknown effects of transgenic products on human health, livestock, poultry, aquatic animals and ecosystem. Statistical analysis was performed with SPSS version 20.

Results:positive response to the questions In proportion to the number of questioned students, undergraduate, postgraduate, doctoral and PHD Respectively was 33,20,56.6,30.16 Also, the level of awareness of female and male was 22.87 and 77.13 respectively

Conclusion: Genetically modified products may cause health problems for consumers, such as infertility , cancers, allergic reactions and Inadequate knowledge about the specific conditions of gene expression, the creation of unknown proteins, bacterial resistance to antibiotics, damage to degradation of ecosystems such as resistance to herbicide and consequently the reduction of biodiversity will result in ethical, social, environmental, bio-safety and commercial concerns.

Keywords: Genetically Modified, Transgenic, Ecosystem

P578 - 509: PREVALENCE OF COAGULASE POSITIVE STAPHYLOCOCCUS AUREUS IN SOME DOMESTIC ANIMALS.

Bahar Malek ghaini[1], mojtaba mohseni[2], rahem khoshbakht[3]

1. Corresponding author: B.Malek@stu.umz.ac.ir
2. Department Microbiology, Faculty of Science, University of Mazandaran, Babolsar, Iran
3. Department Pathobiology, Faculty of Veterinary Medicine, Amol University of Special Modern Technologies, Amol, Iran

Background and Aim: Staphylococcus aureus has been recognized as an opportunistic pathogen in many kinds of domestic animals, especially in dogs and cats. In recent years, occurrence of methicillin resistance in Staphylococcus aureus has increased significantly

Methods: In order to isolate the Staphylococcus aureus, clinical specimens were taken by a sterile swab from the anterior nares of domestic animals including dogs, cats and their owners who referred to veterinary clinics. The specimens were directly inoculated on mannitol salt agar and incubated at 37°C for 48h. Staphylococci were identified by their morphological and physiological characteristics. In addition, oxacillin screening plate method was used for determination of methicillin resistant isolates.

Results: The results of this study showed that in 91 clinical specimens 13 isolates were coagulase positive These results demonstrated that the prevalence of coagulase positive Staphylococc in clinical specimens collected from dogs, cats and pet owners were 8/7, 3/2 and 2/1 percent, respectively.

Conclusion: This study indicated that coagulase positive S.aureus was present in domestic dogs and cats. Due to the constant interaction between these animals and their owners, it is important to prevent the transmission of antibiotic resistant staphylococci between animals and humans.

Keywords: Staphylococcus aureus , Coagulase, Domestic animals

P579 - 510: CLONING AND EXPRESSION TWO RECOMBINANT PROTEIN OF MYCOBACTERIUM BOVIS

Reza Arefpajoohi[1], Taghi Zahraee salehi[2], Nader Mosavar[3], Zahra salehi najaf abadi[4]

1. head of bovine PPD laboratory
2. full professor of microbiology Department
3. head of tuberculine and mallein department
4. assistant professor

Background and Aim: Mycobacterium bovis is agent of bovine tuberculosis that mainly separated from bovidae. The consequences of disease are widely spread including decrease in production, early death and economic losses. Primary diagnosis based on tuberculin skin test that may have false positive. esat-6 and CFP-10 are important protein that secreted in early stage of disease. also these proteins are eliminated in process of PPD-B production. To investigate the functions of that, two genes esat-6 and CFP-10 are cloned and expressed.

Methods: Sequence of esat6 & cfp10 of mycobacterium bovis obtained from bovilst. designed primer with restriction enzymes BamHI and EcoRI synthetize in Macrogen co. After that Polymerase Chain Reaction(PCR) was performed to amplify these genes. In parallel DH5α-pET23a (+) replicated and then isolated the vector. Both vector and PCR product are digested, ligation was done at16 cloned vector transform to DH5α. After being identified with sequencing, cloned vector transformed to expression vector BL21. Expressed protein optimized and analyzed with sodium dodecyl sulfate-polyacrylamide gel electrophoresis(SDS-PAGE) and Western blotting.

Results: The esat6 and cfp10 genes were amplified successfully. Both of them were cloned into expression vector. After identified by sequencing, genes were expressed. Analyzed of proteins expressed showed the molecular weight about 10 KDa.

Conclusion: The esat6 and cfp10 genes were successfully cloned and expressed in E. coli.

Keywords: Mycobacterium bovis,ESAT6,CFP10

P580 - 511: EFFECT OF PROTECTION VACCINE TS11 IN CILINICAL SAMPLES FROM COMMERCIAL AND DOMESTIC POULTRY WITH PCR ASSAYE

Fatemeh Babaahmadi[1], Alireza Mahmodian[2]

1. MS of veternary bacterilogy
2. department of veternary microbiology urmia univercity

Background and Aim: Mycoplasmose a widespread infectious disease that has affected the poultry industry around the world Mycoplasma gallisepticum(MG) belongs to the Mollicutes class and is one of the smallest free living. micro organism that grow in a very nutritious environment. The aim of this study was to investigate and detect Mycoplasma gallisepticum from industrial and domestic broiler chickens in Urmia by polymerase chain reaction (pcr).

Methods: The chickenpox of the suspected poultry was collected by sampling swab. After transferring samples to The bacteriological laboratory was attempting to extract DNA Using mycoplasma galli septicemia specific primers on all samples taken in the gyrb region, the PCR reaction done.

Results: This study experiment randomized 50 samples of broiler commerical poultry with evident clinical manifestations of mycoplasma gallisepticum, 3samples with a specific primer designed, were positive PCR, and in 20 samples from domestic poultr, 6 cases were positive.

Conclusion: The result of the TS11 vaccine is somewhat immune, and contamination in commercial poultry is lower infection than of domestice non-vaccinated individuals

Keywords:poultry, Mycoplasma, gallisepticum, TS11.

P581 - 519: STRUCTURAL ANALYSIS OF THE EFFECT OF MUTATIONS OCCURRED IN A PARTIAL SEQUENCED RDRP GENE OF BOVINE PICOBIRNAVIRUSES.

Ahmad Nazaktabar[1]

1. Amol University of special modern technologies.

Background and Aim: Picobirnavirus (PBV) is a bi-segmented dsRNA-virus living in the alimentary tract of human and various animal species as an opportunist enteropathogen. Because of high mutation rate, this virus is known as a quasi-species. In this study, the effect of nucleotide mutations on the structure of the RdRp gene of PBV was investigated wondering more detail of the biology of this high mutable virus in bovine population.

Methods:PBV was detected in 5 of 485 samples collected from under 2 months old diarrheic calves from 14 provinces of Iran using PAGE assay. Positive samples were submitted to RT-PCR to detect the RdRp gene of PBV. Sequencing of one of PCR amplicons revealed distinctive overlapping peaks investigated to find the effect of nucleotide mutations in the sequence of deduced amino acids by Expresso tool.

Results:43 nucleotides residues were mutated among 153 nucleotides (28%). 25 point mutations were silent. As well, no mutations were seen in the nucleotides encoding 19 amino acid residues (including D--S-D residues of motif A). Mutations of codons encoding 9 amino acid residues may lead to change their amino acids, according to probability rules. In one residue, each of its three coding letters were mutated, a deleterious mutation was probable because of forming the TAG stop codon.

Conclusion: These results reveal that PBV lives as quasi-species in the intestine of bovine similar to swine as other reported and confirmed that despite the high mutation rate of the nucleotide sequence (28%), the amino acid sequence of its RdRp gene highly conserved.

Keywords: Picobirnavirus, Structural analysis, RdRp, calves, Iran

P582 - 520: PREVALENCE OF MYCOBACTERIUM AVIUM SUBSPECIES PARATUBERCULOSIS IS 900 DNA IN BIOPSY TISSUES FROM PATIENTS WITH CROHN'S DISEASE: HISTOPATHOLOGICAL AND MOLECULAR COMPARISON WITH JOHNE'S DISEASE IN FARS, IRAN

Forough Zarei Kordshouli[1], Azizollah Khodakaram Tafti[2], Bita Geramizadeh[3], Masoud Haghkhah[4]

1. Department of Pathology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
2. Department of Pathology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
3. Department of Pathology, Transplant Research Center, Shiraz University of Medical Sciences, Shiraz, Iran
4. Department of Microbiology, School of Veterinary Medicine, Shiraz University, Shiraz, Iran

Background and Aim: The etiology of Crohn's disease is still unknown but seems to be multifactorial. There are reports about the potential link between Crohn's disease in human and the causative agent of ruminants Johne's disease, Mycobacterium avium subspecies paratuberculosis (MAP). The aim of this study was to investigate the prevalence of MAP in the biopsy tissues of Crohn's patients in Fars Province/ Iran

Methods: Intestinal biopsies of 30 patients with confirmed diagnosis of Crohn's disease and 30 patients diagnosed as non-inflammatory bowel disease were studied by molecular, histopathological and histochemical methods. Also, 30 adult goats affected by Johne's disease were studied, comparatively. DNA extractions of tissue specimens were subjected to PCR to amplify a 413-bp sequence of the IS900 gene.

Results: Using IS900-PCR, the overall prevalence of MAP in Crohn's patients and non-inflammatory bowel disease were 47% and 13%, respectively. Also, the prevalence of MAP in goats with Johne's disease was 70%. Using acid fast staining, only 7% of Crohn's patients were scantly positive as paucibacillary and 43% of Johne's disease cases were moderate to severely positive as multibacillary. Histopathologically, granulomatous enteritis (83% and 90%), lymphoplasmacytic enteritis (17% and 14%), edema and lymphangiectasia (67% and 96%), and vasculitis (20% and 73%) were common findings in Crohn's and Johne's diseases, respectively.

Conclusion: Our findings demonstrate a remarkable association between MAP and Crohn's disease in this population. With considering the prevalence of Johne's disease in this province, public health officials may contribute to a better understanding of the potential routes of transmission of MAP to humans.

Keywords:IS900-PCR, Crohn's disease, Johne's disease, Mycobacterium avium subsp. paratuberculosis

P583 - 528: COMPARISION OF SEROLOGICAL TESTS AND ELISA FOR DIAGNOSIS OF BRUCELLOSIS IN SHEEP AND GOATS

Rasa Sheini Mehrabzadeh[1], Masoud Ghorbanpoor[2], Mehdi Pourmehdi-Boroujeni[3]

1. PhD Student of Bacteriology, Department of Pathobiology, Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz, Ahvaz, Iran
2. Professor, Department of Pathobiology, Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz, Ahvaz, Iran
3. Associate Professor, Department of Food Hygiene, Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz, Ahvaz, Iran

Background and Aim: Brucellosis is one of the most important zoonotic diseases which is endemic in Iran. The most widely used methods of diagnosis are based on serology. The aim of this study was to compare serological tests for detection of brucellosis by Rose Bengal test (RBT), Wright, 2-mercaptoethanol and ELISA tests in Khuzestan province.

Methods:A total of 447 sera samples were collected and tested from sheep and goat herds during the time period of July 2017 to February 2018. 45 (10/06%) positive Rose Bengal test, Wright, 2-mercaptoethanol serum samples, ready for slaughter, and 402 negative serum samples were gathered and tested by commercial indirect ELISA ID vet and the results obtained were recorded.

Results: The results showed that out of 45(10/06%) positive Rose Bengal, wright and 2ME samples and 402 negative ones, 179(40/04%) were positive according to ELISA ID vet kit.

Conclusion: The results of this study showed that this ELISA kit is designed for European countries in which their control strategy is slaughter in sheep and goats with serology while in Iran, the strategies of disease control are vaccination, test, and slaughter. Therefore, it is recommended that this method is redesigned for practical use by changing the cut-off point of the commercial kit.

Keywords: Brucellosis, diagnosis, ELISA, Wright test, 2ME test

P584 - 559: THE PREVALENCE OF BRUCELLOSIS IN PATIENTS ADMITTED TO IMAM KHOMEINI HOSPITAL IN ARDABIL

Sahar Sabour[1], Taher Azimi[2]

1. School of Medicine. Ardebil University of medical science. Ardebil.IR Iran
2. Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran

Background and Aim: Brucellosis is one of the most common zoonotic diseases in Iran and is caused by several species of the Brucella genus. The rate of disease is different and most outbreaks have been reported in the spring and summer. The aim of this study was to determine the prevalence of brucellosis in patients admitted in Imam Khomeini Hospital in Ardabil

Methods: In this study, blood samples were collected from 50 patients admitted to different parts of the hospital for a period of 6 months. Rose Bengal and Brucella abortus antigen with 2 ME buffer was prepared and Rose Bengal test was performed on all serum samples. In addition, Wright-Tube test was used for determine antibody titers

Results: Overall, out of 50 blood samples taken from patients, 48 blood samples were positive for brucellosis disease by Rose Bengal test. Result of Wright-Tube test showed that 36 patient have a positive antibody titers. The rate of antibody titers in patient was as follows: 1:80 (12 patient), 1:160 (10 patient), 1:320 (6 patient), 1:640(6 patient) and 1:1280 (2 patient).

Conclusion: The result suggested that there were a high prevalence of the disease and it seems that a large number of the disease is due to lifestyle (close contact with animals and consumption of pasteurized milk products, etc). Specific infection control practices will be important and serious to address this emerging threat.

Keywords: Brucellosis, Bacterial infections, Wright-Tube, Rose Bengal test

P585 - 603: ANALYSIS RISK FACTORS FOR HUMAN CYSTIC ECHINOCOCCOSIS IN MOGHAN PLAIN, AN ENDEMIC REGION OF ARDABIL PROVINCE, IRAN

Hafez MirzanezhadAsl[1]

1. Faculty member of Ardabil University of medical Sciences, Iran

Background and Aim: Cystic Hydatidosis (CE) is a Zoonosis and caused by larval stages of Echinococcus granulosus (metacestode) in the intermediate host, eggs of echinococcus released through the feces from infected dogs and eggs ingesting infects humans.

Methods: So far no survey was conducted to determine analysis risk factors for the human hydatidosis in Ardabil province, so, using ELISA test and for the first HCF-Ag then Ag-5 and Ag-B and questionnaires forms, the prevalence of this disease was detected in the moghan area in this province. Hospital records defined that cystic echinococcosis is frequent in Moghan Area of Ardabil province. The present study designed to determine the seropositive rate and to analyze risk factors of disease for people living in this region. In this survey, 2680 serum samples were randomly collected from the normal population the everywhere of six shingles of Moghan plain. Sera was storage in -70°C in Ardabil medicine. In the first stage of test for screening the sera was tested using enzyme-linked immunosorbent-assay protocol and HCF-Ag.

Results: The serology results + were analyzed by Logistic regression using SPSS 18. Of 2680 serum samples 162 sera (6.9%) and (0.4%), respectively for CE and AE were positive. Women were more than men (21 vs. 11.2%) for CE. The age group of 4-19 showed the lowest rate and the 20-39 and 40-59 showed the highest rate of infection.

Conclusion: The rate of prevalence in this province shows somehow a resemblance with the other cities in Iran. Considering the lifestyle in this province a complementary study is suggested in all related cities.

Keywords: Risk factors, Cystic echinococcosis, Moghan Plain

P586 - 604: SUBTYPE DETECTION OF AVIAN INFLUENZA NEURAMINIDASE WITH NEURAMINIDASE INHIBITION TEST

Najmeh Motamed[1], Abdelhamid Shoushtari[2], MohammadHosein Fallah Mehrabadi[3]

1. Avian Diseases Research department,Razi Vaccine and Serum Research Institute, Agricultural Research,Education and Extension Organization, Karaj,Iran
2. Avian Diseases Research department,Razi Vaccine and Serum Research Institute, Agricultural Research,Education and Extension Organization, Karaj,Iran
3. Avian Diseases Research department,Razi Vaccine and Serum Research Institute, Agricultural Research,Education and Extension Organization, Karaj,Iran

Background and Aim: Neuraminidase(NA) is a glycoprotein expressed on the surface of influenza viruses. There are 9 known subtype of NA based on serological cross reactivity. Characterization of influenza virus isolates is frequently done by both classical and molecular methods. Classical methods such as Hemagglutination Inhibition (HI) assay and neuraminidase inhibition assay are still the reference standards required by OIE. The neuraminidase-inhibition (NI) test is a laboratory and serological procedure for identification and classification of AIVs. Our primary objectives were setting up the NI test for detection of NA subtype in viral or antiserum samples and validate the results with RT-PCR.

Methods: Based on OIE protocol the test was experienced for N1,N2,N6 antigens or their antiserum. we used viral isolates of H9N2 and H9N2 field antiserum and standard H5N1 antigen with its standard and field antiserum, standard H5N6 with standard antiserum. Samples were also investigated for NA subtype by RT-PCR reaction. Fetuin (substrate) was added to virus and unknown antiserum or the revers, after incubation sodium periodate then sodium arsenite , and lastly 2-thiobarbituric acid was added. If no or white color was produced the unknown virus or antiserum was considered to be as same as standard samples. But appearance of pink color mean the sample wasn't the same subtype with standards.

Results:all arranged assays were in one direction with RT-PCR test.

Conclusion: The reagents and the used format of the TBA method described here provide a platform for practical monitoring of NA subtype antibodies or viral isolates.

Keywords: Neuraminidase Inhibition, avian influenza, RT-PCR, NA Subtype

P587 - 615: MOLECULAR DETECTION OF PATHOGENIC AND NON-PATHOGENIC LEPTOSPIRA BASED ON MULTIPLEX PCR

Fatemeh Rahimi zarchi[1], Pejvak Khaki[2], Soheila Moradi Bidhendi[3]

1. Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran.
2. Associate Professor, Department of Microbiology, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
3. Associate Professor, Department of Microbiology, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran

Background and Aim: Leptospirosis is a serious zoonotic infection and the most prevalent disease in the tropical and subtropical region such as the north of Iran. The Leptospiral lipl32 gene expressed only in pathogenic Leptospira. 16S rRNA gene sequences are used to identify the species of Leptospira. The aim of this study was to identify a molecular method to identify pathogenic and nonpathogenic Leptospira by Multiplex PCR based on lipl32 and 16s rRNA genes. This method was also able to differentiate between saprophytic and pathogenic leptospires.

Methods: Saprophytic and pathogenic Leptospira serovars were used in this study. The bacteria were inoculated into the selective culture medium and extraction of the genomic DNA was performed by the standard Phenol-Chlorophorm method. The specific primers for a proliferation of lipl32 and 16SrRNA genes were used. The specificity and sensitivity of the PCR method were evaluated.

Results: The PCR product for the genes of the lipl32 and 16SrRNA was 272bp and 240bp respectively. The sensitivity amplification for the multiplex assay was 10-7 pg for 16S rRNA gene and 10-4 pg for lipl32 gene.

Conclusion: In this study by conducting a simple PCR to spend a minimum of time; were identified as pathogenic and non-pathogenic Leptospira serovars. The results showed that a molecular diagnostic test with high specificity and sensitivity suitable as PCR using 16S rRNA and lipl32 primers for distinguishing between pathogenic and nonpathogenic serovars from each other, very efficient.

Keywords: Leptospirosis, Multiplex PCR, lipl32, detection, 16s rRNA

P588 - 621: STREPTOCOCCOSIS AND ANTIBIOTIC RESISTANCE IN INFECTED RAINBOW TROUT (ONCORHYNCHUS MYKISS) FARMS IN GUILAN PROVINCE

Monireh Faeed[1]

1. Inland Waters Aquaculture Research Center,Iranian Fisheries Sciences Research Education and Extension Organization(AREEO),Bandar Anzali,Iran.

Background and Aim: The aim of this study was to investigate the incidence of streptococcosis and its antibiotic resistance in Guilan province Streptococcosis is one of the most causes of mortality in rainbow trout farms in Guilan province

Methods: The infected fish (168 with an average weight of 25-50 g) with clinical signs such as blurry, exophthalmic eyes and bleeding in the eyes, skin, fins fish were sampled . Samples were taken from the liver, kidney, spleen and some parts of the brain and transferred to the Blood Agar and TSA Agar.

Results: The incidence of Streptococcosis in this study was 39.29%. The streptococcal bacteria were isolated S. iniae (33.3%), S. agalactia (39.4%) and E. faecalis (27.3%) respectively

Conclusion:antibiotic resistance of bacteria in rainbow trout showed the highest resistance to Bacitracin and lincomycin. (92% -100%).

Keywords: Streptococcosis, Rainbow trout , bacteria

P589 - 626: COMPARISON OF IFA AND ELISA TECHNIQUES FOR DIAGNOSIS OF COXIELLA BURNETII

Amin Jaydari[1]

1. Assistant Professor, Department of Pathobiology, Faculty of Veterinary Medicine, Lorestan University, Khorramabad, Iran

Background and Aim:Q fever is a zoonotic disease caused by an obligatorily intracellular bacterium, Coxiella burnetii. This disease, described for the first time among abattoir workers in Australia seems now recognised as being endemic worldwide. Both public health and animal health issues are closely related to Q fever. The aim of this study was to investigate the comparison of IFA and ELISA methods in order to detect the presence of Coxiella burnetii in febrile patients in Khorramabad city

Methods: In this study sampling started in october 2015 and has been continued until may 2016. Totally 100 blood samples were collected from febrile patients in private and public hospitals for comparing ELISA and IFA methods.

Results: In this study, phase II IgG antibodies was 28.41% in ELISA method and 38% in IFA method.

Conclusion: The study demonstrated that the IFA is suitable for diagnosing Q fever and its therapeutic follow-up and is a good candidate for screening sera in large numbers.

Keywords: Coxiella burnetii, Q fever, IFA, ELISA, Febrile patients, Khorramabad

P590 - 627: A SEROEPIDEMIOLOGICAL SURVEY OF Q FEVER AMONG SHEEP AND GOAT BY ELISA METHOD IN ALASHTAR, LORESTAN PROVINCE

Amin Jaydari[1]

1. Assistant Professor, Department of Pathobiology, Faculty of Veterinary Medicine, Lorestan University, Khorramabad, Iran

Background and Aim:Q fever is a worldwide disease that is common between human and livestock. This disease is created by an obligate interacellular rickettsia called Coxiella burnetii. Cattle, sheep and goats are the main carriers of the disease. This study was conducted to identify the amount of Coxiella burnetii prevalence in the sheep and goat's blood in Alashtar, Iran.

Methods: In this cross-sectional study (from January 2016 to June 2016),162 sheep and goat blood samples were collected at random from the villages around the city of Alashtar. These samples were tested for the presence of Coxiella burnetii by the ELISA method.

Results: In this study, 162 samples were tested, that from total 42 samples of goat blood, 15 samples (9.3%) and a total of 120 sheep blood samples, 45 samples (27.8%) were positive for the presence of Coxiella burnetii.

Conclusion: The analysis of the collected data in different seasons and areas revealed that, more than 59.3 percent of the samples were negative and about 37 percent were positive, as well as the remaining 3.7 percent were suspicious in terms of Coxiella burnetii presence. The results of this study showed pollution in the upper area is the sheep and goat populations with regard to zoonotic disease that results of this study should be of interest to health policy.

Keywords:Q fever, Coxiella burnetii, ELISA, sheep, goat, Alashtar

P591 - 631: MOLECULAR IDENTIFICATION OF SHEEPPOX VIRUS (SPV) IN YAZD PROVINCE OF IRAN

Mojtaba Alimolaei[1], Hamid-reza Varshovi[2], Majid Ezatkhah[3], Maryam Amini[4], Mehrdad Shamsaddini Bafti [5]

1. Department of Research and Technology, Kerman branch, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran
2. Department of Animal Viral Vaccine, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran
3. Kerman branch, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran
4. Kerman branch, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran
5. Kerman branch, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran

Background and Aim: Sheeppox virus (SPV) is belongs to Poxviridae family, Chordopaxvirinae sub-family, and capripoxvirus genus. SPV is an endemic disease in Iran and has very important role in agricultural economy. It is included in the notifiable diseases of Office International des Epizooties (OIE). The purpose of this study was molecular identification of SPV in Yazd province of Iran.

Methods:A total of twenty-six biopsy samples from skin lesions of sheep suspected to SPV were collected from different districts of Yazd province. A previous developed capripoxvirus specific PCR assay was applied to identify the P32 gene encoding capripoxvirus immunodominant antigen to identify SPV.

Results: Six samples (23.08%) were shown positive results for 390bp fragment of P32 gene. Spatially, the disease was recorded in 4 out of 14 districts.

Conclusion: Our results revealed that SPV is endemic and dispersed in Yazd province of Iran. Hence, ring vaccination should be undertaken for a period of two to three years, to try to eradicate the SPV. The study also highlights high sensitivity of this PCR in detection of SPV.

Keywords: Sheeppox virus; PCR; P32 gene; Yazd province; Iran

P592 - 641: FIRST REPORT OF ANONCOTAENIA INFESTATION OF ALECTORIS CHUKAR FROM NORTHEAST OF IRAN

Somayeh Namroodi[1], iraj mobedi[2]

1. Assistant professor Department of Environmental sciences, Faculty of fisheries and environmental sciences, Gorgan University of Agricultural Sciences & Natural Resources, Gorgan

Background and Aim: The chukar partridge Alectoris chukar (Phasianidae) is one of the Eurasian species and also one of the most important native game bird in Iran. This species habits in wide range of area, from the Balkans to through Syria and Iraq to Iran and Pakistan. Despite farm- rearing of this species in Iran, wild populations of Alectoris chukar have been decreased significantly causing them to be placed on as Least Concern by IUCN lists of conservation concern in recent years. This study focused on endoparasite infection of 2 Alectoris chukar from North- East of Iran.

Methods:two female partridges, obtained from a hunter in Mazandaran province. The corpses were carefully examined for detection of external and internal parasites. After necropsy, 5 cestodes, up to 1cm in diameter and 30 cm, have been detected in their intestines. The partridges were in good condition and no apparent lesions were observed. Obtained endoparasits were fixed and preserved in 70 % ethanol.

Results: The detected cestodes diagnosed as Anoncotaenia.

Conclusion: This is the first report of Anoncotaenia infection of Alectoris chukar (Phasianidae) or, in general, from any other birds from Iran. Chukar partridge is new host record for this parasite. Relevant data have been described Anoncotaenia infection in different orders of birds such as Dicaeidae, Meliphagida, Muscicapidae). Also current study clarify new order of birds as host of Anoncotaenia

Keywords: Anoncotaenia , Alectoris chukar

P593 - 644: DTECTION OF ZOONOTIC SALMONELLA SPP IN ROAD-KILLED RURAL DOGS

Somayeh Namroodi[1]

1. Assistant professor Department of Environmental sciences, Faculty of fisheries and environmental sciences, Gorgan University of Agricultural Sciences & Natural Resources, Gorgan

Background and Aim: Salmonella spp. which can cause salmonellosis in many species of animals are one of the most important zoonotic bacteria with a worldwide spreading. This bacteria can live for a long time in humid areas such as North Iran. Asymptomatic animals such as dogs may play an important role in salmonella distribution. This study has been planned to survey the role of rural dogs in Salmonella. spp. dissemination.

Methods:50 fecal samples that obtained from 50 road killed rural dogs (Golestan Province) were surveyed by conventional microbial culture tests for salmonella detection. Positive samples were serotyped too.

Results:14 of samples were positive. The isolated were identified as 7 S enteritidis,2 S Dublin, and 5 (20%) S typhymurium

Conclusion:results of this study highlight the important role of healthy animals such as rural dogs in distribution of zoonotic Salmonella spp in North Iran. it seems it is important to make villagers familiar with danger of salmonella contamination through healthy rural dogs.

Keywords:salmonella, rural dogs, Golestan

P594 - 648: DETERMINATION OF TOTAL PROTEIN CONTENT IN BACTERIAL SUSPENSION CONTAINING CLOSTRIDIUM PERFRINGENS TYPE D

Ali Reza Karimabadi[1], Mehrdad Shamsaddini Bafti[2]

1. Department of Research and Development, Razi Vaccine and Serum Research Institute, Kerman Branch, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran
2. Department of Research and Development, Razi Vaccine and Serum Research Institute, Kerman Branch, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran,

Background and Aim: Clostridium perfringens (C. perfringens) secretes at least 17 types of toxins. C. perfringens type D, in addition to secreting major toxins like alpha and epsilon, also produces various alternative toxins. C. perfringens type D, due to the secretion of these toxins, can cause enterotoxemia in domestic livestock and a lot of economic losses to the animal husbandry industry. Accordingly, the study of the amount of secreted toxin, which has the protein nature, is of particular importance.

Methods: For this purpose, at first C. perfringens type D cultured in a nutrient medium in anaerobic conditions then maintained in the incubator so the suspensions that containing toxin were prepared. After centrifuge and preparing various dilution, spectrophotometer was used to measure total protein content in two wavelengths.

Results: The mean amount of toxins that produced from C. perfringens type D isolates was 7.1 mg/ml.

Conclusion: The total protein content obtained from our samples was the significant difference with standard strain.

Keywords: Clostridium perfringens, Toxin, Culture, Total Protein.

P595 - 649: THE MORTALITY RATE OF EPSILON TOXIN CLOSTRIDIUM PERFRINGENS TYPE D

Ali Reza Karimabadi[1], Mehrdad Shamsaddini Bafti[2]

1. Department of Research and Development, Razi Vaccine and Serum Research Institute, Kerman Branch, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran
2. Department of Research and Development, Razi Vaccine and Serum Research Institute, Kerman Branch, Agricultural Research, Education and Extension Organization (AREEO), Kerman, Iran

Background and Aim: Clostridium perfringens (C. perfringens) is classified into five types A to E, based on the secretion of four major toxins, alpha, beta, epsilon, and yota. C. perfringens type D, which secretes the main toxin of epsilon, causes enterotoxemia and mortality in domestic animals, so it is important to discuss for the health of livestock industry and also for providing the meat that is need of the community.

Methods: In this research, the amount of epsilon toxin that released from C. perfringens type D isolated from livestock was investigated. At First, the C. perfringens bacterium type D that was confirmed by multiplex PCR technique cultured on the nutrient medium. After incubating in anaerobe condition and ensuring growth, the supernatant was removed and activated by the enzyme. Then dilutions prepared from 1.10 to 1.200. From each dilution 0.5 ml was injected to N.M.R.I mice intravenously.

Results: The minimum lethal dose of epsilon toxin level was 75.

Conclusion: The mortality rate obtained from our samples was the significant difference with standard strain.

Keywords: Clostridium perfringens, Toxin, Culture, MLD.

P596 - 654: SURVEY ON SALMONELLA CONTAMIATION OF WILD RODENTS IN MAZANDARAN PROVINCE

Somayeh Namroodi[1]

1. Department of Environmental sciences, Faculty of fisheries and environmental sciences, Gorgan University of Agricultural Sciences & Natural Resources, Gorgan-

Background and Aim: Salmonella is a pathogen of worldwide importance, causing disease in a vast range of hosts including humans. Salmonella infection can cause severe disease in animals, which is sometimes associated with high mortality. Salmonella has repeatedly been isolated from wild mice and rats, which represent important reservoir hosts on farms and in food production. Environmental conditions can influence Salmonella spp survival. The study was conducted to determine the frequency of salmonella contamination in the fecal samples of rodents trapped across the different villages and cities in Mazandaran Province.

Methods:A total of 90 Mus musculuses were trapped and their rectal swabs were used for detection of salmonella by conventional microbial culture method. Positive samples were serotyped.

Results: Salmonella spp were detected in 20 fecal samples containing 11 S. typhymurium and 9 S. enteritiddis. There was no difference between male and female ones in salmonella contamination.

Conclusion: Salmonella contamination of trapped Mus musculuses, indicating a potential risk associated with these animals as sampled Mus musculuses originated from locations near the villages. It is therefore imperative that regular rodent control measures should be practiced to reduce risk of salmonella contamination in contaminated areas

Keywords:salmonella, rodent, Mazandaran

P597 - 660: ISOLATION AND IDENTIFICATION OF MYCOBACTERIUM CAPTURED FROM MICE FROM INFECTED FARM BY TUBERCULOSIS

Khashaiar Mansouri[1], Nader Mosavari[2]

1. School of Veterinary, Islamic Azad University, Garmsar Branch, Garmsar, Iran
2. Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran

Background and Aim: Bovine tuberculosis is one of the most important zoonotic diseases in Bovidae. The humans and animals that transit to the farm can transfer Mycobacterium bovis to cattle, so the aim of this study was evaluation the possible role of mice in transferring the Mycobacterium infection in dairy farms.

Methods: From a dairy cattle farm with more than 10 percent infection of Mycobacterium bovis, five mice were captured and their liver, spleen, and lung cultured in the LJ medium. The Acid-Fast staining of the isolates prepared to identify Mycobacterium and PCRs were carried out afterwards.

Results: Three Out of five cultures were positive in direct smear by Acid Fast staining and in PCR-16SrRNA, which indicate that mentioned isolates belonging to Mycobacterium genus. Also positive PCR-IS6110 confirmed that isolates are one of species as Mycobacterium tuberculosis Complex. Currently, we are conducting PCR-RFLP and RD Typing to exact identification of these isolates.

Conclusion: Animals such as mice and cats that live in the farm can harbor Mycobacterium. In this study, it has been proven that mice certainly transfer Mycobacterium to cattle farms.

Keywords: Mycobacterium tuberculosis Complex, Mycobacterium bovis, PCR IS6110, 16SrRNA

P598 - 685: PHENOTYPIC AND GENOTYPIC CHARACTERISTICS OF THE FIRST ESCHERICHIA COLI FECAL ISOLATES REPORTED FOR SEROGROUPS O55, O104 AND O118 ISOLATED FROM LIVESTOCK IN KHUZESTAN, IRAN

Mojdeh Barzan[1], Darioush Gharibi[2], Masoud Ghorbanpoor[3], Mohamad Rahim Haji Hajikolai[4], Mehdi Pourmehdi Boroujeni[5]

1. PhD of bacteriology of Shahid Chamran University of Ahvaz
2. Associate Prof. of Veterinary Microbiology of Shahid Chamran University of Ahvaz
3. Prof. of Veterinary Microbiology of Shahid Chamran University of Ahvaz
4. Prof. of Large Animal Internal Medicine of Shahid Chamran University of Ahvaz
5. Associate Prof. of Veterinary Epidemiology of Shahid Chamran University of Ahvaz

Background and Aim:STEC strains as zoonotic agents are public health concern around the world and domestic livestock are among the most important reservoirs of these strains. Determination of serogroup of isolates can be a useful tool in preventing and treating infections caused by these strains, as well as epidemiological studies.

Methods:A total of 42 STEC were obtained from 205 calves (healthy and diarrheic) and dairy cows. Determination of serogroup, phylogenetic group, class I integron, some of the virulance factors and ESBLs production of these isolates were performed separately by PCR method. Phenotypic ESBL-producing E. coli was determined using the double disk diffusion method too.

Results: Only 5, 4 and 1 isolates were serogroup O55, O104 and O118, respectively. The phylogenetic group B1 was dominant and one O118 isolate from the cow was ESBLs positive and had the blaCTX-M-1 gene alone. All isolates had astA gene and no one had aerobactin and enterohemolysin genes. Two isolates had class I integron gene too.

Conclusion: It seems to be the first report of the presence of these serogroups in Iran. According to the importance of serotype O104:H4 in the development of sudden diarrhea epidemics in the European population such as Germany, the close genetic similarity between serogroup O55 and O157 and the role of serogroup O118 in the case of calf disease, more studies in order to identify the abundance and recognize the characteristics of these serogroups, is recommended.

Keywords: Escherichia coli fecal isolates, serogroups, livestock

P599 - 699: ISOLATION AND MOLECULAR IDENTIFICATION OF MYCOBACTERIUM FROM RAINBOW FISHES IN SABZEVAR

Faezeh Sedighi[1], Nader Mosavari[2], Hassan RavanSalar[3], Keyvan Tadavon[4]

1. Reference Laboratory for Bovine Tuberculosis, Razi Vaccine and Serum Research Institute, Agricultural Research Education and Extension Organization (AREEO), Tehran, Iran
2. Reference Laboratory for Bovine Tuberculosis, Razi Vaccine and Serum Research Institute, Agricultural Research Education and Extension Organization (AREEO), Tehran, Iran
3. Sabzevar University of Medical Sciences
4. Reference Laboratory for Bovine Tuberculosis, Razi Vaccine and Serum Research Institute, Agricultural Research Education and Extension Organization (AREEO), Tehran, Iran

Background and Aim: Fish tuberculosis is a common disease between human and aquatic animals. Several species of Mycobacterium cause tuberculosis in fish. It usually appears as a skin disease, but systemic form of the disease has been reported in human and fish. Due to the possibility of this infection in farmed fish and the risk of public health and nutrition in humans, isolation of these species are necessary. The purpose of this research was isolating and molecular identifying of Mycobacterium from rainbow fishes in Sabzevar.

Methods: In order to carry out of this research, 50 rainbow fishes were randomly collected from seven swimming pools in separate areas of Sabzevar city. Head, fins and internal organs cultured as routine manner. DNA extracted from positive cultures and PCR-16srRNA were accomplished. The PCR product was sequenced for final confirmation.

Results: Out of 50 rainbow fishes, three Acid fast bacteria were isolated. The PCR-16srRNA were positive by specific primers for Mycobacterium. The results of the nucleotide sequencing were analyzed by the BLAST program, which all of these three isolates were identical and similar to Mycobacterium peregrinum.

Conclusion: It is possible that, there is similar source for all of these fishes farming. This research suggests that, there is a possibility of transferring pathogenic Mycobacterium to humans.

Keywords: Fish tuberculosis, Mycobacterium peregrinum, Rainbow, Primer.

P600 - 705: SEROEPIDEMIOLOGY OF LEPTOSPIRA INFECTION IN STRAY DOGS BY MAT DURING A ONE-YEAR PERIOD FROM RURAL COMMUNITIES OF KOOHSAR, ALBORZ, IRAN

Afrooz Fahimipour[1], pejvak khaki[2], Soheila moradi bidhendi[3]

1. Department of Biology, Science and Research Branch, Islamic Azad University,Tehran, Iran
2. Department of Microbiology, Razi Vaccine & Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran Karaj, Iran
3. Department of Microbiology, Razi Vaccine & Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran Karaj, Iran

Background and Aim: Leptospirosis is a worldwide zoonosis disease that has been seen on all continents except the Antarctic. Reservoirs of this disease are companion animals, livestock and wildlife. Dogs are the maintenance hosts of leptospira, so they can be potential sources of infection for dogs owners. Therefore, studying the prevalence of leptospirosis in dogs reduces the disease in other dogs and humans, therfore, the aim of this study was Seroepidemiology of Leptospira infection in stray dogs by Microscopic Agglutination Test (MAT) during a one-year period from rural communities of koohsar, Alborz, Iran.

Methods: The MAT test was performed on 110 serum samples from stray dogs of Koohsar area.We used twenty live antigens of leptospira.

Results: The prevalence of positive MAT test in stray dogs (males and females) were 21.84% (24 cases) for different serovars. The rate of infection in male and female dogs were 20.8% and %22.58, respectively. The lowest antibody titre was observed at 1: 100 and the highest was 1:1600. The most common titers were 1:200 (50%), 1:400 (25%) and 1:100 (12.5%). The dominant serovares in stray dogs were, L.Conicola (33.33%), L.Icterohaemorrhagia (25%), L.Grippotyphosa (20.83%), L.pomona (4.1%) and L.Serjoe hardjo, L.Atumnnalis, each of which (8.33%), respectively.

Conclusion: Our studies showed a relatively high prevalence of leptospirosis in stray dogs in Koohsar area of Alborz province and L.Canicola and L. Icterohaemorrhagiae were the dominant serovars in the dogs of the region.

Keywords: Leptospirosis, MAT, Dog, Seroepidemiology, Alborz

P601 - 713: OPTIMIZATION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNP) ANALYSIS IN THE CLASSICAL PCR MACHINES FOR TYPING OF MYCOPLASMA AGALACTIAE

Khatereh Kabiri[1], Keyvan Tadayon[2], Seiyed Ali Pourbakhsh[3], Jamile Norouzi[4]

1. Department of Microbiology, North Tehran Branch, Islamic Azad University, Tehran, Iran.
2. Department of Veterinary Aerobic Bacteria Razi Institute Karaj
3. Mycoplasma reference laboratory, Razi vaccine and serum research institute, Karaj, Iran
4. Department of Microbiology, North Tehran Branch, Islamic Azad University, Tehran, Iran.

Background and Aim: Contagious agalactia is a chronic infections in small ruminants and remains endemic in many regions of the world, despite intensive and costly eradication programs. To prevent the disease, a vaccine containing three strains of Mycoplasma agalactiae namely Taleghan, Lorestan and Shiraz is currently used in Iran. The present study was aimed to optimize SNP analysis on the basis of P40, P48 and P80genes in order to molecular typing of M.agalactiae for the first time.

Methods: Primer 3 program was used to design specific primers based on P40, P48 and P80 genes of the organism. M. agalactiae Taleghan, as a standard strain, was obtained from the microbial archive of the Razi Vaccine and Serum Research Institute. A universal PCR protocol was developed to enable simultaneous amplification of all genes by conventional PCR machines.

Results: Access of a common PCR protocol, which is able to proceed simultaneously four different reactions in one PCR run, was the primary outcome of this research.

Conclusion:contemplation the fact that goat and sheep farming play an important role in the economy of the Iran, so it is recommended this method used for molecular characterization of strains to other provinces and compare them with vaccine strain.

Keywords:PCR protocol , Iran ,Mycoplasma agalactiae, Standard

P602 - 771: GENOMIC DETECTION OF CHICKEN ANEMIA VIRUS IN LAYING HENS IN ISFAHAN PROVINCE

Azam Mokhtari[1], Milad Parchami[2], Abdolkarim Zamani Moghadam[3], Mohammadreza Mahzounieh[4]

1. Department of Pathobiology, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
2. Department of Pathobiology, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
3. Department of Clinical Sciences, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
4. Department of Pathobiology, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran

Background and Aim: Chicken infectious anemia is an important viral disease of fowl which may cause economic losses in poultry farms. The disease characterized by severe anemia, increasing conversion factor, decreasing body weight, bone marrow apalasia, atrophy of thymus, bursa of fabricius and spleen. Immunosuppression would cause increase susceptibility to other bacterial, viral, fungal and parasitic diseases. Subclinical infection caused high economic losses in laying hens flocks.

Methods: We took liver samples from 70 laying hens wich were 23-44 weeks old. PCR test performed using designed primers.

Results: Of 70 samples were tested, 10 (14.2%) were positive using PCR test. The results showed that there is CIAV in Isfahan.

Conclusion: Considering the immunosuppression due to CIAV, its detection may help to have a better management of poultry farms.

Keywords:CIAV, Immunosuppression, PCR

P603 - 772: THE FIRST SEROLOGICAL STUDY OF COXIELLA BURNETII IN PREGNANT WOMEN WHO WERE REFERRED TO HOSPITAL IN KHORRAMABAD CITY FOR ABORTION

Eiman Azizyari ghobadi[1], Soheila Akbari Torkemani[2], Fariba Hadi Panah[3]

1. Department of Pathobiology,Faculty of Veterinary Science, Lorestan University,Khorramabad,Iran.
2. Associate Professer, Department of Obstetrics and Gynecology,Faculty of Medicine,Lorestan University of Medical Science,Khorramabad.Iran.
3. Asali Hospital, Khorramabad.Iran.

Background and Aim:Q fever is a common, globally distributed, zoonotic infection caused by the obligate intracellular gammaproteobacterial organism,coxiella burnetii. This disease have different clinical symptoms such as spontaneous abortion, premature birth, intrauterine growth retardation, oligoamonios and abnormal pregnancy in pregnant women. The aim of this study was to investigate the coxiella burnetii in pregrant women who were referred to Hospital in khorramabad city for abortions

Methods:A total of 92 samples were collected randomly from pregnant women who were referred for abortion to Asali Hospetal in Khorramabad in 2017. Were examined using indirect ELISA assay kit for the detection of C.burnetii phase II human antibodies in their serum samples.

Results: The total 92 serum samples from pregnant women abortions, that 21sample(22/86%) was positive and 66 sample(71/73%) was negative and 5 sample(5/4%) was suspected.

Conclusion: The present study demonstrated a high seroprevalence of coxiella burnetii. in pregnant women abortions . according to clinical symptoms in pregnant women and risk of abortions in women it is necessary to pay attention to this disease .

Keywords:coxiella burnetii., Women Pregnant, Hospital, Abortion

P604 - 780: FIRST REPORT ON ISOLATION OF CHLAMYDIA FELIS FROM IRAN

Masoud Ghorbanpoor[1], Bahman Mosalanejad[2], Sara barati[3], Babak Barimani[4], Saleh Esmailzadeh[5], Naghmeh Moori Bakhtiari[6]

1. Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz
2. Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz
3. Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz
4. Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz
5. Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz
6. Faculty of Veterinary Medicine, Shahid Chamran University of Ahvaz

Background and Aim: Chlamydiae are gram-negative obligate intracellular bacteria that affects both human and animal health. According to the latest classifications, the order Chlamydiales consists of one family, the Chlamydiaceae, containing one genus, the Chlamydia, which consists of 12 different species that are responsible for a wide range of diseases. Feline chlamydiosis is one of the most important upper respiratory tract diseases of cats. In this paper the successful isolation of C. felis from a cats affected with conjunctivitis is reported.

Methods: Several conjunctival swabs were taken from both eyes of a 2-month-old female kitten with a history of severe bilateral conjunctivitis. The samples were used for direct microscopic examination, microbial cultures, and molecular diagnosis of C. felis infection and the case was treated ophthalmic tetracycline ointment twice daily for 1 week.

Results: Microbiological cultures of swabs did not yielded the growth of extra-cellular pathogenic bacteria or fungi. Molecular diagnosis of C. felis infection by conventional PCR with C. felis specific primers revealed the presence of targeted gene. The Gimsa and imunoperoxidase staining of smears also showed the specific intra-cytoplasmic chlamydial inclusions. Chlamydia felis was isolated from samples by inoculation to cycloheximide-treated L 929 cells. The symptoms and clinical signs of affected kitten disappeared after treatment.

Conclusion: To the best of our knowledge, this is the first reports on isolation of C. felis from Iran. The use of an effective C. felis vaccine for preventing infections in cat populations seem to be necessary and should be recommended.

Keywords: Chlamydia felis, kitten, Conjunctivitis, Isolation, Iran

P605 - 796: SEROLOGICAL SURVEY OF AVIAN INFLUENZA (H9N2) IN INDUSTRIAL POULTRY IN GOLESTAN PROVINCE DURING 2017-2018

safoura tatari[1], fahimeh zarei[2], azam javan[3], hassan arab[4], naser sadri[5]

1. Hospital Veterinary Laboratory Diagnosis Gonbad-E kavous
2. Hospital Veterinary Laboratory Diagnosis Gonbad-E kavous
3. Hospital Veterinary Laboratory Diagnosis Gonbad-E kavous
4. Hospital Veterinary Laboratory Diagnosis Gonbad-E kavous
5. Hospital Veterinary Laboratory Diagnosis Gonbad-E kavous

Background and Aim: Influenza is an acute respiratory disease caused by infection with influenza viruses. Avian influenza (AI) viruses are members of the family Orthomyxoviridae. AI viruses can be classified into two categories: low pathogenicity (LPAI) and highly pathogenic (HPAI) forms, based on the severity of the illness caused in birds. The aim of this study was to monitor mean antibody titer of influenza virus (H9N2) in commercial farms in Golestan province using HI assays.

Methods:in this study we screened the serum antibody level in 17 epidemiologic units and from each unit Collected 15 to 20 samples. Blood samples were collected from the biliary vein by a 2-cc syringe of blood and the syringe was kept at room temperature for 2 hours and transferred to the refrigerator at 4° C. The Hemagglutination Inhibition (HI) test was then performed to determine the titre of antibody.

Results:from the 17 epidemiologic units 9 unit the titre of HI low and need to vaccination for prevention of H9N2 virus. HI tests showed that the lowest and the highest mean antibody titer of AI was 3.63 with C.V 30% and 6.91 with C.V 8.3 %, respectively.

Conclusion: The findings of this study not only reveal low prevalence of AIV (H9N2) antibodies in Poultry farms in Golestan province, but also emphasize for increase the serum antibody level with good vaccination program for improve poultry immune systems.

Keywords:H9N2, HI, Golestan, poultry

P606 - 810: RESISTANT MOTILE SALMONELLOSIS TREATMENT USING TRACHYSPERMUM EXTRACTS WITH YOGHURT IN PEAFOWL'S

Abdolreza Nabinejad[1]

1. Isfahan Res center of Agriculture

Background and Aim: Trachyspermum (Ajowan fruit) is an annual aromatic plant in the family Apiaceae which almost smell like thyme because they contain thymol. The ajwain fruits yields an essential oil consist of thymol, gamma-terpinene , p-cymene and more than 20 trace compounds predominantly terpenoids. Its oils and extracts shows antimicrobial and fungicidal effects as well as stimulant, antispasmodic and carminative properties therefore it would be effective for infective diarrhea and atonic dyspepsia. Since chemical compounds showed some side effects and residues in animal production, herbal medicine will be an appropriate alternative

Methods: Current report goes to 10 Peafowl's infected with motile salmonella sp. in a birds garden. The birds were severely dehydrated , diarrheotic and downer. In differentiative stools culture motile salmonella Sp. were isolated, the antibiogram test for tetracyclines, neomycine, beta-lactam antibiotics, Enrofloxacin , Aminoglycosides, Cephalosoporines and Fosmycine shows 1+ to 4+ resistation.

Results: Finally a 1/4 (V/V) mixture of trachyspermum extracts in yoghurts and ORS powder using gastric tube were used as oral intake 5%-10% BW/birds, the birds fed 4 to 5 times a day . All the birds cured after 4 days and treatment were continued with trachyspermum extracts and yoghurts in their grains for 3 later days.

Conclusion: At the end of herbal therapy the second stool culture showed some gram negative rods and fecal enetercocci and no any motile salmonella were isolated..

Keywords: Salmonellosis, Peafowl, Trachyspermum, Resistant, treatment

P607 - 816: COMPARISON OF CLASSICAL AND ALTERNATIVE PATHWAYS OF SERUM COMPLEMENT OF KHAZAK AGAINST AVIAN PATHOGENIC ESCHERICHIA COLI

Hamed Heidari Mokarar[1], Saeed Salari[2], Hossein Ali Khazaei[3], Mehdi Jahantigh[4]

1. Faculty of Veterinary Medicine, University of Zabol, Iran
2. Department of Pathobiology, Faculty of Veterinary Medicine, University of Zabol, Iran
3. Department of Immunology, Faculty of Medical Sciences, Zahedan University of Medical Sciences, Iran
4. Department of Clinical Sciences, Faculty of Veterinary Medicine, University of Zabol, Iran

Background and Aim: Khazak chicken, as backyard and native poultry, is distributed in Sistan, border of Iran. There has been no investigation about the mechanism of serum of Khazak against Avian Pathogenic Escherichia coli (APEC).The present study was aimed to differentiate the potency of classical and alternative pathways of serum complement of Khazak against APEC.

Methods: Serum was collected, aseptically, from Khazak chickens. Based on pervious references, respectively, EGTA/MgCl2, and 50’ C for 20 min was applied to inactive the classical and alternative pathways of serum complement. Into flat-bottomed 96-well microtiter plates, 104 CFU of APEC was mixed with inactivated alternative or classical pathway of Khazak complement serum, individually, with same volume. The controls were considered. The growth was screened every 30 min for 6 hr, triplicates, at 37’C. The statistical differences of slope value of growth curve was considered at $p<0.05$.

Results: As an interesting finding, there was no statistical significance difference between inhibitory effect of alternative and classical pathways of complement system of Khazak serum against growth rate tested bacterium ($p>0.05$).

Conclusion: As a first report from Iran, about complement system of a native backyard chicken, the knowledge about APEC serum resistance was increased and it could play as a preliminary study to conduct vast investigation, regarding immune system of Khazak, as a potent poultry for investment. The findings could be explained by species-specific or other complement factors found in khazak immune system.

Keywords:khazak, apec, immune system

P608 - 832: THE EFFECT OF COMPLEMENT SYSTEM OF KHAZAK AND BROILER SERUM AGAINST AVIAN PATHOGENIC ESCHERICHIA COLI: AN INVITRO EXPERIMENTAL STUDY

Hamed Heidari Mokarar[1], Saeed Salari[2], Hossein Ali Khazaei[3], Mehdi Jahantigh[4]

1. Faculty of Veterinary Medicine, University of Zabol, Iran
2. Department of Pathobiology, Faculty of Veterinary Medicine, University of Zabol, Iran
3. Department of Immunology, Faculty of Medical Sciences, Zahedan University of Medical Sciences, Iran
4. Department of Clinical Sciences, Faculty of Veterinary Medicine, University of Zabol, Iran

Background and Aim: The pathogenesis of avian pathogenic Escherichia coli (APEC) is different from mammalian E. coli, since in mammals, intestinal form is more prevalent, while the extraintestinal form occurs more in avian. It is logical to consider that two distinct species of poultry, broiler and Khazak, may be act in different manner against APEC. To increase the knowledge about serum resistance mechanism against APEC, the present investigation is aimed to discriminate between the act of complement system of Khazak and broiler, as native-backyard chicken of Sistan and industrial poultry, respectively.

Methods: Serum was collected, aseptically, from Khazak and broiler chicken. The active and inactive (56 ‘C-30 min) serum complement of birds was dispensed, individually, into flat-bottomed 96-well microtiter plate, triplicates, and then, 104 CFU of APEC was inoculated. The growth was screened every 30 min for 6 hr, at 37’C. The statistical differences of slope value of growth curve was considered at $p<0.05$.

Results: Statistical significance difference was observed for inhibitory effect of chicken serum complement in comparison with khazak against APEC ($p<0.05$).

Conclusion: Findings demonstrated that the serum complement of khazak are more inefficient than broiler to APEC and the bacterium may be affect internal organ more easier, and in total, the pathogenesis is different between these two distinct species. Therefore, strategies for treatment and control of colibacillosis in khazak may be differed from broiler, regarding serum complement.

Keywords:broiler, khazak, serum complement, apec

P609 - 853: FIELD INVESTIGATION OF MYCOPLASMA GALLISEPTICUM INFECTION IN BACKYARD AND COMMERCIAL CHICKEN IN URMIA USING PCR METHOD

Fatemeh Babaahmadi[1], Alireza Mahmodian[2], Abdolghaffar ownagh[3]

1. Department of Pathobiology, Faculty of Veterinary Medicine, Urmia University Dep of Pathobiology, Faculty of Veterinary Medicine, Urmia University
2. Department of Pathobiology, Faculty of Veterinary Medicine, Urmia University Dep of Pathobiology, Faculty of Veterinary Medicine, Urmia University
3. Department of Pathobiology, Faculty of Veterinary Medicine, Urmia University Dep of Pathobiology, Faculty of Veterinary Medicine, Urmia University

Background and Aim: Mycoplasma gallisepticum (MG) is the causative agent of chronic respiratory disease (CRD), with a significant economic impact on poultry farms. Asymptomatic infections can make birds susceptible to secondary infections.In field, diagnosis is mainly carried out based on the clinical symptoms by veterinarians. However, to confirm the diagnosis, robust laboratory detection of infection is necessary. Molecular detection using PCR is considered a sensitive method.

Methods: To understand the prevalence of MG infection in the poultry carcases refered to veterinary clinics around Urmia, a PCR assay was developed using the gyrB gene. In total, 80 tracheal swabs from commercial and backyard chicken carcasses with clinical signs were collected and the extracted DNA were investigated using PCR

Results: It had turned out that only 6 out of 50 commercial (12%) and 3 out of 20 backyard samples (15%), which were clinically diagnosed with MG infection found to be MG positive, suggesting that diagnosis made based on the clinical signs is not conclusive and final diagnosis needs to be confirmed by molecular diagnosis for accurate antimicrobial agents and vaccine administration.

Conclusion: diagnosis made based on the clinical signs is not conclusive and final diagnosis needs to be confirmed by molecular diagnosis for accurate antimicrobial agents and vaccine administration

Keywords: Mycoplasma, gallisepticum, Molecular , clinical signs.

P610 - 860: IMMUNOLOGICAL AND PATHOLOGICAL CHANGES IN MICE TOWARDS INFECTION BY PASTEURELLA MULTOCIDA CULTURED IN HIGH AND LOW IRON MEDIA

Elham Hosseini[1], yahya tahamtan[2], nematollah razmi[3]

1. islamic azad university shiraz branch,department of biochemistry
2. shiraz branch,razi vaccine and serum research institute,agricultural research,education and extension organization,shiraz,iran
3. associate professor of islamic azad university shiraz branch,department of biochemistry

Background and Aim: Pasteurella multocida is an important organism that is in charge of upper respiratory tract in human and animals. It has known that growth of this organism at different levels of Iron could influence the pathogenicity of the organism. Present study attempts to evaluate any changes in blood parameters and visceral organs of mice by cultivation of native Pasteurella multocida isolates from south of Iran

Methods:P.multocida was cultured on BHI medium and on the same medium supplemented with bipyridyl and BHI supplemented with Iron. Active and inactivated antigens were prepared from all medium and mice were injected and immunized two weeks apart, respectively

Results: Blood samples were collected to evaluate the antibody against P.multocida. Tissue sections from euthanized mice were also prepared for pathological studies. There were high distraction and necrosis in lung, heart, kidney and spleen in Iron rich. Anti P.multocida antibodies titer did not show significant differences between groups

Conclusion: It seems that Iron depletion would reduce growth and pathogenicity of pasteurella multocida while such condition would not affect its immunogenicity

Keywords: Pasturella multocida, Iron , Bbipyridyl , Immunological pathological

P611 - 34: PREPARATION OF PROBIOTIC MILK USING LACTOBACILLUS BIFIDOBACTERIUM ANGULTUM PTCC 1366 AND ITS EFFECTS ON THE PREVENTION AND TREATMENT OF IBD

Nafiseh Farazandehnia[1]

1. MS

Background and Aim: Probiotic products offer many health benefits and can prevent diseases especially gastrointestinal and infections efficiently. The present work aims to study antibacterial effects of fermented probiotic milk produced by a variety of bacterial strains.

Methods: In this study, a wide variety of items have been investigated including: The stability of probiotic milk in three different temperatures (4 ، 25 ، 37 c^o), different Ph and Antimicrobial effects of manufactured products using two standard bacteria Staphylococcus aureus ATCC 29737 and Salmonella typhimurium ATCC 14028, their potential impacts on improvement and treatment of IBD using animal models (rats). Macroscopic and microscopic evaluations of three inflammatory indices measured in

Results: According to the results, the maximum growth of probiotic bacteria 107 Cfu/ml was observed after 18 hrs which maintained constant rate onward. There was no significant change in the pH. Pathogenic bacteria count was declined by 3 log indicating the antimicrobial effects of probiotic milk. It also reduced the inflamatory factors, which in turn proposes the curative effects of these products in disease improvement.

Conclusion: According to the results, the maximum growth of probiotic bacteria 107 Cfu/ml was observed after 18 hrs which maintained constant rate onward. There was no significant change in the pH. Pathogenic bacteria count was declined by 3 log indicating the antimicrobial effects of probiotic milk. It also reduced the inflamatory factors, which in turn proposes the curative effects of these products in disease improvement.

Keywords: Probiotic, Lactobacillus, Bifidobacter, antimicrobial effect, Staphylococcus.aureus , Salmonella.typhimorium

P612 - 124: STUDY OF THE SURVIVAL RATE OF BIFIDOBACTERIUM BIFIDUM IN DOUGH BY POWDER AND ESSENTIAL OIL OF MENTHA LONGIFOLIA

HAMED KHATAMI[1], MOHAMMAD HADI FAKOOR[2]

1. Department of Food Industry, Hidaj Branch, Islamic Azad University, Hidaj, Iran. (Student of MSc).
2. Department of Microbiology, Hidaj Branch, Islamic Azad University, Hidaj, Iran. (faculty member of Islamic Azad University).

Background and Aim: Probiotics are beneficial bacteria that are present in many fermented foodstuffs and can be used to add to foods due to create the health effects. The Bifidobacteria is one of the most common probiotics of milk products.

Methods: The Mentha longifolia was prepared from Dizajabad village of Zanjan vicinity. It dried under appropriate conditions and the Herbarium Code obtained 1311 from Zanjan Pharmaceutical Faculty. Also, the Duogh was produced with 50-50 (yogurt/water) .Then, Bifidobacterium bifidum was inoculated in it. Duogh divided into 4 groups (samples A, B, C, D) 250 ml. Group A; contains no essential oil and mint powder, B; contains 0.150 gr of mint powder, C; contains 0.3 gr of mint powder, D; contains 0.1 gr of Mentha longifolia essential oil .Then, each 4 groups were counted from Bifidobacterium bifidum in the days (0, 5, 10, 15, 20, 25, and 30). The produced Dough tested by 48 people. The results were analyzed by ANOVA.

Results: The highest quality of color and flavor were in Dough 25 days with 0.150 mg Mentha longifolia (4.69 ± 0.79). Also, the best Dough tissue with 0.15 mg mint was on day 5 (4.88 ± 0.34). In the case of Dough tissue, there was no significant difference with 0.15 mg of Mentha longifolia (4.19 ± 1.05) between 5 to 25 days.

Conclusion: The according to a poll, Dough with 0.15 gr of Mentha longifolia powder had the best results in 25 days.

Keywords: Probiotic, Bifidobacterium bifidum, Mentha longifolia, Dough

P613 - 149: GROWTH OPTIMIZATION OF LACTOBACILLUS PLANTARUM T5JQ301796.1, AN IRANIAN INDIGENOUS PROBIOTIC IN LAB SCALE FERMENTER

Faranak Noori[1]

1. Me

Background and Aim: Lactobacillus plantarum is one of the probiotics species used in functional food products. These bacteria or their purified bacteriocins are used as biological preservatives in food industry. The first step in production of an array of probiotic products is optimizing production in fermentors. This study aimed to examine factors affecting in-vitro growth optimization of Lactobacillus plantarum T5JQ301796.1 in a lab scale fermentor.

Methods: Following 24 hours of anaerobic culture of the lactobacillus at 37°C, the pre-culture was ready and was inoculated to a 5-liter fermentor at 37 °C and stirred at 40 rpm. Then, factors affecting lactobacillus growth, including carbon and nitrogen sources and pH were studied. The results were interpreted using RSM Pro software, and optimal conditions for the device were determined.

Results: For optimal growth of Lactobacillus plantarum T5JQ301796.1 in lab scale fermentor, optimal conditions were 25.96 g/l of glucose, 1.82% of yeast extract, pH of 7.26, stirring at 40 rpm at optimum temperature between 37- 40°C. In this condition maximum viable cell in batch fermentation was 1.25×1010 cfu/ml

Conclusion: The lactobacillus used in the present study was isolated from a traditional fermented dairy product of Iran, called Tarkhineh. Studies have shown probiotic properties of this strain. Thus, optimization of its production in a fermentor is the first step in producing a wide range of probiotic products based on this bacterium Application of CCD for growth optimization of this bacterium led to maximum viable cells equal to 1.25×1010 cfu/ml. So the mentioned features can lead to optimum industrial scale production and usage of this probiotic strain in probiotic products

Keywords: Optimization, Probiotic, Fermentor, Lactobacillus Plantarum T5JQ301796.1, RSM Pro

P614 - 152: IMPROVEMENT OF PROBIOTIC VIABILITY IN YOGURTS CONTAINING CEREAL BRAN

Ali Heshmati[1]

1. Hamadan Uni of Med Sci

Background and Aim: In current years, there is an increasing trend for developing functional foodstuff containing probiotic microorganisms combined with prebiotic ingredients.

Methods: In this study, the effect of incorporation of cereal bran including wheat and barley bran (1, 1.5 and 2%) into yoghurt on probiotic viability during cold storage was studied.

Results: Results showed that Lactobacillus acidophilus and Bifidobacterium animalis count in samples containing wheat and barley bran was significantly higher than the control sample in whole storage period ($p < .05$). High levels of barley and wheat bran (2%) decreased sensory attributes although it led to viscosity increment. Sensory property scores of yoghurt samples containing level s of lower than 1.5% barley and wheat bran was similar control sample, while the number of L. acidophilus and Bifidobacterium animalis in this products was significantly higher than minimal acceptable level (107 CFU/g).in general, addition of barley and wheat bran in level of 1.5% can increase L. acidophilus and Bifidobacterium animalis during cold storage and didn't significant impact on sensory scores.

Conclusion: The finding obtained from this study could be applied by the industry to develop new high-quality functional food.

Keywords: Barley, wheat, bran, Lactobacillus and Bifidobacterium animalis

P615 - 169: EFFECT OF HYPOLIPIDEMIC SUPERNATANT LACTOBACILLUS GASSERI IN HEALTHY AND DIABETIC LABORATORY MICE

Anoosheh Soleimani Rahim Abadi[1], Professor Babak Khalili Hadad[2], Akram Sadat Tabatabaee Bafroee[3], Shaghayegh Pishkari[4]

1. Department of biology, East Tehran Branch , Islamic Azad University , Tehran, Iran
2. Department of medical discipline.school of medicine. CIU.Georgia
3. Department of biology, East Tehran BranchGhiamdasht , Islamic Azad University , Tehran, Iran
4. Department of biology, Tehran Medical Branch , Islamic Azad University , Tehran, Iran

Background and Aim: Diabetes mellitus is a group of metabolic diseases characterized by hyperglycemia. Due to the side effects of hypoglycemic and insulin oral agents, the use of natural products is considered necessary. Probiotics are the natural flora of the body, which has proven the high frequency of hypoglycemic effects of some of them. Also, research has shown the effect of lowering cholesterol in some Lactobacillus species. In this study, the effects of Lactobacillus gasseri supernatant on triglyceride and cholesterol levels in male and female rats, healthy and diabetic by streptozotocin.

Methods: Supernatant Lactobacillus gasseri was treated with intraperitoneal injection at concentrations of 100,150,200,250,300,400 mL / kg of body weight for 20 days. The blood sample was collected after 20 days. Healthy and The diabetic control were treated with saline. Serum cholesterol and triglyceride levels were measured by the enzyme method.

Results: Supernatant Lactobacillus gasseri reduces serum cholesterol and triglyceride in streptozotocin-induced diabetic rats. The results of this study indicate that Hypolipidemic effect is in supernatant Lactobacillus gasseri.

Conclusion: This plant can be considered as a good candidate in Diabetes mellitus disease research. Effective combinations of Supernatant Lactobacillus gasseri are still not known.

Keywords: Lactobacillus gasseri, Hypolipidemic, Diabetes mellitus, Laboratory rat

P616 - 170: EVALUATING THE OF THE EXTRACTED SUPERNATANT OF LACTOBACILLUS GASSERI CONTAIN MEDIUM ON THYROID CANCEROUS CELL LINES; USING MTT METHOD

Anoosheh Soleimani Rahim Abadi[1], Mohammad Ali Mazlomi[2], Mahnaz Farahmand[3]

1. Department of biology, East Tehran Branch , Islamic Azad University , Tehran, Iran
2. Department of biology, East Tehran Branch , Islamic Azad University , Tehran, Iran
3. Department of biology, East Tehran Branch , Islamic Azad University , Tehran, Iran

Background and Aim: Cancer occurs as a result of uncontrolled cell division that is caused by environmental factors and genetic disorders. Thyroid cancer is the most common malignant tumor of the endocrine system. Undifferentiated carcinomas include approximately 10-15% of all thyroid carcinomas. It usually appears in the 7th and 8th decades of life and includes some of the most malign human neoplasms. Probiotics are living organisms that, if consumed, will have effective healing effects for their host. Probiotics are effective in the treatment of cancers. Lactobacillus is one of the most important probiotics. Gram-positive organisms are able to grow under anaerobic or low-oxygen conditions. Lactobacillus gasseri is a probiotic isolated from breast milk.

Methods: First, the supernatant of Lactobacillus gasseri was prepared in different volumes of 7.81, 15.6, 31.25, 62.5, 125, 250, 500 µl of cell suspension in a volume of 1200 µL from the cell culture medium. The effect of supernatant Lactobacillus gasseri on the cancer cell line The thyroid C643 carcinoma were examined by MTT. The survival rate of testicular and thyroid cancer cells was calculated.

Results: Treatment of thyroid cancer cells (C643) with different volumes of probiotic suspension showed that higher volumes of cytotoxicity were higher and the survival rate of cancer cells decreased.

Conclusion: Supernatant Lactobacillus gasseri can be used as a candidate for the treatment of thyroid cancer.

Keywords: Lactobacillus gasseri, MTT, thyroid cancer

P617 - 172: MOLECULAR SEPARATION, PROBIOTIC PROPERTIES AND ANTILISTRIOSTIC BACTERIOCIN PRODUCTION OF ENTEROCOCCUS FAECIUM AND LACTOBACILLUS CURVATUS

Tannaz Mirhadizadi[1]

1. Ferdowsi University Of Mashad

Background and Aim: Bacteriocins have become important preservatives in the food and pharmaceutical industries and today they become important substitutes for chemical antibiotics . The purpose of this study is isolation and molecular identification of Enterococci and Lictobacilli producing bacteriocins with a wide range of antibacterial activity. Enterococcus facium strain had the most antibacterial effect against Listeria monocytogenes 506 and Lictobacillus brevis F 145 and has both bactericidal and Bacteriostatic properties , whereas the lactobacillus curvatus strain had bacteriostatic properties. Bacteriocin lost activiry in presence of trypsin and proteolytic enzymes and maintained its activity against pH changes from 3 to 10 and changes in temperature to 121 Co. The bacteriocin genes of Enterococcus faecium and lactobacillus curvatus ent A, ent P, but L50A and curA were 135, 216 and 542 bp, respectively. The probiotic properties of strains were able to grow in the acidic range and in the presence of bile salts.

Methods: Among the isolated bacteria, two strains with the ability to produce bacteriocin more than other samples were selected for sequencing. DNA extraction was performed based on the kit. PCR reaction was performed using primers of 16S rRNA and PCR products were sequenced after purification.

Results: Identified isolates under the name Lactobacillus curvatus and Enterococcus faecium.

Conclusion: Use as a bio-maintainer in the food industry, Pharmaceuticals and animal feed, as well as an alternative to chemical antibiotics .

Keywords: Bacteriosin, Enterococcus , Lactobacillus ,listeriosis, Bactericidal, Bacteriostatic, Probiotic properties

P618 - 220: THE EFFECT OF ARTEMIA URMIANA POWDER ON INCREASING THE GROWTH OF PROBIOTIC LACTOBACILLUS ACIDOPHILUS AND BIFID BACTERIUM BIFIDIUM ON PROBIOTICS MILK

Fatemaeh Akbarzadeh[1], Ali Ghorbani Ranjbary[2]

1. 1. Department of Biotechnology, Ferdowsi University of Mashhad, Mashhad, Iran.
2. PhD., biotechnology

Background and Aim: Despite significant progress in reducing death rates have occurred from cardiovascular disease, these diseases are still considered as the leading cause of death in many countries. The other probiotic products with a reduced risk of heart attacks and improve favorable microbial flora of the gastrointestinal tract, has a profound effect on the health of consumers.

Methods: To determine effects of different dose of Artemia urmiana, (0 %, 1%,2%,3%) on growth of probiotic bacteria bifid bacterium Bifidium and Lactobacillus acidophilus At a first stage(milk) and at the second stage (yogurt) were produced 0.33 g of lyophilized bacteria Bifid bacterium Bifidium and Lactobacillus acidophilus separately was added to a one liter sterilized low fat milk. Acidity, pH and microbial growth and survival were examined during incubation. The day after the produce, products were examined by sensory evaluation.

Results: The evaluation of microbial cultures showed that probiotic bacteria of Bifid bacterium compared to Lactobacillus acidophilus growth was not very well on MRS Agar medium The investigated of results show that the increasing concentrations of Artemia urmiana has positive effect On probiotic LA and BB bacteria growth in the probiotic milk and the . yogurt. Also groups receiving 3 percent of Artemia urmiana powder had the lowest cholesterol and the highest blood tg levels ($p \leq 0/05$)

Conclusion: Overall we can say that the Artemia urmiana cause the growth of probiotic lactobacilli acidophilus bacteria and Bifidobacterium bacteria in milk and yogurt

Keywords: Artemia urmiana, Lactobacillus acidophilus, bifid bacterium Bifidium, Lipid profile, Probiotic

P619 - 228: FAST AND SIMPLE METHOD FOR DETERMINATION OF CALCIUM PROPIONATE AS PREVENTION OF FORMATION OF MYCOTOXINS IN BREAD SAMPLES BY HPLC

Freshteh Mehri[1], Iraj Khodadadi[2], zohreh Fasihi[3], Ali Heshmati[4], Fatemeh Nazmi[5]

1. Food and Drug Laboratory,Hamadan University of Medical Science, Hamadan, IR Iran
2. Department of Biochemistry and Nutrition, School of Medicine, Hamadan University of Medical Science, Hamadan, IR Iran
3. Food and Drug Laboratory,Hamadan University of Medical Science, Hamadan, IR Iran
4. Nutration Health Research Centeral, Hamadan University of Medical Science, Hamadan, IR Iran
5. Food and Drug Laboratory,Hamadan University of Medical Science, Hamadan, IR Iran

Background and Aim: Moldiness is one of the most common microbiological defects, found in bakery industry. It is estimated that approximately 1-5% of the bread production goes wrong due to fungi activity such as spergillus, Fusarium and Penicillium. Mold contamination determines not only changes in color, taste, but also loss of the food quality as a result of possible formation of mycotoxins. Propionic acid and propionates have been widely used in breads and cakes to prevent development of mold and bacteria. Therefore, a simple, accurate method for determination of propionic acid and propionates would be useful.The objective of the present work was the development and optimization of a sensitive, simple and fast method for determining propionates as propionic acid in some bread samples based on ultrasound-assisted extraction followed and HPLC-UV analysis for the first time in a bread sample and its effect on organoleptic properties of bread.

Methods:A high-performance liquid chromatography (HPLC) method was also developed and validated for comparison. In that bread, the quantity of pH and acidity were measured. Calibration curves of the five compounds ranged from 50-500.The detection limit of these compounds were determined by this method. Twenty-two bread samples from three markets were randomly selected and assayed for calcium propionate using the above developed methods.

Results: Calibration curves of compounds achieved linearity .The detection limit of these compounds were 5ppm. The results showed that 14/30 samples contained calcium propionate<1000 mg/kg.

Conclusion: It is necessary to regulate a periodic monitoring and control program to determine the amount of propionate in a variety of consumable breads.

Keywords:calcium propionate -mycotoxins -bread -HPLC

P620 - 242: ASSESSMENT OF VIABILITY OF BIFIDOBACTERIUM LACTIS(BB12), IN PROBIOTIC SUGAR-FREE CHOCOLATE DAIRY DESSERT

Seyede maryam Noorbakhsh[1], Najmeh Sabahi Mohammadi[2]

1. M.Sc of Microbiology, Department of Microbiology, Olom Tahghighat branch, Islamic Azad University, Tehran,Iran
2. Ph.D Candidate of Food Microbiology. Tabriz University, Tabriz, Iran

Background and Aim: With increasing consumer awareness, demand for sugar-free products and also products containing probiotic bacteria has been increased,in recent years. As a result, the formulation of a non-fermented product which can be a suitable carrier for probiotic bacteria, as well as reduced sugar intake, is of particular importance. The purpose of this study was to formulate and commercialize a kind of sugarless probiotic chocolate dessert containing date sugar

Methods: For this purpose, 17 treatments were prepared according to the experimental design and were kept in the refrigerator until the tests were performed on days 1, 11 and 21

Results: The results showed that probiotic viability decreased with increasing date sugar content and storage time, but did not reach to 107. Also, by examining the results of sensory evaluation, changes in dessert formulation and sugar substitution with date sugar did not have a significant effect on flavor, color, aroma and taste parameters of dessert samples. Acidity increased with increasing storage time

Conclusion: Considering the findings of this study, it is possible to produce probiotic non-sugar chocolate dessert that has no qualitative and sensory properties other than chocolate desserts containing sugar.

Keywords: Bifidobacterium Lactis, Chocolate dairy dessert, Probiotic

P621 - 294: PROBIOTIC APPLICATION IN HONEYBEE BREEDING

Niloufar Soleymani[1]

1. Young Resaerchs Club,Arak Branch,Islamic Azad University,Arak,Iran

Background and Aim:A group of beneficial bacteria have entered marvelous properties in the production process up to the consumption of food. These bacteria are called probiotics. The cycle of agriculture and animal husbandry is important in the food industry. The purpose of this study is the applied importance of probiotic bacteria in honeybee breeding.

Methods: The honeybee's digestive tract is composed of several parts. Honey bag is a place for collecting and storing nectar. This bag contains certain enzymes and acidic conditions. Since microbes exist in the environment, water, soil and plants, it is possible to isolate a group of symbiotic bacteria in the honeybee's digestive tract.

Results: Given the acidic condition of the honey bag, a group of acid-lactic bacteria can be isolated. These bacteria have potential probiotic properties, so these bacteria can be used as nutritional supplements.

Conclusion: The use of isolated bacteria from the honeybee's digestive tract can be a good alternative to medical and antibiotic supplements. It is recommended that probiotics adapted to the digestive tract of honeybees will increase their immune system.

Keywords: Honey Bee,Probiotic,Food

P622 - 372: INVESTIGATION OF THE PRESENCE OF BIOACTIVE PEPTIDES IN TARKHINEH AND THEIR ANTIOXIDANT ACTIVITY

Zohreh Nematollahi[1], Sajad Shokri1[2], Zohreh Nematoallahi[3]

1. Department of Food Hygiene and Control, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
2. M.Sc. in microbiology, Science and Research Branch, Islamic Azad university, Tehran, Iran

Background and Aim: Bioactive peptides have been defined as specific protein fragments that have a positive impact on body functions or conditions and may ultimately influence health. Hydrolytic reactions, such as those catalyzed by digestive enzymes, result in their release. Tarkhineh is a prepared product that usually consists of cracked wheat, yogurt, and vegetables that are fermented. This product considered as probiotic and it is believed that Tarkhineh is the source of bioactive peptides, so the aim of this study was investigation of the presence of bioactive peptides in Tarkhineh and their antioxidant activity.

Methods: Tarkhineh were made in laboratory scale and their aqueous extract were prepared. Protein content of these extracts measured by Bradford method. Extracts were ultra-filtrated with nominal molecular weight exclusion limit of 5000 and 10000Da and the antioxidant activity of these filtrates were investigated by DPPH method.

Results: The protein content of extracts was 1.52 ± 6 mg/ml. The DPPH results showed that antioxidant activity of unfiltered extracts are significantly higher ($p < 0.05$) than the 5000 and 10000 Da fractions. In the other hand, filtrate by molecular weight exclusion limit of 5000 Da showed better antioxidant activity than 10000 Da fractions ($p < 0.05$).

Conclusion: The results of this study suggested that the Tarkhineh can have bioactive peptides with antioxidant activity and therefore can have health effects on consumer.

Keywords:bioactive peptides, Tarkhineh, antioxidant activity, DPPH

P623 - 373: INVESTIGATION OF THE PRESENCE OF BIOACTIVE PEPTIDES IN TARKHINEH AND THEIR ANTIBACTERIAL ACTIVITY AGAINST FOOD BORNE PATHOGENS

Zohreh Nematollahi[1], Sajad Shokri[2], Zohreh Nematoallahi[3]

1. Department of Food Hygiene and Control, School of Veterinary Medicine, Shiraz University, Shiraz, Iran
2. M.Sc. in microbiology, Science and Research Branch, Islamic Azad university, Tehran, Iran

Background and Aim: Tarkhineh is a traditional Iranian fermented product produced from a mixture of doogh and wheat grout. The purposes of the present study were investigation of the presence of bioactive peptides in Tarkhineh and their antibacterial activity against Staphylococcus aureus and E. coli.

Methods: Tarkhineh were made in laboratory scale and their aqueous extract were prepared by maceration in phosphate buffer. Protein content of these extracts measured by Bradford method and then these extracts were filtered through filters with nominal molecular weight exclusion lower than 5000 and 10000Da. These filtrates were used as source of bioactive peptides.

Results: The protein content of extracts was 1.52 ± 6 mg/ml. The results of the antibacterial activity of fractions indicated that none of the extracts didn't have any antibacterial activity against E. coli ($p > 0.05$), but 5000 Da extract fraction could significantly ($p < 0.05$) inhibit the growth of Staphylococcus aureus in comparison with unfiltered extract and 10000Da fraction. In addition results showed higher antibacterial activity against Staphylococcus aureus for unfiltered extract than 10000Da fraction, also this different was not statistically significant ($p > 0.05$).

Conclusion: According to these results it was concluded that Tarkhineh can have bioactive peptides with antibacterial activity against gram positive pathogenic bacteria.

Keywords:bioactive peptides, Tarkhineh, antibacterial activity, food borne pathogens

P624 - 381: THE EFFECT OF LACTOBACILLUS CASEI.ON SKIN WOUND HEALING IN WISTAR DIABETIC RATS BY GAVAGE METHOD ON DAYS 1,3,7,14,21

Atena Bazjo[1]

1. Department of Microbiology, Science Faculty, Islamic Azad University of Arak, Iran

Background and Aim: Probiotics are microorganisms in the digestive tract (Gastrointestinal tract). In addition to helping the digestion of complex molecules, also it helps the immune system and reduces inflammation. The beneficial effects of this bacterium on gastrointestinal ulcer healing have been proven eventhough Quantitative research has been done on the therapeutic effects of these bacteria on skin ulcers, especially the repair of skin lesions in diabetic people. The aim of this study was to investigate the effect of Lactobacillus casei.on skin ulcer healing.

Methods: After isolating the probiotic bacteria strains and examining the production of exopolysaccharides, Lactobacillus casei with the ability of producing exopolysaccharides, were selected. Then, Wistar male rats were divided into 2 groups: 1 group of 10 Control group and one experimental group of 15 experimental groups including gavage control, experimental gavage and then diabetic rats with diabetic streptozotocin, and a square scar in the size of 1.5 × 1.5 cm on mice back was made. . After 24 hours of wound healing, the experimental group of PBS gavage containing Lactobacillus casei but the control group did not receive any treatment. The scar area was measured every 3 days. The skin of the killed rats on days 1,3,7,14,21 were taken and under histological and statistical studies

Results: Thereafter, there was a progressed increase in ulcer healing on day 7 in animals treated with dead probiotics (p= 0.03) as compared to untreated controls

Conclusion:probiotic bacteria consumed decreased inflammation

Keywords: Skin ulcer, Diabetes, Probiotics, Lactobacillus casei, Exopolysaccharide

P625 - 384: EFFECT OF BIFIDOBACTERIUM BIFIDUM ON REDUCING BLOOD SUGAR AND CHOLESTEROLE IN DIABETIC RATS

Shahab Jamaran [1]

1. department of microbiology, science faculty,islamic azad university of arak iran

Background and Aim: Diabetes mellitus is a disease which has affected about 3 million people in Iran. For many years, the use of Phytotherapy in medicine has been common. In the present study, the effects of native probiotic on blood glucose s in diabetic rats were investigated. Probiotics are living microorganisms that administration of sufficient quartiles of them cause health promotion. Since Probiotics modulate the composition of the intestinal microflora, they plays an important role in ameliorating the side effects of diabetes.

Methods:: For this study, 21 male wistar rats aged 12-14 weeks and weighed 110-130 gm was used. After a 1-week adaptation period, the rats were randomly divided into three group positive control, negative control (diabetic), trail 1 (probiotic) . Diabetes was induced through the injection of stereptozotocin (55 mg/kg) into the experimental case and diabetic control . Trail1 group was administrated with 2×109 cells of bifidobacterium bifidum, by oral gavage . After 21 days, rats were anesthetized with ether and blood samples were taken from heart.Then Glucose kit is used for quantitative determination of Glucose in plasma

Results: Our results showed that Glucose level in positive group (268±6.106 mg/dl) was significantly increased compare to negative control(92.29±2.697 mg/dl), (Pvalue < 0.0001). It also became clear that receiving probiotics in first trial group caused a significant decrease in Glucose concentration to(124.6±1.478mg/dl), (Pvalue < 0.0001).

Conclusion: The results of these tests indicate that the probiotic bifidobacterium bifidum as a probiotic can reduce the negative effects of diabet and reduce levels of Glucose blood significantly .

Keywords: Diabetes,Probiotic, glucose, rat

P626 - 414: EFFECT OF LIVE OR HEAT-KILLED L. ACIDOPHILUS ON FREE AFLATOXIN M1 IN DOOGH

Zahra Sarlak[1], Milad Rouhi[2]

1. Students' Research Committee, Department of Food Science and Technology, National Nutrition and Food Technology Research Institute, Faculty of Nutrition Sciences, Food Science and Technology, Shahid Beheshti University of Medical Sciences.Email: sarlak.zhr@gmail.com
2. Corresponding author: Department of Food Science and Technology, Faculty of Nutrition Sciences, Food Science and Technology, Kermanshah University of Medical Sciences. Email:milad.rouhi@kums.ac.ir

Background and Aim: Aflatoxin is one of the most important contaminants in milk and dairy products. Therefore, more efforts must be performed due to reduce or remove the Aflatoxin in dairy products. In this study, the effects of live or dead L.acidophilus on the reduction in 0.500 ppb of free aflatoxin M1 in Doogh during fermentation and refrigerated storage were studied.

Methods: Immunoaffinity column and HPLC with fluorescence detector were used for extraction and measurement of free AFM1, respectively.

Results: Treatment containing dead (heat-killed) L.acidophilus significantly binded more AFM1 than live L.acidophilus treatment. However, the live probiotics were more effective in the reduction of AFM1 at day 14 and 28 of storage ($p<0.05$).

Conclusion: Although the mechanism of probiotics action on aflatoxin has not been clarified yet, it has been suggested to be a physical adhesion to the bacterial cell-wall components, rather than covalent binding or degradation by bacteria metabolism. Both polysaccharides and peptidoglycans are expected to be greatly affected by heat treatment, which can cause denaturation of proteins, in turn increasing hydrophobic nature of surface or forming products of a Maillard reaction. Such disturbances allow aflatoxins to bind to the bacterial cell wall and plasmatic membrane components,which are unavailable when the cell wall is intact. In contrast, at days 14 and 28, AFM1 reduction was significantly increased in treatment with live probiotics. Viable inoculated probiotics exhibit reproduction activity during fermentation and refrigerated storage; this could be responsible for increases in both live and dead cell populations in Doogh, resulting in higher AFM1 removal comparing to dead probiotics treatment.

Keywords: Aflatoxin, Reduction, Milk, Dairy products

P627 - 424: THE EFFECT OF PROBIOTIC BACTERIA AND PREBIOTICS ON THE GROWTH OF E.COLI ATCC23922 AND ENTEROCOCCUS FAECALIS ATCC 29212

Akram Asadi[1], Dr.Rouha Kasra Kermanshahi[2], Dr.ZahraMoosavi-nejad[3]

1. Tehran, Alzahra university,Faculty of Biology
2. Tehran, Alzahra university,Faculty of Biology
3. Department of Biotechnology,Faculty of Biological sciences

Background and Aim: Intestine is the habitat of a large and diverse population of microbes,including a variety of anaerobic bacteria .these bacteria participate in the catabolismes of a wide range of compounds and generates secondary toxic compounds. Often these secondary compounds are toxic to the host.the consumption of probiotic bacteria and prebiotics in the diet can balance the number and the type of intestinal flora.

Methods: In this study,100 microliter of 0.5 McFarland concentration of over night probiotic bacteria that grown in MRS broth (Lactobacillus acidophilus ATCC 4356,L.casei ATCC 39392, L.fermentum ATCC 9338 , L plantarum ATCC 8014 ,L.reuteri ATCC 2372,L.rhamnosus ATCC 7469) were incubated in three cultured medium ,pure MRS broth and MRS broth containing 2% w/v trehalose and MRS broth containing 2% w/v sorbitol.then after 48 hours,to obtain supernatant of probiotic bacteria,all cultures were centrifuged at 6000 rpm and -4 centigrade degree for 20 minutes and the supernatant was passed through a filter 0/22 micrometer and its effect on growth of E.coli ATCC23922 and Enterococcus faecalis ATCC 29212 was determied by MIC(minimum inhibitory concentration)and MBC(minimum bactericidal concentration).

Results: The result showed that the MIC of free supernatant of L.casei that grown in MRS broth containing 2% w/v terhalose on E.coli and L.casei that grown in MRS broth containing 2% w/v sorbitol and L.casei that grown in control culture medium on Enterococcus faecalis were 12/5% .

Conclusion:we can use L.casei's supernatant with Terhalose and Sorbitol as dietary supplement to modulation intestinal flora.

Keywords:probiotic , prebiotic,MIC-MBC , Intestinal flora

P628 - 426: COMPARISON OF PROBIOTIC PROPERTIES OF LACTOBACILLUS PARACASEI AND LACTOBACILLUS PLANTARUM ISOLATED FROM TRADITIONAL SEMNAN CHEESE

Mahnoosh Parsaeimehr[1], Ashkan Jebellijavan[2], Maedeh Hashemi[3], Zahra Dehghan[4], Negin Mahravan[5], Fatemeh Manteghi[6], Mansure Kanaani[7]

1. Food Hygiene Department, Faculty of Veterinary Medicine, Semnan University, Semnan, Iran
2. Food Hygiene Department, Faculty of Veterinary Medicine, Semnan University, Semnan, Iran
3. Food Hygiene Department, Faculty of Veterinary Medicine, Semnan University, Semnan, Iran
4. Food Hygiene Department, Faculty of Veterinary Medicine, Semnan University, Semnan, Iran
5. Food Hygiene Department, Faculty of Veterinary Medicine, Semnan University, Semnan, Iran
6. Food Hygiene Department, Faculty of Veterinary Medicine, Semnan University, Semnan, Iran
7. Food Hygiene Department, Faculty of Veterinary Medicine, Semnan University, Semnan, Iran

Background and Aim: Probiotics are defined as live microorganisms, which when administered in adequate amounts, confer a health benefit on the host. In fact, the beneficial effects of probiotics are exerted by improving microbial balance. The acid and bile tolerances are two fundamental properties that indicate the ability of a probiotic microorganism to survive the passage through the gastrointestinal tract, resisting the acidic conditions in the stomach and the bile acids at the beginning of the small intestine. New probiotic strains should be resistant to the severe condition of human gastrointestinal tract.

Methods: In this study, the probiotic ability of Lactobacillus paracasei and Lactobacillus plantarum isolated from traditional Semnan cheese was evaluated. At first, the ability of isolates to bile resistance and acid tolerance was determined by culturing in MRS broth previously adjusted to pH values (3.5, 4.5 and 5.5) and bile concentrations (0.3, 0.5 and 1%). Then comparing the bacterial growth was monitored by measuring absorbance with a spectrophotometer at 600 nm during 24 hours incubation at 37 C.

Results: Based on the comparison of the growth outcomes, Lactobacillus plantarum showed better resistance to Lactobacillus paracasei in PH and different concentrations of bile salts ($p<0.05$).

Conclusion: Therefore, the mentioned Lactobacillus can be considered as a native probiotic for simultaneous application with commercial cultures to increase the health of probiotic dairy products.

Keywords: Lactobacillus plantarum, Lactobacillus paracasei,Probiotic, Traditional cheese

P629 - 434: THE EFFECT OF LACTOBACILLUS PLANTARUM AND HONEY-DERIVED LACTOBACILLUS RHAMNOSUS ON GASTRITIS CAUSED BY HELICOBACTER PYLORI IN C57BL/6 MOUSE MODEL

Behnoush Asgari[1]

1. 1Student research committee, School of Medicine, Alborz University of Medical Sciences, Karaj, Iran

Background and Aim: Helicobacter pylori is one of the most common pathogenic bacteria in the human gut, which is one of the most important factors in causing digestive disorders such as chronic inflammation, gastric ulcers and even gastric cancer. Since the use of various antibiotics to treat H. pylori infection is associated with development of resistance in this bacterium, therefore, the aim of this study was to determine the antimicrobial effects of Lactobacillus rhamnosus(L. rhamnosus) and Lactobacillus plantarum(L. plantarum) as probiotic compounds on H. pylori induced gastritis in C57BL / 6 mouse model.

Methods: Materials and Methods: In this experimental study, the mice were infected 4 weeks after the last infection with standard strain of H. pylori (ATCC 43504). Fourteen days after the last exposure, responses to the treatments and the efficacy of the compounds were evaluated by H. pylori stool antigen test and tissue staining

Results: Based on ELISA results and histological findings, reduction of inflammation was observed after exposing H. pylori infected mice with L. plantarum and L. rhamnosus. So that L. rhamnosus exposure group and exposure group containing all two strains of Lactobacillus showed the highest antimicrobial effect on H. pylori

Conclusion: According to the results of this study L. plantarum and L .rhamnosus as a probiotic compound can be beneficial as a pharmaceutical supplementation which can have useful effects in the elimination of bacteria.

Keywords: Helicobacter pylori, Lactobacillus, Probiotic, Gastritis

P630 - 462: EFFECT OF PROBIOTIC STRAINS OF LACTOBACILLUS SP. ON ENTEROPATHOGENIC ESCHERICHIA COLI O SEROGROUPS ISOLATED FROM CLINICAL SPECIMENS

Morteza Mohajeri Amiri[1], Ali Navabzadeh[2]

1. Department of Biology, Science and Research branch, Islamic Azad University, Tehran, Iran.
2. Department of Microbiology, Islamic Azad University, North branch of Tehran, Iran.

Background and Aim: Enteropathogenic Escherichia coli (EPEC) are common intestinal pathogens of adults and young children. Many methods have been employed to control these bacteria, including the use of probiotic strains specially Lactobacillus species. The aim of this investigation was to evaluate the antagonistic influences of probiotic Lactobacillus species, including L. plantarum, L. acidophilus and L. casei on the enteropathogenic E.coli O serogroups.

Methods:A total of 188 clinical specimens from E.coli bacteria were isolated from medical centers of Tehran and O serogroup profiles of each isolate were determined. The inhibitory influence of pure cultures and two pooled cultures supernatants of Lactobacillus strains on the growth of every serogroup of E.coli were assessed by the spot agar design and by monitoring turbidity.

Results: The clinical specimens belonged to 11 serogroups of enteropathogenic E. coli including O18, O20, O26, O44, O86, O111, O112, O119, O125, O126 and O142. In non-neutralized culture, all of the strains and the pool of Lactobacillus strains were antagonistic towards serogroups O18, O20, O111, O125 and O126. Other microbial antagonism profiles were between 47% and 81%. The combination of Lactobacillus strains indicated greater inhibitory activity toward all E.coli serogroups than the individual media.

Conclusion: All strains of Lactobacillus assessed in this study indicated bactericidal influences on enteropathogenic E.coli O serogroups. Thus, the strains of Lactobacillus studied could be employed as antibacterial supplements to control pathogenic bacteria such as enteropathogenic E.coli.

Keywords: Enteropathogenic E.coli, Lactobacillus, probiotic, microbial antagonism.

P631 - 482: THE EFFECT OF NATIVE IRANIAN PROBIOTIC BACILLUS COAGULANS 6068 AND MEDICAGO SATIVA EXTRACT ON LOWERING BLOOD SUGAR AND HEPATIC ENZYMES ACTIVITY IN DIABETIC RATS

Parisa Mohammadi Hezaveh[1]

1. Islamic Azad University of Arak

Background and Aim: Diabetes is a chronic disease which is caused by lack of insulin production or the inability of cells in using insulin.There are lots of methods for its treatment although they'll be encountered with many problems, so in this case the importance of integrating new method for treatment and also its prevention are implicated. The aim of this research is using native Iranian probiotic and sativa extract on reducing blood sugar levels in diabetic rats.

Methods:. In this study 35 male rats are injected and characterized by Streptozotocin which is utilized for diabetic.They were divided into five groups The: normal control , diabetic control, diabetic receiving probiotics diabetic receiving sativa , group V: diabetic received probiotic and sativa. Bacillus coagulans6068 is employed with concentration of 109 cfu/ml .Probiotic and sativa extract was given daily by gavage to groups

Results:. After 21 days from cardiac puncture blood samples were taken and serum markers including blood sugar, Hepatic Enzymes were analyzed and studied. The results demonstrated significant reduction in blood glucose(61%), sgpt(50%), and sgot (35%)

Conclusion: Consumption of probiotic Bacillus coagulanse 6068 with Sativa extract has a significant effect on the control of blood glucose and other liver factors.

Keywords:probiotic(Bacillus coagulans 6068) , blood glucose, Hepatic Enzymes , sativa extract

P632 - 513: THE SPORE-FORMER PROBIOTICS REDUCE THE EFFECTS OF SALMONELLA ON THE GUT MICROFLORA POPULATION

Somaye Mazkour[1], Seyed Shahram Shekarforoush[2], Sara Basiri[3]

1. Department of Food Hygiene and Public Health, School of Veterinary Medicine, Shiraz University, Shiraz, Iran.
2. Department of Food Hygiene and Public Health, School of Veterinary Medicine, Shiraz University, Shiraz, Iran.
3. Department of Food Hygiene and Public Health, School of Veterinary Medicine, Shiraz University, Shiraz, Iran.

Background and Aim: The intestinal lumen is a major way for pathogens entrance such as Salmonella. But in the gut lumen, the pathogens face a dense microbiota. This community confers health benefits. The probiotics cause the enhancement of colonization resistance and direct inhibitory effects against pathogens which are important in reduction the incidence and duration of gastroenteritis.

Methods: In this study 60 rats were randomly divided into three groups (each group consists of 5 subgroups- 4 rats in each subgroup) as follows: Group 1: Control. Group 2 (Pro.+Sal.): Receiving water containing 5×107 spore/ml Bacillus subtilis and 5×107 spore/ml Bacillus coagulans for 29 days and intragastric gavage of 109 CFU of Salmonella Typhimurium at day 22. Group 3 (Salmonella): Receiving intragastric gavage of 109 CFU of Salmonella Typhimurium at day 22. At day 23, 25, 27 and 29 of the experiment, the total aerobic and anaerobic microorganisms, lactic acid bacteria (LAB) and Coliforms were counted in the feces samples in each subgroup.

Results: Salmonella caused no change in aerobic bacteria enumeration, but in Pro.+Sal. group it reduced and returned to the normal range in 5 days. In Salmonella group anaerobic and Coliform count increased, but probiotic reduced these enhancements and the population were kept close to the control group values. Also, probiotics inhibited the reduction in LAB population following Salmonella infection.

Conclusion:B. subtilis and B. coagulans help the maintenance of gut microflora population when expose to the pathogen, which, causes the reduction of pathogen effects and early recovery.

Keywords: Spore-forming probiotic, Gut microflora, Salmonella Typhimurium

P633 - 516: THE EFFECT OF BACILLUS SUBTILIS AND BACILLUS COAGULANS SPORES AS PROBIOTIC ON SALMONELLA CONCENTRATION IN THE INTESTINE AND ORGANS

Somaye Mazkour[1], Seyed Shahram Shekarforoush[2], Sara Basiri[3]

1. Department of Food Hygiene and Public Health, School of Veterinary Medicine, Shiraz University, Shiraz, Iran.
2. Department of Food Hygiene and Public Health, School of Veterinary Medicine, Shiraz University, Shiraz, Iran.
3. Department of Food Hygiene and Public Health, School of Veterinary Medicine, Shiraz University, Shiraz, Iran.

Background and Aim: Salmonella infection has become a great concern in recent decades due to the high prevalence and antibiotic resistance. So finding novel preventive methods can be helpful. Recently, uses of probiotics, especially spore-forming bacteria such as Bacillus spp. have been growing up.

Methods: In this study 40 rats were randomly divided into two groups as follows: Group 1: Receiving water containing 5×107 spore/ml Bacillus subtilis and 5×107 spore/ml Bacillus coagulans for 29 days and intragastric gavage of 109 CFU of Salmonella Typhimurium at day 22. Group 2: Receiving intragastric gavage of 109 CFU of Salmonella Typhimurium at day 22. At day 23, 25, 27 and 29, five rats were chosen randomly from each group and Salmonella was counted in the liver, spleen, mesenteric lymph node, content of ileum and cecum and feces.

Results: On the first day of sampling the number of Salmonella in the liver, spleen and mesenteric lymph node was zero. At day 25, 27 and 29 the Salmonella count had been reduced by up to 0.5, 0.8 and 1.4 log in the liver, 0.4, 0.6 and 0.7 log in the spleen and 0.4, 0.6 and 0.7 log in the mesenteric lymph node respectively. At day 23, 25, 27 and 29 the Salmonella count had been reduced by up to 0.9, 0.2, 0.1 and 0.7 log in the ileum, 0.4, 0.2, 0.3 and 0.7 log in the cecum and 0.4, 0.2, 0.1 and 0.7 log in the feces respectively.

Conclusion: Spore-forming probiotics can be mentioned as a preventive method for Salmonella infection.

Keywords: Spore-forming probiotic, Bacillus subtilis, Bacillus coagulans, Salmonella Typhimurium

P634 - 524: EVALUATION ANTIMICROBIAL EFFECTS OF PROBIOTIC EXTRACT OF LACTOBACILLUS FOR TREATMENT OF INFECTIONS CAUSED BY SALMONELLA

Zahra moghimi[1], Dr.Golshan Sheikhi[2], Abdolghain Ameri[3], Dr. Sepide Sayadi[4]

1. Student of pharmacy,Ahvaz Jundishapur University of Medical sciences,Ahvaz,Iran
2. Pharmacist,Ahvaz Jundishapur University of Medical sciences,Ahvaz,Iran
3. Microbiology Research Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
4. Pharmacist,Ahvaz Jundishapur University of Medical sciences,Ahvaz,Iran

Background and Aim: Salmonella is one of the most common bacterium causing gastrointestinal infections. Nowadays the resistance of Salmonella against current antibiotics is increasing day by day. Nowadays tendency toward using the natural, biologic and probiotic products as substitutions of antibiotics have been increased due to prevalent side effects of using antibiotics and resistance against them. Probiotic bacteria are living microorganisms which fight against pathogens using different mechanisms.

Methods: The lactobacillus .Casei was cultured in MRS media under microaerophile conditions and its extract was gathered by centrifuge. At first its acidity and salmonellosis effect in comparison with neutral and alkaline states was examined by method of cup plate. The minimum restrainability concentration of probiotic extract was examined using method of serial micro dilution in concentration range of 0.0625 – 1 mg/ml. A comparison had been made using anti biogram test between anti pathogen effect of probiotic extract and common antibiotics in treatment.

Results: The results of the minimum restrainability concentration showed that the stable extract had more antibacterial effect in comparison with supernatant (P<0/01). Using anti biogram test and comparing anti pathogen effect of probiotic extract and common antibiotics revealed that the effect of stable extract is more than supernatant and some antibiotics.

Conclusion: This research shows that useful effect of probiotic against salmonella is related to its metabolites and the stability and effect of stable extract is more than supernatant.

Keywords: Probiotic – lactobacillus – Salmonella

P635 - 526: EFFECT OF OLIGOFRUCTOSE ON VIABILITY OF BIFIDOBACTERIUM LACTIS AND SENSORY PROPERTIES IN SYNBIOTIC YOGURT

Motahare Broughani[1], Rezvan pourahmad[2], ali akbarian moghari[3]

1. M.Sc. Student, Department of Food Science and Technology, College of Agriculture, Varamin-Pishva Branch, Islamic Azad University, Varamin, Iran
2. Department of Food Science and Technology, , College of Agriculture, Varamin-Pishva Branch, Islamic Azad University, Varamin, Iran (Corresponding Author)*
3. Department of Food Science, Technology and Engineering, Faculty of Agricultural Engineering and Technology, Tehran University, Karaj, Iran

Background and Aim: Due to the occurrence and spread of various diseases, the use of functional food, because of having health effects, seems to be more necessary. The purpose of this study was to investigate the effect of oligofructose on viability of Bifidobacterium lactis and sensory properties in synbiotic yogurt.

Methods:t. The amounts of 3 and 5 percent of oligofructose were used in probiotic yogurt containing Bifidobacterium lactis. The viability of probiotic bacteria and sensory properties of synbiotic yogurt were investigated at intervals of 1, 11 and 21 days.

Results: Compared to control sample (without oligofructose), the viability of probiotic bacteria of test samples increased significantly ($p < 0.05$). The number of probiotic bacteria decreased significantly during storage time ($p < 0.05$) but population of probiotic bacteria in all treatments was higher than the minimum required for health effects.According to the result of this research sensory scores (odor, texture, and overall acceptance) of the samples increased significantly ($p < 0.05$). However, teste of the majority of samples did not change significantly ($p > 0.05$). The sample containing 3% oligofructose had the highest sensory score (overall acceptance) which also had a high population of probiotic bacteria (3×106 cfu/ml) at the end of the maintenance period.

Conclusion: Therefore, it can be said that the compound of prebiotic with a positive effect on survival of probiotic bacteria in symbiotic yoghurt samples can improve the health properties of probiotic product.

Keywords:synbiotic yogurt, oligofructose, Bifidobacterium lactis, sensory properties

P636 - 543: PRIMARY EVIDENCE ON THE POTENTIAL OF THREE IRANIAN ENDEMIC PROBIOTICS IN TREATMENT OF HEPATOCELLULAR CARCINOMA

Fatemeh Karami[1], Maryam Aminaee [2], Maryam Tajabadi Ebrahimi [3], Fattah Sotoudehnejad [4]

1. Department of Medical Genetics, Applied Biophotonics Research Center, Science and Research Branch, Islamic Azad University, Tehran, Iran
2. Department of Biology, School of Basic Science, Science and Research Branch, Islamic Azad University, Tehran, Iran
3. Department of Science, Islamic Azad University, Central Branch, Tehran, Iran
4. Department of Biology, School of Basic Science, Science and Research Branch, Islamic Azad University, Tehran, Iran

Background and Aim: Hepatocellular carcinoma (HCC) is the 6th human cancer with high morbidity and mortality rate. Owing to the recent significance of anticancer effects of probiotics in various types of human cancers, current study was conducted to assay the potential of three Iranian endemic probiotics in inhibition of HCC cell growth.

Methods: HepG2 cell line was treated with different concentration of supernatant isolated from L. paracasei, L. acidophilus and L. rhamnosus compared to MRL/MRS broth mediums as negative control. MTT assay was performed to assess cell viability within 24, 48 and 72 hours following treatment.

Results:MTT results demonstrated significant decrease in HepG2 cells viability when treated with each of probiotics and was directly correlated with concentration of bacterial supernatant.

Conclusion: Similar to the other human cancers, lactobacillus can be considered as a potential anticancer probiotics in restriction of HCC cells growth. Further studies are needed to clarify active components of three lactobacillus strains supernatant and their potential as adjuvant therapy in HCC patients' treatment, as well.

Keywords:lactobacillus, HepG2, cell line, treatment

P637 - 564: STUDY ON ANTAGONIST ACTIVITY OF LACTOBACILLI ISOLATED FROM BUFFALO MILK AND YOGHURT AGAINST SOME BACTERIAL PATHOGENS

Neda kouroshzadeh[1], Ania Ahani Azari[2], Sahar Baei[3], Farzaneh Bagheri[4], Rozhin ahmadi Livani[5]

1. Gorgan Branch, Islamic Azad University, Gorgan, Iran
2. Department of Microbiology, Gorgan Branch, Islamic Azad University, Gorgan, Iran
3. Gorgan Branch, Islamic Azad University, Gorgan, Iran
4. Gorgan Branch, Islamic Azad University, Gorgan, Iran
5. Gorgan Branch, Islamic Azad University, Gorgan, Iran

Background and Aim: To overcome the increasing incidence of bacterial infections in humans as well as the rising resistance of pathogens to available antibiotics, there is a need for biological agents to control microbial pathogens. Considering that there has been no research on the antagonistic activity of Lactobacilli isolated from buffalo milk and yoghurt against some important pathogenic bacteria in Golestan province, the aim of this study was to evaluate their antagonistic activity against 9 of them.

Methods: Samples were collected from west of Golestan province (suburbs of Bandar Gaz) under sterile conditions. The samples were cultured in MRS media and incubated under anaerobic conditions for 48 hours at 37°C. After purification, the isolates were identified by Gram staining, catalase and oxidase tests, and fermentation pattern of carbohydrates. Then, their antimicrobial effects were evaluated against the studied pathogenic bacteria. For this purpose, the well diffusion method was used. After 24 hours of incubation at 37°C, the inhibitory zone around the wells was measured.

Results: Six strains belonging to lactic acid bacteria including Lactobacillus plantarum, Lactobacillus casei and Lactobacillus Composti were isolated. L. Casei had the highest inhibitory effect on Klebsiella pneumonia. L. Plantarum had the most antagonistic activity against Staphylococcus aureus and Shigella flexneri. L. Composti had a similar inhibitory effect on S. aureus, S. Flexeneri and Salmonella typhimurium.

Conclusion:: Based on the result, lactobacilli isolated from the buffalo milk and yogurt samples showed a variable range of antagonistic activity against pathogens studied in this research.

Keywords: Antagonistic, Buffalo, Lactobacilli, pathogens.

P638 - 570: EFFECT OF SACCHAROMYCES CEREVISIAE ON EXPRESSION TOXIN GENE STX1 IN ENTEROHAEMORRHAGIC ESCHERICHIA COLI EHEC

Maryam Kopayee[1], Maryam Koopayee[2], parviz Owlia[3]

1. Shahed university
2. Shahed university

Background and Aim: Enterohaemorrhagic Escherichia coli (EHEC) is an important pathogen in the world that cause acute disease such as Hemolytic-Uremic Syndrome (HUS).EHEC produces Stx1 that cause this disease. Consumption of Probiotics is a new method to curing some illnesses. Probiotic Saccharomyces cerevisiae can decrease microorganisms or their effects. The aim of this study is to evaluate the effect of Saccharomyces cerevisiae on the expression of the produced toxin gene (Stx1) by EHEC.

Methods: Supernatant and lysate of Saccharomyces cerevisiae were prepared so dried. The level of Stx1 toxin genes expression was measured by Real Time technique in the present of concentrations of 1/2 MIC of supernatant and the highest concentrations for lysate.

Results: Supernatant and lysate reduced the gene expression by 77% and 61% respectively.

Conclusion: The both of Supernatant and Lysate decreased the expression of Stx1 but Supernatant was more effective than Lysate.

Keywords: Saccharomyces cerevisiae- Enterohaemorrhagic Escherichia coli- Probiotic

P639 - 578: THE PRELIMINARY EFFECT OF DAIRY PRODUCTS' PROBIOTIC LACTOBACILLI ON THE CELL VIABILITY OF U937 CELLS

Nadia Karimi[1], safoura sameni[2], elham moazamian[3]

1. Department of Biochemistry, College of Science, Agriculture and Modern Technologies, Shiraz Branch, Islamic Azad University, Shiraz, Iran
2. Department of Biochemistry, College of Science, Agriculture and Modern Technologies, Shiraz Branch, Islamic Azad University, Shiraz, Iran
3. Department of Microbiology, College of Science, Agriculture and Modern Technologies, Shiraz Branch, Islamic Azad University, Shiraz, Iran

Background and Aim:one of the main concepts of modern food biotechnology is related to probiotics. By affecting the intestinal flora, these bacteria may stimulate the immune responses and prevent the activity of pathogenic and harmful microorganisms, providing the host's health. Probiotics, through the anti-carcinogenic properties, neutralize the poisoning of substances that can potentially damage gene. In several studies, the influence of probiotics on cancer treatment has been shown to be related to stimulation of inflammatory and cellular responses. Lactobacillus is a known subtype of probiotics which is found naturally in humans and foods. The purpose of this study was to isolate and identify the probiotic Lactobacilli extracted from the dairy products of Fars province, Iran

Methods: Dairy products are one of the key sources of lactobacillus production. Native dairy products of Fars province including milk, yogurt, cheese, whey, dough, butter were collected and cultured. After identification and sonification, the effect of different parts of Lactobacilli strains was detected with the U937 cells, by the MTT assay

Results: In this study, different strains of Lactobacillus were identified from native dairy products of Fars province and each bacterium has shown different and significant effect on the U937 cell viability

Conclusion: As a myeloid cell lineage, it is important to know the reaction of U937 cell viability against natural product-extracted lactobacilli and their wall components. This primary screening of their action may provide better insights for further biochemical, immunological and clinical experiments on the immune system

Keywords:probiotics, G-CSF, U937

P640 - 579: MOLECULAR IDENTIFICATION AND ISOLATION OF DAIRY PRODUCTS' PROBIOTIC LACTOBACILLI FROM FARS, IRAN

Nadia Karimi[1], safoura sameni[2], elham moazamian[3]

1. Department of Biochemistry, College of Science, Agriculture and Modern Technologies, Shiraz Branch, Islamic Azad University, Shiraz, Iran
2. Department of Biochemistry, College of Science, Agriculture and Modern Technologies, Shiraz Branch, Islamic Azad University, Shiraz, Iran
3. Department of Microbiology, College of Science, Agriculture and Modern Technologies, Shiraz Branch, Islamic Azad University, Shiraz, Iran

Background and Aim: Probiotics are live microorganisms that can be found in the natural flora of the human intestine. Lactobacilli as a type of probiotics are useful for human health. Several studies have reported the effects of lactobacilli and their products including toxins, LTA, LPS and glycoproteins on the metabolism, inflammation, cellular and immune response, skin restoration, improvement of cancer and HIV. The purpose of this study was to isolate and identify the probiotic Lactobacilli extracted from the dairy products of Fars province, Iran.

Methods: This bacterium is naturally present in dairy products, therefore, native dairy products of Fras province, Iran were collected. The bacteria of these products were cultured in MRS broth and MRS agar media. After the growth, in order to identify and purify the bacteria, chemical methods including Gram staining and TSI and other tests to evaluate the Catalase and oxidase activity were performed. Thereafter, several strains of lactobacillus were identified using the molecular method PCR analysis (16S rDNA).

Results:: Different strains of lactobacilli were identified, purified and replicated from the native dairy products of Fars province.

Conclusion: Regarding the fact that probiotic-extracted lactobacilli and their products can be used for biomedical and healthcare applications, it is important to identify the dairy products bacterium strains of any specific area for further researches.

Keywords:probiotics, lactobacillus, dairy products

P641 - 589: ANALYSIS OF STREPTOCOCCUS THERMOPHILUS COMMUNITY PROFILES OF DAIRY PRODUCTS FROM FARS, IRAN

Sara Sadeghi[1], Safoura Sameni[2], Elham moazamian[3]

1. Department of Microbiology, College of Science, Agriculture and Modern Technologies, Shiraz Branch, Islamic Azad University, Shiraz, Iran
2. Department of Biochemistry, College of Science, Agriculture and Modern Technologies, Shiraz Branch, Islamic Azad University, Shiraz, Iran
3. Department of Microbiology, College of Science, Agriculture and Modern Technologies, Shiraz Branch, Islamic Azad University, Shiraz, Iran

Background and Aim: Streptococcus thermophilus is an optional, non-pathogenic, aerobic lactic acid bacterium, with a long history of application in locally fermented food and modern industrial products, especially yogurts. This species is known as "safe bacteria" and is defined as probiotic bacteria. Probiotics prevent the presence of harmful microorganisms in the body by connecting to the binding sites on the coating cells, competing with pathogenic bacteria to get nutrients, lowering pH, producing bacteriosin and H2O2.

Methods: Methods: Ten grams of 50 samples of different dairy products were weed out on SM17 medium and incubated at 42 ° C. The initial identification were done according to the colony morphology, followed by the gram staining, oxidase and catalase enzyme tests. Different strains of Streptococci were later identified by the molecular method PCR analysis (16S rDNA)

Results:: Based on the enzyme assays and the analysis of 50 samples, identification of different strains of Streptococci were identified, purified and replicated from the native dairy products of Fars province

Conclusion:: On average, 50 samples of 19 bacteria were isolated. The results of this study indicate that the frequency of this bacterium was 38% in dairy samples. It can be argued that Streptococcus thermophilus is easily isolated as a probiotic in dairy products and is used as a safe and safe bacterium in dairy products

Keywords: Streptococcus thermophilus, dairy, safe bacteria

P642 - 622: IDENTIFICATION OF LACTOBACILLUS GASTROINTESTINAL WHITE PERCH FISH (SANDER LUCIPERCA)

Monireh Faeed[1], Roha kasra -kermanshahi [2]

1. Inland Waters Aquaculture Research Center,Iranian Fisheries Sciences Research Education and Extension Organization(AREEO),Bandar Anzali,Iran.
2. - Department of Microbiology, Faculty of biological Sciences, Alzahra University, Tehran, Iran

Background and Aim: Lactic acid bacteria are beneficial bacteria in the intestinal tract of humans and animals .LAB improve the intestinal micro flora and increase the growth and health of animal.

Methods: The samples (30) were collected from sander luciperca intestinal tract and the isolates were obtained by growing on MRS agar . Identification of bacteria was based on biochemical and molecular (16s rDNA) methods.

Results:the bacteria were detected lactobacillus brevis and lactobacillus plantarum. Which can be used as probiotics in fish feed.

Conclusion: Phylogenetic results showed that Lactobacillus spp Had the highest genetic similarity with strains of China and Iran.

Keywords: Lactobacillus, sander luciperca, intestinal tract

P643 - 637: DISCRIMINATION OF LACTOBACILLUS SPECIES EXTRACTED FROM TRADITIONAL DAIRY PRODUCTS USING RAPD-PCR MOLECULAR MARKER

Seyed mostafa Hosseini[1], Mohammad Reza Arabestani[2]

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: Probiotics are non-pathogenic useful microorganisms with positive effects on the hos health.the aim of the present study was to discriminate Lactobacillus species extracted from traditional dairy products

Methods: This study was conducted on twenty-six specimens were collected from traditional dairy products in Bukan. Lactobacillus species were separated and purified by employing biochemical tests. Then, the intra/inter-species diversity was investigated using the RAPD-PCR technique.

Results:PIC value varied between 15.9 and 34.4 % with the maximum value of 34.4 percent associated with the 1254 primer. The mean of MI for the 6 primers was 4.52, in which the maximum and minimum values belonged to the 1254 and OPA-02 primers, respectively. UPGMA clustering method based on Jaccard similarity coefficient categorized the isolates into four main clusters. Principle Coordinates analysis (PCoA) demonstrated that the first and second components explained 30.59% and 22.48% of variances, i.e. 53.07% of variances in total. the results of RAPD marker indicated that the intra-species diversity was greater inter-species diversity. The intra-group variance explained 94 percent of the all variance, while inter-group variance explained 6 percent of the all variance. Moreover, the results of AMOVA indicated that the highest level of discrimination was occurred at the 16 groups cut-off point with a similarity coefficient of 0.56.

Conclusion: It can be concluded from the present study that are an enriched source of probiotic bacteria which can ensure the health of general population and enhance their immune systems. Moreover, RAPD-PCR is an appropriate method for detection and classification of lactobassiluses.

Keywords: Probiotic, Lactobacillus, RAPD-PCR

P644 - 640: ISOLATION, CHARACTERIZATION AND PRESERVATION OF LACTIC ACID BACTERIA (LAB) FROM MAZANDARAN PROVINCE TRADITIONAL FOODS AND SURVEY OF THEIR IN-VITRO PROBIOTIC ACTIVITY

Shahrzad Tavanania[1], Mohammad ali Amoozgar[2], Mohaddaseh Ramezani[3], Azam Haddadi[4], Naser Harzandi[5]

1. Department of Microbiology, Karaj Branch, Islamic Azad University Karaj, Iran.
2. Microorganisms Bank, Iranian Biological Resource Center, Alborz provience, Iran.
3. Microorganisms Bank, Iranian Biological Resource Center, Alborz provience, Iran.
4. Department of Microbiology, Karaj Branch, Islamic Azad University Karaj, Iran.
5. Department of Microbiology, Karaj Branch, Islamic Azad University Karaj, Iran.

Background and Aim: Probiotics are defined as live microorganisms, which when administered in sufficient amounts, admit a health benefit on the host. Health benefits have mainly been associated with specific probiotic strains from lactic acid bacteria. Because of the benefits that probiotics brings to their host, isolation and identification of them from fermented food sources are in great consideration these days. In addition, the flavoring and nourishing properties of native bacteria are more desirable for native consumers. Therefore, we try to isolate and introduce probiotic native species from traditional foods of north province, Mazandaran, Iran.

Methods: In this study, we isolate LAB on MRS and M17 agar under anaerobic condition. Microscopic and macroscopic morphological analysis were then carried out on isolated strains and Non-LABs are omitted at this step. In-vitro probiotic assay like bile and acid tolerance, hemolysis and catalase activity, tolerance to gastric juice, etc was determined according to INSO19459. Finally, the positive probiotic strains were preserved using cryopreservation technique.

Results:339 LAB strains were isolated and examined in this study. Morphological analysis showed that 50, 91 and 198 of the isolates have coccid, coccobacilli and bacilli morphology respectively. Bacilli strains were selected for probiotic assay and the resulted positive ones are 25 isolate.

Conclusion:: Rich biodiversity of natural dairy products can be considered as good sources of new LAB species. Therefore, we can focus on local dairy products for new LAB strains, which their nourishing properties are more desirable for native consumers.

Keywords: Mazandaran province, Lactic acid bacteria, probiotic, Traditional food.

P645 - 703: IMMUNOLOGICAL EFFECT OF LACTOBACIILUS CASEI IN RAT WITH CANDIDA ALBICANS INFECTION

Behnazsadat High-tech zavareh[1], Behnazsad haghayeghzavare[2], Mahboobeh madani[3], Fereshte Ghandehari[4]

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

Background and Aim: Abstract: Immunological effect of Lactobaciilus casei in rat with Candida albicans infection Behnaz Haghayegh1, Mahboobeh Madani1* ,Fereshte Ghandehari1. 1. Department of Microbiology, Falavarjan Branch, Islamic Azad University, Isfahan, Iran Objective: Probiotic organisms are claimed to offer several functional properties including stimulation of immune system. Candida albicans is the most common type of yeast infection that found in skin and mucous membranes such as mouth, intestinal tract and vagina. This study was undertaken to evaluate the humoral immunologic effect of Lactobaciilus casei in rat with Candida albicans infection.

Methods: Material and Methods: 25 rats were randomly divided in 4 groups including two treatment, positive and negative groups. Treatment groups were recieved Lactobacillus casei within 20 days, every other day. In 11 day one treatment and positiv groups were received Candida albicans. Negative control received distilled water respectively. Blood samples were collected and serum proteins were determined.

Results: Results: According to the results, gamma globulin was increased, whereas alfa and beta globulin were not affected. Conclusion: These findings suggested that Lactobaciilus casei has potential use as a functional food ingredient to improve the immune response agalst candida albicans.

Conclusion: Conclusion: These findings suggested that Lactobaciilus casei has potential use as a functional food ingredient to improve the immune response against candida albicans.

Keywords: Keyword: Lactobacillus casei, Candida albicans, immune system, gamma globulin.

P646 - 724: SURVEY AND COMPARISON OF THE EFFECT OF MULTIPLE LACTOBACILLUS ON THE FUNCTION OF LIVER ENZYMES IN THE VISTAR MATURE NAFLD RATS

Mohammadjafar Begoo[1], fatemeh foroohi[2], taher mohammadian[3]

1. Department of microbiology, Shahr-e-Qods Branch, Islamic Azad University, Tehran, Iran.
2. Department of microbiology, Shahr-e-Qods Branch, Islamic Azad University, Tehran, Iran.
3. Department of microbiology, Shahr-e-Qods Branch, Islamic Azad University, Tehran, Iran.

Background and Aim: In recent years, changes in lifestyle have led to an increase in plasma lipids and a change in the level of Non-Alcoholic Fatty Liver Disease (NAFLD) and cardiovascular disease. Considering the beneficial and non-pathogenic effects of lactobacillus, we used this study.

Methods: In this research, rats were used, first, hypercholesterolemia and then NAFLD disease. Then the amount of cholesterol and triglyceride serum levels of enzymes AST, ALT and ALP were examined. Then, the effects of L.Casei and L.Plantarum strains suspension were studied.

Results: The effect of L.Casei strain on the other is more in reducing the level of cholesterol and triglyceride. In contrast to the hepatic enzymes, L.Casei strain showed a significant difference in the level of AST and ALT enzymes, but in relation to The ALP enzyme was not significantly different.

Conclusion: Lipid metabolites had significant reductions, indicating the potent effects of probiotic bacteria on continued use of cholesterol, triglyceride and liver enzymes in rats. This point indicates that lactose in the diet of organisms and lactic acid is produced positive by the presence of the beta-galactosidase enzyme in probiotic bacteria, thus preventing the storage of fat and adipose tissue in the body.

Keywords:L.Casei, L.Plantarum, NAFLD, Cholesterol, Triglyceride

P647 - 735: STUDY OF THE SURVIVAL RATE OF LACTOBACILLUS ACIDOPHILUS IN DOUGH BY POWDER AND ESSENTIAL OIL OF MINT

Hesam Eskandari[1], Mohammad Hadi Fakoor[2]

1. Department of Food Industry, Hidaj Branch, Islamic Azad University, Hidaj, Iran. (Student of MSc).
2. Department of Microbiology, Hidaj Branch, Islamic Azad University, Hidaj, Iran. (faculty member of Islamic Azad University).

Background and Aim: Herbal essential oil is volatile compound of plants which have been used to produce food up to now. On the other, Probiotics are beneficial bacteria that are present in many fermented foodstuffs and can be used to add to foods due to create the health effects. Therefore, our research was conducted on the survival of Lactobacillus acidophilus in dough by powder and peppermint essential oil.

Methods: The peppermint used in this study after drying, received herbarium code and it was analyzed by the GC and GC/MS. Then, the production of Dough and inoculation of Lactobacillus acidophilus bacterium were divided into 4 groups of 250 cc. A, contains no essential oil and mint powder. B, containing 0.15 grams of mint powder. C, contains 0.23 grams of mint powder. D, contains 0.1 gram of peppermint essential oil. Each 4 groups were counted from Lactobacillus acidophilus in the days (0, 5, 10, 15, 20, 25, and 30).

Results: The best quality of color was in the Duogh containing 0.3 mint and on the 20th and 25th day of production. The best quality of the texture in the Duogh was 0.3 gr of mint and on the 5th day of production. There was a significant difference with the Duogh which was produced on day 20th and contains 0.3 gr mint.

Conclusion: By combining the results of flavor changes and time, Dogh with 0.3 grams of mint and on production 20th day has the best quality in color and texture for consumers.

Keywords: Probiotic, Lactobacillus acidophilus, Peppermint, Dough

P648 - 784: ANTIBIOTIC SUSCEPTIBILITY OF YOGURT`S PROBIOTICS

Narges Aghajanian[1], Mina Gholami[2], Mozhgan Kheirandish[3], Farzaneh Rafiee[4], Davoud Afshar[5]

1. BS of laboratory medical science, Department of Medical laboratory sciences, School of paramedical sciences, Zanjan University of Medical Sciences, Zanjan, Iran,n1.aghajanian@yahoo.com, http://orcid.org/0000-0001-7661-4103
2. MSC of medical microbiology, Department of Microbiology and Virology, faculty of medicine, Zanjan University of Medical Sciences, Iran,m.gholami137052@yahoo.com,http://orcid.org/0000-0002-0405-3762
3. MSC of medical microbiology, Department of Microbiology and Virology, faculty of medicine, Zanjan University of Medical Sciences, Iran, M.Kheirandish73@gmail.comhttp://orcid.org/0000-0003-1159-4599
4. . MSC of medical microbiology, Department of Microbiology and Virology, faculty of medicine, Zanjan University of Medical Sciences, Iran, farzaneh.rafiee021@gmail.com,https://orcid.org/0000-0002-3300-3713
5. PhD of medical bacteriology, Department of Microbiology and Virology, faculty of medicine, Zanjan University of Medical Sciences, Iran,afshar.d@zums.ac.ir , http://orcid.org/0000-0002-3259-3790

Background and Aim: Probiotics are mainly belonged to Lactobacillus spp. and useful for humans in appropriate amounts. The present study aimed to determine antibiotic resistance patterns of probiotic bacteria isolated from probiotic yogurts of Iran.

Methods:7 yogurt samples were cultured in MRS medium and isolated species identified by conventional methods and then confirmed using polymerase chain reaction (PCR) technique. Antibiotic susceptibility test was performed by disc diffusion test in order to determine isolates antibiotic resistance patterns.

Results:8 isolates were recovered from 7 yogurt samples and PCR also showed that the isolates belong to Lactobacillus delbrueckiisubsp. bulgaricus. Antibiotic susceptibility testing showed that three isolates from three brands were resistance to Vancomycin and Gentamicin. Other species were susceptible to all tested antibiotics.

Conclusion: Low resistance rate to antibiotics among Iranian probiotic bacteria indicate that the consumption of their products is safe but their clearance following antibiotic therapy cannot be an acceptable trait. Hence, we suggest that applying probiotics strains with non-transferrable resistance elements in Iranian probiotic yogurts can be a useful strategy to make stable probiotic products.

Keywords: Probiotics, Lactobacillus, yogurt, antibiotic resistance

P649 - 785: EVALUATION OF THE PERFORMANCE OF PLANTAGO PSYLLIUM, PLANTAGO MAJOR AND LALLEMANTIA IBRICA LOCAL PREBIOTICS ON LACTIC ACID BACTERIA

Shima Babaei[1], Gholamreza Zarrini[2], Farzam Shikhzadeh Hesari[3], Majid Mahdavi[4]

1. Department of Animal Biology, Faculty of Natural Science, University of Tabriz
2. Department of Animal Biology, Faculty of Natural Science, University of Tabriz
3. Department of Animal Biology, Faculty of Natural Science, University of Tabriz
4. Department of Animal Biology, Faculty of Natural Science, University of Tabriz

Background and Aim: Prebiotics are resistant to inappropriate conditions of the stomach and are often as nondigestible dietary ingredients that beneficially affect the host by selectively stimulating the growth and or activity of one of a limited number of bacteria in the colon, thus improve host health. In recent years, a new strategy has been developed using the combination of probiotics with prebiotics, called synbiotics. Synbiotic function is more effective than probiotic and prebiotic function alone in improving the quality of life in patients with ulcerative colitis, in preventing colorectal cancer or in microbiota positive regulation. In this research the effect of local prebiotics on lactobacillus bacteria to achieve new synbiotic formulation has been investigated.

Methods: Three samples of prebiotic including Plantago psyllium, Plantago major and Lallemantia ibrica were selected and their effects on 4 Lactobacillus strains including UT1, ST1, CT2 and JTa1, as well as some antimicrobial testing clinical strains were investigated by standard agar well-diffusion method.

Results: The results showed that all three prebiotics were studied not effective against lactic acid bacteria while they showed antimicrobial effects on gram positive and gram negative clinical strains.

Conclusion: The results of this study indicate that the prebiotic compounds studied are usable with lactobacilli with the aim of providing effective synbiotics.

Keywords:prebiotics, lactic acid bacteria, synbiotic

P650 - 793: CYTOTOXICITY EFFECT OF BACTERIOCIN LIKE INHIBITORY SUBSTANCE (BLIS) PRODUCED BY PROBIOTIC LACTOBACILLUS CASEI TA0021 ON COLORECTAL CANCER CELL LINES (HT-29

Elham Norouzi[1], Naheed Mojgani[2], Elahe Motevaseli[3], mohammad Hossein Modarressi[4], Majid Tebyanian[5]

1. Science and Research Branch, Islamic Azad University (srbiau), Tehran, Iran
2. Razi Vaccine and Serum Research Institute- Agriculture Research. Education and Extension Organization, Karaj, Iran..
3. Departeman of Molecular Medicine ,School of Advanced Technologies in Medicine, Tehran University of Medical Sciences.Tehran ,Iran.
4. Departeman of Medical Genetics ,Tehran University of Medical Sciences , Tehran ,Iran.
5. Razi Vaccine and Serum Research Institute- Agriculture Research. Education and Extension Organization, Karaj, Iran..

Background and Aim: Colorectal cancer (CRC) is known as the third most common form of cancer. Diverse therapies such as chemotherapy, immunotherapy and radiation have shown beneficial effects, but are limited due to their adverse effects on the target. Probiotic bacteria and their metabolites are long known to have significant role in decreasing the viability of colorectal cancer cells. This study provided evidence for the anti-cancer effect of a bacteriocin like inhibitory substance produced by a locally isolated L.casei TA0021 strain on colorectal cancer cells HT-29 cell lines invitro.

Methods: The supernatant fluid of L.casei TA0021 showing inhibitory effects towards Salmonella typhimurium, S.enteriditis and E.coli K99, were subjected to catalase and proteolytic enzymes. The inhibitory proteins in the supernatant fluids were precipitated by 60% ammonium sulphate, dialyzed and ultra-filtered using 10KDA filter membranes. The inhibitory proteins accumulated in the filtrate were concentrated using PEG(6000) and saved recorded as BLIS.

Results: Non- denaturing gel indicated a band of approximately 9 KDa to be responsible for the activity. Confluently grown HT-29 cell lines were treated for 72 h with 1%,3%,5%,10% (v/v) of BLIS, incubated at 37˚C under 5% CO2 condition. Cell growth inhibition was measured by MTT assay kit and IC50 values calculated.

Conclusion: Based on the results, the supernatant fluids of L.casei possessed inhibitory actions towards the indicator strains, sensitive to the action of proteolytic enzymes, while unaffected by acidic pH and catalase enzyme. IC50 valve of BLIS against HT-29 cells was 5%(v/v), and significant (86%) cytotoxicity levels on the cancer cells were recorded.

Keywords: bacteriocin , Lactobacillus casei , colorectal cancer (CRC), cytotoxicity , HT-29 cell line.

P651 - 798: ANTIMICROBIAL ACTIVITY AND ANTIBIOTIC SUSCEPTIBILITY OF BIFIDOBACTERIUM SPP ISOLATE FROM HUMAN MILK AGAINST HOSPITAL , ENTEROPATHOGENIC AND FOOD-BORNE PATHOGENS

Soda Amini[1], Ali Aminifazl[2], Hojjat Alizadeh Mamaghani[3]

1. Bacteriology , Islamic Azad university , Mahabad branch , Iran
2. Assistant Professor,Microbiology ,Department of veterinary, Islamic Azad university , Mahabad branch , Iran
3. young researchers and elite club , Islamic Azad university , Mahabad branch , Iran

Background and Aim: Human breast milk consists of high amounts of necessary nutrients and various bioactive for infants . Among these bioactive agents, probiotic bacteria were isolated from human milk.The research comprises isolation and identification of Bifidobacterium strains from Human Milk.

Methods:samples cultured in MRS broth, Bifido agar under anaerobic conditions.Identification of Bifidobacterium isolates was performed by biochemical and PCR technique using species specific Primers . An agar well diffusion assay , disc diffusion method and Elisa method was used for detection of antimicrobial activity,Antibiotic susceptibility and Aflatoxin B1 detoxification potential respectively.Statistical analyses were performed with SPSS software.One-way ANOVA with post-hoc Tukey HSD was used for statistical analysis. Results were regarded as statistically significant at $p< 0.05$

Results: The examined strains were identified as B. Longum , B. Breve .All Isolate showed good probiotic potential.The majority of the strains exhibited antagonistic activity towards Bacillus Cereus , salmonella , Campylobacter , E.coli , shigella , staphylococcus areus respectively . all strains tested were susceptible to penicillin G, amoxicillin, piperacillin, ticarcillin, imipenem, chloramphenicol, rifampicin and vancomycin . all strains tested were resistant to gentamicin, sulfamethoxazole and polymyxin B . Most isolates were resistant to fusidic acid .

Conclusion: This study showed that Bifidobacterium strains with good probiotic potential could be isolated from Human milk and suggest Bifidobacterium strains with probiotic potential may be useful for prevention or treatment of diarrhea and Supportive therapy in Aflatoxicosis but further in vitro and in vivo studies on these strains are still required.

Keywords: Bifidobacterium, human milk, Probiotics, Antimicrobial Activity

P652 - 811: ANTIMICROBIAL ACTIVITY AND ANTIBIOTIC SUSCEPTIBILITY OF BIFIDOBACTERIUM SPP ISOLATE FROM THE FECES OF HEALTHY INFANT AGAINST HOSPITAL , ENTEROPATHOGENIC AND FOOD-BORNE PATHOGENS

Soda Amini[1], Ali Aminifazl[2], Hojjat Alizadeh Mamaghani[3]

1. Bacteriology , Islamic Azad university , Mahabad branch , Iran
2. Assistant Professor,Microbiology ,Department of veterinary, Islamic Azad university , Mahabad branch , Iran
3. young researchers and elite club , Islamic Azad university , Mahabad branch , Iran

Background and Aim: The human intestinal microflora is complex with total counts of 1011-1012 bacteria per gram of stool.The research comprises isolation and identification of Bifidobacterium strains from the feces of healthy infant.

Methods:samples cultured in MRS broth, Bifido agar under anaerobic conditions.Identification of Bifidobacterium isolates was performed by biochemical test and PCR technique using species specific Primers . An agar well diffusion assay , disc diffusion method and Elisa method was used for detection of antimicrobial activity,Antibiotic susceptibility and Aflatoxin B1 detoxification potential respectively.Statistical analyses were performed with SPSS software.One-way ANOVA with post-hoc Tukey HSD was used for statistical analysis. Results were regarded as statistically significant at $p< 0.05$

Results: The examined strains were identified as B. Longum , B. bifidum and B. Breve .All Isolate showed good probiotic potential.The majority of the strains exhibited antagonistic activity towards Bacillus Cereus , salmonella , Campylobacter , E.coli , shigella , staphylococcus areus respectively . all strains tested were susceptible to penicillin G, amoxicillin, piperacillin, ticarcillin, imipenem, chloramphenicol, rifampicin and vancomycin . all strains tested were resistant to gentamicin, sulfamethoxazole and polymyxin B . Most isolates were resistant to fusidic acid .

Conclusion: This study showed that Bifidobacterium strains with good probiotic potential could be isolated from fecal of healthy infant and suggest Bifidobacterium strains with probiotic potential may be useful for prevention or treatment of diarrhea and Supportive therapy in Aflatoxicosis but further in vitro and in vivo studies on these strains are still required.

Keywords: Bifidobacterium, Infant , Fecal flora , Probiotics, Antimicrobial Activity

P653 - 818: ISOLATION AND IDENTIFICATION OF PROBIOTICS FROM MARAGHEH LOCAL YOGURT

Mona Kordloo[1], Behnush Dinarvand[2], Parisa Fathi Rezaei[3], Neda Akbari[4]

1. MSc student,Microbiological Biotechnology University of Maragheh
2. MSc student,Microbiological Biotechnology University of Maragheh
3. Department of Biology, Faculty of Science, University of Maragheh, Maragheh, Iran.
4. Department of Microbiology, Faculty of Science, Islamic Azad University of Arak, Arak, Iran

Background and Aim: Probiotics¬ are living microorganisms that when administered in adequate amounts in humans and animals have beneficial effects on the host through restoring the intestinal microflora balance. The most common probiotics are lactobacilli and bifidobacteria. These organisms are present in foods, often dairy fermented products such as yogurt. Yogurt is a cultured or fermented milk product that is rich in probiotic strains stimulate healthy digestive function, and help produce vitamin B12 and K. ¬The aim of this research is to isolate and identify probiotics from local yogurt sources in Maragheh.

Methods: Ten samples collected from different areas in Maragheh. Then, enrichment on MRS broth, serial dilution and culture of different dilutions on MRS agar were performed. For identification, biochemical tests including gram, catalase and oxidase activity, acid and bile salts resistance were done.

Results: Based on the results, 67 probiotic strains were isolated.

Conclusion: Lactobacillus is one of the most abundant probiotics that comes from yogurt. Now further studies are running.

Keywords: Biochemical tests- Dairy products- Lactobacillus-probiotic

P654 - 836: DETECTION OF A BENZOAT DEGRADATION GENE (BOX-B) IN L. CASEI ISOLATED STRAIN IN CHEESE

Narges Dadfarma[1], Mojgan Bandehpour[2], Bahram Kazemi[3], Jamileh Norozi[4]

1. Islamic Azad Universityof Tehran North Branch
2. Cellular and Molecular Biology Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
3. Cellular and Molecular Biology Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
4. Islamic Azad Universityof Tehran North Branch

Background and Aim: Aromatic compounds like benzoate belong to the second most abundant class of organic growth substrates. Depends on the availability of oxygen, several types of aromatic metabolism are known. Under microaerobic conditions, facultative aerobes use hybrid type of aerobic metabolism of benzoate, These pathways use coenzyme A and do not require oxygen for ring cleavage, rather they use an oxygenase/reductase to dearomatize the ring. We examine presence of BoxB (benzoyl-CoA oxygenase) in Lactobacillus casei isolated from cheese

Methods:: In order to identification of lactobacillus of traditional cheese, one sample of cheese diluted in MRS broth. Then plated on MRS Agar medium and incubated at 37ºc for 48- 72h. To identified species the biochemical analysis was prepared the following conventional tests like carbohydrate fermentation. For screening this gene, after DNA extraction presence of boxB ,the benzoat degradation gene, was confirmed by PCR with specific primers.

Results:: This strain isolated from cheese recognized as lactobacillus casei. The isolates were found to be gram positive, rod shaped, catalase negative bacteria and were found to harbor the BoxB gene, responsible for benzoat degradation.

Conclusion: Studies have demonstrated that some strains of lactic acid bacteria were able to reduce the absorption of toxic substances by the gastrointestinal tract. The use of lactic acid bacteria in remediation processes has shown to be effective. Previous studies performed praised the use of this bacteria in the remediation of heavy metal-contaminated water. Moreover, some of these bacterial species are able to bind to heavy metals due to specific structures found on their cell wall.

Keywords: L. casei, traditional cheese , BoxB , benzoat degradation, bioremediation

P655 - 854: ISOLATION AND IDENTIFICATION OF PROBIOTICS FROM LOCAL WHEY WATER IN MARAGHEH

Behnush Dinarvand1[1], Mona Kordloo[2], Parisa Fathi Rezaei[3], Neda Akbari[4]

1. MSc student,Microbiological Biotechnology University of Maragheh
2. MSc student,Microbiological Biotechnology University of Maragheh
3. Department of Biology, Faculty of Science, University of Maragheh, Maragheh, Iran
4. Department of Microbiology, Faculty of Science, Islamic Azad University of Arak, Arak, Iran

Background and Aim: Probiotics are the healthy living bacteria when administered in adequate amounts results in health benefits in the host. The main objective of this present study is to screen the bacterial strains for potential probiotic characters from whey water in Maragheh. Whey water is the by-product of paneer or cottage cheese which is well known source for probiotic.

Methods: In order to isolate of probiotic strains, five local whey samples were collected. In next step, MRS medium was used for enrichment and isolation of bacteria. Subsequently, biochemical identification and some probiotic properties including catalase, oxidase, hemolysis and resistance to bile salts and acid were studied.

Results: Based on the results, 13 strains of gram-positive Lactobacillus with potency of probiotic were isolated.

Conclusion: The extended investigations about ¬industrial and medical enzyme production of the isolated probiotics are going on.

Keywords: By-products- Probiotic bacteria- Identification- Cheese

P656 - 863: ISOLATION AND IDENTIFICATION OF LACTIC ACID BACTERIA FROM CARP FISH SPECIES IN GUILAN

Hosein Alipour[1], amir mozafari [2]

1. the leader author
2. the counsalter

Background and Aim:solation and identification of lactic acid bacteria from carp species in Guilan province and their probiotic evaluation

Methods: In this study, the effectiveness of lactobacilli isolated from different types of carp in Lahijan city in laboratory environment on E.coli and Listeria monocytogenes to select acid and bile acid resistant strains as well as their susceptibility to antibiogram test. Was investigated. In this study, 10 carp samples were used, divided into 3 series, and 6 different lactose bacillus species were obtained from them. The separation of Lactobacillus was done in the MRS environment by purplate method. In this study, two high acidity tolerance and bile salts resistance tests were used to determine the probiotic potential of isolated strains

Results: Probiotics are basically living microbes that are used to treat and prevent certain infectious diseases. So that if it be possible to establish a beneficial organism in the body we can prevent the colonization of various microbial infections.

Conclusion: This study, in line with the continuation of research in 1977, has proven that it is better to use probiotics and biotherapy instead of antibiotics to prevent and treat enterotoxigenic infections, which could be a new strategy for biochemical control of E.coli without The use of antibiotics and also helps maintaining the balance of bacterial ecosystems

Keywords:probiotic,carp fish,lactic acid

P657-ANTIMICROBIAL EFFECT OF SILVER-NANOPARTICLES ON BACITRACIN-POLYMIXIN-GENTAMYCIN-CLINDAMYCIN AND ERYTHROMYCIN AGAINST BACILLUS SUBTILIS- BACILLUS CEREUS- PSEUDOMONAS AERUGINOSA- E-COLI

Nastaran Ghobadi[1] , Prof. Seyed Reza Hosseini Doust [2]

1-Islamic Azad University, Pharmaceutical Sciences Branch
2-Islamic Azad University, Pharmaceutical Sciences Branch

Background and Aim: Although the majority of infections are now curable, but their effectiveness have been blocked with progressing phenomenon of worldwide Antibiotic resistance among microbial pathogens. Probably, the best solution is to increase their effects by means of various Nanoparticles
Methods: Bacterial spp. were prepared from National collection and cultured on standard bacteriological medium. The antimicrobial effects of AgNPs and Antibiotics against each strains were tested individually and the MIC were calculated. Finally, different combination ratio of each Antibiotic/AgNPs were prepared, and the activity of each combination were achieved against each bacterial spp. Triplicately and the data were analysed statistically.
Results: The inhibition zone of AgNPs against E.coli, P.aeruginosa, B.subtilis and B.cereus were 23, 17, 10, 10 mm. The inhibition zone of Combination of 25% AgNPs: 75% Clindamycin against gram positive spp. Was above 33mm and the same ratio of AgNPs and Gentamycin for gram negative spp. Was above 20mm.
Conclusion: According to the final results of current research project, we concluded that the ratio of 25% AgNPs with 75% Antibiotics had better Antibacterial activities against our research bacterial spp. rather than Antibiotics or AgNPs solus.

Keywords: AgNPs, Antibiotics, Antibiotc resistancy

P658- SIGNIFICANT HEMOLYTIC ACTIVITY OF A BACILLUS STRAIN ISOLATED FROM AQUACULTURE WATER OF SHRIMPS FARM

Shukufeh Ghasemian[1], Mansour Mashreghi [2]

1- M.Sc. Student of Microbiology, Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran
2- Affiliation 2:Professor, Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran

Background and Aim: Hemolysin as a pore forming toxin is an important virulence factor in many bacteria especially Bacillus species. This toxin causes lysis of erythrocytes by destroying cell membrane. According to its concentration, hemolysin can induce apoptosis or necrosis in host cells. The aim of this study was to evaluate the hemolytic activity and hemolysin characteristics of a naturally occurring bacterium isolated from shrimp's farm for further anticancer studies.
Methods: shrimp farm samples had been collected in previous studies and kept in laboratory stock cultures. After recultivation of samples, hemolysin screening was performed on blood agar medium and bacteria with highest alpha zone were selected, purified and designated as HGM96. Bacterium (HGM96) was molecularly identified by 16S ribosomal RNA gene sequencing. Then HGM96 hemolysin was extracted by ammonium sulphate precipitation. Bradford assay was performed for measuring the protein concentration and Zymogram and SDS-PAGE methods were respectively used to purify and measure the molecular weight of hemolysin.
Results: molecular identification showed up to %99 homology of HGM96 strain with Bacillus zhangzhouensis. The hemolysin was successfully extracted and its lysis properties were confirmed. SDS-PAGE method showed that HGM96 is able to produce two hemolysins with molecular weights of 54 and 18 kDa.
Conclusion: isolated bacillus strain from aquaculture water of shrimp presented a strong hemolytic activity and the ability of this toxin in pore formation and apoptosis induction can be a valuable tool in cancer studies.
Keywords: Bacillus, hemolytic activity, hemolysin, shrimp farm