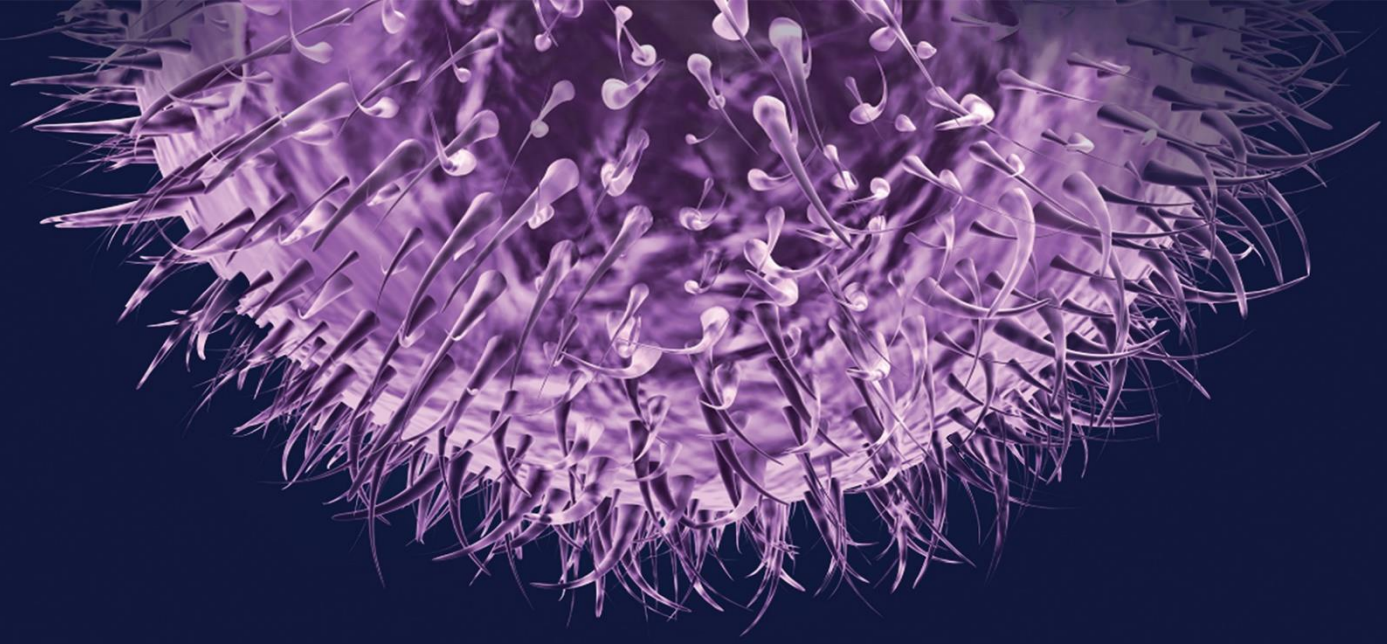

THE 21st INTERNATIONAL VIRTUAL CONGRESS OF MICROBIOLOGY

انجمن علمی میکروب شناسی ایران
Iranian Society of Microbiology

17-20 Auguest 2020

Tehran University of Medical Sciences

APPRaise
Appraise To Raise

Fasa University of Medical Sciences

Razi Vaccine and Serum Research Institute

جامعه علمی آزمایشگاهیان ایران
ISACL
Iranian Scientific Association of Clinical Laboratory

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فهرست مطالب

پیام رئیس انجمن

President of Committee of Iranian Society for microbiology

Iranian Society for microbiology with the purpose of upgrading scientific level and presenting the most novel scientific and research achievements, is going to hold the 21th International congress of Microbiology of Iran. According to the necessity of improvement in microbiology science among microbiologist community of our country in regard to the latest scientific achievements around the world; this congress has an important role in sharing experiences and up to date discoveries among Iranian and international researchers. Therefore, it is a great honor for me to invite you to the 21th International Congress of Microbiology to be held from the 17th till the 20th of August 2020 in Tehran, Iran. The 21th congress of Iranian microbiology society is going to be held with the support of Tehran University of Medical Sciences, Razi Vaccine and Serum Research Institute and Fasa University of Medical Sciences, and with retraining points for community of therapeutic and health services (Medical Doctors, dentists, pharmacist, laboratory scientists staff, nurses and midwifes, therapeutic and health services experts and specialists) as well as microbiologists and infectious disease and laboratory specialists. The innovative aspects of technologies in applied microbiology will be in debate among expert scientists in symposiums and seminars. We hope that we will provide a suitable atmosphere in order to share national and international achievements with the support and collaboration of other executive and scientific committees of our country. I strongly hope that this congress will have a great impact on improving the health and hygiene quality of our lives.

Dr. Mohammad Mehdi Feizabadi

پیام دبیر اجرایی کنگره

Executive Secretary of the Congress

The 21th International congress of Microbiology of Iran will be held on 17-20 August 2020 in Tehran University of Medical Sciences. In this scientific event, the most novel scientific achievements and investigations will be considered in different section including keynote lectures, educational panels, and oral and poster presentation with the presence of prominent international scientists in various subject areas. Celebration in honor of our veteran professors is one of the routine programs as former congresses.

On behalf of the Executive Committee, I kindly appreciate the valuable participation of dear Professors and Microbiologists in this event.

I hereby would like to thank the president of School of Medicine of Tehran University of Medical sciences, financial supporters and all of the executive members for their sincere collaborations with preparation of holding the forthcoming congress.
Besides I would like to highlight the important role of productive and knowledge based companies, which will be introduced in exhibition section of the congress, in providing research materials and equipment in our country.

Dr. Abbas Abdollahi

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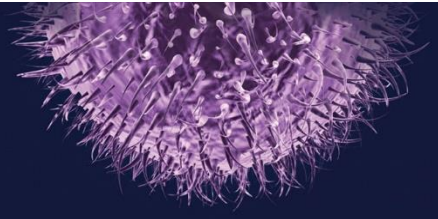
- مهدی نوروزی / دانشگاه علوم پزشکی تهران



- مجتبی نوفلی / موسسه تحقیقات واکسن و سرم سازی رازی
- محمد نیاکان / دانشگاه علوم پزشکی شاهد
- ایرج نیکوکار / دانشگاه علوم پزشکی گیلان
- غلامرضا هاشمی تبار / دانشگاه فردوسی
- مجتبی هدایتی / دانشگاه علوم پزشکی گیلان
- زویا هژبری ماهانی / دانشگاه علوم پزشکی سمنان
- فرزام وزیری / انستیتو پاستور ایران
- جلیل وند یوسفی / موسسه تحقیقات واکسن و سرم سازی رازی
- یوسف یحیی پور / دانشگاه علوم پزشکی بابل
- سمیه یسلیانی فرد / دانشگاه علوم پزشکی البرز
- رسول یوسفی مشعوف / دانشگاه علوم پزشکی همدان

کمیته داوری

رئیس کمیته: دکتر رامین عبیری

اعضای کمیته داوری:

- **دکتر عباسعلی ایمانی فولادی**
- **دکتر پژواک خاکی**
- **دکتر عباس عبداللهی**
- **دکتر بیژن نعمان پور**
- **دکتر پرویز افروغ**
- **دکتر سیمین معروف**
- **دکتر فاطمه فرد صانعی**
- **دکتر آوا بهروزی**
- **دکتر نازنین عطایی**
- **دکتر جلیل کاردان یامچی**
- **دکتر محمد علی ملکان**

اعضای کمیته اجرایی

- دکتر پرویز افروغ
- سمانه دهقان
- الهه احمدی
- محمد قائدی
- هستی حدادیان
- مهندس زهره صادقی
- حسین خدامرادی
- ملیحه علاءالدینی
- علی صیادی
- آریا تنها
- مهراوه راعی
- نازنین پورنصیری
- آزاده احمدی

حامیان کنگره

- دانشگاه علوم پزشکی تهران
- موسسه تحقیقات واکسن و سرم ساز رازی
- دانشگاه علوم پزشکی فسا

برنامه های روزانه

بیست و یکمین کنگره بین المللی میکروب شناسی ایران

بیماری های عفونی نوپدید و بازپدید

۱۳۹۹/۵/۲۷

دبیر علمی وبینار : دکتر محمد مهدی گویا

اعضای پانل: دکتر محمد مهدی گویا، دکتر احسان مصطفوی، دکتر خاویر گارائو، دکتر مجید مختاری، دکتر طلعت مختاری آزاد، دکتر مصطفی صالحی وزیری، دکتر پیمان همتی، دکتر صابر اسمعیلی

زمان	موضوع سخنرانی	سخنران	تخصص
۱۵-۱۵:۱۵	بررسی پاندمی کووید-۱۹ و آینده آن	دکتر محمد مهدی گویا	متخصص بیماری های عفونی، مرکز مدیریت بیماری های واگیر
۱۵:۱۵-۱۵:۳۰	تازه های اپیدمیولوژی بیماری کووید-۱۹ در ایران	دکتر احسان مصطفوی	دکترای اپیدمیولوژی- انستیتو پاستور ایران
۱۵:۳۰-۱۵:٤۵	COVID-19مدیریت در	دکتر خاویر گارائو	دکترای میکروب شناسی-دانشگاه بارسلونا- اسپانیا
۱۵:٤۵-۱٦	عوامل تعیین کننده سندرم کروناویروس خاورمیانه در تقابل انسان و حیوان	دکتر المباشر ابوبکر عبد فاراگ	دکترای اپیدمیولوژی-قطر
۱٦-۱٦:۱۵	مدیریت درمان و پیشگیری در کووید-۱۹	دکتر سیدعلی دهقان منشادی	متخصص بیماری های عفونی
۱٦:۱۵-۱٦:۳۰	سیری بر گذشته و آینده اپیدمی بیماری کووید-۱۹	دکتر مجید مختاری	متخصص بیماری های عفونی
۱٦:۳۰-۱٦:٤۵	تغییرات کورونا ویروس ها در طول زمان	دکتر طلعت مختاری آزاد	دکترای ویروس شناسی
۱٦:٤۵-۱۷	تازه های بیماری تب هموراژیک ویروسی در ایران	دکتر مصطفی صالحی وزیری	دکترای میکروب شناسی، بخش آربوویروس انستیتو پاستور ایران
۱۷-۱۷:۱۰	کنترل بهداشت بین المللی در برابر بیماری های عفونی نوپدید	دکتر پیمان همتی	متخصص بیماری های عفونی
۱۷:۱۰-۱۷:۲۰	بیماری های ریکتزیال در ایران	دکتر صابر اسمعیلی	دکترای میکروب شناسی ، انستیتو پاستور ایران
۱۷:۲۰-۱۷:۳۰	*پرسش و پاسخ*		

کنترل عفونت ها

۱۳۹۹/۵/۲۸

دبیر علمی وبینار: دکتر محبوبه حاج عبدالباقی

اعضای پانل: دکتر محبوبه حاج عبدالباقی، دکتر آرش سیفی، دکتر عباس بهادر، دکتر شیرین افهمی، دکتر اسماعیل محمدنژاد، دکتر نگین اسماعیل پور

زمان	موضوع سخنرانی	سخنران	تخصص
۱۵:۱۵-۱۵	اپیدمیولوژی عفونت های بیمارستانی در ایران	دکتر محبوبه حاج عبدالباقی	متخصص بیماری های عفونی
۱۵:۳۰-۱۵:۱۵	عفونت های بیمارستانی برنامه استواردشیپ آنتی بیوتیک ها و تاثیر آن ها بر بهبود کیفیت کنترل عفونت ها	دکتر آرش سیفی	متخصص بیماری های عفونی
۱۵:۴۵-۱۵:۳۰	نقش مواد ضدعفونی کننده و وسایل حفاظت شخصی در کنترل عفونت ها	دکتر عباس بهادر	دکترای میکروب شناسی
۱۶-۱۵:۴۵	پیشگیری و کنترل از ایجاد عفونت های باکتریال چند مقاومتی در مراکز درمانی	دکتر شیرین افهمی	متخصص بیماری های عفونی
۱۶:۱۵-۱۶	عفونت های ادراری مرتبط با سوند و کنترل و پیشگیری آن	دکتر اسماعیل محمدنژاد	دکترای پرستاری
۱۶:۳۰-۱۶:۱۵	عفونت های خونی مرتبط با کاتترهای وریدی و تشخیص و پیشگیری آن	دکتر نگین اسماعیل پور	متخصص بیماری های عفونی
۱۶:۴۵-۱۶:۳۰	*پرسش و پاسخ*		

توبرکلوزیس و سایر عفونت های مایکوباکتریال

۱۳۹۹/۵/۲۹

دبیر علمی وبینار : دکتر پیام طبرسی

اعضای پانل: دکتر پیام طبرسی، دکتر دانیلا ماریا کریلو، دکتر تانیل کوچاگز، دکتر افشین منیری، دکتر محمد جواد نصیری، دکتر مجید مرجانی، دکتر محمد مهدی فیض آبادی

زمان	موضوع سخنرانی	سخنران	تخصص
۱۵:۱۵-۱۵	درمان توبرکلوزیس مقاوم به درمان	دکتر پیام طبرسی	متخصص بیماری های عفونی
۱۵:۳۵-۱۵:۱۵	استفاده از تکنیک WGS در ردیابی انتقال مایکوباکتریوم توبرکلوزیس	دکتر دانیلا ماریا کریلو	متخصص بیماری های عفونی
۱۵:۵۵-۱۵:۳۵	تشخیص شخصی توبرکلوزیس در افراد	دکتر تانیل کوچاگز	دکتری میکروب شناسی
۱۶:۱۰-۱۵:۵۵	توبرکلوزیس و ایدز	دکتر افشین منیری	متخصص بیماری های عفونی
۱۶:۲۵-۱۶:۱۰	درمان عفونت های مایکوباکتریوم آویوم کمپلکس (MAC)	دکتر محمد جواد نصیری	دکتری میکروب شناسی
۱۶:۴۰-۱۶:۲۵	تشخیص و درمان توبرکلوزیس غیرفعال	دکتر مجید مرجانی	متخصص بیماری های عفونی
۱۶:۵۵-۱۶:۴۰	نقش افلوکس پمپ و موتاسیون نقطه ای در ایجاد مقاومت در توبرکلوزیس	دکتر محمد مهدی فیض آبادی	دکترای میکروب شناسی
۱۷:۱۰-۱۶:۵۵	*پرسش و پاسخ*		

مقاومت در برابر عوامل ضد میکروبی

۱۳۹۹/۵/۳۰

دبیر علمی وبینار : دکتر فرشته شاهچراغی

اعضای پانل : دکتر ژوزف آنه، دکتر کریستین گیسکه، دکتر محمدرضا صالحی، دکتر فاطیما کلیم، دکتر فرزاد بادمستی، دکتر محمد ایمان عینی

زمان	موضوع سخنرانی	سخنران	تخصص
۱۵:۲۰-۱۵	استراتژی ها و اهداف جدید در درمان باکتری های مقاوم	دکتر ژوزف آنه	دکترای میکروب شناسی
۱۵:۴۰-۱۵:۲۰	مقاومت های دارویی در باکتری های گرم منفی	دکتر کریستین گیسکه	دکترای میکروب شناسی
۱۵:۵۵-۱۵:۴۰	مقاومت های دارویی و نسخه های دارویی در دوران اپیدمی کووید-۱۹	دکتر محمدرضا صالحی	متخصص بیماری های عفونی
۱۶:۱۵-۱۵:۵۵	احیای مجدد آنتی بیوتیک های قدیمی و فراموش شده در درمان عفونت های مقاوم	دکتر فاطیما کلیم	دکترای میکروب شناسی
۱۶:۳۰-۱۶:۱۵	نگاهی بر اسنیتوباکتربومانی	دکتر فرزاد بادمستی	دکترای میکروب شناسی
۱۶:۴۵-۱۶:۳۰	مقاومت های رایج در کوکسی های گرم مثبت	دکتر محمد ایمان عینی	دکترای میکروب شناسی
۱۷-۱۶:۴۵	*پرسش و پاسخ*		

واکسن

۱۳۹۹/۶/۱۸

دبیر علمی وبینار : دکتر مجتبی نوفلی

اعضای پانل: دکتر نیکول گیزو، دکتر بهرام کاظمی، دکتر رضا بنی هاشمی، دکتر علی خامسی پور، دکتر مجتبی نوفلی

زمان	موضوع سخنرانی	سخنران	تخصص
۱۵:۵۰-۱۵:۳۰	اهمیت انطباق برنامه های واکسیناسیون در دوران اپیدمی کرونا	دکتر نیکول گیزو	دکترای میکروب شناسی -انستیتو پاستور فرانسه
۱۶:۱۰-۱۵:۵۰	چالش های تشخیصی در کووید-۱۹	دکتر بهرام کاظمی	دکترای انگل شناسی- دانشگاه علوم پزشکی شهید بهشتی
۱۶:۳۰-۱۶:۱۰	چالش های پیشرو در تولید واکسن کووید-۱۹	دکتر رضا بنی هاشمی	دکترای ایمنی شناسی
۱۶:۵۰-۱۶:۳۰	تولید واکسن: از آزمایشگاه تا بالین	دکتر علی خامسی پور	دکترای میکروب شناسی
۱۷:۱۰-۱۶:۵۰	طراحی کاندید واکسن های جدید در شرایط غیربالینی	دکتر مجتبی نوفلی	دکترای میکروب شناسی
۱۷:۲۵-۱۷:۱۰	*پرسش و پاسخ*		

بیماری‌های مشترک انسان و دام

۱۳۹۹/۶/۲۰

دبیر علمی وبینار : دکتر تقی زهرائی صالحی

اعضای پانل: دکتر خاویر گارائو ، دکتر گرازیا گرکو، دکتر بهزاد امیری، دکتر محمدرضا شیرزادی، دکتر محمد زینعلی، دکتر کریم امیری، دکتر نادر مصوری، دکتر محسن مقدمی

زمان	موضوع سخنرانی	سخنران	تخصص
۱۵:۴۵-۱۵:۳۰	مدیریت بیماری های تب کیو	دکتر خاویر گارائو	دکترای میکروب شناسی-دانشگاه بارسلونا-اسپانیا
۱۶-۱۵:۴۵	بررسی عفونت های زئونوز بارتونلا در سگ و گربه در کشور ایران و ایتالیا	دکتر گرازیا گرکو	دکترای میکروب شناسی -دانشگاه باری-ایتالیا
۱۶:۱۵-۱۶	تب خونریزی دهنده کریمه کنگو	دکتر بهزاد امیری	متخصص بیماریهای عفونی-رئیس گروه بیماری زئونوز مرکز کنترل بیماریهای واگیر
۱۶:۳۰-۱۶:۱۵	مروری بر لشمانیوز در ایران	دکتر محمدرضا شیرزادی	متخصص بیماریهای عفونی-کارشناس ملی حیوانات وحش
۱۶:۴۵-۱۶:۳۰	اپیدمیولوژی تب مالت در ایران	دکتر محمد زینعلی	متخصص انگل شناسی پزشکی-کارشناس ارشد مرکز کنترل بیماریهای کنترل بیماریهای واگیر
۱۷-۱۶:۴۵	نقش نظارت بر دام ها در بیماری های زئونوز در ایران	دکتر کریم امیری	دکترای دامپزشکی - معاون بهداشت و درمان بیماری های زئونوز
۱۷:۱۵-۱۷	بررسی سرواپیدمیولوژی سطح G و I خون در بیماران بهبود یافته کووید-۱۹	دکتر نادر مصوری	دکترای میکروب شناسی-رئیس گروه سل و غده، پژوهشکده واکسن و سرم سازی رازی
۱۷:۳۰-۱۷:۱۵	آخرین یافته های تشخیصی و درمانی بروسلوزیس	دکتر محسن مقدمی	متخصص بیماریهای عفونی
۱۷:۴۵-۱۷:۳۰	*پرسش و پاسخ*		

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O1-29: New Spoligotypes of Mycobacterium tuberculosis isolates in west of Iran

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Background and Aim : Spoligotyping can assay the transmission of mycobacterium tuberculosis strains. We aimed to study the geneotyping of M. tuberculosis isolated from patients with tuberculosis from west of Iran by spoligotyping.

Methods : a total of 47 M. tuberculosis isolates were collected from west of Iran. All sample cultures on Lowenstein-Jensen medium and incubated at 37 °C for 8 weeks. Bacterial isolates were identified as M. tuberculosis using standard biochemical tests. Drug resistance patterns of M. tuberculosis were to rifampicin and isoniazid determined and multi drug resistance (MDR) strains isolated. After DNA extraction, Spoligotyping was performed.

Results : This study revealed new spoligotypes 4162 and 4163 that correlated to Atypic lineage. Atypic and Unknown lineages also hah correlation with MDR-TB rate (4%). The most prevalent (Spoligotyping international types) SIT were Orphan (34%), 2669(23.4%) and 127(14.8%) types. The most prevalent clade were Ural-2 (NEW-1) (25.53%) and Atypic (23.40%) lineages.

Conclusion : The predominant clade were Ural-2 (NEW-1) and Atypic lineages lineage that restricted to Iran. Also the rate of MDR were so low. A good control program need to know the dynamic transmission of local isolates, therefore this study present the circulating isolate in west of Iran.

Keywords : Iran; Mycobacterium tuberculosis; spoligotyping

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O2-73: Viral safety issues for biological products

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Background and Aim : Approaches to viral safety issues for biological products have evolved during the past 50+ years. The first cell culture products (viral vaccines) relied largely on the use of in vitro and in vivo virus screening assays that were based upon infectivity of adventitious viral agents. The use of Cohn fractionation and pasteurization by manufacturers of plasma derivatives introduced the concepts that purification and treatment with physical and chemical agents could greatly reduce the risk of viral contamination of human albumin and immunoglobulin products

Methods : But the limitations of such approaches became clear for thermolabile products that were removed early in fractionation such as antihemophilic factors, which transmitted hepatitis viruses and HIV-1 to some product recipients. These successes and limitations were taken into account by the early developers of recombinant DNA (rDNA)-derived cell culture products and by regulatory agencies, leading to the utilization of cloning technology to reduce/eliminate contam- ination due to human viruses and purification technologies to physically remove and inactivate adventitious and endog- enous viruses, along with cell banking and cell bank characterization for adventitious and endogenous viruses, viral screening of biological raw materials, and testing of cell culture harvests, to ensure virus safety.

Results : Recent advances in polymerase chain reaction (PCR) technology have allowed preharvest testing for specific viral agents to reduce the risk of cell culture contamination by specific viruses in the harvest material. Examples of each of these stages in the evolution of virus detection methods are described and assessed in this paper.

Conclusion : These measures have proven very effective at preventing iatrogenic infection of recipients of biotechnology products; however, viral contamination of production cell cultures has occasionally occurred.

Keywords : Viral safety, In vivo virus screening, In vitro virus screening, Adventitious viral agents, Viral clearance, Viral inactivation, PCR testing, Biological products

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O3-368: Simple and modified method for evaluation of antimicrobial effects of porous polymers

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Background and Aim : Antimicrobial agents are used extensively for different purposes. Non-drugs agents such as some polymers are used to inhibit or kill microbes in environments such as hospital isolation and operating rooms. Some of these polymers are very porous hydrophile or hydrophobe and also after surface functionalizing antimicrobial agent, their porosity changes. So antimicrobial assay of them is error-prone. This article was focused on the set up of the methods for the in vitro investigation of one hydrophilic porous polymer, as a sample for the preparation of antimicrobial agents. The method of this article can be also used for very porous hydrophobic polymers.

Methods : In this method, the first agar slurry inoculum with the hydrophilic polymer was placed on the surface of the glass slide. E.coli ATCC 25922 strain was used as a test microorganism. Then the cassette was placed on the upside plate, inside the petri dish containing water to prepare humidity. After overnight incubation, in proper temperature, the whole slide cassette was submerged in saline for dilution. After the preparation of serial dilution and culturing, CFU counting was done.

Results : Statistical analysis showed a significant difference between CFU count of this modified method and the control. The control sample was prepared according to the unmodified and standard method; ASTM: E 2180 – 07.

Conclusion : Tow modification was performed on standard protocol ASTM: E 2180 – 07. One the whole slide cassette was submerged in saline for dilution and the other humidity providing with a petri dish containing water. These two modifications prevented bacterial losing and then correct CFU counting for antimicrobial polymers in comparison with control polymers.

Keywords : Antimicrobial Activity, hydrophilic, hydrophobic, porous polymers

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O4-127: Anti-adherent activity of Althaea officinalis L. extracts on in-vitro biofilm formation of Streptococcus mutans and Candida albicans

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Background and Aim : Denture stomatitis is an inflammatory condition that affects the mucosa underlying complete dentures with a prevalence of about 30% among the Iranian population. In the current study, we evaluate the in-vitro anti-adherent property of alcoholic and aqueous extracts from Althaea officinalis L. (Marshmallow) on biofilms formed by Streptococcus mutans (S. mutans) and Candida albicans (C. albicans) strains which isolated from denture-related stomatitis.

Methods : The effect of the extract of Althaea officinalis L. at concentrations of 0.5,1, 2 and 4 mg/mL on S. mutans and C. albicans adherence were survived using broth microdilution method (CLSI and M27-S4). After formation of biofilms in microplates, the extracts were added. Subsequently, the minimum inhibitory concentration (MIC) was determined to evaluate the anti-adherent potential of Althaea officinalis L. extracts.

Results : After 24h, MIC of adhesion was observed. The inhibitory effect of the alcoholic extract on C. albicans with a concentration of 1mg/mL was similar to that of MIC of nystatin. Moreover, the aqueous extract caused significant inhibition of adhesion at 2mg/mL. Finally, the best effect of both extracts was observed at 0.5 mg/mL on S. mutans.

Conclusion : The extracts of Althaea officinalis L. showed better anti-adherent activity against S. mutans rather than C. albicans by decreasing MIC. The interaction of S. mutans with other microorganisms like C. albicans on the denture biofilms may contribute to the increased resistance of these strains to antibiotic agents. More studies should consider the action of the herbal on biofilm of clinical strains in the oral cavity.

Keywords : Streptococcus mutans, Candida albicans, Biofilm, Denture, Stomatitis, Herbal extracts, Adherence

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O5-180: Overexpression of efflux pumps in Mycobacterium tuberculosis can contributes in drug resistance development

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Background and Aim : Active extrusion of anti-tuberculosis drugs via efflux pumps (EPs) has been considered as an alternative mechanism for drug resistance in Mycobacterium tuberculosis. Expression of drug efflux transporters in a series of drug-susceptible/resistant M. tuberculosis isolates was investigated in the present study.

Methods : Thirty-one M. tuberculosis isolates were studied. Drug susceptibility testing of rifampicin and isoniazid was performed using proportion method. The cDNA was synthesized from extracted RNA and expression analysis of 14 efflux pumps genes was evaluated by real-time quantitative reverse transcriptase PCR. Minimum inhibitory concentrations (MICs) of rifampicin and isoniazid were evaluated with and without of an EPs inhibitor, carbonyl cyanide 3-chlorophenylhydrazone (CCCP).

Results : Among the 21 drug-resistant isolates were detected, 14 were over expressed (>4 fold) in at least one of the efflux pumps genes. The drrA, Rv1218c, and Rv1410c were found to be the most commonly overexpressed, being in 7 isolates followed by stp and Rv1273c in 5 and 4 isolates, respectively. However, no elevation was observed in the expression of mmr, Rv1250, Rv1634 and Rv1258c genes in any of the isolates. MICs of rifampicin, but not isoniazid, were decreased from 2 to 8 folds in the presence of CCCP.

Conclusion : Overexpression of EP genes can contribute in the development of resistant-phenotypes in M. tuberculosis strains. Inhibition of efflux transporters can provide a promising target for drug discovery and improve tuberculosis treatment.

Keywords : Mycobacterium tuberculosis, Drug resistance, Efflux pumps, Expression, CCCP

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O6-241: Isolation and In Vitro evaluation specific bacteriophage against methicillin-resistant Staphylococcus aureus and of its antibacterial effects compared to methicillin assay

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Background and Aim : Staphylococcus aureus is an important causative agent of infections in various hospital wards. Today, antibiotic-resistant strains, especially methicillin-resistant Staphylococcus aureus (MRSA), are spreading rapidly, causing many problems in infection control and treatment. Bacteriophage (phage) is a group of viruses that can infect their host cells and multiply inside them, eventually causing cell lysis. Phage cannot infect eukaryotic cells and therefore can be used in infection therapy. The present study aims to evaluate the antibacterial and lytic activities of isolated bacteriophage against MRSA.

Methods : The standard strain of MRSA (ATCC 25923) was obtained from the Department of Bacteriology, Pasteur Institute of Iran. The specific bacteriophage was isolated from hospital sewage using Soft agar. The morphology of isolated bacteriophages was evaluated using electron microscopy (TEM). The susceptibility of MRSA to the isolated bacteriophage was assessed by the Spot test. To obtain the appropriate titer for bactericidal results, different concentrations of bacteriophage were evaluated against MRSA. The binding and pathogenicity of MRSA on HEP-2(Human epithelial type 2) cell lines were evaluated.

Results : The isolated bacteriophage was specific for S. aureus and had no lytic activity against other pathogenic bacteria. The binding and pathogenicity of MRSA to HEP-2 cell line was evaluated, and as expected, the lytic activity of specific bacteriophage was observed following inoculation.

Conclusion : Given the increased antibiotic resistance rate among S. aureus strains and growing concerns about the treatment of infections associated with these strains, this bacteriophage may be used as an effective therapeutic agent as well as a preventive measure in hospital environments.

Keywords : Staphylococcus aureus, antibiotic resistance, methicillin, lytic bacteriophage

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O7-269: Genotypes of New Delhi Metallo-beta-lactamase-Producing Escherichia coli among Clinical Isolates around the World: The First Review

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Background and Aim : New Delhi Metallo-beta-lactamase (NDM)-producing Escherichia coli (E. coli) is allegedly perceived as one of the most indispensable multidrug-resistant bacteria causing infections in hospitals and clinic domains. The nobility of the present study was evaluation of epidemiology, genotypes and the most prevalent sequence types (STs) of NDM-producing E. coli among clinical isolates worldwide.

Methods : Several international databases including Medline, Embase, and Web of sciences were searched from March 2018 to June 2018 to discern studies addressed the prevalence of NDM-producing E. coli around the world

Results : Of the 974 records identified from the databases, 110 studies fulfilled the eligibility criteria ostensibly. The analyses manifested that the prevalence of NDM-producing E. coli were 82.6%, 12.9%, 1.4%, 0.9% and 1.9% in Asia, Europe, America, Africa and Oceania continents, respectively. According to our results, the most common reported STs among NDM- producing E. coli were ST101, ST167, ST131, ST405, ST410 and ST648.

Conclusion : The dissemination of NDM variants among E. coli strains is a serious threat to global public health. In addition, the most prevalent E. coli clonal groups such as ST101 and ST167 are one of the main causes of E. coli infection in different countries. Then the control of the spread of NDM variants-producing E. coli especially in the most common E.coli clonal groups, is very important to prevent the spread of antimicrobial resistance around the world.

Keywords : New Delhi Metallo-beta-Lactamase, E. coli, Sequence Type

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O8-334: Evaluation of the presence of IMP1 gene in clinical isolates of Klebsiella pneumoniae patients of Shohadaye ashayer and Shahid Rahimi hospitals in Khorramabad using PCR

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Background and Aim : The presence of resistance layers of bacteria against different types of antibiotics, due to some of the support genes, which can survive through plasmid to other bacteria in a hospital environment, can be problematic for general health of patients. Recognizing the prevalence of these genes is important and the aim of this study was to identify the genes of antibiotic resistance in the clinical isolates of Klebsiella pneumoniae producing IMP1 β-lactamase

Methods : In this study, 100 samples of carbapenem isolated from patients of Shohada and Shahid Rahimi hospitals in Khorramabad were identified using standard biochemical methods and were used to determine the phenotypic ESBLs. In the Antibiogram method, the antibiotic resistance of isolates was determined and the prevalence of IMP-1 gene was determined by PCR method

Results : In this research, a total of 73 isolates (73%) Were ESBLs and 27 isolates (27%) Were non-ESBL. Of these 22 samples had IMP1 genes

Conclusion : The results showed high antibiotic resistance in Klebsiella pneumoniae bacteria. Given that there was IMP1 in a large number of resistant samples, the use of conventional antibiotics could not help reduce the infectious effects of Klebsiella pneumoniae bacteria and further studies are needed in this area

Keywords : Klebsiella pneumoniae, IMP1, antibiotic resistance.

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O9-19: The role of quorum sensing genes in antibiotic resistance of Pseudomonas aeruginosa isolated from burned patients

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Background and Aim : Pseudomonas aeruginosa, a gram-negative bacillus, and opportunistic pathogen, is an important microorganism involved with infections in burn patients worldwide. It produces biofilms by Quorum-sensing signals and makes an antibiotic resistance. The aim of this study to reveal the role and effect of Quorum-sensing genes in antibiotic resistance.

Methods : From April to September 2018, 100 samples of burn injuries were collected from the Central Hospital of Shahid Beheshti in Kashan. The samples were identified in terms of biochemical and phenotypic tests and a definitive diagnosis of P.aeruginosa species was examined based on a toxA gene by the PCR method. The positive samples were analyzed for antibiotics of amikacin, ciprofloxacin, norfloxacin, gentamicin, cefepime, aztreonam, meropenem, ceftazidime, colistin, and piperacillin-tazobactam. Then, samples were analyzed for lasR and pqsR (quorum-sensing genes) by PCR.

Results : We verified eighty-five (85%) isolates as P. aeruginosa. According to antibiograms, 92% of the isolates were considered as multidrug-resistant (MDR), of which 85.5% were extensively drug-resistant (XDR) and none of the pan drug resistance (PDR). Also, in MDR isolates, there was one nonsense mutation. In XDR samples, two isolates had a missense mutation and nonsense mutation was seen in one strain.

Conclusion : The results of our study show that with increasing resistance rates, more mutations occur in lasR and pqsR genes and the possibly can play a key role in antibiotic resistance. Given the mutations found in the quorum sensing genes, it can be concluded that these genes are mutagenic genes that will be effective in changing bacterial behavior and adaptability to environmental conditions.

Keywords : quorum sensing, antibiotic resistance, Pseudomonas aeruginosa, burned patients

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O10-90: Determination of multi- drug resistant (MDR) and extensively drug-resistant (XDR) clinical isolated Pseudomonas aeruginosa and Acinetobacter baumannii phenotypes in Northeast of Iran.

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Background and Aim : Multi and extensively drug- resistant, Pseudomonas aeruginosa (PA) and Acinetobacter baumannii (AB) as two main causative agents of nosocomial infections are considered as health threats in hospitalized patients. Choosing a proper antibacterial regime plays a critical role in the prevention and eradication of mentioned bacterial related infections. Evaluation of the MDR and XDR AB and PA frequencies in clinical specimens are the main objectives of this survey

Methods : : In this cross-sectional study, clinical isolates of AB and PA strains were collected using traditional bacteriological tests during 2017-2018. Susceptibility patterns of isolates were assessed by disc diffusion methods according to the Clinical Laboratory Standard Institute (CLSI) guidelines.

Results : Out of 3248 clinical samples, AB and PA strains were detected in 309(9.51%) of them, 94 (30.42%) females and 215 (69.58%) males. Susceptibility testing indicated that (16.50%) and (15.53%) of the PA and (74.75%) and (73.13%) of the AB isolates were screened as the MDR and XDR strains, respectively. The frequency of MDR isolates was higher in wound samples 222 (71.8%). This rate in Behavioral Intensive Care Unit (BICU) 187(60.5%) and restoration ward 63(20.4%), were detected respectively. The frequency of XDR isolates in BICU 187 (59.54%), restoration 58 (18.77%), and burns 30 (9.70%) were assessed as well.

Conclusion : considering high isolation rates of MDR and XDR AB and PA strains, it is necessary to apply prevention criteria for eradication of the mentioned bacteria from hospital wards.

Keywords : Multi-drug resistant (MDR), extensively-drug resistant (XDR), Pseudomonas aeruginosa, Acinetobacter baumannii, Carbapenem resistant A. baumannii, nosocomial infections.

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O11-91: Prevalence of Enterobacteriaceae spp. and its multidrug-resistant (MDR) rates in clinical isolates: A two-center cross-sectional study

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Background and Aim : Enterobacteriaceae spp. are fermentative Gram-negative bacilli, which, owing to their high durability, various virulence factors, and antibiotic-resistant mechanisms, are described as an eminent part of health treatments in hospital-acquired infections. This study aimed to estimate the prevalence of Enterobacteriaceae spp. to characterize antibiotic susceptibility, and to explore the frequency of each genus

Methods : In this cross-sectional study, over two years (2017-2019), clinical isolates were collected and Enterobacteriaceae spp. were identified using the Analytical Profile Index (API 20E) from two centers (main educational hospitals) in northeastern Iran. Isolates were confirmed by targeting the rpoB gene. Moreover, the susceptibility patterns of isolates were assessed using disc diffusion methods according to the Clinical Laboratory Standard Institute (CLSI) guidelines.

Results : : Out of 2645 clinical specimens, 297 (11.2%; 4.96% and 6.28% belonging to Boali and Zareh hospitals) Enterobacteriaceae spp. containing E. coli 94 (48.9%), Citrobacter freundii 65 (21.9%), Klebsiella pneumoniae 48 (16.2%), Enterobacter spp. 43 (14.5%), proteus spp. 23 (7.7%), and 25% of other spp. were identified. C. freundii 65 (37.95%) and Enterobacter spp. 33 (19.88%) more isolated than another bacterial specimen in Zareh hospital wards. E. coli 68 (51.9%) and K. pneumoniae 45 (34.35%) have higher rates of isolation in other hospitals as well. The frequency of isolate was higher in urine samples (117, 39.4%) and wounds (114, 38.4%) than other clinical specimens. Multidrug-resistance (MDR) strains are more isolated in the behavioral intensive care unit (BICU) than other wards as well. In Boali, 65 (49.61%) isolates were screened as MDR isolates. This frequency at Zareh hospital was 130 (78.31%). Amikacin (81.1%) has been shown to be an improper drug of choice for the isolates. Moreover, the lowest incidence of resistance among isolates was associated with nalidixic acid (34.3%).

Conclusion : Considering the high isolation rates of MDR Enterobacteriaceae spp., it is necessary to apply prevention criteria for the eradication of the mentioned bacteria from hospital wards.

Keywords : : Enterobacteriaceae, Hospital-acquired infections, Susceptibility testing, Multi-Drug resistant.

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O12-94: The Study Effects on Aqueous Extract of Ammi visnaga on the Pseudomonas aeruginosa Exo A and Exo S Genes

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1. *Negin Bahmanpoor*

Background and Aim : Abstract Background: Pseudomonas aeruginosa is one of the important factors in many secondary diseases and infections including burns. The aim of this study was to investigate the effect of Ammi visnaga extract on the expression aeruginosa pathogenic genes. Materials and Methods: In this experimental study. Antimicrobial effects of Soxhlet extract using microdilution technique in sequential dilutions. Also, expression of exotoxin A and S genes as pathogens of Pseudomonas aeruginosa was evaluated by Real Time PCR method. Results: The results showed that expression of Exotoxin A and S genes of Pseudomonas was significantly (P <0.001) lower than the expression level of reference gene (16s). Also,it had significant effect on inhibition of bacterial growth at different concentrations and the lowest inhibitory concentration was observed at 500. Conclusion:The extract of ammi visnaga can decrease the expression of Exotoxin A and S genes of Pseudomonas aeruginosa and consequently decrease the number of bacteria.

Methods : 2. Methodology 2-1- preparation of plant 2-2-Bacterial strains and storage methods 2-3-Cultivation of Pseudomonas aeruginosa bacterium for the production of exotoxins 2-4-Determining the minimum MIC growth concentration of toothpaste extract 2-5- Investigating gene expression, RNA extraction, primer design and PCR reaction

Results : 3. Results 3-1-MIC and MBC test results and well, The lowest concentration in which no turbidity was observed was considered as the MIC, which was 500. The MBC test results and MIC test wells are also presented. 3-2-Product Replication Curve shows: at the end of the reaction, a standard linear reaction curve based on Ct and logarithm of DNA concentration was drawn to confirm the proliferation of the PCR product. 3-3-Real-Time PCR results shows the effect of toothpaste extract on the expression of exoA and exoS genes of Pseudomonas aeruginosa.

Conclusion : 4- Discussion and conclusion The results showed that the plant extract reduced the expression of these genes, which are pathogenic bacteria. Also, the results of MIC test showed that the lowest bactericidal concentration of toothpaste extract is 500. There is very little research done in this field, so that the discussion and comparison of the present study was difficult. However, some research in this area has yielded close and similar results, which we will examine.

Keywords : Ammi visnaga, Pseudomonas aeruginosa, Exotoxin A, Exotoxin S

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O13-170: Monitoring, quantification and invasion assessment of Legionella in hospital water sources by culture, real-time PCR and cell culture

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Background and Aim : Legionella is a heterophilic bacterium in the water supply network, which can normally survive in the biofilm or planktonic form in freshwater and is an optical intracellular bacterium and will be found only after proliferating within macrophages and rip them out in large numbers in the alveolar spaces and the lower respiratory secretions. the bacteria enter the lungs through the formation of aqua aerosol and contamination with Legionella species includes the spectral of disease that is the Pontiac fever, self-limited influenza-like disease in one hand, and systemic and legionnaire's disease depends on the contamination of water sources and susceptibility. The aim of this study was to Using culture, quantitative PCR for Legionella monitoring in hospital water samples, and risk assessment by an invasion of the HeLa cell.

Methods : In this study 100 water samples collected from hospitals of Iran university medical sciences, from head-showers, humidifier bottles, and laboratory water baths and were examined. To prevent the growth of fast-growing bacteria and saprophytic fungi, all samples were treated with acid. Then they were cultures on selective media such as GVPC. To confirm the primary identity of the isolates colonies, gram staining, and lack of growth after insemination to conventional laboratory environments such as blood agar and BCYE without L-CYS. DNA of the samples was extracted, and then the PCR reaction for 16srRNA genes was done using proprietary primers. Eventually, after electrophoresis an determination of PCR products, they were analyzed. After that real-time PCR to measuring the number of bacterial was done and invasion of isolates was asses by the HeLa cell culture.

Results : Out of 100 water samples were collected, 12 cases (12%) were positive by culture method and 42 cases (42%) were positive by the PCR method, and results of culture were confirmed. Quantification of bacteria in 23 cases (54/56%) was with 104GU/L and 2 cases (4/76%) were with <104 GU/L. Finally, the invasion of isolates was assessed by the HeLa cell culture.

Conclusion : Despite the use of refined water resources for the urban distribution system, 12% of the samples taken from hospital water sources were contaminated with legionella bacterium; on the other hand, because the legionella bacterium was resistant to disinfectant such as chlorine with common concentration.

Keywords : Legionella - hospital water sources - hela cell culture - real time PCR

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O14-281: Molecular analysis of Methicillin-Resistant Staphylococcus aureus isolated from pemphigus patients

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Background and Aim : Pemphigus is an autoimmune bullous disease that affects the skin and mucosas. Colonization of these skin wounds with MRSA can delay the healing process of the wound and increase the rate of infection and mortality in these patients. We therefore decided to conduct this study to determine the SCCmec and dru types, toxins, MSCRAMM and biofilm genes of MRSA isolated from Pemphigus patients.

Methods : In total, 118 S. aureus isolates were collected from wound infection of pemphigus patients. In order to detect MRSA isolates, the mecA gene was amplified through the polymerase chain reaction (PCR) method. Multiplex-polymerase chain reaction (MPCR) assay was performed for the characterization of the staphylococcal cassette chromosome mec (SCCmec). The dru region was sequenced and thereby, dru types and dru repeats were identified. A similarity matrix was used to create minimum spanning tree (MST). All MRSA isolates were assayed for the presence of the sea, seb, sec, tst, eta, pvl, hla, hlb, MSCRAMMs and ica genes by PCR.

Results : Our study results illustrated that the prevalence of MRSA among S.aureus isolated from patients with pemphigus was 43.2% . Thirty-four (35.3%) of MRSA strains were SCCmec type II and Eighteen (35.3%) of MRSA strains were SCCmec type III. The successful dru typing of isolates revealed seven different dru types. There was a new dru type, namely dt9ca. the prevalence rates of the hla،sea ،sec genes among MRSA isolates were 54.9%, 27.4% and 1.9%, respectively. The hlb, seb, eta and pvl genes were not detected in any of the MRSA isolates. Our results revealed that 1 isolate from pemphigus wound infection expressed the tst gene. The prevalence rate of MSCRAMM genes such as fib, eno, ebpS, were 21.5%, 31.3% and 9.8%, respectively. The fnbB, fnbA and cna genes were not detected in any of the MRSA isolates. Moreover, 3.9% and 5.8% of the isolates harbored the icaA and icaD genes respectively.

Conclusion : This study shows the high prevalence of toxin genes such as hla, sea among MRSA strains with SCCmec II and III isolated from Pemphigus wounds in a dermatology centre in Tehran, Iran.

Keywords : MRSA, SCCmec type, MSCRAMMs, Toxin genes, Pemphigus

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O15-275: Study of oral microbiome in MS patient compared with healthy people.

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Background and Aim : Word " microbiome" was used by Lederberg for definition of commensal, symbiotic ecologic population and pathogenic microorganism. Microorganisms in oral cavity are called oral microflora, Researchers believe that oral microbiome is important in systemic diseases. Oral cavity is suitable for microbiome because of its temperature (almost 37degree), PH (7.5) and humidity. Oral microorganisms include different genera of bacterium. Interaction between host and microorganisms is important in nervous diseases such as Autism, Alzheimer, Parkinson and Multiple Sclerosis (MS) . Recently researchers studied on bacterial infection as one of environmental factors of MS. Importance of bacteria is their role in increase of Th17. Th17 increase production of IL-21, IL-17, IL -22 that are inflammatory cytokines. In this study for first time is studied oral microbiome in MS patients and is compared with healthy people.

Methods : Sampling was performed in MS patients center of Kermanshah University of Medical Sciences during October to March 2019. 30 samples were recruited from MS patients and 30 samples were obtained from healthy people. From each person was taken 2 swab samples from on and side of mouth that one swab was sunk into PBS and another one into Thioglycollate broth for increase turbidity in aerobic and an aerobic condition. Brucella blood agar supplemented hemin and vitamin K was used for this studing, After pure cultures were obtained , identification of bacteria was performed by Phenotypic tests including gram staining, catalase, nitrate, Aerotolerance test, Antibiogram test, bile esculin agar test.

Results : In this study Staphylococcus, Streptococcus, Enterococcus, Peptostreptococcus, Actinomyces, Lactobacillus, Fusobacterium, Bacteroides, Porphyromonas, Prevotella, Veillonella, Propionibacterium and Bifidobacterium genera were isolated that in all cases the number of bacteria were more in patient group except Peptostreptococcus and Lactobacillus and Prevotella and Propionibacterium genera were found just in patient samples.

Conclusion : It seems oral microbiome composition is important in MS disease development as the effect of gut microbiome in MS disease was confirmed in previous studies. High number of useful genera such as Lactobacillus in healthy group shows that take a meal containing useful bacteria can help in control of inflammatory conditions and as a result control of MS disease development.

Keywords : Microbiome, Multiple Sclerosis and Bacteria.

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O16-86: Engineering of a PTX inactivated Bordetella pertussis strain isolated from clinical specimens in Iran

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Background and Aim : One of the important reason of the resurgence of whooping cough (pertussis) caused by Bordetella pertussis is difference between genomic profile of circulating and vaccine strains. Genetically inactivated B. pertussis is one of the new strategies to generate live attenuated vaccine against pertussis. The aim of this study was to construct a PTX inactivated B. pertussis strain based on predominant profile of circulating Iranian isolates.

Methods : According to the results of genomic and virulence profile of 100 clinical B. pertussis strains from Pasteur Institute of Iran, a B. pertussis strain with predominant pattern was selected. R9K and E129G mutations in ptxS1 were conducted by the site directed mutagenesis and substitution of mutant ptxS1 gene were done by homologous recombination. Genetic stability and antigen expression of S1 mutant strain (S1mBPIP91) was tested by serially in vitro passages and western blot assay, respectively. Toxicity reduction was also analyzed by Chinese Hamster Ovary (CHO) cells clustering test.

Results : In this study all constructs were well confirmed via restriction enzyme analysis and sequencing. Our results showed stability of the mutations of S1mBPIP91 after in vitro serially passages. The virulence factors expression was also shown in S1mBPIP91 strain. CHO cell clustering test was demonstrated reduction of PTX toxicity in S1mBPIP91 mutant strain.

Conclusion : A PTX inactivated B. pertussis strain with predominant genomic and virulence profile in Iran was successfully created and characterized in this study. This attenuated B. pertussis strain should be tested in animal model to use in further studies of both whole cell and acellular pertussis vaccines strategies.

Keywords : Bordetella pertussis, attenuated vaccine, pertussis toxin, homologous recombination

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O17-49: Bacteriophages and their role in the treatment of common bacterial infections

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Background and Aim : Bacterial infections are one of the most common types of infections that occur in many people of all ages. And in many cases, they can be fatal. Apart from that, they cause a lot of damage to the healthcare system and the economy of any country. Today, antibiotic resistance or drug interactions cause bacterial infections in some cases to have more destructive effects. Therefore, new therapeutic approaches can be an effective way to fight bacterial infections and minimize mortality and reduce the economic costs of treatment and hospitalization. Bacteriophage therapy is one of these approaches. Bacteriophages are viruses that attack bacteria and are specific to bacteria and can kill them. These viruses cannot attack eukaryotes due to their specificity and therefore can be considered as one. Modern methods of treatment should be considered. Therefore, this study aimed to investigate the characteristics of bacteriophages and their role in the treatment of common bacterial infections.

Methods : Articles related to the subject were searched on two websites, Pubmed, science direct, and systematic review articles that examined the effects of bacteriophages on the prevention and reduction of common bacterial infections.

Results : The results of various studies indicate the role of lytic bacteriophages in eliminating or reducing bacterial infections. Animal studies also seem to confirm the effective role of bacteriophages in reducing bacterial infections. The positive effects and reduction of bacterial infection in strains containing antibiotic resistance are seen after the use of bacteriophages.

Conclusion : The results of studies show that to reduce bacterial infections, especially antibiotic-resistant strains, the use of bacteriophages can play an effective role, which is confirmed in both invitro and invivo conditions, and it is hoped that with the right perspective, approach The use of bacteriophages has been instrumental in both reducing mortality and improving economic conditions in communities.

Keywords : Bacterial infections,Bacteriophage,Bacteria

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O18-55: Bioactive compounds of Lactobacillus casei as anti-virulence agents against Pseudomonas aeruginosa

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Background and Aim : Probiotics are among new agents that can target quorum sensing (QS) systems of drug-resistant bacteria. QS is a cell-to-cell signaling mechanism that enables gene regulation to control diverse physiological functions in bacteria. QS is a highly attractive target for the development of novel therapeutics. The present study investigated whether Lactobacillus casei might interfere with the pathogenic properties of Pseudomonas aeruginosa, in vitro.

Methods : The minimum inhibitory concentration (MIC) of Lactobacillus casei subsp. casei PTCC 1608 filtrate (acid filtrate) was determined against P. aeruginosa ATCC 27853 and P. aeruginosa PAO1. Filtrates were tested for their effects on the production of P. aeruginosa virulence factors controlled by the QS system (biofilm formation, pyocyanin and rhamnolipid production, swarming, swimming and twitching motilities). Besides, the effect of filtrate on the expression of QS genes including lasI/R, rhlI/R, pqsA/R as well as pelF (pellicle/biofilm glycosyltransferase PelF), lasB (elastase LasB) and toxA (exotoxin A) was evaluated by quantitative real-time polymerase chain reaction.

Results : The MIC value was 6.25 mg/ml. Sub-MICS (3.125-1.562 mg/ml) demonstrated a statistically significant reduction of virulence factors including pyocyanin and rhamnolipid production. Biofilm formation, swarming, swimming and twitching motility were also reduced after treatment. rhlI/R, pqsA/R, pelF and lasB genes were down-regulated after treatment.

Conclusion : The present research demonstrated that natural bioactive compounds of L. casei could reduce virulence in P. aeruginosa strains and may be introduced as prophylactic and/or therapeutic agents in P. aeruginosa infections.

Keywords : L. casei, bioactive compounds, P. aeruginosa, QS-controlled virulence factors

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O19-104: Antibacterial and antifungal activity of Onosma essential oils compared to four common antibioticsMON ANTIBIOTICS

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Background and Aim : Essential oils are recommended to treat infectious diseases, but data about their efficacy in scientific literature are insignificant. Antibacterial and antifungal activity of the essential oils from Onosma microcarpum and Onosma chlorotricum against Staphylococcus aureus, Pseudomonas aeruginosa, Escherichia coli and Candida albicans and Candida glaberata evaluated

Methods : Plants were collected in September 2015 from the suburb of Koohdasht, Lorestan province. Essential oil extracted by hydro distillation method, the antimicrobial effects of these essential oils was determined by disc diffusion method and microdilution method. Results were compared with the Vancomycin, Amikacin, Fluconazole and Nystatin by SPSS software.

Results : The results showed that both essential oils possess antimicrobial activity against all tested microbes, however essential oil of O.chlorotricum has antimicrobial activity stronger than O.microcarpum. the mean inhibitory diameter of growth (mm) of S.aureus (24±1.2), E.coli (22.5± 0/6) P.aeruginosa (20.5±0.16) in the presence of O.chlorotricum essential oil was higher than O.microcarpum. Also O.chlorotricum showed more antifungal activity with 21 and 19.3 mean of inhibition zones (mm) for C.albicans and C.glaberata respectively. The MIC assay of the O.chlorotricum essential oil showed antibacterial and antifungal activity stronger than O. microcarpum, The lowest MIC for S.aureus and C.albicans was 32.03 and 64.06 ?g/ml respectively. The highest MIC for P.aeruginosa and C.glaberata was 128.12 512.5 ?g/ml respectively. essential oils often, have a more antibacterial and antifungal activity rather than tested antibiotics.

Conclusion : The obtained results suggest that, O.chlorotricum and O.microcarpum essential oils are potentially a good source of antimicrobial agents which can be used for supporting primary health care and alternative treatment of common antibiotics.

Keywords : Essential Oil, Antibacterial, Antifungal, Onosma, Antibiotics

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O20-105: Evaluation of the phenolic contents and antibacterial activity of different concentration of Onosma chlorotricum Boiss

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Background and Aim : Increasing resistance to antibiotics, drug side effects and extracting new and low-risk compounds from medicinal plants, caused researchers to more studies treatment effects of plants active secondary metabolites. The aim of the this study is to evaluate the total phenolic and flavonoid contents and antibacterial activities of different concentrations of various extracts of Onosma Chlorotricum compared with two standard Antibiotics.

Methods : Total phenolic and flavonoid contents and the antibacterial activity of methanol, n-hexane and aqueous extracts (5 mg/ml to 0.156 mg/ml final concentration) of Onosma chlorotricum against Staphylococcus aureus, Pseudomonas aeruginosa and Escherichia Coli were evaluated using disc diffusion and microdilution methods. Antibiotics Vancomycin and amikacin were used as Positive control and DMSO as negative control. Total phenolic and flavonoid contents of these extracts were determined according to the Folin-ciocalteu procedure and Aluminum chloride colorimetric assay respectively.

Results : The results showed that the total phenolic and flavonoid contents of these extracts ranged from 74.12± 0.05 to 56.10±0.13 mg GAE/g dry extract and from 23.20±0.41 to 19.3±0.6 mg QE/g dry extract, respectively. The methanol extract with the highest phenolic and flavonoid content showed the highest antibacterial activity against all tested bacterial strains with the highest inhibition zone of (21±0.7) and the lowest MIC and MBC values 78.12 ?g/ml for S.aureus.

Conclusion : The antibacterial effects and the total phenolic content of Onosma chlorotricum Boiss were remarkable and should be investigated more in future studies. we offer the effects of this extracts on wound healing in an animal model and to be investigated via in vivo and clinical models.

Keywords : Phenolic content, Flavonoid content, Antibacterial, Onosma chlorotricum

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O21-131: production of egg yolk immunoglobulin (IgY) against chimeric recombinant protein TCPA-CTXB-OMPW and investigating its protective effect on Y1 cell line against CT and LT toxins

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Background and Aim : Cholera is a severe diarrheal disease causes severe dehydration in infected persons with gram-negative bacteria called vibrio cholera. Cholera is still one of the main causes of death in children under 5 years old. Applying of specific chicken egg yolk immunoglobulins (IgY) is an innovate technology to produce antibodies for passive immunotherapy and prophylaxis. In this study we produced egg yolk antibody (IgY) against a chimeric antigen from 3 different proteins of OMPW-TCPA-CTB from vibrio cholera o1. The inhibitory effect of on CT and LT toxins was investigated.

Methods : The pET28a plasmid containing the chimeric gene OmpW, ctxB and TcpA, was expressed in the E coli BL21 (DE3). The recombinant antigen was purified via Ni-NTA chromatographic column. After immunizing chickens with the recombinant protein, polyclonal antibodies (IgY) were purified from the egg yolk by water dilution method and analyzed on SDS-PAGE. The activity and specificity of the IgY antibody was analyzed by the indirect and the whole cell ELISA. Inhibitory effect of IgY against CT toxin was tested on the Y1 cell line. Due to the structural and functional similarity of CT and LT toxins, the inhibitory effect of IgY produced against chimeric protein was also investigated on the inhibition of LT toxin.

Results : Indirect ELISA data showed that injection of 100 mg of protein for four times into the chicken produced a significant amount of IgY. CT toxin affects the Y1 cells by changing the shape of the cell from elongated to round one and 250micro gr of IgY in PBS inhibited the effect of this toxin. The inhibitory effect of IgY on LT toxin was 100 micro gr.

Conclusion : The chimeric antigen could stimulate the immune response effectively and increase the antibody titer significantly with four injection. In addition, the IgY produced against chimeric protein could effectively inhibit the effects of LT and CT toxins.

Keywords : CT toxin, LT toxin, vibrio cholera, IgY Immunoglobulin, Y1 assay, chimeric proteins

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O22-147: Identification of nano-lipid system containing curcumin extract in order to prevent tooth decay by Mozaffari method

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Background and Aim : The aim of this study was to characterize the nano-lipid system containing curcumin extract in order to prevent tooth decay. For this purpose, a lipid system containing curcumin extract has been developed for optimal anti-streptococcus mutans by Muzaffari method.

Methods : The aim of this study was to characterize the nano-lipid system containing curcumin extract in order to prevent tooth decay. For this purpose, a lipid system containing curcumin extract has been developed for optimal anti-streptococcus mutans by Muzaffari method.

Results : The average particle diameter was about 60 nm and its zeta potential was -16 mV. The loading rate in nanoparticles was 91%, which was calculated by reading the absorption of light from the standard curcumin curve. In addition, minimum inhibitory concentration (MIC) of nanoparticles against Streptococcus mutans, was 0.204 and 0.438 mg/mL for starch nanoparticles and pure curcumin, respectively. It was also found that starch nanoparticles had inhibitory effect on bacterial biofilm.

Conclusion : nano-particles improve adhesion properties and interactions with enamel and prevent dental caries of Streptococcus mutans.

Keywords : Streptococcus mutans, Curcumin, Dental caries.

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O23-280: The efficacy of pulsed and continuous ultrasound against Staphylococcus aureus population in chronic rhinosinusitis patients

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Background and Aim : Staphylococcus aureus is one the most important bacterial pathogens involved in chronic rhinosinusitis (CRS) may result in treatment failure. Ultrasound as an alternative therapy is able to destroy bacterial population in sinus cavities and hence improving treatment efficacy.

Methods : Twenty-six patients with CRS and 20 healthy controls were included in this study. Clinical specimens were collected before and after ultrasound treatment. Serially diluted samples were used for bacterial isolation and DNA was extracted for bacterial detection using quantitative PCR.

Results : : S. aureus was detected in 14 and 17 patients using phenotypic tests and qPCR respectively. However, 6 out of 20 healthy controls were also positive for S. aureus. Among the 6 patients, 4 of them were completely recovered after pulsed ultrasound therapy and 9 out of 11 patients showed significant reduction of S. aureus population after continuous ultrasound treatment.

Conclusion : Both the pulsed and continuous ultrasound strategy have been quantitatively decreased the S. aureus population in chronic rhinosinusitis patients ($p < 0.05$). This was a hopeful basis for doing more studies with ultrasound therapy as an alternative option of CRS patient's treatment.

Keywords : : Chronic rhinosinusitis, Ultrasound treatment, Staphylococcus aureus, quantitative PCR

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O24-345: In vitro and in vivo efficacy and toxicity assessments of Melittin antimicrobial peptide produced in the yeast system

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Background and Aim : Some studies introduced the Melittin peptide, the main component of honeybee venom, as an antimicrobial peptide. The aim of the present study was to produce Melittin peptide using yeast system and evaluate its efficiency as well as toxicity in both in vivo and in vitro systems.

Methods : The chemically synthesized Melittin was obtained by cloning its sequence in the pPIC9 vector and then transformed it into the Pichia pastoris GS115. Minimum inhibitory concentration (MIC) of Melittin (range 0.5-32 µg/ml) was determined by the microwell dilution method against an extensively drug-resistant (XDR) Acinetobacter baumannii. Human primary fibroblast cells were used to assay in vitro toxicity of Melittin by 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) test. Acute and sub-acute in vivo toxicity doses were determined using BALB/c mouse model.

Results : The MIC of Melittin against an XDR A. baumannii was 16ug/mL, Its half maximal inhibitory concentration (IC50) value on primary fibroblast cells was 7.5ug/mL, the single intraperitoneal median lethal dose (i.p. LD50) was 5.4 mg/kg and repeated i.p.LD50 (8h interval) was 4.2 mg/kg.

Conclusion : The results of present study, for the first time clearly demonstrate that despite valuable antimicrobial activity of melittin, we could not prescribe it as a systemic agent because in therapeutic doses it has different levels of in vivo and in vitro toxicities.

Keywords : Mellitin, toxicity, Acinetobacter baumannii

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O25-355: The impact of Melittin monotherapy versus combination therapy with Imipenem or ceftazidime against Carbapenem-sensitive and Carbapenem-resistant Acinetobacter baumannii strains

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Background and Aim : Acinetobacter baumannii is one of the predominant pathogens involved in hospital-acquired infections worldwide. There are limited treatment options for carbapenem-resistant Gram-negative infections such as Acinetobacter baumannii. Several ways including loading dose, higher maintenance dose, adjunct local administration and combination therapy are proposed to enhance conventional drugs efficiency. The aim of this study was to evaluate the effectiveness of a new emerged antibacterial peptide melittin alone or in combination with imipenem and ceftazidime conventional antibiotics against clinically isolated carbapenem-sensitive (CSAB) and carbapenem-resistant (CRAB) acinetobacter baumannii strains.

Methods : Clinically isolated CSAB and CRAB strains were used to test minimum inhibitory concentration (MIC) by microbroth dilution method. Combination therapy was evaluated by checkerboard titration methods. The drugs dilution range used for peptide and the mentioned antibiotics were 0.5-32 and 0.125-128 µg/ml, respectively.

Results : MIC of Melittin, ceftazidime and Imipenem against CSAB were 16, 0.5, 0.25 µg/ml, respectively, and the MIC of Melittin, ceftazidime and Imipenem against CRAB were 16, 128 ? and 16 µg/ml, respectively. The fractional inhibitory concentration (FIC) index for combinations of Melittin and ceftazidime against CSAB and CRAB were 1.3 and 2.0 µg/ml respectively. Moreover, the FIC index for the combination of melitin and imipenem against the CSAB and CRAB were 1.05 and 2.03 µg/ml, respectively.

Conclusion : The data exhibited that the combination therapy of Melittin with ceftazidime or imipenem had no synergistic effect against CSAB and CRAB strains.

Keywords : Melittin, monotherapy, combination therapy, carbapenem-resistant bacteria

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O26-411: Comparison of antimicrobial and wound healing properties of mouse adipose tissue- and bone marrow-derived mesenchymal stem cells in fibrin scaffold on burn wound infection triggered by Pseudomonas aeruginosa

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Background and Aim : Burn is a leading cause of injury and the most devastating forms of trauma. Pseudomonas aeruginosa has become a common cause of burn wound infection. Recently, a new method using mesenchymal stem cells has been developed for the recovery of burn wounds. Fibrin hydrogel scaffold has been addressed to release mesenchymal stem cells.

Methods : The stem cells were extracted from mouse adipose and bone marrow tissues and then were confirmed by the surface markers using flow cytometry analysis. The possibility of differentiation of the stem cells into bone marrow and adipose were also checked. The extracted stem cells were encapsulated in the fibrin scaffold. Fibrin-encapsulated mesenchymal stem cells were used to dress wound following induction of burn infection in mice. The microbial load was measured by the colony count method in sacrificial mice.

Results : In vivo studies showed that the adipose-derived mesenchymal stem cells had strong antimicrobial characteristics on P. aeuroginosa-induced burn wound, while the bone marrow-derived mesenchymal stem cells improved wound regeneration/healing

Conclusion : We showed that the fibrin-encapsulated mesenchymal stem cells could regenerate lost wound tissue and significantly reduced the load of bacteria

Keywords : Burn wound infection, Fibrin scaffold, Mesenchymal stem cells, Pseudomonas aeruginosa

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O27-32: SARS-CoV-2 (COVID-19): The new pandemic and the challenges ahead

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Background and Aim : Emerging of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2 / Covid-19) has caused widespread worldwide outbreaks and a major public health problem. The aim of this study is to provide an overview of the origin, symptoms, transmission, pathogenesis, diagnosis, and treatment of the virus.

Methods : Search the databases of PubMed, Scopus, Science Direct, and Google scholar search engine with keywords 2019-nCoV, COVID-19, SARS-CoV-2, and Novel coronavirus, and search the results were evaluated.

Results : Studies have shown that the virus may has originated from the bat. It has also been shown that the virus receptor is ACE2 which is also the SARS virus receptor and is expressed in most tissues. The most common way of virus transmission is through respiratory droplets and close contact. It is also transmitted by asymptomatic patients, but vertical transmission from mother to fetus has not been confirmed. Since it is the gold standard for RT-PCR detection, but a chest CT is more sensitive to detect positive cases.

Conclusion : Since no effective vaccine or drug for prevention and treatment of this disease has not yet been identified and also because of the high incubation period, the relatively long infection period, easy transmission and the lack of complete recognition of the characteristics and stability in different environments, the best way to control is to prevent the spread of the infection in different ways and take seriously personal and public hygiene.

Keywords : Coronavirus, 2019-nCoV, COVID-19, SARS-CoV-2, Novel coronavirus, Emerging viruses, pathogenesis

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O28-124: TRANSMISSION OF SEVERE ACUTE RESPIRATORY SYNDROME COVID-19 TO ANIMALS: AN Updated REVIEW

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Background and Aim : The novel coronavirus (SARS-CoV-2), the etiology of COVID-19, outbreak that originated in Wuhan (Hubei province, China) during late 2019. It has spread across the globe affecting nearly 7 million people with a toll of 0.4 million deaths and restricting the movement of the most of the world population during past three months. COVID-19 became the leading health, economic, and humanitarian challenges of the 21st century. In addition to the considerable COVID-19 cases, hospitalizations, and deaths in humans, several cases of SARS-CoV-2 infections in animal hosts (dog, cat, tiger, lion, mink) have been reported. Thus, the concern of pet owners is increasing. Moreover, the dynamics of the disease requires further explanation, mainly concerning the transmission of the virus from humans to animals and vice versa.

Methods : Therefore, this study aimed to gather information about the cases of transmission of COVID-19 in animals already reported, through a literary review of works has been published in scientific journals and performing genomic analysis of SARS-CoV-2 virus isolates from animal hosts.

Results : Although many instances of transmission of the SARS-CoV-2 have been reported, caution and further studies are necessary to avoid the occurrence of maltreatment in animals and to achieve a better understanding of the dynamics of the disease in the environment, in men and animals.

Conclusion : Future research in animal-human interface can help in formulating and implementing apt preventive measures combating the further transmission of COVID-19.

Keywords : Coronavirus; COVID-19; SARS-CoV-2; pandemic; zoonoses; pet animals; animals; epidemiology; one health

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O29-165: Relationship between human breast cancer and bovine leukemia virus in women of Iran

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Background and Aim : Breast cancer is one of the most common cancers in the world particularly among Iranian women. Although the mortality rate decreased in developed countries, there were increased changes in breast cancer incidences. Bovine leukemia virus (BLV) is an enzootic, exogenous, and oncogenic retrovirus that causes B-cell leukosis in 1-5% of infected cattle. Recently, some epidemiological studies have reported BLV infectivity in humans. The current study aimed at evaluating the correlation between BLV infection and breast cancer in Iran.

Methods : In the cross-sectional study, the presence of BLV in breast cancer-suspected tissues was evaluated for the first time in Iran and Qom Province. A total of 400 samples including 200 breast cancer-suspected tissue samples and 200 blood samples of women without breast cancer, were collected from July 2017 to October 2018 from women referred to two general hospitals in Qom Province, Iran. The nested PCR technique was performed to determine the presence of tax and gag genes of BLV in the collected samples.

Results : Based on nested PCR technique, tax and gag genes of BLV were detected in 30% and 8% of breast cancer-suspected tissue samples, respectively. The frequency of BLV in blood samples collected from women without breast cancer was 16.5%. It is notable that BLV DNA was identified even after chemotherapy in some breast cancer samples. Most BLV-positive people were from relatively poor hygienic regions and/or rural areas of Qom Province. The consumption of unpasteurized raw milk and dairy products is common in these areas due to their lower cost than the cost of pasteurized milk and dairy products. This facilitates the transmission of BLV infection from the cattle to human. Also, this report of BLV in the human blood adds important information which could be useful to elucidate possible routes of transmission of these viruses to humans and to prevent further human infection.

Conclusion : The results of the current study demonstrate a possible relationship between human breast cancer and bovine leukemia virus in women of Iran. BLV is one of the major risk factors for breast cancer.

Keywords : Bovine leukemia virus (BLV); Human Breast cancer; Nested PCR technique

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O30-189: Repurposing drugs for inhibitory activity against nonstructural proteins catalytic complex from COVID-19 by molecular modeling

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Background and Aim : Nonstructural proteins (NSPS) is a piece of multisubunit machinery that catalyzes the synthesis of viral RNA and plays a central role in the replication and transcription cycle of the COVID-19 virus. NSP12 is considered a primary target for nucleoside analog antiviral inhibitors, which shows the potential treatment of COVID-19 viral infections. To discover new inhibitor this target we run virtual screening workflow for discovery new potential drugs.

Methods : For all molecular modeling, the Small-Molecular Drug Discovery Suite 2015-2 (Schrodinger, LLC, New York, NY, 2016) was used. The molecular modeling was subjected using the Glide application in the Schrödinger drug discovery suite. More than 5000 drugs downloaded from ZINC15 were prepared with Ligprep application; proteins were obtained from a protein data bank (PDB). The Protein Preparation and Prime application were performed to minimize the protein strains state.

Results : The results of molecular modeling showed that compounds with ZINC ID 85552114 (Maltotetraose), 2522868 (Nystatin) and 60183170 (Paromomycin) demonstrated docking score -14.250, -12.214 and -12.013 Kcal.mol-1 had the highest inhibitory activity on NSPS catalytic complex and RNA dependent RNA polymerase replication activity, respectively.

Conclusion : Regarding the importance of finding a safe, cheap, easy to industrialize as fast as a possible cure for the worldwide pandemic, COVID-19, the inhibitory activity of maltotetrose, nystatin and Paromomycin against NSPS catalytic complex has been investigated by molecular docking and could be carried on in future researches. all authors were equally contributed.

Keywords : Repurposing, Molecular modeling, COVID-19, NSPS complex

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O31-307: Physicochemical inactivation of SARS-CoV 2 versus SARS and MERS

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Background and Aim : SARS-CoV-2 could be spreading via respiratory droplets or through direct and indirect contact with incubation times between 2h-14 days. In the present study, we reviewed all available information about the susceptibility and persistence of SARS-CoV 2.

Methods : The entire related studies were collected and analyzed according to keywords including persistence on inanimate and animate surfaces, virucidal compounds and physical treatments from valid databases.

Results : In comparison to the SARS- CoV and MERS-CoV, SARS-CoV2 can remain infective only 30 min to 2h on different types of materials dependent on the other physical conditions. Notably, it is much more sensitive than SARS-CoV and MERS-CoV to the heat treatment and is completely inactivated in less than 5 min at 70°C. Contrary to expectations, coronaviruses have shown resistance to a wide range of disinfectants. Hydrogen peroxide 0.5 %, sodium hypochlorite 0.5% and alcohol-based solutions have scored higher disinfection activity due to their effectiveness in less than 1 min contact time, easy access and reasonable price.

Conclusion : The existence of different variants of this strain can differentiate it from SARS-CoV and MERS-CoV. The mutations in the spike protein of SARS-CoV 2 can increase its multiplication and transmission up to 3 to 9 times. The susceptibility assessment of its different variants to physical and chemical treatments can aid in developing new disinfection formulations and efficient control of the transmission and spread of this virus.

Keywords : SARS-CoV-2, Persistence on inanimate surface, Physical treatment, Chemical inactivation, Disinfection

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O32-183: Comparison of Morphometric and Molecular Methods in The Identification of Fasciola Species in Golestan Province

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Background and Aim : The genus Fasciola parasite causes Fascioliasis infection. Fascioliasis is widespread all around the world and is found in abundance in the northern provinces of Iran. Cattle and sheep are the main hosts of the Fasciola parasite . Two main species of this genus are F. hepatica and F. gigantica. The aim of this study is to identify Fasciola through morphometric and molecular methods in Golestan province

Methods : Fasciola worms taken from infected livestock livers then small sections from worms separated and kept in Ethanol 70°. In order to extract DNA samples, phenol-chloroform technique was used. A part of ITS-1 genome was amplified by a special primer. To separate the two species from each other, TasI enzyme was utilized for amplified fragments. All worms were stained with carmine acid. After staining, the worms were measured morphologically by calibrated microscope which had True Chrome II camera.

Results : A morphologic study carried out to isolate 271 samples including 107 Fasciola hepatica (39.48%), 137 Fasciola gigantica (50.55%) and 27 Fasciola sp. (9.96%). Through PCR-RFLP, it was indicated that of 271 worms taken from infected sheep and cattle with Fasciola, 126 were identified as Fasciola hepatica (46.49%), 145 as Fasciola gigantica (53.50%) .

Conclusion : This study showed the main two species of worms, that is F.hepatica and F.gigantica were found in abundance in Golestan province. It was also found that molecular method works well in detecting genus of Fasciola than morphological methods.

Keywords : Morphometric, Molecular, Fasciola and Golestan

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O33-370: Seroprevalence of brucellosis in Famenin city, Hamadan, west of Iran : Famenin Brucellosis Cohort Study

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Background and Aim : Brucellosis is endemic in Iran with higher level of endemicity at western areas including Hamadan province. This study aims to define the seroprevalence of brucellosis and it,s risk factors in general population of Famenin, a city of Hamadan province, in west of Iran.

Methods : This survey was conducted on 2367 participants in Famenin and its villages from September to November, 2016. After receiving written consent from subjects, demographic information was entered into the questionnaires and also 10cc blood samples were taken from the participants. Blood samples were sent to the Core facility of Hamadan University of Medical Sciences and were tested using Wright and 2ME kits (Pasteur Institute, Iran) for brucellosis serological detection. The seroprevalence of brucellosis was reported as percentage with 95% confidence interval.

Results : 2367 individuals with the mean age (SD) of 34.6 (20.9) (range: 2 to 95) years were enrolled. Of these, 1060 (44.8%) were men and 1610 (68.0%) lived in rural areas. The seroprevalence of brucellosis according to the Wright titer, equal or greater than 1:80, was 6.6% (95% CI: 5.62% -7.66%). The corresponding prevalence based on 2ME titers, equal or greater than 1:40 in the subjects with positive Wright test was 37.2% (95% CI: 29.5%-44.84%). We saw a significant association between the incidence of brucellosis and the occupation ($p<0.001$) and type of contact with livestock ($p= 0.009$) as two important risk factors.

Conclusion : The seroprevalence of brucellosis in Famenin population was considerable. Contact with livestock, animal husbandry, farming and history of brucellosis were risk factors for brucellosis infection.

Keywords : Brucellosis; Seroprevalence; Zoonotic Infectious Disease; Famenin; Iran

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O34-182: Studying Vibrio Genus in Surface Waters of Khuzestan Province after the Flood in Spring of 2019

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Background and Aim : Vibrio genus are halophilic bacteria, negative gram and curved bacilli, which are usually found in seawater and fresh water. At least 40 species of this genus have been identified, 12 of which are pathogenic to humans and the type species is Vibrio cholerae. The aim of this study is to identify pathogenic species of Vibrio in Khuzestan province surface waters after the flood in the spring of 2019.

Methods : Ten samples of surface water and rive water from 5 cities of Khuzestan province (Ahvaz, Ramhormoz, Masjed soleyman, Izeh, and Baghmalek) were collected and Thiosulfate-citrate-bile salts-sucrose agar and Alkaline Peptone Water culture methods were used for the primary isolation of Vibrio. The exact species identification was done by performing biochemical tests. The V.cholerae strains isolated were serotype by using specific antisera test to identify V.cholerae O1.

Results : Of ten samples, 9 were of non-O1 Vibrio cholerae and 1 was identified to be Vibrio cholerae O1 whose strain was Ogawa.

Conclusion : This study showed that Vibrio pathogenic species was observed in the surface waters of Khuzestan province after the flood.

Keywords : Vibrio, Surface Waters, Khuzestan

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O35-36: Antimicrobial Effect of Au Nanoparticle against Streptococcus mutans and Candida albicans biofilms on Denture Stomatitis

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Background and Aim : Background: Denture stomatitis (DS) is an oral biofilm–associated inflammation of the denture-bearing mucosa. DS has been reported in 10–70% of complete denture wearers. It is more common on the palatal mucosa. In past decades, research has focused on newer targeted agents with the aim of decreasing the rates of side effects of current antimicrobial. Nowadays the field of nanotechnology becomes one of the most topics of interest. The aim of this study was to evaluate the antimicrobial efficacy of gold nanoparticle (Au-NP) against Streptococcus mutans and Candida albicans biofilms.

Methods : Materials and Methods: Here, we evaluated the effect of Au-NP against ten biofilms of Streptococcus mutans and Candida albicans isolated from patients with stomatitis. The standard strain of C. albicans (ATCC 10231) and Streptococcus mutans (PTCC 1683) as a control were used in this study. The Au-NP were applied on mature biofilms and after 24 h of treatment their antibiofilm activities were assessed by crystal violet staining. Biomass quantification was defined and according to classification, recorded no, weak, moderate and high biofilm producer the isolates.

Results : Results: The data indicated that Au-NP had excellent antibiofilm activity against Streptococcus mutans, but this activity against Candida albicans was dependent on the nanoparticle concentrations used.

Conclusion : Conclusion: The results of this study suggest that the Au-NP may have clinical implications in the treatment of denture stomatitis. However, further studies are needed before recommending the use of these drugs safely in clinical situations.

Keywords : Key words: Gold nanoparticles, Candida albicans, Streptococcus mutans, antimicrobial effect.

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O36-89: Nanoporous iron oxide nanoparticle: hydrothermal fabrication, human serum albumin interaction and potential antibacterial effects

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Background and Aim : Nanoporous iron oxide (Fe3O4) nanoparticles (NIONPs) have been widely used as promising agents in biomedical applications.

Methods : Herein, the NIONPs were synthesized by one-step hydrothermal method and well-characterized by FESEM and TEM investigations. Afterwards, their interaction with human serum albumin (HSA) was studied using a range of biophysical approaches, including intrinsic and extrinsic fluorescence, far and near UV- CD, and UV-Vis spectroscopic methods as well as molecular docking investigation. Also, the antibacterial effect of NIONPs was examined on pathogenic bacteria such as Staphylococcus aureus (ATCC 25923), Klebsiella penumoniae (ATCC 33883), Enterococcus faecalis (ATCC 29212) and Pseudomonas aeruginosa (ATCC 27853) standard strains.

Results : The results showed the feasible fabrication of spherical-shaped NIONPs with an average diameter of around 100 nm. Intrinsic fluorescence spectroscopy data depicted that NIONPs formed a complex with HSA by a KSV value of 0.092 (µg/ml)-1. Extrinsic fluorescence, near UV-CD and UV-vis spectroscopic methods revealed that NIONPs induced some changes on the quaternary structure of HSA, whereas Tm measurement and far UV-CD spectroscopy showed some slight changes on the secondary structure of HSA even in the presence of high concentration of NIONPs. Molecular docking study disclosed that Fe3O4 nanoclusters with varying morphologies and dimensions could interact with different residues on the surface of HSA molecules. In addition, antibacterial assays exhibited a significant inhibition on both Gram-positive and Gram-negative pathogenic bacteria.

Conclusion : In conclusion, these NPs can be used as promising antibacterial agents.

Keywords : spectroscopy, docking , HSA

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O37-140: Chemical Assessment of Active Ingredients, Anti-oxidant and Anti-microbial Effects of Trachyspermum Copticum's Seeds harvested in Yazd Province

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Background and Aim : Trachyspermum copticum as a medicinal plant has many therapeutic properties including; anti-flatulence, anti-emesis, anti- rheumatism and expectorant. The aim of this study was to identify active compounds, anti-oxidant and anti-microbial effects of Trachyspermum Copticum's seeds harvested in Yazd province.

Methods : The essence of the seeds was first extracted by Clevenger apparatus. The active components of the essence were then separated and identified by gas chromatography (GC) and gas chromatography-mass spectrometry (GC-MS) methods. The anti-oxidant effect was determined by DPPH (2, 2diphenyl-1-picrylhydrazyl) test as the half maximal inhibitory concentration (IC50) and the total amount of phenolic components of the essence was quantified utilizing the Follin-Ciocalteu method and measurement of MIC (minimum inhibitory concentration) of the product, anti-microbial activity.

Results : Our study shows that thymol (64.9%) and ?-Terpinene (11.1%) were the most prevalent components of the essence. Also, the anti-oxidant activity and the total amount of phenolic component of the essence were 0.809µg/ml-1 and162.62mg/g-1 resepectively and the standard AATCC microbial test showed inhibitory effect of bacteria, especially E. coli and S. aureus indicated acceptable properties.

Conclusion : The result of this research indicated that the active ingrediebts of native Trachyspermum copticum harvested in Yazd province were much higher than the ones found in Trachyspermum copticum harvested in other places.

Keywords : Trachyspermum Copticum, Therapeutic Effects, Seed essence, Antioxidant, Antimicrobial, Active ingrediernts.

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O38-142: Investigation of the effect of antibacterial nano-lipid system containing Trachyspermum Copticum's essential oil by Mozaffari method

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Background and Aim : The aim of this study was to investigate the antibacterial effect of nano-lipid system containing Trachyspermum Copticum's essential oil. For this purpose, the lipid system containing Trachyspermum Copticum's essential oil has been synthesized for gram-positive (Staphylococcus aureus) and gram-negative (E.coli) antibacterial methods.

Methods : The type of study is laboratory research. The nanoparticle synthesis method is Mozaffari method. Particle characterization has been performed in terms of size and charge with DLS and morphology with the Atomic Force Microscope (AFM) and the amount of loading and release with the spectrophotometer. MIC tests were then performed to evaluate the performance of nanoparticles containing Trachyspermum Copticum's essential oil on Staphylococcus aureus and Escherichia coli.

Results : The average particle diameter was 58 nm and its zeta potential was -14.9 mV. The loading rate in nanoparticles was 57%, which was calculated by reading the absorption of light from the standard Trachyspermum Copticum curve. The minimum inhibitory concentration (MIC) of Staphylococcus aureus and E.coli for nanoparticles was 15.625 and 31.25 mg / ml.

Conclusion : Nanoparticles containing Trachyspermum Copticum's essential oil kill gram-positive (Staphylococcus aureus) and gram-negative bacteria (E.coli) and can be used as antibacterial nano-systems.

Keywords : Trachyspermum Copticum, Antibacterial, Staphylococcus aureus, Escherichia coli

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O39-430: A green nano-dressing with potent antibacterial effect

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Background and Aim : Skin is the body's first defense line against environmental pathogens. However, open skin wounds can interfere with the normal function of the skin and the entry of opportunistic bacteria into the body. Recently, the development of nano-dressing containing green antibiotics has been received much attention around the world.

Methods : Ingredients of essential oil of Citrus sinensis (CSEO) the used antibacterial agent were identified by GC-MS analysis. Its half-maximal inhibitory concentration (IC50) against four important human bacteria strains were investigated. After that, a nanogel impregnated nanodressing was also prepared.

Results : The five major components were included as limonene (61.83%), trans-p-2, 8-menthadien-1-ol (4.95%), trans-limonene oxide (2.29 %), cis- limonene oxide (2.58 %), and trans-carveol (2.90%). The IC50s were observed as follows, Staphylococcus aureus (1.0 mg/mL), Escherichia coli (10 mg/mL), Pseudomonas aeruginosa (4.7 mg/mL), and Klebsiella pneumonia (5.8 mg/mL). The nanogel was prepared by the addition of a gelling agent (carbomer 940 2%) to nanoemulsion with a particle size of 125 ± 4 nm. After that, the nanogel was impregnated on the surface of the electrospun nanofibers of polycaprolactone with a mean diameter of 186 ± 36 nm. Interestingly, the prepared nanodressing completely inhibited (~ 100%) the growth of all examined bacteria at the concentration of 15 mg/mL.

Conclusion : The prepared prototype can be used as a potent antibacterial agent. Furthermore, this work introduced an effective and new method for the preparation of green antibacterial agents as well as antibiotic-free wound dressings.

Keywords : Citrus sinensis; Essential oil; PCL nanofibers; Electrospinning; Nanogel; Antibacterial activity.

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O40-200: Cloning and expression of Aspergillus niger PEP in Saccharomyces cerevisiae .

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Background and Aim : Background: It appears for most patients with CD, that a lifelong gluten-free diet alone is required for CD treatment. There are a variety of fungal PEPs such as Aspergillus niger PEP, with therapeutic applications, which destroy internal pralines. Significantly, Aspergillus niger PEP reduces gluten peptides concentration in food and plays an important role in patients with CD. Aim: The aim of this study was to evaluate the expression of Aspergillus niger _ Proline-specific endoprotease in a ura3 auxotroph strain of Saccharomyces cerevisiae

Methods : Methods: The AN-PEP amino acid sequence was synthesized.The plasmid Pyes2 was utilized as expression vector. We were codon optimized the complete amino acid sequence of endoprotease AN-PEP according to S. cerevisiae codon usage. Saccharomyces cerevisiae auxotrophic was used as a host for the expression of the gene encoding endoprotease AN-PEP.

Results : Results In this study, Aspergillus niger PEP gene was cloned in the PYes2 expression vector and expressed in Saccharomyces cerevisiae. The Aspergillus niger PEP was expressed in secretary form and was confirmed by SDS-PAGE analysis and western blotting. The enzyme activity was determined using the Z-Gly-Pro-pNA substrate Results: The Aspergillus niger PEP the enzyme was expressed in the secretory form in The recombinant auxotroph strain of S. cerevisiae.

Conclusion : Conclusion: The findings showed that the expression of the engineered protein may have potential applications in the production of gluten-free bread.

Keywords : Keywords: Aspergillus niger _ Proline-specific endoprotease _ Expression _ Saccharomyces cerevisiae

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O41-80: Effect of bacteriophages in cancer

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1. *banafsheh kiani*
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Background and Aim : Targeted gene therapy of cancer is of paramount importance in medical oncology. Bacteriophages, viruses that specifically infect bacterial cells, offer a variety of potential applications in biomedicine. Their genetic flexibility to go under a variety of surface modifications serves as a basis for phage display methodology. These surface manipulations allow bacteriophages to be exploited for targeted delivery of therapeutic genes.

Methods : Moreover, the excellent safety profile of these viruses paves the way for their potential use as cancer gene therapy platforms. The merge of phage display and combinatorial technology has led to the emergence of phage libraries turning phage display into a high throughput technology. Random peptide libraries, as one of the most frequently used phage libraries, provide a rich source of clinically useful peptide ligands. Peptides are known as a promising category of pharmaceutical agents in medical oncology that present advantages such as inexpensive synthesis, efficient tissue penetration and the lack of immunogenicity.

Results : Phage peptide libraries can be screened, through biopanning, against various targets including cancer cells and tissues that results in obtaining cancer-homing ligands.

Conclusion : Cancer-specific peptides isolated from phage libraries show huge promise to be utilized for targeting of various gene therapy vectors towards malignant cells. Beyond doubt, bacteriophages will play a more impressive role in the future of medical oncology.

Keywords : Bacteriophage Cancer Targeting Phage display Peptide library Gene therapy

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O42-146: Determination of the frequency of infection caused by herpes virus human type 8 (HHV-8) in patients with breast cancer

ELAHEH FOZOUNI[1] *

1. *ELAHEH FOZOUNI*

Background and Aim : Breast cancer is one of the most common malignancies and cause of death among women worldwide. The aim of this study was to investigate the prevalence of HHV-8 DNA in women with breast cancer was detected using Real-Time PCR.

Methods : In study, to investigate non-familial and viral factors in breast cancer, Real Time PCR was used to diagnose herpes virus type 8 in 138 patients with breast cancer.

Results : Of the 138 paraffin blocks in breast cancer patients, 17 were positive for HHV8. The most positive cases in the age group of 40 to 60 years were 7.25% (10 people). Among the positive viral cases, the most cases are related to the type of Intermediate grade tumor with 5.9% (8 people). There was no relation between tumor grade and age group with HHV8 positive. The highest rate of lymph node tumor involvement is in the group (the number of lymph nodes involved is less than three) and is 71%. While the most pollution of HVV8 in the lymphatic group is related to the number group (lymph nodes involved 6 to 9) with a rate of 14 cases of 10.140%.

Conclusion : There is a relation between the number of Tumor lymph node and the HV88, The frequency of HHV8 is directly related to the tumor as the number of lymph nodes involved increases. it is possible that lymphocytes infected with the HHV8 virus are the source of the cancer cell. Infected cells may spread to other parts of the body, making treatment more complicated.

Keywords : Herpes virus type 8, breast cancer, Real Time PCR, Kerman, Iran

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O43-396: The prevalence of Mucosa-Associated adherent-invasive Escherichia coli isolated from Colorectal Cancer patients

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Background and Aim : Among the pathogenic bacteria AIEC (Adherent Invasive E.coli) pathovars have special attention in colorectal cancer. It was identified in 1999 by Boudeau. According to the WHO, 25% of cancers are caused by infections, wich colorectal cancer being the second leading cause of death in 2018. AIEC is an effective pathogen in CRC.Ability to bind and invade the M epithelial follicle-associated (FAE) cells, the ability to survive and replicate within macrophages allow the bacterium to the formation of granulomas and malignancy (1). Therefore, we decided that by isolating and diagnosing AIEC pathovars from CRC patients and compare with control.

Methods : 60 biopsy samples (30 from CRC, 30 from control) were taken. Samples lysed with Triton 100-X% to release intracellular E. coli isolates. The isolates confirmed by phenotypic and molecular methods. To distinguish AIEC pathovar, phenotypic tests; Adhesion assays, Invasion assays, Gentamicin protection assays, and survival and replication in macrophage (2).

Results : We analyzed 60 biopsies (30 CRC and 30 controls). Bacterial growth, following overnight incubation, was detected in tissue specimens from 17 out of 30 CRC and 7 out of 23 controls. For AIEC identification, adherent isolates were assayed for invasiveness, and the capacity of the adhesive-invasive isolates to survive and replicate intracellularly was determined over macrophages J774. In this way we identified 19AIEC- isolates. Interestingly, their relative abundance was significantly higher in CRC patients (46.6%; 14/30) than in controls (16.6%; 5/30).

Conclusion : The studies indicated that Mucosa-Associated AIEC strains are more frequently in CRC than the control. One explanation of the high prevalence of AIEC in CRC could be that changes in the host mucosa receptor repertoire have an effect on the bacterial population associated with mucosa. Previous studies reported higher numbers of AIEC in CRC than controls (3, 4). In conclusion, our study showed a high prevalence of AIEC in biopsies of colon cancers.

Keywords : Mucosa-Associated adherent-invasive Escherichia coli , Colorectal cancer,

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O44-421: Cytotoxicity effect and Changes in the expression of BAX, BCL-2 and CASPASE-9 genes in breast cancer cell line (MCF-7) treated with hydroalcoholic Rosmarinus officinalis extract

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Background and Aim : Today, due to the high prevalence of cancer in Iran and the world, the need for drugs with fewer side effects and better therapeutic effects has been considered by researchers. So that more than 60% of anti-cancer compounds for the treatment of cancer patients are obtained from plant sources. The aim of this study was to investigate the effect of hydroalcoholic extract of rosemary (Rosmarinus officinalis) on the expression of BAX, BCL-2 and CASPASE-9 genes in breast cancer cell line (MCF-7).

Methods : In this experimental study, the hydroalcoholic extract of rosemary was made qualitatively by Soxhlet apparatus. Cells were treated with doses of 5,10,25,50 and 100 micromole rosemary extract for 24,48 and 72 hours. Then, using MTT method, the effect of different concentrations of the extract on cell life was investigated. Using Real Time PCR, the expression of BAX, BCL-2 and CASPASE-9 genes in the groups treated with different amounts of rosemary extract was measured.

Results : This study showed that with increasing concentration and time, cell viability decreased significantly and significantly compared to control samples. The results of Real-Time PCR showed that the expression of CASPASE-9 gene at 48 hours increased significantly compared to the control sample. Also, the expression of BAX and BCL2 genes at 48 and 72 hours increased and decreased significantly compared to the control sample.

Conclusion : Rosemary hydroalcoholic extract has anti-cancer effects in breast cancer, can inhibit the growth and proliferation of cancer cells and may be an effective factor in preventing the growth and spread of cancer cells.

Keywords : Rosmarinus officinalis, BAX, BCL-2, CASPASE-9, cell line

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O45-93: Lip-sub protein fusion acts as a biological wastewater treatment

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Background and Aim : Nowadays Wastewater sufficent and perfect treatment is an important point which attract the attention of all countries .instead of using of chemicals and complicated methods and high expenses .researchers got to use of natural microbial enzymes which works better ,economical,less time and not hazardous for ecosystems .in this study by the use of genetic engineering and molecular methods a new recombinant protein was created with component of Pseudomonas putida and subtilisin protease in order to treat wastewater.

Methods : At first Gene sequences of lipase of Pseudomonas putida and subtitlisin of Bacillus subtilis got from Gene bank. The restriction enzymes xhoI at the 3´ and Bamh1 at the 5´were chosen. PET22b vector was choosed for the cloning vector.the designed protein was checked by ITASSER,GOR4,EXPASY online protein prediction software for its structure and function. The calcium chloride method was used for the competence cells of this bacterium. the transformation of pet22b + Lip-Linker-Subtilisin was performed on E.coli BL21DE3.The confirmatory test of designed structure was done with primers which designed and covered all the sequence and electrophoesis. The expression of recombinant proteins is mediated by the transfer of recombinant vector to host cell and induction of protein production in these cells. In lactose-inducible or IPTG-induced pET system. For confirmation of recombinant protein after 24h induction, SDS-PAGE was performed to observe the expression of recombinant protein. The Western-blot was performed according to the Bumatte method. The purification steps of recombinant protein were performed by the Native method using a histidine tag. The Bradford method used for the protein concentration checking.

Results : The bioinformatical results conveyed that the structure is suitable and functional for the aim of the study.for confirmatory test The results of amplifying Amplicon with size 750 bp for confirming of gen fusion lipase-subtilisin. The induction reached its optimum within 24 hours. Western blot results indicate protein expression and confirm it. Concentration of recombinant fusion protein LIP-SUB with Nanodrop. The recombinant protein produced with a concentration of 4.11 mg/ml.

Conclusion : According to the results the new recombinant protein has a good and suitable structure for the aim of this study.

Keywords : lipase -subtilisin-protease-wastewater

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O46-83: Relationship between Demodex count and acne vulgaris

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Background and Aim : Demodex folliculorum is a parasite of the human pilosebaceous follicle. D.folliculorum inhabits in the hair follicle and D.brevis in the sebaceous and meibomian glands. Follicle mites are quite motile, and migrate from follicle to follicle and transport different bacteria as a vector. Acne is a chronic inflammatory disease of the pilosebaceous units. The objectives of this study were to assess the rate of Demodex infestation in acne and normal groups.

Methods : Patients, 180 case with average 29.37 years old, show acne feature on the facial skin. Control group were consist of 186 case with normal skin. We took sebum sample of facial skin with acne tool from five different areas then counted mites under light microscope. Positive Demodex test means above five mites per cm2.

Results : Demodex test was positive in 81 patients (45%) and 26 controls (13.1%). The average of Demodex density in acne group was 11.76 mites per cm2. Demodex test was positive in 12 men (6.66%) and in 69 women (38.3%) in acne group. Cases with acne had higher odds of being infested with Demodex compared to those without.

Conclusion : People with oily or mixed skin seems to favour Demodex proliferation. Demodex could be associated with acne vulgaris as a bacterial vector. Demodex mites show a predilection for areas of high sebum production and they have been shown to contain lipase. It seems people with acne vulgaris are prone to infested with Demodex.

Keywords : Demodex folliculorum, Demodex Brevis, Acne Vulgaris

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O47-145: Determine Of The Prevalence of human papillomavirus (HPV-16) infection in lesions of lichen planus in comparison with oral lichenoid using PCR

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Background and Aim : human papiluma virus (HPV) cause oral, cervical, and any other keratinocyte cancers and are of 2 groups based on the risk of carcinogenesis; high-risk and low-risk HPVs. Oral lichen planus (OLP) is a common chronic autoimmune disorder, which causes damages to the keratinocytes of the oral mucosa. Although the etiology of OLP is still unknown, it is generally accepted to be a T-cell-mediated inflammatory disease. The reaction of these specific CD8 T cells is similar to what occurs during a viral infection, in which a virus can act as a cytoplasmic antigen or induce the expression of host cell proteins. Oral lichenoid lesions (OLLs) are a group of lesions with different etiologies but common clinical and histopathological features. Considering the previous studies, it was reported that the premalignant potential of OLLs could be more than that of OLPs. Since the HPV virus in OLLs has not ever been studied this research aimed at investigating the presence of HPV-16 (human papillomavirus) in Oral lichenoid in order to evaluate a possible association between premalignant potential of HPV in lichenoid lesions in comparison to Oral lichen planus.

Methods : fifty formalin fixed paraffin wax embedded tissue blocks 25 paraffin block of OLPs as well as 25 formalin fixed paraffin wax embedded tissue blocks of of OLLs, which were previously diagnosed, were gathered from patients who had referred to the Department of Pathology, Faculty of Dentistry of Islamic Azad university, Isfahan (Khorasgan) Branch during 2013-2018. DNA extraction from formalin fixed paraffin wax embedded tissue blocks was performed using GEN ALL extraction kit. Confirmation of the extracted DNAs was conducted using β-globin gene. The samples were tested for the presence of HPV-16 genome by PCR .

Results : In the two experimental groups, the presence frequency of HPV-16 was detected respectively at 0 and 6.7 % of OLLs and OLPs. Fisher's test did not show this difference statistically significant (P value> 0.05).

Conclusion : Based on the findings of this study it is conceivable that HPV-16 plays a role in the creation of OLLs. According to the obtained results, performing further studies in this field is recommended.

Keywords : PCR, Oral lichenoid, HPV-16

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O48-237: High genetic diversity of Mycobacterium tuberculosis concurrent with low genetic diversity among Mycobacterium bovis reveals their distribution patterns in northeast of Iran using 24 loci MIRU-VNTR for the first time

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Background and Aim : For the first time in Iran, Mycobacterium tuberculosis complex isolated from human and livestock populations, in the province of Khorasan Razavi, were simultaneously investigated using the standard 24 loci MIRU-VNTR. The aim of this study was to evaluate the genetic diversity of Mycobacterium tuberculosis complex (Tuberculosis and Bovis).

Methods : One hundred and twenty Mycobacterium tuberculosis were collected a year period. A total of 123 samples from lymph nodes and tissues of reactor cattles were collected. All samples were then cultured in pyruvate and glycerol enriched Lowenstein Jensen media. To extract the DNA, boiling method was used. The 24-loci MIRU-VNTR was performed for all Mycobacterium tuberculosis and bovis.

Results : Among 120 investigated isolates, detected patterns included genotypes NEW-1 (53.3%), CAS/ Delhi (24.1%), Haarlem (5%), Beijing (4.16%), Uganda I (4.16%), S (3.3%), Ural (0.83%), TUR (0.83%), Uganda II (0.83%), Lam (0.83%) and Cameroon (0.83%). The HDGI rate was 0.9981 and the rate of clustering was 10.83%. In addition, recent TB transmission rate was 6.66%. The allele diversity was high in 6 loci, moderate in 10 loci and the rest of the loci showed a low allele diversity. QUB26 had the highest allele diversity (h: 0.76) and the loci Mtub29 and MIRU24 had the lowest (h: 0). Among 123 collected tissue samples, 21 (17%) grew on the culture media. The HGDI rate was 0.71 and the rate of clustering was 85.7%. Also, recent bovine tuberculosis transmission rate was estimated to be 71.4%. Two loci had moderate allele diversity and other loci had low allele diversity. The locus ETRC had the highest allele diversity (h: 0.45).

Conclusion : Since results suggest a high diversity in circulating Mycobacterium tuberculosis in human population, latent infections are reactivated. Thus, screening and treating individuals with latent tuberculosis is important in decreasing tuberculosis outbreaks. Moreover, the highest number of tuberculosis cases in livestock population are caused as a result of recent transmission, which makes it advisable for cattle farms to be under the supervision of veterinary organization for performing periodic tuberculin tests and eliminating reactor cattle to prevent the spread of the disease.

Keywords : Tuberculosis, Mycobacterium tuberculosis, Mycobacterium bovis, MIRU-VNTR,

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O49-290: A prion-derived peptide successfully reduced the intracellular levels of ROS and Ca2+ in neuroblastoma cells after treatment with Aβ42 oligomers

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Background and Aim : Alzheimer's disease (AD) is the most prevalent form of dementia caused by accumulation of senile plaques formed by AB. Cellular prion protein (PrPC) is a membrane protein and that has a high binding affinity for Aβ42 oligomers. The levels of reactive oxygen species (ROS) and Ca2+ were investigated in human neuroblastoma cells after treatment with Aβ42 oligomers (ADDLs) in presence and absence of short prion-derived peptide.

Methods : SH-SY5Y neuroblastoma cells were seeded on glass coverslip in 6 well plates. After 24 h, 600 µl of various samples were added to cells and after washing, cells loaded with Fluo-4 AM and CM-H2DFDA specific probe for Ca2+ and ROS, respectively. Cell image acquisition was performed using the TCS SP8 confocal system and analysis was done using Image J software.

Results : The quantification of the intracellular Ca2+ and ROS derived fluorescence shows that the treatment of the cells with A?42 ADDLs causes an increase of intracellular Ca2+ and ROS compared with untreated cells and when cells were treated with A?42 ADDLs + synthetic peptides ROS and Ca2+ levels were significantly lower than those observed after treatment with A?42 ADDLs alone.

Conclusion : The present study shows the synthetic peptide can effectively protect the SH-SY5Y cells against the oxidative stress and Ca2+ influx induced by Aβ42 ADDLs and has potential therapeutic value for the treatment of AD.

Keywords : Prion protein, AB oligomer, Alzheimer's disease, ADDLs

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O50-299: Investigation of antibiotic profile and biofilmogenic ability in Klebsiella pneumonia isolates with carbapenem resistance

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Background and Aim : Klebsiella pneumoniae, a gram-negative bacillus, is a member of the enterobacteriaceae family that is capable of causing various infections. Infections caused by Klebsiella pneumoniae with carbapenem resistance as an important treatment problem are increasing worldwide. The aim of the present study was to investigate the antibiotic profile and the ability of biofilm production of Klebsiella pneumoniae isolates to have carbapenemase resistance in 1398.

Methods : 73 isolated Klebsiella pneumonia were collected from patients in hospitals and laboratories in Tehran province, and after confirmation of the samples with standard biochemical experiments, the samples with the enzyme method of carbapenemase enzyme were screened with the help of the phenotypic method. Then, the antibiotic profile of the obtained samples, along with the ability to form biofilm by microplite method in laboratory conditions were examined.

Results : Of the 73 samples, 23 (31%) had carbapenemase enzyme. The highest antibiotic resistance was observed with ampicillin, chloramphenicol and ciprofloxacin antibiotics, and the lowest resistance was related to gentamicin, amikacin and cotrimoxazole. Most samples were able to form biofilm.

Conclusion : The present study suggests that, unfortunately, the insulin resistance of Klebsiella pneumonia is increased compared to carbapenem antibiotics, and that the samples studied have a higher resistance to antibiotics such as phosphomycin compared to previous studies. It is recommended that these isolates be evaluated for the presence of resistance genes to Colistin and phosphomycin.

Keywords : Klebsiella pneumoniae, carbapenemase, Biofilm, Antibiogram

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O51-300: Evaluation of antibiotic profile and biofilmogenicity ability in Klebsiella pneumoniae isolates with broad-spectrum beta-lactamase (ESBL) resistance

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Background and Aim : Klebsiella pneumoniae is a gram-negative bacterium that can cause a variety of infections, including nosocomial infections. Various infections caused by Klebsiella pneumoniae with annual carbapenemic resistance cause high mortality and treatment costs in various countries around the world. The aim of the present study, which was conducted as part of the dissertation project, is to investigate the antibiotic profile and the biofilmability capacity of Klebsiella pneumoniae isolates with ESBL resistance in 1398

Methods : 73 isolated Klebsiella pneumoniae were collected from patients in hospitals and laboratories in Tehran province and after confirmation of the samples with standard biochemical experiments, ESBL isolates were screened by combined phenotypic combination method. Then, the antibiotic profile of the obtained samples, along with the ability to form biofilm by microplite method in laboratory conditions were examined.

Results : Of the 73 samples, 44 (60%) had broad-spectrum beta-lactamase enzymes. The highest antibiotic resistance was observed with ampicillin, chloramphenicol and ciprofloxacin antibiotics, and the lowest resistance was related to gentamicin, amikacin and cotrimoxazole. Most samples were able to form biofilm.

Conclusion : Comparing the present study with previous studies, we saw an increase in antibiotic resistance in the studied isolates, and unfortunately the prevalence of isolates with high beta-lactamase resistance was high. It is recommended that the isolates be tested for ESBL resistance genes.

Keywords : Klebsiella pneumoniae, ESBL, Biofilm, Antibiogram

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O52-320: Frequency of aacC2 gene in clinical isolated of Klebsiella pneumoniae in Khorramabad

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Background and Aim : Klebsiella pneumoniae is a gram-negative intestinal bacilli and is a member of Enterobacteriaceae family and forms part of the natural microflora of the human body. Klebsiella causes 5 to 7-5% of all hospital infections and infections caused by it in the pediatric and intensive care sector are a major problem. Reports around the world emphasize resistance to aminoglycoside antibiotics in recent years. The aim of this study was to determine the frequency of aacC2 gene in clinical isolates of Klebsiella pneumoniae in Khorramabad.

Methods : In this study, the patients were referred to hospitals in Khorramabad city during 7 months. Samples were subjected to molecular evaluation after biochemical and antibiotic tests. DNA extraction was performed by boiling method and detection of genes by specific primers was performed using PCR technique.

Results : After molecular studies, using PCR technique, 100% of the isolates studied had 17.1% of the aacC2 gene.

Conclusion : Due to the 17.1% prevalence of the gene aacC1, one of the most effective genes in resistance to aminoglycoside antibiotics. It was determined that in the future, antibiotics resistance should be increased in clinical isolates and resistant to resistant isolates.

Keywords : Klebsiella pneumoniae, molecular diagnosis, aminoglycoside antibiotics, aacC2

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O53-326: Isolation and molecular identification of ultraviolent resistant soil bacteria indigenous to south of Iran

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Background and Aim : Harmful environmental factors such as high temperature, salinity and high levels of solar radiation are constant challenges for living organisms which inhabit extreme environments like high attitudes, deserts and hot springs. However, there are various microorganisms that they cope with damaging factors and they are adapted to the extreme situations. Enzymes and secondary metabolites that are produce by UVB resistant bacteria can be used in biotechnological and medical industries as anticancer, antioxidants and skincare products.

Methods : Eight soil samples were collected from Shiraz and Ahwaz, southern cities of Iran, which are exposure to high solar radiation, to study bacterial resistance to UVB radiation. Soil samples were cultured on the Tryptone Soy Agar and Luria Bertani Agar medium and 108 pure colonies with various colors and shapes were in exposure to UVB lamp (Philips/20w) with wavelength of 312 nm, from 30 centimeters distance for 20 to 90 minutes. Then to avoid photoreactivation they were wrapped in foils and incubated at 30◦ C. Also, photo reactivation was tested by incubating UVB irradiated colonies under photo-active radiation lamps at 30◦ C. All of experiments were repeated three times.

Results : At last four bacteria were highly resistant to UVB radiation which include: 1. A coccoid, gram positive, catalase and oxidase positive and nonmotile bacterium with orange pigmentation was isolated from a soil sample of Shiraz, 2. A coccoid, gram positive, catalase and oxidase positive and motile bacterium with orange pigmentation, 3. A coccoid, gram positive, catalase and oxidase positive and nonmotile bacterium with yellow pigmentation , 4. A rod shaped, gram positive, spore forming, catalase and oxidase positive and nonmotile bacterium which were isolated from Ahwaz soil samples and they could tolerate 50, 60, 50 and 70 minutes of UVB radiation, respectively.

Conclusion : UVB resistant bacteria were isolated from southern cities of Iran. These bacteria may have secondary metabolites that can be used as sunscreen and other skincare products.

Keywords : ultra violet, antioxidant, UVB, resistant bacteria

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O54-367: Prevalence and molecular characterization of Mycobacterium tuberculosis resistance to aminoglycosides in the Northeast of Iran

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Background and Aim : Tuberculosis is an important cause of death with an increased antibiotic resistance. Kanamycin and amikacin are among the most effective aminoglycosides for multidrug-resistant strains. We investigated the resistance to these two antibiotics in 111 susceptible and 9 resistant specimens.

Methods : Phenotypic method was used to assess the resistance, PCR method was performed for rrs and eis genes and the results confirmed by sequencing.

Results : No resistance against kanamycin and amikacin was observed in susceptible specimens and only three resistant samples had such resistance. Two had mutations at A1401G nucleotide, and the nucleotide change of G→A was observed at 1484 position in one sample. Mutations at A514C, A907C, G1332A positions were observed in one sample. eis gene sequencing revealed that one sample had mutation in promoter region at A-13G position.

Conclusion : The most important mutation was at nucleotide A1401G in rrs gene and a low prevalence of aminoglycoside resistance was observed in northeastern Iran.

Keywords : Tuberculosis, Resistance, Aminoglycosides, MDR-TB

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O55-413: Bioinformatics can change phylogenetic relations of bacterial strains: a case study on pathovars of Xanthomonas campestris

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Background and Aim : Xanthomonas campestris pathovars are phytopathogenic bacteria which are classified into numerous categories based on their selective and specific hosts. Complete genome sequences of different bacteria are increasingly available due to the advent of high-throughput sequencing technologies and the development of bioinformatics tools. This provides new opportunities for investigating phylogenetic relations of Xanthomonas campestris pathovars at the genome level.

Methods : Available genome sequences of sixty Xanthomonas campestris strains from different pathovars were retrieved from GenBank and were submitted to RAST to use a uniform methodology for genome annotation. Taking Xanthomonas campestris pv. campestris ATCC 33913 as a reference, ANI was calculated by JSpecies and dDDH was determined using Web tool GGDC for intergenomic distance analysis. For phylogenomic analysis, sequences of 20 universal housekeeping genes were extracted from Xanthomonas campestris genomes and then were aligned and concatenated by CLUSTALW and SeaView, respectively. A maximum likelihood phylogenomic tree was constructed using IQ-TREE. The phylogenomic tree was displayed by TreeGraph 2.

Results : ANI and dDDH are the similarity indices for genome comparison which are used to confirm the taxonomic hierarchy at the species level. ANI and dDDH values for 45 strains of Xanthomonas campestris were above the species cutoff values (95% and 70%, respectively). The G+C content of each genome was also determined and was compared with Xanthomonas campestris pv. campestris ATCC 33913. A genome was considered to belong to species campestris if it showed less than 1% difference in G+C content with the reference strain. Relatedness of these 45 strains to reference, Xanthomonas campestris pv. campestris ATCC 33913 in the phylogenomic tree was confirmed the species status of them as Xanthomonas campestris and they were restricted to three pathovars including campestris, incanae and raphani.

Conclusion : According to the results of present study, it is suggested that comparison of related genomes using bioinformatics tools can be considered as a new approach for biosystematics study of different bacteria as well as Xanthomonas campestris pathovars and may be avoided ecological and evolutionary misinterpretation in subsequent studies of these industrially and agriculturally important bacteria.

Keywords : Xanthomonas campestris, bioinformatics, phylogenetic, phylogenomic tree, genome, pathovar

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O56-420: Alteration in the expression levels of Matrix Metalloproteinase -1, MMP-7 and MMP-9 following Helicobacter pylori infection in the gastric epithelial cell

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Background and Aim : Matrix metalloproteinases (MMPs) are a large family of zinc endopeptidases that play important roles in the degradation of extracellular matrix (ECM) and various inflammatory diseases. Also, they affect cancer development processes, such as apoptosis, cell proliferation, and immune system. Therefore, this study aimed to investigate the induction of MMP2, -7, and -9 by different H. pylori strains in the MKN-45 cell line. We also determined correlation of MMPs mRNA expression levels with virulence factors of the strains and type of disease.

Methods : Nineteen H. pylori strains which were isolated from biopsy specimens of dyspeptic patients with different histopathological status were selected. Fresh colonies of H. pylori were co-cultured with MKN-45 cells at a multiplicity of infection of 100 for 1 and 6 hours. Then, the expression of MMP-2, -7, and -9 messenger RNA was measured by a quantitative real-time PCR method. The presence of virulence genes, including cagA, vacA (s/m), babA (A2), and sabA was performed using PCR analysis as well

Results : Histopathological status consisted of 10.5% intestinal metaplasia (IM), 26.3% chronic gastritis (CG), and 63.2% severe active gastritis (SAG) that 68.41% and 31.59% of them were non-ulcer diseases (NUD) and peptic ulcer disease (PUD), respectively. Status of cagA, vacA s1, vacA s2, vacA m1, vacA m2, iceA1, iceA2, iceA1+A2, babA2 and sabA genes in isolates were 78.9%, 73.7%, 26.3%, 5.3%, 94.7%, 36.8%, 5.3%, 47.4%, 100%, and 94.7%, respectively. Upregulation of MMP2, MMP7 and MMP9 genes were detected at ranges of 15.73%, 5.26%, 15.78% (1 hour co-culturing), 21.05%, 26.31%, 15.78% (6 hour co-culturing) respectively. Further, downregulation of MMP2, MMP7and MMP9 genes were respectively detected at ranges of 36.84%, 10.52%, 15.78% (1 hour co-culturing), 36.84%, 0%, 10.52% (6 hour co-culturing).

Considering, the results indicated that the infection of MKN-45 cells with H. pylori did not lead to an increase or decrease in levels of MMPs messenger RNA significantly. Furthermore, the induction of MMPs wasn't correlated with virulence factors of the strains and type of disease.

Conclusion : Our finding showed a variation in the induction of MMP2, -7, and -9 gene expression in MKN-45 cell by different strains of H. Pylori. As a result, further studies are needed to evaluate the possible role of H. pylori on the induction of MMP2, -7, and -9 in human gastric.

Keywords : H. Pylori, MKN-45 cell line, Matrix metalloproteinase, quantitative Real-time PCR

خلاصه مقالات پوستر

P1-4: Evaluation of incidence of Ch.trachomatis and N.gonorrhoeae in women with endoservitis by PCR method

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Background and Aim : Introduction and Objectives: Neisseria gonorrhoeae and Chlamydia trachomatis are the two most common bacterial sexually transmitted infections that manifest primarily as urethritis in males and endocervicitis in females. Recently molecular amplification assays like Polymerase Chain Reaction (PCR) and Ligase Chain Reaction (LCR) have been found to be highly sensitive and specific methods for detection of N. gonorrhoeae and C. trachonmatis not only in urethral and cervical specimens but also in urine. In women, the cervix is the most common site of gonorrhea, resulting in endocervicitis and urethritis, which can be complicated by pelvic inflammatory disease (PID). The study aimed to assess the prevalence of N.gonorrhoeae and C.trachomatis infections rate in women with endoservisit.

Methods : Materials and Methods: In this study endocervical smears and urine samples collected from 150 women with genitourinary infections were analyzed after DNA extraction by using PCR technique and special primers (KL1,KL2 and SL59,SL67) to determine the C.trochomatis and N.Gonorrhoea.

Results : RESULTS: In our study prevalence of Chlamydia infection in urine samples was 8.1% and in Endoservical swab (ESS) was 9.8% and prevalence of N.gonorrhea was 1% in urine samples and 0.7% in ESS samples. Coinfection prevalence was 0.4% with analyzing urine samples and it was 0.6 in ESS samples.

Conclusion : In conclution in sexually transmitted diseases two most important pathogens, C. N .gonorrhoea which are difficult to diagnosis with conventional culture me more comfortable for the patients PCR-based methods are seen to be p: samples of cervical swab which have smilar sensitivity, although these easy, inexpensive, and highly sensitive.

Keywords : Key worlds: C.trochomatis, N.gonorrhoea, Endocervitis, PCR

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P2-30: Antifungal activity of Rosemary oil extract against in the Aspergillus flavus fungus and its effect on the AFL.1 Gene expression by Real Time-PCR

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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. 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 Aspergillus flavus and Candida albicans in sabouraud dextrose agar and Trichophyton verrucosum and Epidermophyton floccosum on 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 minimum density of deterrence rosemary extract or MCI for Candida albicans is approximately 4 to 6 mg per liter, for Asperjillus flavus is 3 to 5 mg per liter and dermatophyte fungu Epidermophyton floccosum and Trichophyton verrucosum s 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 : Aspergillus flavus, Rosemary, AFL.1, Real Time-PCR

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P3-72: Bacteriological examination and diagnosis of root canals associated with dental periapical abscesses

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Background and Aim : The aim of this study was to identify microorganisms from root canals with periapical abscesses and to ascertain the susceptibility of Peptostreptococcus prevotii and Fusobacterium necrophorum to antimicrobials. Study design Thirty root canals were microbiologically sampled by using sterile paper points. The concomitant microorganisms were identified through the use of established methods. The susceptibility of P prevotii and F necrophorum to antimicrobials was evaluated by using the E test method.

Methods : Culture procedures have traditionally been used in the assessment of the microbiota associated with vari- ous infectious diseases, including infections of endodontic origin. The culturing techniques have a reasonable degree of agreement in terms of the identification of oral microorganisms compared with that of the "checkerboard" DNA-DNA hybridization method. The major advantage of the culture procedure is its ability to enable the detection of unexpectedly viable cells (molecular procedures enable the detection of only target microbial species). Many molecular techniques assist in the identification of cultivable microorganisms.

Results : A total of 117 different bacterial strains were recovered, including 75 strict anaerobes or microphilic species. The most frequently isolated strict anaerobes were P prevotii, Peptostreptococcus micros, and F necrophorum. Facultative bacteria such as Gemella morbillorum and Streptococcus mitis were also found, albeit less frequently.

Conclusion : Gram-positive anaerobic bacteria predominate in the mixed microbiota of root canals with periapical abscesses. Moreover, P prevotii and F necrophorum are susceptible to the tested antibiotics.

Keywords : Bacteriological,periapical abscesses,root canals,

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P4-92: Study on differentiation of pathogen-nonpathogen Mycobacterial infections using ESAT6-CFP10 in ELISA system

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Background and Aim : Pathogenic mycobacteria, including the causative agents of tuberculosis, are responsible for considerable morbidity and mortality worldwide. The availability of a laboratory method that can distinguish between two groups of pathogens; Mycobacterium tuberculosis complex (MTC or MTBC), nontuberculous mycobacteria (NTM) and those who have only had a history of dealing with nonpathogenic or recently vaccinated individuals is of great importance.

Methods : In this regard, different strains of mycobacteria were cultured in the Dorset-Henley liquid medium and the inactivation of the cultures is carried out by the heat. The bacteria were separated from the liquid medium containing secreted proteins with EKS filters. Low molecular weight proteins in Mycobacterium tuberculosis precipitated with ammonium sulfate were purified by Sephadex-G50 gel chromatography and crude antigens in other mycobacteria precipitated with TCA. Protein concentrations determined with lowry protein assay, antigens coated on the ELISA plate and the results were analyzed with SPSS software and investigated.

Results : In this study, all antigens had more than 92% detection ability in healthy livestock in the ELISA method. The highest specificity was related to ESAT-6/CFP10 and M. avium subsp. Paratuberculosis antigens were 83.66% and 95.83% respectively and the highest efficiency of diagnostic tests were over 83% concerning these two antigens.

Conclusion : It concluded that the two antigens ESAT-6/CFP10 and M. avium subsp. Paratuberculosis are suitable candidates for the design of the diagnostic ELISA system due to their sensitivity, specificity and efficiency and also reliable detection of healthy livestock from sensitized livestock.

Keywords : Mycobacteria, ELISA, Tuberculosis, livestock

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P5-96: Validation Approach (TaqMan) Real Time PCR in the Diagnosis of Tuberculosis-Related Patients (with an emphasis on TB negative) in Mashhad City

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Background and Aim : Mycobacterium tuberculosis (TB) is a species of pathogenic bacteria in the family mycobacteriaceae and the causative agent of tuberculosis, remains the leading cause of death worldwide. Sometimes due to a small number of tuberculosis in some cases, in addition to smear and culture as gold standard, Real time PCR (TAq Man) is very helpful in diagnosis due to high sensitivity and specificity. The purpose of this study was to investigate the validation approach (TaqMan) Real Time PCR in the diagnosis of tuberculosis-related patients (with an emphasis on TB negative).

Methods : Of all patients referred to Mashhad University of Medical Sciences hospitals referring to the similar symptoms of tuberculosis by the physician, pulmonary (lavage or phlegm) samples and extrapulmonary were taken. At first, patients' basic information was recorded for age, type, sex and type of preparation. The specimens were then evaluated for smear and culture and it was determined that the smear or culture was negative. DNA extraction was carried out to determine the molecular properties of the samples using a DNA isolation kit (Qiagen), then primers and probes were designed using the Beacon designer software and the real-time PCR method was optimized. In this research, the Real-Time PCR Taqman probe was used for IS6110 for diagnosis of tuberculosis. In this research, optimization of methods for use in TB diagnostic laboratories was studied.

Results : The sensitivity of the real-time PCR Taqman probe designed to detect Mycobacterium tuberculosis complex was 100%. In this study, 294 samples were taken, 20 samples were smeared and positive culture, and 213 samples were smeared and negative culture, from 233 samples 49 samples of TaqMan positive and 184 negative TaqMan test samples. 61 samples were unculturable, of which 1 sample was positive by performing TaqMan test.

Conclusion : Classical methods are used to detect Mycobacterium tuberculosis, so in this study, Real-time PCR was described as the fastest method. According to the results of this study, the Real-Time PCR Taqman probe method can be used as a standard method for diagnosis and confirmation of tuberculosis

Keywords : Mycobacterium tuberculosis, TB (Tuberculosis) and Real-time PCR Taqman probe

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P6-112: Ionizing Radiation Resistant Microorganisms: Opportunities and Challenges

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Background and Aim : The microorganisms that thrive in extreme environmental conditions, such as different levels of ionizing radiation, are known as extremophiles. The secondary metabolic reserves including extremozymes and extremolytes play an important role in the survival of extremophiles in high levels of radiation. The biotechnological advances in the field of genomics, proteomics and, metabolomics have opened new perspectives on the use of extremolytes in the treatment of diseases. Therefore, it is important to study the therapeutic and industrial potential of these Microorganisms.

Methods : This review article aims to discuss the defensive mechanisms, therapeutic and industrial implications, opportunities and challenges associated with radiation-resistant microorganisms. PubMed, Ovid Medline, and Embase were the sources of research in this article.

Results : Radiation resistance in extremophiles includes several strategies such as scavenging of free radicals, limitation of ROS production, efficient DNA repair, Synthesis of pigment and protection of proteins against oxidation. The compounds that have been extracted from extremophiles including, melanin, bacterioruberin, scytonemin, sphaerophorin, and ectoine are widely used in the production of anticancer drugs, cell-cycle-blocking agents, antioxidants and sunscreens. Also, extremophiles as a microfactories have the ability of Bioremediation of radioactive waste. Extraction and Purification of extremolytes, optimization of production efficiency and economic profitability are the challenges in this field.

Conclusion : Extremophiles have great potential in the pharmaceutical industry, biotechnology and, bioremediation of toxic and radioactive compounds. However, increased research efforts need to be made for evaluating the unique characteristic of radioresistant extremophiles.

Keywords : Ionization radiation, Microorganisms, Extremophiles, Extremolytes

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P7-125: Use of touch-down polymerase chain reaction to enhance the sensitivity of Brucella melitensis detection in raw milk

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Background and Aim : Brucellosis is a highly contagious bacterial zoonotic infectious disease which severely affects the public health and economic features of the endemic and non-endemic countries. The aim of this study assessed the potential of using the touch-down polymerase chain reaction (TD-PCR) compared with the conventional PCR and culture methods in order to detect Brucella melitensis (B. melitensis) in raw milk.

Methods : In the present study, 100 samples of raw milk obtained from 55 sheep and 45 goats were first cultured and then the DNA of each milk sample was extracted with a Blood Genomic DNA Extraction Mini Kit and evaluated using conventional PCR and TD-PCR methods. To this end, the primers were derived from the omp31 element of the Brucella genome.

Results : In addition, nine isolates of B. melitensis were identified using the culture method. No positive cases were found in sediment samples while the testing of the fatty tap layer by conventional PCR and TD-PCR revealed 6 and 16 positive samples, respectively. Based on the survey of the limit of detection by TD-PCR and conventional PCR, TD protocol had the detection threshold three logs higher than the conventional protocol under the experimental condition.

Conclusion : The developed protocol in this study was highly sensitive and fast. Thus, this TD-PCR protocol could detect a very low number of bacteria in the milk samples. To the best of our knowledge, this is the first report on the use of a TD-PCR assay for the identification of B. melitensis in raw milk.

Keywords : Brucellosis, TD-PCR, Conventional PCR, B. melitensis, omp31

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P8-130: Evaluation of Brucella melitensis MLVA Genotyping for sheep and goats Milk in Iran.

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Background and Aim : In Iran brucellosis is an endemic disease characterized by high infection rate in both humans and animals. Overall, data on the epidemiological situation of brucellosis in the country are limited. The aim of this study was to evaluate MLVA (multiple-locus variable-number tandem repeat (VNTR) analysis) for diagnostic and epidemiological use in animal brucellosis.

Methods : Isolates of Brucella melitensis (B. melitensis) collected in sheep and goat milk samples from six provinces of Iran. To identify B. melitensis biovars, omp2a and omp2b genes was amplified by TD-PCR, and PCR products digested with PstI and HinfI restriction enzymes. Genotyping was performed using MLVA-8 and MLVA-11, panel 1 for species identification and MLVA-16 panels 2A and 2B for further subspecies differentiation.

Results : PCR-RFLP analysis confirmed the 64 strains isolated as belonging to B. melitensis biovar 1 and single strain being a B. melitensis biovar 2. Using panel 1 (MLVA-8) two genotypes were observed namely genotype 47 and genotype 63. The genotypes 47 belonged to the American group and genotype 63 belonged to East Mediterranean group.And using the combination of panels 1 and 2A loci (MLVA-11), five genotypes were obtained while using the complete panels 1, 2A and 2B (MLVA-16), 25 genotypes were obtained.

Conclusion : This study showed that the prevalence of B. melitensis bv. 1 was the biovar most frequently isolated in small ruminants. Also representing the first MLVA typing results of animal Brucella isolates from Iran, indicated that B. melitensis isolates were most closely related to the the isolates included in the American group.

Keywords : MLVA, RFLP, B. melitensis, sheep, goat, Milk

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P9-167: The prevalence of NetB and TpeL genes in Clostridium perfringens type A isolated from Iranian animals

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Background and Aim : Clostridium perfringens is anaerobic and Gram-positive bacteria, which are found in the intestinal tract of mammals and birds. C. perfringens causes different disease in humans and animals including enterotoxaemia, lamb dysentery, avian necrotic enteritis, and neonatal haemorrhage due to their major and minor toxins. The aim of this study was to evaluate the prevalence of NetB and TpeL genes in C. perfringens type A among Iranian isolates.

Methods : In total, 61 archive isolates obtained from intestinal and feces samples (sheep, cattle, calf, goat and hen suspected to clostridial disease) all over the country, were subjected for detection by traditional test (microbiological and biochemical tests). Then, isolates were evaluated using polymerase chain reaction (PCR) to diagnostic molecular of CPA, NetB and TpeL genes. C. perfringens type B, C, D and C. septicum were included as the reference strains.

Results : In bacterial culture 27 out of 61 isolates were tested positive. C. perfringens was detected in all isolates by microbiological and biochemical tests. Genotyping results showed all isolates belonged to C. perfringens type A. Eighteen and sixteen isolates (66.66% and 59.2%) were positive for NetB and TpeL genes respectively.

Conclusion : The results indicate that the role of NetB and TpeL genes in pathogenesis and also needs to be further investigated.

Keywords : Clostridium perfringens, PCR, biochemical tests, genotyping, NetB, TpeL

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P10-231: Identification and study of vaginal Infectious fungi using Pap smear test

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Background and Aim : Vaginal and cervix fungal infections are one of the most important health problems of women all over the world. Uterus fungal infection also is one of the common problems of women of fertility age.

Methods : Several tests are using today for identification of vaginal and uterus infections. Investigation of cells during Pap smear test, beside its diagnostic value for cancerous alterations, would be helpful for identification of other alterations such as inflammation (vaginitis), fungal infections and also some sexual transmitted diseases.

Results : Such infections could happen due to the presence of a wide range of microbial agents such as pathogenic bacteria and fungi. Maximum incidents of vaginitis have been recorded due to infection by the three organisms of Candida albicans, Gardnrella vaginalis and Trichomonas vaginalis.

Conclusion : It has been clear that the occurrence of frequent infections of vagina could affect the cells for cancerous alterations. Due to the importance of the subject, the present manuscript will introduce the infectious agents of the vagina and the cellular alterations of the region.

Keywords : Vaginitis, Pap smear, Candida albicans

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P11-234: In-vitro antibacterial activity of Eucalyptus extract against clinical isolates of Acinetobacter baumanni

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Background and Aim : Acinetobacter baumannii are causes of nosocomial-acquired infections that are related to the biofilms forming talent of this microbe. The immediacy of the drug resistance challenge demanded important treatment, among that was the explore for new antibacterial agents. From nature, that harbors plants, a lot of have been used for therapeutic targets. The goal was to In-vitro antibacterial activity of Eucalyptus extract against clinical isolates of A. baumanni.

Methods : A total of 39 clinical isolates of A. baumannii were provided by streak on MacConkey agar, Blood agar, EMB, Gram staining, and different microbiology identification tests. In-vitro antibacterial activities of pathogens were analyzed by typically used microbroth dilution method.

Results : Isolates from different departments Shahid Beheshti Hospital were included: 20 (51.3 %) intensive care units, 9 (23 %) general surgery, 7 (18%) emergency, and 3 (7.7%) pediatric. Samples collected of A. baumannii were isolated from patients; 20 (51.3 %) males and 19 (48.7 %) females. Outcomes have gotten considering that Eucalyptus extract was active for isolates bacteria with minimal inhibitory concentration ranging from 128 to 256 mg/ mL.

Conclusion : According to important antimicrobail property of aqueous extracts of Eucalyptus on pathogenic microorganism, which supply to the expansion of various types of infectious and nosocomial infection. This extract makes use of natural products.

Keywords : Eucalyptus extract, Acinetobacter baumannii, Method, Kashan

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P12-248: Comparison of four Invasive Methods for Diagnosis of Helicobacter pylori Infection: Fluorescence in Situ Hybridization, Histology, Culture, Rapid Urease Test

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Background and Aim : Helicobacter pylori (H.pylori) is one of the most prevalent pathogenic bacteria globally. Choosing reliable methods will lead to a correct diagnosis of infection. The aim of this study was to evaluate four H.pylori infection diagnostic methods from dispeptic patients.

Methods : In this descriptive cross-sectional study, 165 antrum biopsy specimens were obtained from dyspeptic patients referred to the endoscopy unit of Shariati Hospital, Isfahan, Iran, and collected in 2018. Four diagnostic methods of H. pylori, namely histology, culture, rapid urease test (RUT) and fluorescence in situ hybridisation (FISH) were tested for each patient. The gold standard of the study was for positive confirming one of the two tests, RUT or histology.

Results : According to the predefined criteria, the prevalence of H.pylori infection was 55.2%. Among the four diagnostic methods, the most sensitive ones were FISH and RUT, respectively (95.7% and 92.3%). Despite the high specificity of the histological examination (100%), its NPV was lower than the other methods (88%). The kappa coefficient of agreement between the gold standard and the tested techniques was perfect. ($P < 0.001$)

Conclusion : FISH and histology are recommended in combination with diagnosis of H.pylori infection, which can manage its complications in the most optimal manner.

Keywords : Helicobacter pylori; Fluorescence In Situ Hybridization; Histology; Culture; rapid urease test

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P13-256: Molecular detection of Theileria annulata in dairy cattle of Qazvin province, Iran

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Background and Aim : Theileria annulata is one of the most important parasitic diseases in Iran which causes severe economic loss such as the reduction of dairy products. Diagnosis of theileriosis is based on microscpic and clinical examination. Nowadays, molecular detection methods are used for detection such as polymerase chain reactions (PCR) using specific primers. Despite the existence of bovine theileriosis in Iran, no comprehensive study has been done in this matter. So, the aim of this study was detection the cases of T. annulata in dairy cattle from Qazvin province.

Methods : A total of 68 dairy cattle with clinical symptoms were taken from blood samples. The blood samples were transported to the laboratory immediately. Then the blood smears were prepared and stained with Giemsa method. Positive samples were incorporated for molecular detection. So, DNA of blood was extracted using phenol-chloroform method and performed PCR using specific primers of Tams1 and 18SrRNA genes. Vaccine strain of bovine theileriosis and sterile buffer was used as the positive and negative control, respectively. Then, the PCR product of one sample was sent for direct sequencing.

Results : The result showed the ring form of Theileria infection in 28 (41.18%) of blood smears. The PCR result indicated that all of the samples were infected with T. annulata. BLAST analyses based on the 18S rRNA gene sequence of the Iranian isolate determined the 99.1% identity.

Conclusion : Based on the obtained results, it is concluded that T.annulata had a high frequency in dairy cattle of Qazvin province.

Keywords : Molecular detection, Theileria, annulata, Qazvin, dairy cattle

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P14-288: Evaluation of the prevalence of Theileria annulata, Babesia and Anaplasma in cattle Alborz province by direct examination and PCR

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Background and Aim : Babesia and Theileria are intraerythrocytic parasites of the phylum Apicomplexa which infect wild and domestic animals. Detection of these pathogens is important in an epidemiological study. In spite of the existence of these pathogens in Iran, little study has been done up to now. So, the aim of this study was the evaluation of the prevalence of Theileria, Anaplasma and Babesia and in cattle Alborz province using the conventional and molecular method.

Methods : A total of 130 cattle were taken blood samples and transported to the laboratory immediately. Then the blood smears were observed with Giemsa staining. Positive samples were confirmed using PCR. So, DNA of blood was extracted using the phenol-chloroform method and performed PCR using specific primers of Tams1 and 18SrRNA genes for confirmation of Theileria and Anaplasma respectively. Vaccine strain of bovine theileriosis and the sterile buffer was used as a positive and negative control, respectively.

Results : The result showed the Theileria and Anaplasma infection in 7 (5.38%) and 5 (3.85%) of blood smears respectively. Also, one blood sample simultaneous has been infected by Anaplasma and Theileria. But there is no case of infection with Babesia. Based on the PCR assays, all of the 11 blood samples showed the predicted PCR fragments sizes for Theileria and Anaplasma in presence of the two primer pairs, 871 and 577bp for Tams1 and 18SrRNA respectively.

Conclusion : Based on the results, T.annulata and Anaplasma have been found in cattle of Alborz province. But no cases of Babesia have been observed in cattle.

Keywords : PCR, Theileria annulata, Babesia, Anaplasma, Alborz, cattle

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P15-310: Design of Multi-epitope based Vaccine on N-Ag of 2019 novel coronavirus (SARS-CoV-2) by Immunoinformatics Methods

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Background and Aim : Coronaviridae is a family of enveloped, positive-sense, single-stranded RNA viruses which can infect animals and humans and has caused a large number of deaths with thousands of confirmed cases worldwide. People of all ages can be infected by the 2019 novel coronavirus. Older people, and people with pre-existing medical conditions appear to be more vulnerable to becoming severely ill with the virus. As regards, there is no drug for treatment, it seems to be the most effective way to prevent and treat vaccinations. The aim of this study was design of epitope-based vaccine against SARS-CoV-2 in based on In silico analysis to determine the most conserved B and T-cell epitopes of N protein that could be able to stimulate a remarkable immune response.

Methods : Sequence of N protein was collected from protein databases (NCBI & Uniprot) and analyzed by In silico tools (IEDB – ABCpred) for recognizing the most conserved immunogenic epitopes to trigger the T and B cell immune response. These suitable epitopes were evaluated in terms of toxicity and allergenicity and immunogenicity with used of Toxinpred and AllerTop and Vaxigen servers, respectively. Finally, the chimeric protein as a novel epitope-based vaccine was designed and assayed in terms of 2D and 3D structures by Prabi garland & Swiss-model servers, respectively.

Results : In base of Immunoinformatics study was predicted the most immunogenic epitopes (FTALTQHGK) and (VPINTNSSPDDQIGY) to stimulate TCD8 and TCD4 respectively, by IEDB server, also was predicted a suitable epitope (INTNSSPDDQIGYY) by ABCpred server, to motivate B cells. These peptides were bound to the largest number of alleles. Also they weren't toxigenic and allergenic epitopes that were investigated by Toxinpred and AllerTop servers. Designed chimeric protein was suitable in terms of physicochemical properties and stability.

Conclusion : Immunoinformatics study showed that, predicted epitopes were with high efficiency and stability that can be used as a therapeutic peptide vaccine to be selected for prevention of SARS-CoV-2 infection.

Keywords : SARS-CoV-2 - Immunoinformatics - Vaccine

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P16-333: Capsular Typing by PCR Method for Streptococcus agalactiae Isolated from pregnant Women in Yasuj , Iran

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Background and Aim : Background: Group B Streptococcus (GBS) is major cause of serious life threatening infections including sepsis, pneumonia and meningitis in neonates as well as in pregnant women. Capsular polysaccharide typing is significant and essential for epidemiological studies of GBS. Objectives: The aim of the current study was to differentiate genotypes of GBS clinical isolates based on the polymerase chain reaction (PCR) to acquire information about distribution of GBS types in Yasuj, Iran.

Methods : : In this experimental study we used 37 GBS clinical strains isolated from vaginal swabs (n = 18) and Rectal swabs (n = 19) of patients, who had referred to private clinic centers during one year from June 2017 to June 2018 in Yasuj, Iran, for genotyping using PCR assay.

Results : : Among the 37 GBS isolates examined, all capsular types except for III,VI, VII and VIII were found. Types II and V were the most prevalent types with a sum of 26 isolates (70.27%). Type V was the predominant type with 19 (51.35%) isolates, followed by type II (9 isolates; 24.32%), type I (2 isolates; 5.4%) .

Conclusion : The results of the current study demonstrated that type V is the predominant type in Yasuj, followed by types II, type I respectively. Use of the molecular serotyping (MS) method such as PCR assay as an alternative to conventional serotyping (CS) method leads to accurate, sensitive, specific, and fast typing of GBS isolates.

Keywords : Capsular Typing , Streptococcus agalactiae , GBS , Pregnant Women

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P17-364: Development, optimization, and validation of an in-house Dot-ELISA rapid test based on SAG1 and GRA7 proteins for serological detection of Toxoplasma gondii infections

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Background and Aim : The aim of the present study was to develop a simple, portable, and rapid assay for serodiagnosis of toxoplasmosis based on recombinant Toxoplasma gondii (T. gondii) SAG1 (rSAG1) and GRA7 (rGRA7) proteins.

Methods : The rSAG1 and rGRA7 proteins were expressed in Escherichia coli (E. coli) and purified in a single step by immobilized metal ion affinity chromatography. The immunoreactivity of the recombinant antigens was tested in an in-house IgG and IgM Dot enzyme-linked immunosorbent assay (Dot-ELISA) for potential use in serodiagnosis of T. gondii infection.

Results : Results from the comparison of in-house rSAG1-Dot-ELISA with ELISA for the detection of anti-Toxoplasma IgG and IgM include sensitivity of 83.7% and 81.2%, specificity of 90.2% and 89.3%, positive predictive values of 85.9% and 68.4%, and negative predictive values of 88.6% and 94.3%, respectively. Sensitivity of 66.2%, specificity of 81.2%, positive predictive values of 71.6%, and negative predictive values of 77.1% were concluded from in-house IgG rGRA7-Dot-ELISA. The sensitivity and specificity of IgM rGRA7-Dot-ELISA included 87.5% and 83.9%, respectively. Sensitivity and specificity of in-house Dot-ELISA for a combination of rSAG1 and rGRA7 included 87.5% and 91.1% for IgG and IgM, respectively. Sensitivity and specificity of a combination of rSAG1 and rGRA7 for the detection of IgM in suspected sera to acute toxoplasmosis were higher than those for the detection of IgG in sera with chronic infections (90.6% and 92% instead of 86.2% and 91.6%, respectively).

Conclusion : The highlighted parameters of combined recombinant proteins were more significant than those of single recombinant proteins in in-house Dot-ELISA. These data suggest that the in-house Dot-ELISA based on rSAG1 and rGRA7 combination is a promising diagnostic tool with a similar sensitivity to the native antigens of T. gondii, which can be used for the serodiagnosis of toxoplasmosis in fields as well as less equipped laboratories.

Keywords : Toxoplasma gondii RH strain, in-house Dot-ELISA, rSAG1, rGRA7, soluble tachyzoite antigen (STAg), recombinant proteins

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P18-369: The first report of identification of clinical isolates of Alcaligenes xylosoxidans and Alcaligenes faecalis by phenotypic and genetic methods in Iran

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Background and Aim : Alcaligenes is a non-fermentative Gram-negative bacillus which as an opportunistic pathogen causes nosocomial infections, including urinary tract infections, pneumonia, and sepsis, and may be confused with Pseudomonas species. Diagnosis of Alcaligenes infections in hospital medical diagnostic laboratories is usually done by phenotypic methods and biochemical tests. However, due to possible errors and similarities with Pseudomonas, accurate diagnosis with phenotypic tests is not sufficient, and molecular methods for accurately identifying are more effective.

Methods : In a six months descriptive-analytical study, we analyzed all 36 isolates collected from hospitalized patients which were phenotypically identified as Alcaligenes. Using the PCR method and tracking AX and 77F-r genes, we identified A. xylosoxidans and A. faecalis respectively, and the antibiotic resistance of each isolate was distinguished by the disc diffusion method.

Results : Of 36 samples of Alcaligenes identified by phenotypic methods and biochemical tests, only 13 (36.11%) were A. xylosoxidans and 3 (8.33%) were A. faecalis. among A. xylosoxidans the highest susceptibility (92.3%) was seen to Cephalosporin and the highest resistance (76.92%) was seen against Ciprofloxacin. Among A. faecalis isolates the most susceptibility (100%) was seen to Ceftazidime, Piperacillin/Tazobactam, Imipenem, Meropenem, and Cefepime and the most resistance (66.66%) was against Gentamicin and Ceftriaxone.

Conclusion : Since Alcaligenes species are a known cause of nosocomial infections with increasing prevalence in recent years, it seems that with phenotypic methods and biochemical tests, there is a possibility of error in their diagnosis, so using the PCR method, each species can be determined more accurately.

Keywords : Alcaligenes, A. xylosoxidans, A. faecalis, molecular detection, PCR method

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P19-374: Seroprevalence of Cytomegalovirus Antibodies by Electrochemiluminescence Method in Young Women Referred to the Clinical Laboratory, Sanandaj, Iran

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Background and Aim : Maternal primary and recurrent infection of cytomegalovirus (CMV) may be transmitted to the fetus during pregnancy and may have complications such as death or growth, along with the development retardation of the fetus and infant. The aim of this study was to determine the prevalence of immunoglobulin G (IgG) and immunoglobulin M (IgM) antibodies against CMV in young women, Sanandaj, Iran.

Methods : To this end, 90 women (15-40 years old) referring to a clinical laboratory were randomly selected and announced their informed consent to participate in this cross-sectional study. Demographic information and women's data were collected, including pregnancy, history of abortion, and history of blood transfusion. Then, women's sera were measured for CMV IgG and IgM antibodies using the electrochemiluminescence technique. Finally, the data were analyzed by SPSS statistical software.

Results : The prevalence of IgG and IgM antibodies against CMV in women was 92.2% (95% CI = 86.5-97.8) and 0%, respectively. In addition, the average CMV IgG antibody level was about 137.52 ± 85.215 SD IU/mL. The results revealed a significant statistical association between IgG antibody and pregnancy (P value = 0.012) while there was no association between CMV IgG antibody and other demographic data.

Conclusion : In general, high percentages of women had CMV IgG antibody whereas 7.8% of them were susceptible. They are expected to acquire CMV primary infection, and therefore, the screening of antibodies to CMV is suggested for prenatal care.

Keywords : Seroprevalence, Cytomegalovirus, Electrochemiluminescence, Women, Sanandaj, Iran

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P20-381: Evaluation of Anticancer Activity of Enterocin A-Colicin E1 Fusion peptide in Gastric Cancer Cell

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Background and Aim : Cancer is one of the most causes of deaths all over the world, although improvements in its treatment and recognition. Due to the limitations of common anticancer methods, including surgery, chemotherapy and radiotherapy, attention has been drawn to other anticancer compounds, especially natural peptides such as bacteriocins.

Methods : In this study, we used a combination of two bacteriocins, colicin E1 and enterocin A, against AGS gastric cancer cell lines. After conducting bioinformatics design and confirming the expression of the desired peptide with Western blot, in the next step, we applied MTT assay, real-time PCR and flow cytometry tests to investigate the anticancer properties of fusion peptide. This is the first report that the cell growth inhibitory activity of the enterocin A in combination with colicin E1 against AGS human cancer cells.

Results : The results of this study showed that this fusion peptide at a concentration of 60 µg/ml and 24 hours was able to kill half of the tested cancer cells, and treatment of the cells with this concentration increased the expression of bax and caspase 3 genes and reduced the expression of bacl-2 in 24 hours. Flow cytometry analysis of annexin V-FITC/propidium iodide results also showed that our peptide was able to induce apoptosis in treated cells compared with control.

Conclusion : Taken together, enterocin A-colicin E1 (ent A-col E1) can be considered as a good candidate for anticancer therapies.

Keywords : Bacteriocins; Enterocin A; Colicin E1; Anticancer activity; Apoptosis

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P21-382: Evaluation of antibacterial activity of enterocin A-colicin E1 fusion peptide

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Background and Aim : Bacterial resistance to most common antibiotics is a harbinger of the requirement to detect novel anti-infective, antimicrobials agents, and increase innovative strategies to struggle them. Numerous bacteria produce small peptides with antimicrobial activities called bacteriocin. This study aimed to investigate the antibacterial properties of the fusion protein of Enterocin A and Colicin E1 modified against pathogens.

Methods : Analysis of recombinant bacteriocin Enterocin A and Colicin E1 (ent A-col E1) was done to assay the stability and antibacterial activity of this fusion protein. The pET-22b vector was employed to express the coding sequence of the ent A-col E1 peptide in E. coli BL21 (DE3). Minimum inhibitory concentration (MIC), disk diffusion, and time-kill tests were performed to evaluate the antibacterial activity of the ent A-col E1 against Pseudomonas aeruginosa (ATCC 9027), Escherichia coli (ATCC 10536), Enterococcus faecalis (ATCC 29212), and Staphylococcus aureus (ATCC 33591).

Results : The suggested recombinant peptide had good antibacterial activity against both Gram-negative and Gram-positive pathogens. It has also good stability at various temperatures, pH levels, and salt concentrations.

Conclusion : Because bacteriocins are harmless compounds, they can be recommended as therapeutic or preventive supplements to control pathogens. According to the obtained results, the ent A-col E1 peptide can serve as an efficient antibacterial compound to treat or prevent bacterial infections.

Keywords : Bacteriocins, Fusion peptide, Enterocin A, Colicin E1, Antibacterial activity

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P22-412: Associations of a NLRP3 rs10754558 polymorphism with Helicobacter pylori-infected patients with gastritis and peptic ulcer disease

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Background and Aim : Diseases caused by Helicobacter pylori infection, including gastritis and gastric ulcer, can be harmful to epithelial cells in gastric mucosa. Furthermore, pro-inflammatory cytokines can affect the severity of some diseases caused by H. pylori infection. NLRP3 inflammasome can detect H. pylori and trigger caspase-1 activation and thus IL-1β release in the stomach. Since genetic variations such as polymorphisms might be responsible for the expression of genes, the present research aimed to explore the effect of NLRP3 rs10754558 polymorphism in pathogenesis of H. pylori infection.

Methods : genotyping was performed on 464 Iranian patients (300 patients infected with H. pylori and 164 patients uninfected with H. pylori) using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP). Cytokine mRNA and protein expression were evaluated in patients infected with different genotypes of NLRP3 rs10754558 using real time-PCR and western blotting, respectively.

Results : The NLRP3 rs10754558 gene polymorphism was not associated with H. pylori infection or diseases caused by this bacterium. It was found that the IL-1β level in infected patients with gastritis was more than in the uninfected individuals. Moreover, no relation was found between these single nucleotide polymorphisms (SNP) and cytokine expression in H. pylori infected subjects. The findings of this study show that NLRP3 rs10754558 polymorphism may be related to the severity of acute inflammation in these patients.

Conclusion : Our findings show that NLRP3 rs10754558 polymorphism may be involved in the severity of some diseases caused by H. pylori infection.

Keywords : Helicobacter pylori, gastritis, peptic ulcer disease, polymorphism, NLRP3 rs10754558.

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P23-415: Investigating The Associations of Between Gene Polymorphism NLRP3 rs10754558 and IL-18 Expression Level In Patients With Ulcers And Gastritis Caused By Helicobacter pylori

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Background and Aim : Helicobacter pylori (H. pylori) is one of the most common bacterial pathogens in humans. The bacterium has been colonized in the stomachs of at least half of the world's population. H. pylori infection is associated with gastrointestinal ulcers, inflammation, and gastric cancer. Several cytokines are secreted from these inflammatory cells, resulting in localized inflammation, which spreads and persists. Interleukin-18 (IL-18) is one of the most important cytokines associated with inflammation of gastric mucosal tissue.The aim of this study was to investigate the expression of IL-18 mRNA in patients with gastritis with H. pylori infection compared to patients with gastric inflammation without H. pylori infection.

Methods : In this case-control study, biopsies were collected from 464 patients with indigestion referred to the endoscopic ward. The genotype of NLRP3 rs10754558 polymorphism was analyzed by RFLP-PCR. Mucosal expression level of IL-18 was measured by Real-Time PCR. The expression of this cytokine in both infected and non-infected groups with H. pylori were statistically analyzed.

Results : In current study, IL-18 mRNA expression in biopsy of infected H. pylori patients was significantly higher than non-infected individuals but there was no significant relationship between them.

Conclusion : IL-18 may play an important role in the innate immune response to inflammation and the progression of the Th1 response to H. pylori infection, and play an major role in multiple different clinical outcomes.

Keywords : H. pylori, IL-18, Polymorphism, NLRP3, Gastritis

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P24-427: Current applications of the microbiome engineering and its future

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Background and Aim : In the human body there are many microorganisms with a variable genetic content. These microorganisms play an important role in metabolism, homeostasis, the immune system and in general human health (1). Over millions of years of evolution, different microorganisms adapted to each other, and different environmental communities formed on Earth. Microbial communities, known as microbiome, can exist in living or non-living environments, such as the human body, animals, and plants, as well as in soil, oceans, and air (2). The term microbiome refers to all microorganisms (archaea bacteria, eukaryotes and viruses), their genome and environmental conditions, and the term "biome" it is an environmental community it has a special climate, plants and animals where they live. More precisely, the microbiome is a combination of metagenomic, metabolomic, metatranscriptomic, metaproteomic that is described with comprehensive environmental or clinical information. The main purpose of microbiome engineering is mostly human microbiome and is now used in the treatment of diseases such as Clostridium difficile, inflammatory bowel disease, obesity, etc (3).

Methods : The research data in this thesis are drawn from four main sources Web of science google scholar, Pubmed, Scopus. Articles on microbiome have been selected, some articles from 2010 to 2019 have been reviewed, and these studies have focused on the interaction of bacteria and some fungi.

Results : The Human Microbiome Project (HMP) was launched around the world with the aim of understanding its role and impact on human life, and the term microbiome was used by Joasholderberg in 2001 (2, 4). The widespread impacts of the microbiome on the ecosystem and the increased attention to microbiome recognition are factors contributing to the creation of microbiome engineering science, and recent advances in genome sequencing and metagenomic science have made microbiome analysis apart from cultivation process (2).

Conclusion : Although microbiome engineering is a relatively new field, there has been much progress in recent years that can be an important strategy for improving human health by continual effort and microbial manipulation as well as by the changing microbial population (2).

Keywords : Microbiome, healthy human microbiome, Microbiome engineering, Microbiota

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P25-2: Evaluation of effective antibiotics against extend-spectrum beta-lactamase (ESBLs) enzymes producing Enterobacteriaceae in outpatients referred to Nobel Laboratory, Isfahan 2017-2019

ali ajami[1] , ensieh kheirolahi[1] , dariush shokri[1] *

1. *nobel laboratory*

Background and Aim : Introduction: Extended-spectrum beta-lactamases enzymes (ESBLs) cause resistance to many beta-lactams whose prevalence among Enterobacteriaceae is a serious threat to the successful treatment of infections with these enzymes and limits effective antibiotics. The aim of this study was to evaluate the frequency of ESBLs enzymes in Enterobacteriaceae family bacteria in outpatients referred to Isfahan Nobel Laboratory during 2017-2019 and to introduce antibiotics effective on them.

Methods : methods: After detection of Enterobacteriaceae family, ESBLs enzymes with initial resistance to ceftazidime and ceftriaxone discs were examined by confirmatory tests using clavulanic acid. On the other hand, in order to find the most effective antibiotics, antibiotic susceptibility testing was performed with 14 different antibiotics.

Results : Results: A total of 580 strains of Escherichia coli, 72 strains of Enterobacter, 362 Klebsiella, 22 strains of Serratia and 35 strains of Citrobacter were isolated, with ESBL enzymes frequency of 30, 38, 45, 52 and 56%, respectively. The most effective antibiotics in all ESBL-containing bacteria were imipenem, meropenem, fosfomycin, amikacin and nitrofurantoin.

Conclusion : Discussion & Conclusion: The rate of ESBL enzymes in outpatients was high, which is a cause for concern about their spread in the community. Citrobacter strains also had higher levels of these enzymes. Both antibiotics fosfomycin and nitrofurantoin are recommended as the best treatment options for these outpatient patients.

Keywords : beta-lactamase,Enterobacteriaceae ,antibiotics,resistance

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P26-8: CP and CO Antimicrobial Susceptibility Patterns of Pseudomonas aeruginosa Isolated from Hospitalized patients

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Background and Aim : In examinations of clinical samples in hospitals, continuous surveillance of antibiotic resistant patterns is a significant method for successful patient management. This survey aimed to evaluate drug CP and CO resistant patterns of Pseudomonas aeruginosa bacterial isolates of patients from educational hospitals of Urmia City at the Urmia University of Medical Sciences, Iran.

Methods : A total of 100 clinical isolates of Pseudomonas aeruginosa were assembled from urine, wound, trachea, eye swab… etc. then evaluated by standard tests and antibiotic susceptibility was determined by the Kirby-Bauer disc diffusion method.

Results : Among culture positive patients, 100 bacterial isolates were recovered, as Pseudomonas aeruginosa. Of the Pseudomonas aeruginosa isolates, 63% were from urine cultures, 10% from sputum, 8% from wound and 6% from tracheal aspirates and remained cases from other body aspirates. The result shows higher resistance of Pseudomonas aeruginosa isolates toward CP and CO. However, in compared two examined antibiotic there was more susceptible pattern toward CO versus CP.

Conclusion : Overall, it is suggested that similar studies should be conducted in various hospitals to obtain certain antimicrobial resistance pattern. In addition, recommending precise medications is important to avoid further resistant toward bacteria including Pseudomonas aeruginosa.

Keywords : antibiotic resistant patterns,Pseudomonas aeruginosa ,antibiotic

P27-26: Detection of pathogenicity islands encoding the P fimbriae from E.coli strains in patients with urinary tract infections

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Background and Aim : Urinary tract infection is a common term used for infections which may involve any part of urinary tract especially ureters, bladder, urethra and kidney. Moreover, urinary tract can divide into lower and upper tract. Among different kinds of bacteria, E.coli is the predominant uropathogen isolated in uncomplicated UTIs in children and adults. The UPEC strains consist of blocks of DNA, termed as a pathogenicity island (PAIs) which can contribute to their virulence. Three different PCR assays were developed to detect three various PAIs in 195 E.coli isolate. Among 195 isolates, 69% of isolates (135 isolates) carried PAI I CFT073 and from these isolates 27 of them were boy and 108 of them were girl. In addition, 39% of these isolates (76 isolate) contain PAI II CFT073 and among these numbers 15 isolates were boy and 61 were girl. It is important to note that PAI I j 96 was not detected in any isolates.

Methods : Bacterial isolates ESBL Confirmation Antibiotic Tests DNA Extraction and PCR

Results : Therefore, the results were submitted after loading the PCR products in the agarose gel electrophoresis. Then, the final results were analyzed by SPSS software.

Conclusion : Isolation and detection of ESBL producing strains are essential for the selection of the most effective antibiotic for treatment and also infection control. Moreover, the emphasized pathogenicity islands in UPEC strains could be uncommon in urinary tract and when they present can be highly virulent so further in-vivo studies are needed to fully establish and clarify this hypothesis.

Keywords : Pathogenicity islands; E.coli; Fimbriae; Urinary tract infection; Antibiotics Resistance

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P28-27: Multi-drug Resistant Citrobacter freundii Isolates in a Burn Hospital in Northeast of Iran: A Single-Center Cross-sectional Study

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Background and Aim : Multi-drug resistant (MDR) Citrobacter freundii (C. freundii) as a causative agent of nosocomial infections is a health threat, especially in hospitals. This study was conducted to determine the prevalence of MDR C. freundii, considering isolation sites and a variety of utilized antibiotics.

Methods : In this cross-sectional study, the clinical samples of C. freundii strains were collected and screened using traditional bacteriological tests in Zareh Hospital, Sari City, Iran, during 2016-2017. We used disk diffusion methods to assess the susceptibility patterns of isolates according to the Clinical Laboratory Standard Institute (CLSI) guidelines.

Results : Out of 3248 clinical samples, C. freundii strains were detected in 109 samples (32.1% females and 67.9% males). Susceptibility tests indicated that 89 isolates (81.65%) were MDR strains. Frequencies of MDR C. freundii strains were higher in the Behavioral Intensive Care Unit (BICU) (37.61%) and restoration ward (29.35%) compared with other hospital wards.

Conclusion : Considering the MDR C. freundii strains detected from burn hospital wards, it is necessary to implement prevention criteria for their eradication from burn hospitals. The results indicate the urgent need to design more practical methods for controlling infection in hospital wards.

Keywords : Citrobacter freundii , MDR ,antibiotic resistance

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P29-31: High frequency of integrons and efflux pump in Uropathogenic Escherichia coli isolated from Iranian kidney and non-kidney transplant patients

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Background and Aim : Due to the important role of integrons and efflux pumps in increasing drug resistance, the aim of this study was to investigate the frequency of integrons and efflux pump in UPEC isolated from Iranian KTPs and non-KTP.

Methods : A case-control study was performed on 111 UPEC isolates obtained from 46 KTPs (group A) and 65 non-KTP (group B) who were diagnosed with a UPEC-associated UTI between June 2019 to October 2019 at three laboratory center and two nephrology private clinic in Isfahan, Iran. These isolates were further confirmed as E. coli based on phenotyping and genotyping test. Antimicrobial susceptibility was determined using the disc diffusion method, and the presence of integron and efflux pump genes was detected by polymerase chain reaction.

Results : In this study, a total of 111 confirmed UPEC were isolated, in group A, 69.6% and 30.4% isolates were collected from female and male, while 69.2% and 30.8% isolates were obtained from female and male in group B, respectively. The frequency of integron genes was as follows: 60.9% and 28.3% isolates of group A and 47.7% and 21.6% isolates of group B carried int1 and int2, respectively. In both groups with int1-positive, the highest resistance was to co-trimoxazole with (89.3%) and (67.7%), respectively. The lowest antibiotic resistance rates in groups A and B with int1-positive were seen against piperacillin/tazobactam (14.3%) and nitrofurantoin (9.7%), respectively. All three genes acrA, acrB, and tolC were present simultaneously in 68.5% (76/111) isolates, 71.8% (33/46) isolates of group A, and 66.2% (43/65) isolates of group B.

Conclusion : Our data indicated a significant relationship between the presence of integrons and several antibiotics such as co-trimoxazole and cefixime. Furthermore, RND efflux pumps such as AcrAB-TolC play an important role in gram-negative bacteria in the removal of toxic substances and antibiotics.

Keywords : Urinary tract infection, Escherichia coli, kidney transplantation, Integron, Efflux pump

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P30-40: Antibacterial effects of alcoholic extracts of Caracrol, thyme and Ferulago

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Background and Aim : Background and purpose: Antibiotic resistance of bacteria is one of the most common problems in medical sciences. In this study, the antibacterial effect of alcoholic extract of caracol, thyme and ferulago plants on four bacteria of Escherichia coli pathogen, Klebsiella pneumoniae, Staphylococcus aureus and Streptococcus agalactia was examined under laboratory conditions

Methods : Materials and Methods: In this experimental study, the alcoholic extract of three plants, caracrol, thyme and ferulago, was used. The total extract of the mentioned plants in different concentrations (100 mg / ml, 200, 400, 800) was affected by the method of propagation in agar and tube dilution on Escherichia coli, Klebsiella pneumoniae, Staphylococcus aureus and Streptococcus agalactia. Tetracycline and gentamicin antibiotics were used as positive control and DMSO as negative control, and the minimum inhibitory concentration (MIC) and the minimum lethal concentration (MBC) were determined. One-way analysis of variance and Duncan's test and SAS software were used to compare the mean data.

Results : Results: Based on the results of this study, the alcohol extract of all three dose-dependent plants caused a significant increase in the diameter of the zone , preventing the growth of bacteria, especially gram-positive bacteria, compared with the negative control group P(<0/005) Among the extracts studied, ferulago extract had the greatest inhibitory effect on the growth of S.oureus bacteria.(P<0/05)(25±0/57)

Conclusion : Conclusion: The results of this study showed that all three plants have a growth inhibitory effect on all four bacteria.ferulago extract has more antibacterial activity than other extracts, and Staphylococcus oureus is known to be the most sensitive strain to the extracts used.

Keywords : Keywords: savory, Hollyhocks, ferulago , minimum inhibitory concentration, antibacterial effect

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P31-42: The effect of Wi-Fi electromagnetic waves on on the Antibacterial Susceptibility of some Pathogenic Bacteria

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Background and Aim : Nowadays, the increasing resistance of pathogenic bacteria creates a major problem in public health, and the reason for this problem is the overuse of antibiotics among the people. On the other hand, the use of Wi-Fi modems has increased so much that Wi-Fi-emitted waves can affect eukaryotic and prokaryotic cells. The aim of this study was to investigate the effect of Wi-Fi (2.4 GHz) on changes in antibiotic resistance of pathogenic bacteria P.aeruginosa, E.Coli, S.aureus strains, A.baumani.

Methods : Two plates from each strain(test and controls) were cultured in Muller Hinton agar medium (Oxoid) according to the National Committee for Clinical Laboratory Standards. The test plates were incubated for 24 h with Wi-Fi exposure, and controls were in normal atmosphere incubation (37°C for 24 hours).Then, the inhibition diameters was evaluated using the macroscopic method.

Results : According to the results, after the bacteria were exposed to GHz 2.4 radiofrequency for 24 hours, the diameter of the inhibition zones in P.aeruginosa increased significantly ($P < 0.05$). However, the diameter of the inhibition zones of other bacteria exposed to Wi-Fi did not differ significantly from the control groups.

Conclusion : These results show that Wi-Fi radiation can reduce the sensitivity of P.aeruginosa. Therefore, using this method can be useful in controlling and managing infectious diseases related to this bacterium.

Keywords : Wi-Fi, E.coli, P.aeruginosa, S,aureus, A.baumani, antibacterial Susceptibility.

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P32-45: investigating the prevalence of nosocomial bacterial infections and the bacterial antibiotic resistance pattern in patients admitted to Poursina Hospital in Rasht

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Background and Aim : Controlling nosocomial infections is especially important due to increasing convalescence and death caused by hospital infections. The purpose of this study was to investigate the prevalence of nosocomial bacterial infections and the antibiotic resistance pattern of bacteria in patients admitted to Poursina Hospital in Rasht.

Methods : This study was performed using available data and census methods on all patients with nosocomial infections from February to July 2019 at Poursina Hospital in Rasht, and SPSS 26 software was used for statistical analysis.

Results : Out of 285 patients with positive bacterial culture, 59.3% were male. Six types of bacteria were found, Klebsiella and Pseudomonas were the most prevalent agents of nosocomial infections. The highest infection rate was observed in urine and tracheal intubation. The highest age group with Klebsiella was 36-50 years old. The highest antibiotic resistance was found in 67.0% of men and 67.9% in the 66-80 age group. Klebsiella showed the highest resistance to trimethoprim/sulfamethoxazole (84.1%) and ceftriaxone (83.6%). Klebsiella and Pseudomonas are the main pathogens of nosocomial infections.

Conclusion : Therefore, the incidence of these nosocomial infections can be greatly reduced by using the methods of controlling nosocomial infections. Findings show that improper use of antibiotics, gender, and age can be effective in creating antibiotic resistance. These findings could indicate special attention to the methods of controlling nosocomial infections and help physicians to have better treatment options against bacterial nosocomial infections.

Keywords : nosocomial infections, Klebsiella, Pseudomonas, bacterial culture, antibiotic resistance, Hospital

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P33-46: Investigation of Drug Resistance, Presence of ompA and Oxacillinases Genes in Acinetobacter baumannii Isolated from Guilan Hospitals

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Background and Aim : Acinetobacter baumannii is one of the most important emerging multi drug-resistant bacteria. Several factors are involved in resistance to the drug and its pathogenicity. Of these factors, OmpA and Oxacillinases genes play an important role. The aim of this study was to assess resistance to drugs and also ompA and Oxacillinases genes existence in A. baumannii isolated from clinical sources from Guilan hospitals.

Methods : Clinical samples were collected from clinical sources of Guilan hospitals during the 2017-2018 and the final confirmation were done by using biochemical methods. Then, susceptibilities to antibiotics of different classes were determined by the disc diffusion method, and the presence of ompA and Oxacillinases genes were checked by using the PCR method.

Results : The results show that of 150 clinical samples, 40 (26.66%) of isolates were formed of A. baumannii and mostly showed resistance to different classes of antibiotics. 84.95% of isolates were Multi Drug Resistance (MDR) and 79.53% were Extremely Drug Resistance (XDR). All of them contained ompA and 80% contained Oxacillinases genes.

Conclusion : The presence of multidrug resistance in most isolates, as well as the existence of ompA in all and Oxacillinases genes in 80% samples, can cause bacterial virulence and drug resistance. It seems essential to provide continuous monitoring and determination of antibiotic susceptibility of clinical A. baumannii.

Keywords : Acinetobacter baumannii, Multi Drug Resistance, ompA and Oxacillinases genes

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P34-51: Inhibitory effect of Nardostachys jatamansi plain aqueous and alcoholic extract of fungus Malassezia

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Background and Aim : The opportunistic yeasts of the Malassezia genus are naturally inhabited by human beings and warm-blooded animals. These yeasts, under certain conditions, can produce diseases such as tinea versicolor, seborrheic dermatitis and even systemic infections. In recent decades' opportunistic fungal infections caused by Malassezia species such as Malassezia fur fur, which is caused by the significant increase in the incidence of disease Nardostachys jatamansi plant has numerous health benefits.

Methods : In this study, aqueous, ethanol and methanol extracts of Nardostachys jatamansi using on the fungus Malassezia, in disk and plate method, in the well method, a minimum growth inhibitory concentration (MIC) and minimum fungicide concentration (MFC) was studied.

Results : In the disc method, the lowest diameter of the aqueous extract in 10 µl was 7.33± 0.33 mm and the largest diameter was methanol extract with a length of 14.66±0.33 mm at a concentration of 50 µl. In the well method, the lowest diameter was ethanolic extract at a concentration of 80 µl with a diameter of 15 ± 00 mm and the largest diameter was aqueous extract with a length of 22.33±0.31 mm at a concentration of 110 µl.

Conclusion : The results of this study showed that ethanolic, methanolic and aqueous extracts of the Nardostachys jatamansi plant had an antifungal effect on Malaysia in laboratory conditions. According to these results, in the future, more research should be done on this plant in vitro and in vivo conditions and its antimicrobial compounds should be identified and extracted. Due to the fact that herbal medicines have fewer side effects, to reduce the side effects and drug resistance caused by chemical drugs, it is hoped that the effective compounds of this plant can be used in the future to treat fungal diseases as a suitable alternative to chemical drugs.

Keywords : Nardostachys jatamansi, Malassezia, anti-fungal effect

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P35-54: Antibacterial effects of aqueous extracts of Hypericum perforatum and Myrtus communis on Escherichia coli producing ESBL

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Background and Aim : The increasing incidence of infections caused by extended-spectrum beta-lactamase (ESBL) producing Escherichia coli in Iran is of serious concern. The aim of study was to investigate the effect of aqueous hypericum perforatum extract on Escherichia coli producing ESBLs.

Methods : 40 strains of Escherichia coli bacteria ESBLS from clinical purified samples were taken from Arak medical university microbial research center infectious diseases and E. coli ATCC25922. Antibiogram and Biochemical tests were taken in order to verify Escherichia coli bacteria. The hypericum perforatum plant is prepared freshly from farm herb. Before drying plant in a traditional way, it should be washed with water for several times, hypericum perforatum aqueous extracts were excavated by means of reflux device with distillation and investigating the antibacterial effects of hypericum by disk diffusion method, minimal inhibitory concentration (MIC) and minimal bactericidal concentration (MBC).

Results : Result showed that hypericum perforatum extract to Escherichia coli ESBLs in the concentrations of 8, 4 and 2 mg/ml, 57.5 percentages of bacteria out of %100 have halo and 42.5 percentages of bacteria out of %100 are non-halo. In these concentrations 1, .5, .25, .125, .0625, .0312, .0156 mg/ml, the percentage of sensitive bacteria (having halo) is decreased and the percentage of resistant bacteria (non-halo) increased. MIC against Escherichia coli taken in different concentrations, which concentration 0.0078mg/ml was lowest among them.

Conclusion : The findings demonstrate that by making a suitable herbal medicine, it is possible to hope for the treatment of resistant infections.

Keywords : hypericum perforatum, E. coli, Drug resistance, ESBL

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P36-56: The morphological analysis by bright field and transmission electron microscopy of Escherichia coli producing ESBL with a Hypericum perforatum aqueous extract

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Background and Aim : The increasing resistance of microorganisms to conventional chemicals and drugs is a serious and evident worldwide problem that has prompted research into the identification of new biocides with broad activity. Plants and their derivatives are often used in folk medicine. aqueous extract and their components have activity against a variety of targets, particularly the membrane and cytoplasm, and in some cases, they completely change the morphology of the cells. The aim of study was to investigate the effect of aqueous Hypericum perforatum extract on the morphological properties of Escherichia coli producing ESBLs (extended-spectrum beta-lactamases).

Methods : 40 strains of Escherichia coli ESBLs from clinical purified samples were taken from Arak medical university microbial research center infectious diseases and E. coli ATCC25922. Antibiogram and Biochemical tests were taken in order to verify Escherichia coli. The Hypericum perforatum plant is prepared freshly from farm herb. Before drying plant in a traditional way, it should be washed with water for several times, Hypericum perforatum aqueous extracts were excavated by means of reflux device with distillation and investigating its morphological investigation, taken by the use of electronic microscope and light microscope.

Results : Obtained result showed that aqueous extract of Hypericum perforatum leading to an increased in coccobacilli status, increased degradation and changes in bacterial pigmentation properties.

Conclusion : The action of aqueous extract and their components on bacteria remains a focal area for future research.

Keywords : Hypericum perforatum, E. coli, Microbial morphology, Drug resistance

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P37-57: Investigating the antibiotic resistance pattern of calves with coli basilosis diarrhea

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Background and Aim : Today, antibiotic resistance is one of the problems of human health, which is increasing day by day, and unfortunately, with poor management and treatment systems, especially in cattle and poultry, this problem has become bigger and more widespread. Bacteria are one of the most common diseases in industrial dairy cows. Irregular and unscientific treatments by veterinary medicine have made these bacteria resistant to various antibiotics. In this study, we tried to measure the resistance of this bacterium by isolating the cause of diarrhea in dairy calves and testing antibiotic susceptibility, and by taking it, we took a step towards controlling the antibiotic resistance of infectious agents.

Methods : In this study, 100 samples of calves with diarrhea were taken. In 70 cases, the bacterium was isolated using a dedicated culture medium. After the bacteria isolated in the environment, brain broth was cultured and 5% McFarland was prepared. The bacteria were then cultured in the Muller Hilton culture medium and the five antibiotic enrofloxacin ampicillin, gentamicin, trimethoprim sulfonamide and seftiofour were injected into the environment by disc herniation.

Results : As a result of the above test, the strain of the strain bacterium was more sensitive to immediate stiffness than others and was resistant to gentamicin and trimethoprim sulfonamide.

Conclusion : Due to the antibiotic resistance that has become one of the human problems today, many tests are performed based on antibiotic sensitivity. In this test, we examined the antibiotic resistance of strain bacteria and found that the drugs of choice for this disease were used every day. It has not been effective and the bacterium is resistant to gentamicin and sulfate, but it is still sensitive to immediate stiffness. It is recommended that further research be done to control the growing trend of antibiotic resistance in the future.

Keywords : Antibiotic resistance ,calve, coli basilosis diarrhea.

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P38-58: Investigating the effect of yarrow extract on Candida albicans growth compared to ketoconazole

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Background and Aim : Medicinal plants are a good option for the treatment and even prevention of many diseases, and due to their lower side effects and more economical efficiency and high internal production potential, they are a good alternative to chemical drugs

Methods : In this study, a fungal isolate sample prepared from the genital tract of people with genital infection was cultured during the diagnostic and final confirmation tests in the Muller-Hilton culture medium. We impregnated the prepared disks with the extract. In the culture of Muller Hilton Agar containing Candida albicans fungus, the extract disks and a disk containing 2% ketoconazole were placed and then the growth halo diameter was examined.

Results : : The findings showed that yarrow did not have good inhibition at low dilutions compared to ketoconazole, but at concentrations of 100, 90, 80, and 70 mg / ml had a 70% inhibition.

Conclusion : : According to the above findings, yarrow extract plant has been successful in preventing the growth of Candida albicans in the above concentrations, but it cannot be definitively introduced as an alternative to ketoconazole, and ketoconazole is still a suitable drug for the treatment of Candida albicans.

Keywords : Herbal extracts, yarrow extract, ketoconazole, Candida albicans.

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P39-78: Antibacterial effects of Extract of Rosemary (Rosmarinus officinalis) compared with five common antibiotics against E coli responsible for avian colibacillosis

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Background and Aim : Antimicrobial therapy is an important tool in reducing colibacillosis. Nowadays, the increased use of synthetic antibiotics leads to the incidence of resistant strains and high side effects. Therefore, The use of antimicrobial properties of medicinal plants can solve common problems in the use of antibiotics. Rosemary (Rosmarinus officinalis) is a medicinal plant uses in traditional medicine that can considered as an appropriate alternative of antibiotics.

Methods : The objective of present work was to evaluate antibacterial effects of Rosemary (Rosmarinus officinalis) on Escherichia coli isolated from broiler flocks with colibacillosis. The antimicrobial effects of alcoholic extract of Rosemary was obtained on the E. Coli isolates in a culture medium and Mueller Hinton agar using disc diffusion and microdilution methods and determination of microbial susceptibility was also performed by Bauer and Kirby method.

Results : The antibiotics flomequine, neomycine, trimethoprim-sulfamethoxazole, doxycycline and lincospectin were used as positive control. The hydro-alcoholic extracts of rosemary at higher concentrations was active against Escherichia coli. The test results Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC) Determined that Rosemary Extracts ompared with some this antibiotics are better antibacterial effect.

Conclusion : The results showed that Rosemary has antimicrobial activity. Considering the increasing resistance to synthetic antibiotics, Rosemary as a potential source of new antibacterial substances can replace chemical drugs for treat infections.

Keywords : Antibacterial effects, Rosmarinus officinalis, E. Coli, MIC

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P40-95: Prevalence of Extended-spectrum ß-lactamases among Acinetobacter Baumannii Strains Isolated from University Hospitals of Qazvin, Iran

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Background and Aim : Acinetobacter baumannii is a major cause of health care-associated infections. Extended-spectrum beta-lactamase (ESBL)-producing A. baumannii is spreading worldwide. We aimed to determine the frequency of ESBL encoding genes in clinical isolates of A. baumannii and to access their clonal relationship by repetitive extragenic palindromic-PCR (rep -PCR).

Methods : In this descriptive cross-sectional study, 203 isolates of A. baumannii were collected from Qazvin teaching hospitals. These isolates were identified using standard laboratory methods and by detection of the intrinsic blaOXA-51-like and gltA genes. To verify ESBL production, all isolates were screened by disk agar diffusion and confirmed using the combined disk method. Subsequently, ESBL encoding genes were isolated by PCR and sequencing. Possible clonal association of ESBL-producing isolates was evaluated by rep-PCR.

Results : In total, 200 (98.5%) isolates showed reduced susceptibility to one of the antibiotics used in the ESBL screening test, of which 127 isolates (62.6%) produced ESBL. PCR results showed that 26 (20.5%) isolates carried the blaOXA-1 gene as the most common gene followed by blaTEM-1 (20%), blaGES-1 (15.7%), and blaCTX-M-15 (7.9%), and blaPER-1 (1.6%). Rep-PCR results showed that ESBL-producing isolates belonged to three distinct clones A (85%), B (13.4%), and C (1.6%).

Conclusion : The findings of this study showed the significant presence of blaOXA-1, blaTEM-1, blaGES-1, and blaCTX-M-15, and blaPER-1 genes in ESBL-producing A. baumannii isolates in the studied hospitals. This is the first report of the presence of blaOXA-1 gene in these isolates in Iran. The use of comprehensive antimicrobial treatment guidelines based on laboratory data and appropriate infection control strategies to prevent further infection by these organisms are essential.

Keywords : Acinetobacter baumannii, ESBLs, repetitive extragenic palindromic-PCR

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P41-106: Genetic diversity based on 24-locus MIRU-VNTR typing method among first and second line drugs-resistant Mycobacterium tuberculosis isolates in Isfahan, Iran

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Background and Aim : We aimed to determine the genetic diversity of first and second-line drugs resistant Mycobacterium tuberculosis isolates based on 24-locus MIRU-VNTR genotyping method in Isfahan, Iran.

Methods : A set of 482 patients with tuberculosis among referrals of Mollahadi Sabzevari Tuberculosis Center, Isfahan, Iran, from 2014 to 2017 were studied. Drug susceptibility testing was done for the first-line drugs (Isoniazid, Rifampin, and Ethambutol) on all culture-positive specimens and second-line drugs (Ofloxacin, Amikacin, Kanamycin, and Capreomycin) only on the multi-drug resistant (MDR) and rifampin-resistant (RR) isolates using the proportion method on the Lowen-stein Jensen medium according to the 2014 WHO guideline. We also did a similarity search and phylogenetic tree analysis based on the (http://www.miru-vntrplus.org) website.

Results : Of 482, 32 (6.63%) isolates were resistant to the first-line drugs and 13 (2.6%) MDR/RR isolates were also resistant to second-line drugs. Two lineages (Lineages 3 and 4) of seven global lineages was observed. Lineage 3 including Delhi/CAS sub-lineage (n=17; 53.1%), and lineage 4 including NEW-1 (n=11; 34.3%), H37Rv-like (n=2; 6.2%), LAM (n=1; 3.1%) and URAL (n=1; 3.1%) sub-lineages identified among first-line drugs-resistant isolates and NEW-1 (n=6; 46.1%), Delhi/CAS (n=5; 38.4%) and H37Rv-like (n=2; 15.3%) sub-lineages identified among second line drugs resistant isolates.

Conclusion : We did not detect any XDR isolates; however, MDR and pre-XDR isolates were observed and can be alarming. Delhi/CAS and NEW-1 genotypes were the most prevalent among first and second-line drugs resistant M. tuberculosis isolates, respectively. Also, the frequency of isoniazid-resistant isolates was significantly higher in Delhi/CAS genotype.

Keywords : Tuberculosis, Drug resistance, Iran, Mycobacterium tuberculosis, MIRU-VNTR

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P42-119: Effect Of Turmeric Ethanolic Extract On Group A Streptococcus β Hemolyticus

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Background and Aim : Mohammad ebrahim Goli mehdi abadi* Introduction : Pharyngitis is one of the most common infection that general practitioners handled. It is estimated in one year there are 15 million people with pharyngitis will come to the doctor. American Society of Microbiology said that 94,3 % from 402 patient who were suspected pharyngitis received antibiotic therapy even without indication of antibiotic therapy. Antibiotic resistance is becoming a great threat for the world today. Turmeric domestica is a plant that is widely used in all over the world and some research said that it has anti -inflammatory, antioxidant, and antimicrobial effect. Aim: The aim of this study is to find the antibacterial effect of Turmeric (curcuma) domestica ethanolic extract on Group A Streptococcus β hemolyticus and find the Minimum Bactericidal Concentration (MBC) value.

Methods : This was in vitro experimental study with broth microdilution method and inoculation on agar blood media to find the MBC. Treatment group consisting of, media (Mueller Hinton Blood Broth), Group A Streptococcus β hemolyticus bacteria, and 5 concentrations (312.5 µg/ml, 625 µg/ml, 1250 µg/ml, 2500 µg/ml, 5000 µg/ml) of Turmeric(Curcuma) domestica extract.

Results : There is no bacterial growth at 5000 ?g/ml concentration on solid media, but there are less bacterial growth at 2500 ?g/ml than at concentration 312.5 ?g/ml, 625 ?g/ml, 1250?g/ml.

Conclusion : There is an antibacterial effect of Turmeric(Curcuma) domestica ethanolic extract on Group A Streptococcus β hemolyticus with MBC value in range 2500 – 5000 µg/ml.

Keywords : Group A Streptococcus β hemolyticus ,MBC,Turmeric

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P43-126: Does selenium nanoparticles prevent the adherence of Candida parapsilosis and Enterococcus faecalis to urinary catheters?

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Background and Aim : Catheter related urinary tract infections continue to be a major cause of morbidity in hospitalized patients. The prominent role of biofilm in the pathogenesis of these infections has been suggested in the past few years. The aim of this study was to evaluate in vitro effect of selenium nanoparticles (SeNPs) on the formation of Candida species and Enterococcus species biofilms on urinary catheters.

Methods : In order to prepare yeast and bacterial suspensions (0.5 McFarland), 0.5 cm pieces from catheter were incubated at 37°C in tryptic soy broth medium. Then, the pieces were washed with PBS to remove nonadherent microorganisms. After biofilm formation, the effect of SeNPs at concentrations of 64 to 0.125 µg/mL were investigated using broth microdilution method (CLSI, M27-S4).

Results : Minimum inhibitory concentration (MIC) was determined to evaluate the anti-adherent effect of SeNPs on microorganisms. Totally effect of SeNPs on E. faecium strains adherence was lower than C. parapsilosis strains, significantly ($p < 0.01$).

Conclusion : The pathogenicity of multiple Candida species and Enterococcus species is mainly associated with their ability to form biofilms; so that, early steps in the establishment of infections are adherence and biofilm formation. Furthermore, we concluded that SeNPs has a considerable anti-adherent activity against C. parapsilosis by decreasing MIC. This study suggests that coating catheter with SeNPs could be effective to prevent catheter related urinary tract infection through inhibition of microbial adherence.

Keywords : Candida parapsilosis, Enterococcus faecalis, Selenium nanoparticles, Adherence

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P44-132: The effect of alcoholic extract of chicory on the bacteria Staphylococcus aureus and Salmonella typhimurium causes food poisoning.

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Background and Aim : Due to the many problems that chemical drugs, especially antibiotics, have in terms of many side effects and the resistance of pathogens to them, human society towards nature and the use of natural resources have medicinal properties and extensive studies and research. They have done it in this regard

Methods : In this experimental study of plants, chicory Cichorium intybusL.) Was selected for study. Using the Disc Diffusion Method, as well as determining the minimum inhibitory concentration of microbial growth (MIC = Minimum Inhibitory Concentration) and the minimum bacterial strain concentration (MBC = Minimum Bactericidal Concentration) using the Macro Dilution Method It was performed agains two bacteria, Staphylococcus aureus and Salmonella typhimurium

Results : The results showed that the alcoholic extract in both tubular dilution and disc release had antibacterial effects on Staphylococcus aureus, but no significant changes were observed in Salmonella typhimurium. The method of diluting the tube was 29.50 and the minimum lethal concentration was 51.32, which was not a significant amount and was not significantly different from the inhibition rate of chemical drugs. Prevent the growth of this bacterium

Conclusion : According to the above findings, the conclusion that can be made is that the medicinal plant chicory could not have a good response in eliminating and preventing the growth of bacteria

Keywords : Medicinal plant, alcoholic extract, Staphylococcus aureus, Salmonella typhimurium

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P45-135: Antimicrobial Stewardship in the Treatment of Asymptomatic Bacteriuria (ASB)

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Background and Aim : Unnecessary antibiotic treatment is associated with acquisition of drug-resistant pathogens, Clostridium difficile infection, and other drug-related adverse events. Antimicrobial stewardship designed to promote the optimal use of antimicrobial agents, including their choice, dosing, route, and duration of administration. The primary goal of antimicrobial stewardship is to optimize clinical outcomes while minimizing unintended consequences of antimicrobial use. Additional benefits include reducing antimicrobial resistance. Asymptomatic bacteriuria (ASB) is the presence of 1 or more species of bacteria growing in the urine at specified quantitative counts, irrespective of the presence of pyuria, in the absence of signs or symptoms attributable to urinary tract infection (UTI).

Methods : The present study on Antimicrobial stewardship programs have identified the treatment of ASB as an important contributor to inappropriate antimicrobial use, which promotes resistance. Guidelines from the Infectious Diseases Society of America recommend treating ASB only in pregnant women or immediately prior to a urologic procedure likely to involve mucosal injury.

Results : Clinical distinction between UTI and ASB in some populations with a high prevalence of bacteriuria is difficult. Obtaining urine cultures when not clinically indicated, including for routine screening, promotes inappropriate antimicrobial use. Laboratory evidence of pyuria and bacteriuria is necessary for the diagnosis of ASB in patients without symptoms which benefit from antibiotic treatment.

Conclusion : Educational interventions are effective ways to reduce rates of inappropriate ordering of urine cultures and the treatment of ASB.

Keywords : Antimicrobial Stewardship, Asymptomatic Bacteriuria, UTI, Drug resistance

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P46-137: E.coli is a common cause of urinary tract infections in the town of Nir in 2019

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Background and Aim : Increasing resistance of bacteria to antimicrobial agents is a major problem worldwide. Therefore, it is important to know the strains status of urinary tract infections versus common antibiotics in treatment. Different types of bacteria lead to infection. This study was conducted in 2019 with the aim of investigating the bacterial causes of urinary tract infections and determining their antibiotic resistance in urban and rural population visitors to Nir Health Center.

Methods : This descriptive cross-sectional study was performed on 337 people referred to Nir Health Center in 2019. The morphology and detection of isolated bacteria were performed using hot staining and differential biochemical experiments were performed. Antibiotic susceptibility testing was performed by the Karbi-Baer method. And antibiotic disks such as cotrimoxazole, nalidixic acid, gentamicin, nitrofurantoin, tetracycline, ceftizoxime, ampicillin, ciprofloxacin, and amikacin were used.

Results : Of the 337 patients studied, 94.2% were women and 5.8% were men. In the statistical studies, it was observed that 73.2% of positive cases are in terms of cultivation in rural areas and 26.8 cases are in urban areas.The most common causes of infection include E.coli (44.2%), Staphylococcus aureus (31.2%), Staphylococcus epidermis (11.2%), Staphylococcus saprophyticus (4.6%), Proteus (3.4%), respectively. The species were Enterobacteriaceae (3.2%). Regardless of the type of bacterium, the highest resistance was to septicemia (38.2%) and the lowest resistance to nitrofurantoin (8%). E.coli has been shown to be the most common cause of urinary tract infections.

Conclusion : According to the results of this study, the most common cause of urinary tract infection in adults is E.coli. The rural population is more polluted than the urban population, and the species have the highest resistance to septicemia and the lowest resistance to nitrofurantoin.

Keywords : Urinary tract infection, antibiotic resistance, nir

P47-143: Investigation of tetracycline resistance genes in Escherichia coli isolates from Patients with Urinary Tract Infection; Yasuj City, Southwest Iran

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Background and Aim : Urinary tract infections (UTIs) are the most disregarded diseases in both developing and developed countries and accountable for one fourth of the health care related infections. Microbial resistance to antibiotics due to treatment of bacterial pathogens and extended use of different antibiotics is an increasing public health problem worldwide. The aim of this study was to determine the prevalence of tetracycline resistance genes (tetA and tetB) in Escherichia coli isolates that cause urinary tract infections.

Methods : Totally, 129 strains of Escherichia coli isolated from UTIs patients, using bacterial culture method. Isolates were tested for susceptibility to 10 antimicrobial drugs by using disk diffusion method and the presence and identification of tetA and tetB genes were determined by Polymerase Chain Reaction (PCR). Data were statistically analyzed using SPSS v.18 (SPSS Inc.,Chicago, IL, USA).

Results : Among tetracycline-resistant isolates, 77 (59.7%) isolates with tetA and 86 (66.7%) isolates with tet B gene and 61 isolates with both genes were identified.There was a statistically significant association between tet A gene and resistance tetracycline (P = 0.006) and tet B gene and resistance tetracycline (P = 0.037).

Conclusion : The results of this study showed that the percentage of tetracycline resistance genes is high in patients with urinary tract infections. This can indicate an overdose of antibiotics. Therefore, due to the prevalence of urinary tract infections with Escherichia coli in the community and the spread of resistance and pathogenic factors, it is necessary rapid and accurate identification of this bacterium and its resistance factors to treat such infections.

Keywords : Antibiotic Resistance, tetracycline,tetA and tetB ,Escherichia coli, Urinary Tract Infection, Uropathogenic

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P48-144: Phylogenetic group distributions in Uropathogenic Escherichia coli Strains Isolated from Patients with Urinary Tract Infection; Southwest Iran

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Background and Aim : Urinary tract infections (UTI) are the most commonly encountered infections in clinics and outpatient settings and are mainly caused by Uropathogenic Escherichia coli (UPEC). Phylogenetic analyses have shown that Escherichia coli isolates fall into four main phylogenetic groups A, B1, B2, and D. Biofilm formation is the pathogenic process that allows E. coli to be maintained in the urinary system and prevents the loss of bacteria. The aim of this study was to identify the phylogenetic groups of UPEC strains using Clermont's triplexPCR method and to assess Biofilm formation of E. coli isolates from UTI cases in Yasuj, Iran

Methods : A total of 130 E.coli isolates were collected from patients with UTI during July to November 2017. Biochemical and standard microbiological techniques were used to identify E.coli and the presence of phylogenetic groups' genes was investigated by multiplex polymerase chain reaction (PCR). Antimicrobial resistance pattern was performed by Kirby-Bauer method and Biofilm formation was detected by Congo Red Agar (CRA) phenotypic assay

Results : The phylogenetic analysis of the UPEC isolates revealed that most of the isolates belonged to groups B2 and D. The isolates from UTI cases were distributed within phylogroups B2 (74.61%), D (15.38%), B1 (6.15%), and A (3.84%). There was a significant association between the formation biofilm and antimicrobial agents tested including Ampicilin (p-value=0.020) and Co-Trimoxazole (p-value=0.038).

Conclusion : The phylogroups of E. coli isolates from UTI cases showed that groups B2 and D are prevalent in in E. coli strains isolated from patients with UTI in Yasuj. Therefore, phylogenetic group B2 plays a more effective role than other phylogenetic groups in urinary tract infection caused by Escherichia coli bacteria in this area. Detection Phylogenetic group distributions, biofilm in E. coli and its resistance to commonly prescribed antibiotics in the clinical practice is essential in improving the efficacy of empirical treatment.

Keywords : Antibiotic Resistance, Biofilm, Escherichia coli, phylogenetic group, Urinary Tract Infection, Uropathogenic

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P49-166: Distribution and drug resistance of pathogens causing spontaneous bacterial peritonitis in patients with cirrhosis: A cross-sectional study

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Background and Aim : Introduction: Spontaneous bacterial peritonitis (SBP) is defined as bacterial infection of a previously sterile ascitic fluid with unknown source of infection. The current study aims to assess the microorganism distribution and their antibiotic resistance profile causing spontaneous bacterial peritonitis among patients with ascites hospitalized in a tertiary referral hospital, southern Iran from January 2019 to January 2020.

Methods : This cross-sectional study included 1261 patients with ascites that sample for gram stain and culture from their ascitic fluid were gathered. Data was analyzed using IBM SPSS version 24 and descriptive statistics were conducted.

Results : : Among study participants with ascites, 154 patients (12.2%) were diagnosed with SBP(Spontaneous bacterial peritonitis). The most common pathogen found in the ascitic fluid culture in these patients was Escherichia coli (29.2%), followed by Staphylococcus epidermidis (26%). E. coli organisms isolated in this study showed high rate of resistance to most of cephalosporin family antibiotic; while they were sensitive to gentamycin, carbapenems and vancomycin. Similarly, isolated Staphylococcus epidermidis organisms were sensitive to gentamycin and carbapenems.

Conclusion : To the high morbidity and mortality rate of SBP(Spontaneous bacterial peritonitis), early detection and prompt administration of appropriate empirical antibacterial regimen are highly crucial. A series of investigations as well as our study suggest that pathogenic resistance to the conventional antibiotics has been increased; therefore, changes in conventional prophylaxis and treatment strategies should be done. Such studies are demanded to be aware of antibiotic resistance pattern to prevent infections from spreading.

Keywords : Ascites / complications*, Peritonitis / diagnosis*, Ascitic Fluid / microbiology

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P50-173: Study of frequency of Methicilin and Vancomycin resistant Staphylococcus aureus strain isolated from clinical samples of Kerman Hospitals by genotypic and phenotypic methods in 2017-18

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Background and Aim : Staphylococcus aureus is associated with different infections ranging from skin and soft tissue infections to endocarditis and fatal pneumonia. Today, methicillin resistant S. aureus (MRSA) isolates are present in the hospitals of most countries and are often resistant to several antibiotics. The present study was conducted to investigate the frequency of MRSA and MSSA (Methicillin-sensitive Staphylococcus aureus) strains, and antibiotic susceptibility patterns of these strains from university teaching hospitals of Kerman.

Methods : From August 2018 to November 2019 a total of 65 S. aureus isolates were collected from Afzalipour, and Bahonar Hospitals in Kerman. All isolates were tested by disk diffusion method for susceptibility to 13 antibiotics and MIC of Vancomycin was evaluated by micro broth dilution method. The MRSA isolates were detected by the combination of phenotypic (susceptibility to cefoxitin) and genotypic (mecA gene amplification) methods. The presence of vanA gene in vancomycin resistant isolates was determined by PCR.

Results : Among, total 65 S. aureus strains isolated, 33 (50.7 %) were MRSA. All S. aureus isolates except one were susceptible to vancomycin and the highest rates of resistance were detected for tetracycline (69.2%) and erythromycin (58.5%). The antibiotic sensitivity results showed that all MRSA isolates were significantly more resistant to erythromycin, tetracycline, gentamicin, amikacin, tobramycin, trimethoprim/sulfamethoxazole, ciprofloxacin, levofloxacin as compared to MSSA (Methicillin-sensitive Staphylococcus aureus) isolates ($p<0.05$). All but one cefoxitin-resistant isolate carried mecA gene. The vancomycin resistant isolate possessed the vanA gene.

Conclusion : Given the alarming rate of resistance among the MRSA isolates, the monitoring of antibiotic resistance should be performed to reduce treatment failure in patients with staphylococcal infections. Although vancomycin remains a drug of choice for MRSA, our study suggests that its efficacy may be limited by resistance development.

Keywords : Staphylococcus aureus, Methicillin, Vancomycin, antibiotic resistance

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P51-185: Inducible Clindamycin resistance of Staphylococcus aureus isolates among burn patients in Motahari hospital, Tehran, Iran

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Background and Aim : Background and aim: Inducible resistance to Clindamycin, an effective antibiotic against Staphylococcus aureus (S. aureus) in infections of skin and soft tissue, can lead to in vivo therapeutic failure. The aim of this study was to investigate the outbreak of inducible resistance to Clindamycin in S. aureus isolates.

Methods : Material and Methods: A total number of 21 S. aureus isolates from burn wound swabs which were confirmed by standard bacteriologic tests were subjected to antimicrobial susceptibility test (AST) and inducible Clindamycin resistance using D-test in accordance with Clinical and Laboratory Standards Institute 2019 (CLSI).In D test, a 5 µg erythromycin (E) disk and a 2 µg clindamycin (C) disk placed 15 to 20 mm apart on an agar plate that has been inoculated with the clinical isolate. Then the plate incubated at 37°C for 24h. Then the figuration of a D shape around clindamycin of inhibition were evaluated. A standard S. aureus ATCC 25923 were evaluated simultaneously.

Results : Results: The majority of isolates (80.95%) were constitutively resistant to common antibiotics. Based on AST, 97.9% of isolates were resistant to: 84.4% to erythromycin, 80% to cefoxitin, 75% to gentamicin and 66% to Clindamycin . Only 4.76% of the isolate was D-test positive (inducible resistance to Clindamycin) in this study.

Conclusion : Conclusion: The increasing prevalence of resistance to different therapeutic options including Clindamycin in the treatment of S. aureus infections, could cause treatment failure. Therefore D-test, which is an easy and inexpensive text, is needed for clinicians to choose an appropriate treatment.

Keywords : Staphylococcus aureus, Inducible Resistance, D-test, Clindamycin, Erythromycin

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P52-188: Detection of some plasmid Qinolones resistance genes (qnrA, qnrB, qnrS, qnrC, aac(6')-Ib-cr) in salmonella isolates from poultry

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Background and Aim : The presence of qnr plasmid genes in the Enterobacteriaceae family is a major cause of quinolone resistance. Due to the increased fluoroquinolones resistance due to the prevalence of plasmid genes, the aim of this study was to determine the frequency of plasmid genes (qnrA, qnrB, qnrS, qnrC, aac (6 ') - Ib-cr) which are present in poultry salmonella

Methods : Fifty specimens were collected from bacteriological collections of Ferdowsi University of Mashhad, Faculty of Veterinary Medicine. These samples were first tested for antibi gram suseptibility and then all of them for presence of genes (qnrA, qnrB, qnrS, qnrC, aac (6 ') - Ib-cr) using PCR.

Results : In this study, the highest resistance to nalidixic acid was observed in 16% of samples and then to 14% of flomcquin. 2% of isolates had intermediate resistance to flomcquin and 4% to Enrofloxacin. PCR tests were performed, no strains showing the presence of genes (qnrA, qnrB, qnrS, qnrC, aac (6 ') - Ib-cr).

Conclusion : The conclusion of this study suggest that the rate of antibiotic resistance of Salmonella to quinolones by plasmid (qnr) genes is not very common in the studied poultry. But there is some antibiotic resistance that may be due to the other mechanisms, including mutations, are involved in resistance formation. Using proper antibiotic administration, it could be to treat salmonella infections and to prevent the spread of resistance by bacteria in the future.

Keywords : Salmonella, Quinolones, Antibiotic Resistance, Gene

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P53-195: EVALUATION OF ANTIBIOTIC RESISTANCE PATTERN AND EFFICACY OF MODIFIED HODGE TEST FOR DETECTION OF CARBAPENEM-RESISTANT KLEBSIELLA PNEUMONIAE STRAINS ISOLATED FROM CLINICAL SAMPLES

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Background and Aim : Klebsiella pneumoniae is a gram-negative opportunistic pathogen belonging to the Enterobacteriaceae family and can cause several infections with high rates of morbidity and mortality in human. Nowadayes, the emergence of carbapenem-resistant Klebsiella pneumoniae strains has become a big threat for public health. The aim of this study was to evaluate the prevalence of carbapenemase producing Klebsiella pneumoniae strains among various clinical specimens at Imam Khomeini Educational and Treatment Center of Sarab.

Methods : In this study, 130 different clinical samples were collected from patients included 73 (56%) females and 57 (44%) males at Imam Khomeini Educational and Treatment Center of Sarab. K. pneumoniae strains were isolated by different culture techniques and standard biochemical tests. Standard disk-diffusion method was used for evaluate antibiotic resistance pattern and The Modified Hodge Test was performed for detection of KPC-producing strains based on the instructions of Clinical Laboratory Standards Institute (CLSI).

Results : The highest and the lowest rate of resistance in isolated strains were observed for Piperacillin (78%) and Ertapenem (44%) respectively. The Modified Hodge Test was positive for 73 (56%) isolates that the highest rate of resistance was observed for piperacillin (88%) and cefotaxime (79%).

Conclusion : The results of this study represent increasing prevalence of carbapenemase producing Klebsiella pneumoniae isolates. Therefore, it is necessary to modify the antibiotic consumption pattern for effective therapy

Keywords : Klebsiella pneumoniae, Carbapenemase, Modified Hodge Test

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P54-197: EMERGENCE OF VANCOMYCIN-RESISTANT COAGULASE-NEGATIVE STAPHYLOCOCCI IN AN EDUCATIONAL AND THERAPEUTIC HOSPITAL OF SARAB IRAN

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Background and Aim : Coagulase-negative staphylococci (CoNS) are major opportunistic pathogens causing nosocomial infections due to use of medical devices and implants. Today, increasing prevalence of antibiotic resistant, especially vancomycin resistant CoNS is a warning problem and can lead to failure in treatment. The aim of this study was to determine the prevalence of Vancomycin-resistant clinical isolates of coagulase-negative staphylococci at Imam Khomeini Educational and Treatment Center of Sarab

Methods : The clinical specimens (blood, urine, wound) were collected from patients included 285)62%(females and 175 (38%) males during the study. The strains were isolated by routine culture techniques and microbiological methods. The antibiotic resistance pattern of the isolates was detected by disk diffusion method and susceptibility testing to vancomycin was performed by E-test method according to Clinical and Laboratory Standards Institute guidelines

Results : Out of 460 clinical samples, 82% of isolates were identified as Staphylococcus epidermidis. Also 18% of isolates were Staphylococcus saprophyticus. Among the S.epidermidis isolates, 81% and 19% of them were resistant to Co-trimoxazole and Vancomycin, while 53% and 6% of S. saprophyticus isolates were resistant to Co-trimoxazole and Vancomycin, respectively

Conclusion : Significant increase in the prevalence and emergence of Vancomysin-resistant coagulase-negative Staphylococci is a concerning public health problem. Therefore, determining the antimicrobial susceptibility profile of CoNS strains is necessary before the treatment.

Keywords : Staphylococci, Coagulase-negative, Vancomycin, Resistance

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P55-199: DETECTION OF MECA GENE AMONG METHICILLIN RESISTANT STAPHYLOCOCCUS AUREUS ISOLATED FROM BLOOD INFECTION IN AN EDUCATIONAL AND THERAPEUTIC HOSPITAL OF SARAB IRAN

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Background and Aim : Methicillin-resistant Staphylococcus aureus (MRSA) is one of the clinically significant pathogens that cause various nosocomial and community acquired infections in human. Nowadays, high prevalence of MRSA among bloodstream infections is concerning and its resistance to different types of common antibiotics has limited treatment options. MecA gene that encodes a protein called penicillin binding protein 2a (PBP2a) is responsible for resistance to methicillin in staphylococci. The present study aimed to determine the prevalence of MRSA and antibiotic susceptibility patterns of the isolates at Sarab Imam Khomeini Educational and Medical Center

Methods : In a period of one year (Aug. 2018 to Aug. 2019) S. aureus strains were isolated by conventional culture techniques and standard biochemical tests from patients at Sarab Imam Khomeini Educational and Medical Center. Susceptibility of the isolates against several antibiotics was evaluated by disk diffusion method. Methicillin resistant isolates were subjected to PCR analyze for the presence of mecA gene.

Results : Out of 110 blood samples, 22% of isolates were identified as S.aureus. Among S.aureus strains, 30% were resistant to cefoxitin disk and 6 strains were positive for mecA gene, according to the guidelines of Clinical and Laboratory Standards Institute (CLSI). According to results, polymerase chain reaction (PCR) assay is a useful and reliable way for rapid detection of MRSA strains and plays a big role in prognosis of blood stream infections

Conclusion : Findings in this study indicate the high prevalence of MRSA among the isolates at Sarab hospital

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

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P56-213: Helicobacter pylori antibiotic resistance and correlation with cagA motifs and homB gene

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Background and Aim : Helicobacter pylori (H. pylori) infection caused by antibiotic-resistant strains represents a major public health threat that aggressively promotes gastric cancer progression. Antibiotic resistance evaluation is immensely important to counteract its emergence. Here we merely determine the prevalence of antibiotic resistance in H. pylori isolates and its correlation with cagA motifs and the homB gene.

Methods : The antibiotic resistance pattern was investigated on 128 H. pylori isolated strains utilizing the disk diffusion method and study the correlation between it and the presence of pathogenic genes, cagA EPIYA motifs and homB gene, were accurately detected using the PCR.

Results : The resistance rates to four antibiotics were 70.1% for metronidazole, 35.5% for amoxicillin, 7.2% for clarithromycin and 8.2% for tetracycline. Resistance phenotypes were separated into two groups, single resistance (63.2%) and multi-resistance (12.5%). The prevalence of cagA-ABCC resistant strains and homB+ resistant strains was significantly higher in cancer ($p = 0.04$ and $p = 0.01$, respectively) than those of other diseases. The prevalence of cagA-homB+ resistance strains was 21.8% and had a significant correlation with PUD. A significant relationship was observed between amoxicillin resistant rate with ABC-homB ($p = 0.0006$).

Conclusion : The Resistance rate to selected antibiotics in Shiraz is higher than years ago. The presence of cagA-homB+ is associated with antibiotic resistance and also homB can be used as a marker to antibiotic resistance status prediction in H. pylori isolated in this area.

Keywords : Helicobacter pylori; antibiotic resistance; cagA-motifs; EPIYA-motifs; homB

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P57-220: Determining of bacterial species and their antibiotic resistance from UTI patients referred to Yazd Central Laboratory in 2019

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Background and Aim : Urinary tract infection (UTI) is one of the common infections that affect human health. This infection is caused by pathogenic microorganisms in the urinary tract with or without the appearance of symptoms. Bacteria commonly involved in UTI include E. coli, Klebsiella, Pseudomonas, and Staphylococcus. UTIs are often treated with a variety of broad-spectrum antibiotics, so regular identification of resistance patterns is essential in improving empirical antibiotic treatment. The aim of this study was to determine the prevalence of bacteria that cause UTIs and their antibiotic resistance pattern in patients referred to Yazd Central Laboratory in Yazd, Iran.

Methods : This cross-sectional study was performed in 2018-2019. Bacterial culture results and antibiotic resistance pattern were collected from all positive urine cultures. Data were analyzed by the software SPSS 16 ver.

Results : Of the 2560 positive urine culture samples, 88.8% were from females and 11.2% were from males. The highest frequency of infection was in the age group 21-40 years. E. coli (53.9%) was the most isolated bacterium and Acinetobacter (0.2%) was the least isolated. The isolated E. coli had the highest resistance to amoxicillin-clavulanic acid (62.9%), nalidixic acid (61.9%) and trimethoprim/sulfamethoxazole (56.9%), and the highest sensitivity to nitrofurantoin (93.1%) and gentamicin (84.7%).

Conclusion : Since the frequency of antibiotic resistance varies over time and different regions, and because of the high resistance rate in E. coli, as the most common pathogen in UTI, periodic monitoring of antibiotic resistance to infection control is recommended.

Keywords : Drug Resistance, Urinary Tract Infections, Bacterial Species, Iran, Yazd

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P58-223: Purification and isolation of SHV beta-lactamase enzyme from the Klebsiella pneumoniae and effect of Thyme essence on its expression by Real Time PCR and SDS PAGE methods

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Background and Aim : Klebsiella pneumoniae is a gram-negative bacteria of Enterobacteriaceae family.Increasing the resistance of this bacteria to many antibiotics has caused serious problems in treatment of its infections .Today, antibiotic resistance is high in pathogenic bacteria and the number of deaths is increasing with these infections. The aim of this study is to investigate antibacterial effects and mechanism of action of Thyme essence against SHV beta-lactamase expression in Klebsiella pneumoniae strains which have a SHV gene by using Real-time PCR method.

Methods : In a descriptive cross-sectional study, 12 isolates of Klebsiella pneumoniae were collected. Subsequently, the presence of SHV β-lactamase gene were evaluated in all strains by using PCR method. Then, in in vitro situation, Thyme essence activity was investigated against all isolates which have SHV gene by micro broth dilution method. Then the SHV beta -lactamase expression in strains which treated with Thyme essence and non-treated strains of Klebsiella pneumoniae were evaluated by using Real Time PCR and SDS-PAGE methods.

Results : The results of this study showed that 2 isolates had SHV beta-lactamase gene. The results of the Real-Time PCR test showed that the expression of SHV gene in Klebsiella pneumoniae strains which treated with Thyme essence, was about 41% lower than non-treated strains.

Conclusion : Thyme essence has a strong anti-beta-lactamase activity against Klebsiella pneumonia strains which have a SHV gene. This essence can be used alone or beside the antibiotic treatments in order to have a better effect of antibiotic treatment.

Keywords : Thyme essence, Klebsiella pneumoniae, SHV gene, Real-time-PCR

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P59-239: Phenotypic identification of metallo-beta-lactamase (MBL) in non-infectious children under three years old in Khuzestan province

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Background and Aim : Commensal Escherichia coli, one of the most important bacteria of the gut microflora, is a reservoir of antimicrobial resistance (AMR) that able transfer resistance genes especially carbapenemase genes to the pathogenic microorganisms. The aim of the current study was phenotypic identification of metallo-beta-lactamase (MBL) among E. coli strains isolated from feces of non-infectious children under three years old in Khuzestan province.

Methods : Two hundred one E. coli strains were collected and examined after culture in the proprietary media. The imipenem and meropenem resistance isolates were evaluated by phenotypic methods including combined disc test (CDT), double disc synergy test (DDST), modified carbapenem inactivation method (mCIM) and EDTA-CIM (eCIM) for the presence of MBL.

Results : Out of 201 isolates, 4 (1.99%) strains were identified as MBL producer. Two and one isolates were positive by DDST and CDT respectively and identified as MBL producer. One isolates with eCIM not been identified as a producer of MBL. One E. coli isolate was negative by CDT and DDST, and it was positive by mCIM and eCIM. Therefore four isolates were considered as MBL-producers.

Conclusion : The resistance against carbapenems, the last-line group of antibiotics against MDR Gram-negative bacteria, is increasing worldwide. The emergence of the strain MBL-producing commensal E. coli isolates that are not associated with any infectious diseases has thrown light on the fact that these isolates can act as a reservoir of antibiotic resistance genes and transfer them among commensal microorganisms, including into pathogens.

Keywords : Commensal Escherichia coli, CDT, DDST, mCIM, eCIM, carbapenemase, MBL

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P60-254: Heavy-metal and antibiotic resistance co-existence in an isolated native heavy-metal resistance bacteria

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Background and Aim : The relationship between metal tolerance (or resistance) and AR has been known. Certain metals, albeit toxic at high concentrations, contribute to the biochemical health of microorganisms. Therefore, understanding the link between antibiotic resistance (AR) and environmental conditions remains crucial. However, clinically relevant infections have been found resistant to multiple antimicrobials, including metals, by susceptibility assays, suggesting that a link between genetic traits exists.

Methods : In order to investigation the heavy metal resistance effect on AR profile of an isolated bacteria, at the first some commercial antibiotic discs were applied to determine antibiotic resistance profile. After MIC and MBC determination to selenate, a suitable selenate concentration was used to preparation of MHA medium.

Results : The results of separate cultivation on MHA medium and MHA medium supplemented with Se oxyanion were compared and showed that presence of 25mM selenate oxyanion has been resulted in change of antibiotic resistance pattern of Cefotaxime, Ciprofloxacin, Gentamycin and Chloramphenicol and mainly cause the strain become sensitive.

Conclusion : Co-contamination of antibiotics and heavy metals prevails in the environment, and may play an important role in disseminating bacterial antibiotic resistance, but the selective effects of heavy metals on bacterial antibiotic resistance is largely unclear. The linkage between antibiotic resistance and metal exposure has been known for many decades, when it was first discovered that penicillinase was linked with mercury exposure. Therefore, determination of the heavy-metal effect on AR profile could be useful before field applications of the heavy-metal resistance strains for bioremediation purposes.

Keywords : Antibiotic, resistance, heavy metal, bacteria

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P61-267: Interaction of eugenol and voriconazole against genital isolate of Candida tropicalis and Candida krusei from the mares.

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Background and Aim : Due to the limited range of antifungals available to treat genital Candida infections and the emergence of resistant isolates, attention has focused on the antifungal potency of natural compounds with promising biological properties. To examine whether eugenol synergises the in vitro efficacy of voriconazole against Candida strains isolated from the genital tract of mares.

Methods : The antifungal activity of eugenol and voriconazole was evaluated using the broth microdilution assay (CLSI- M27-A3). Synergism of eugenol and voriconazole was evaluated by the microdilution checkerboard method

Results : Minimum inhibitory concentration (MIC) values for eugenol and voriconazole ranged from 400 to 800 µg/mL and 1 to 8 µg/mL, respectively, for C. tropicalis isolates, and from 200 to 400 µg/mL for eugenol and 2 to 16 µg/mL for voriconazole against C. krusei isolates. Eugenol decreased the arithmetic mean MIC for voriconazole against C. tropicalis and C. krusei isolates from 2.66 to 0.46 µg/mL and 7.77 to 0.41 µg/mL respectively. The fractional inhibitory concentration index (FICI) values for the eugenol-voriconazole combination ranged from 0.25 to 0.88 and 0.19 to 0.63 for C. tropicalis and C. krusei isolates respectively. A synergistic effect of eugenol in combination with voriconazole was observed for 83.3% of C. tropicalis and 77.7% of C. krusei isolates.

Conclusion : Eugenol showed fungistatic and fungicidal effects against genital Candida isolates and, in combination, synergised the antifungal effects of voriconazole. The eugenol-voriconazole combination can lay the foundation for a therapeutic approach against isolates in which azole resistance has increased over time.

Keywords : Eugenol, voriconazole,antifungal activity, Candida tropicalis, Candida krusei

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P62-285: Detection of blaIMP4, bla CTX-M, tetA and aadB genes among Acinetobacterbaumanii clinical strains isolated from Imam Khomeini, Bahman, Bu-Ali and Momenin hospitals in Tehran by PCR

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Background and Aim : Acinetobacterbaumannii is an opportunistic bacterial pathogen responsible fora wide range of hospital-acquired infections. These bacteria take a variety of factors for resistance to different antibiotics, including resistance to β-lactams, aminoglycosides, and tetracyclines. The aims of this study were to determine the antimicrobial susceptibility pattern and prevalence of blaIMP4, bla CTX-M, tetA and aadBgenes in A.baumannii strains obtained from Imam Khomeini, Bahman, Bu-Ali anda Amir Al-Momenin hospitals.

Methods : In this cross-sectional study, 100 clinical Acinetobacterbaumannii isolates were collected from various hospitals in Tehran. After identification of Acinetobacterbaumannii isolates by biochemical tests, the antibiotic susceptibility test (Kirby-Bauer method) was done according to CLSI advice against 9 antibiotics. Finally, the blaIMP4, bla CTX-M, tetA and aadB genes were determined among the antibiotic resistant isolates using PCR.

Results : The disc diffusion results showed resistance rates of 90% for ciprofloxacin, 32% ceftazidime, 25% imipenem, 36% gentamicin, 34% streptomycin, 28% piperacillin, 5% polymyxin B and 63% tetracyclin. All isolates were susceptible to colistin. PCR results forblaIMP4, bla CTX-M, tetA and aadB genes were detected in 63%, 62%, 76% and 71% of resistant isolates respectively.

Conclusion : This study detected clinical A. baumannii isolates harboring antibiotic resistance genes. Identification of antibiotic resistance patterns in A. baumannii and investigation of molecular epidemiology are critical to control the rapid spread of antimicrobial resistant strains.

Keywords : Acinetobacterbaumannii, antibiotic resistance, Antibiogram, PCR

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P63-296: Investigation of the frequency of bacteria in positive cases of blood and urine culture tests in patients referred to Besat Hospital in Sanandaj during the autumn of 2019

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Background and Aim : Blood infections are a leading cause of death in hospitalized patients. Urinary tract infections are also one of the most common bacterial infections. Knowledge about variety of bacterial agents of infection is important. The aim of this study was to determine the frequency of bacteria in the positive cases of blood and urine culture in patients.

Methods : This study was descriptive-retrospective using data from 3230 samples of urine culture and 1100 blood culture samples taken from patients referred to Sanandaj Besat Hospital during the autumn of 2019. Cultures specimen's and laboratory microbiological methods for bacteria detection and disk diffusion were performed. For statistical analysis, SPSS 20 software, Chi-square test was used ($p \leq 0.05$).

Results : 8% of blood culture samples and 7.19% of urine culture samples were positive. Bacteria isolated from blood culture and urine culture include, respectively. Escherichia coli (3.40% and 71.55%), Staphylococcus saprophyticus (2.27% and 1.72%), Enterobacter (3.40% and 3.44%), Citrobacter (1.13% and 4.31%), Staphylococcus epidermidis (36.36% and 3.44%), Klebsiella (0.6% and 6.03%), Serratia (0.1% and 1.3%), Proteus (1.13% and 2.5%), Streptococcus (5.69% and 0.43%), Acinetobacter (5.69% and 0.42%), Staphylococcus aureus (2.27% and 2.15 %), Pseudomonas (1.13% and 2.59%) and Stenotrophomonas maltophilia (40.90% and 0%) have been reported.

Conclusion : Pathogens of Stenotrophomonas maltophilia and Staphylococcus epidermidis are the most common causes of blood infection and Escherichia coli is the most common cause of urinary tract infection. Proper diagnosis of pathogens causing infection is essential.

Keywords : Urine culture, Blood Culture, Bacteria

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P64-298: Investigating the Rate of Antibiotic-Resistant Bacteria in Positive Cultures

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Background and Aim : Microbiological cultures of different specimens such as urine, stool, blood, tissue and wound in for detection of infection and antibiotics is common methods in laboratory. Antimicrobial resistance has been as a threat to the public health. Laboratory had a important role in detection of infection and antimicrobial resistance. The aim of this study was to detection of positive culture and antimicrobial resistance in Besat hospital.

Methods : This report was performed in Besat hospital, Kurdistan province, Sanandaj city (Spring 2020). Common cultures specimen's and laboratory microbiological methods were performed. Disk diffusion also was applied for detection of antibiotics resistance. For statistical analysis, SPSS 20 software, Chi-square test and t-test analysis of variance were used ($p \leq 0.05$).

Results : 598 Microbiological cultures of different specimens (urine: 60.36%, blood: 31.43%, stool: 6.02%, wound: 2.1%) were performed. 101 positive culture were detected (urine: 38.61%, blood: 56.43%, stool: 0, wound: 1.98%). 22 of positive culture were defined as positive antibiotics resistance, 13 (59.09%) Extended-spectrum beta-lactamases (ESBL), 6 (27.27%) Methicillin-resistant Staphylococcus aureus (MRSA), 3 (13.63%) multidrug resistant (MDR) were detected. No vancomycin-resistant Staphylococcus (VRSA) was detected. It was directly related between number of positive culture and antibiotic resistance (p?0.05).

Conclusion : High antibiotic resistance in bacteria observed. The importance of testing antibiotic sensitivity before prescribing the drug in the treatment and control of drug resistance should be performed.

Keywords : Antibiotic-Resistant, Positive Cultures, Bacteria

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P65-305: Antibacterial resistance of Acinetobacter baumannii isolated from Mostafa Khomeini Hospital to selected antibiotics

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Background and Aim : Acinetobacter baumannii is an opportunistic pathogen, related with nosocomial infections such as bacteremia, urinary tract infections (UTIs), and ventilator associated pneumonia. A. baumannii strains are first line cause of infection, especially in patients hospitalized at intensive care units (ICUs). The aim of the current study was the evaluation of pattern of antibacterial resistance of A. baumannii isolates .

Methods : This study was performed on 72 A. baumannii isolates collected from Mostafa Khomeini Hospital in Tehran,Iran. The antibiotic susceptibility pattern was examined using Kirby-Bauer disk diffusion susceptibility test.

Results : According to the antibiogram test, among the 72 isolates from patients admitted to the ICU, the pattern of antibiotic resistance were respectively: cefipime (97.2%), ceftriaxone (95.8%), amikacin (94.4%), imipenem (80%), pipracilin-tazobactam (71.4%), meropenem (68.6%), gentamicin (62.8%), tobramycin (57.1%) and tetracycline (48.6%).

Conclusion : our results show that antimicrobial resistance of A. baumannii in Iran has increased. according to the findings, novel prevention and treatment strategies against A. baumannii infections are necessary. Furthermore, these data may assist in revising and updating treatment guidelines in hospitals to reduce the emergence of antimicrobial resistance.

Keywords : Acinetobacter baumannii,antibacterial resistance, nosocomial infections

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P66-313: Genetic characterization and occurrence of aminoglycoside resistance among Uropathogenic Escherichia coli isolates in the North of Iran

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Background and Aim : Community-acquired urinary tract infection (UTI) and a large portion of nosocomial UTIs are mainly caused by Uropathogenic Escherichia coli (UPEC) which increases substantial morbidity and mortality. The widespread usage of antibiotics has led to an increase in the emergence and spread of resistant strains, that this is a serious public health problem worldwide, particularly in developing countries. The present study aimed to investigate the genetic diversity and prevalence of aminoglycoside-resistant strains of E. coli isolated from inpatients with urinary tract infection.

Methods : This cross-sectional study was conducted during September 2018 to March 2019 on a total of 83 non-susceptible aminoglycosides E. coli in the North of Iran. Antimicrobial susceptibility test was performed by disk diffusion method. The presence of genes encoding aminoglycoside modifying enzymes (AMEs) were detected by PCR. The clonal relatedness of E. coli isolates was investigated by ERIC-PCR.

Results : Totally, 66.3% and 43.4% of isolates were non-susceptible to gentamicin and amikacin, respectively. The most common AME gene was aac(6′)-Ib (49.4%) followed by aac(3)-II (39.8%), ant(3″)-I (8.4%) and aph(3′)-VI (1.2%). Moreover, aac(6′)-II gene was not found among studied strains. All of the extended-spectrum beta-lactamases (ESBLs) producing isolates (55 isolates) were tested by ERIC-PCR. These isolates were classified into 10 ERIC types, and ERIC type A were the predominate type containing 52.7% of isolates.

Conclusion : Findings showed a substantial proportion of AMEs among aminoglycosides-resistant UPEC isolates. Moreover, the clonal analysis showed that a remarkable rate (52.7%) of aminoglycosides-resistant and ESBL-producing isolates were closely related.

Keywords : Aminoglycosides, Urinary tract infection, ESBL, ERIC-PCR

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P67-348: The effect of microbial omega 3 and 6 against pathogenic bacteria

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Background and Aim : Human health and development have been related to dietary intake of essential fatty acids (omega 3, 6 and 9) and important for brain development, immune system function, and blood pressure regulation. Essential oils are plant or microorganism-derived compounds that may view as more natural and safer alternatives to synthetic preservatives. These oils have been demonstrated to have antibacterial activity within food systems and may be ideal additives to food formulations. The increasing resistance of traditional antibiotics against pathogen infections provided the attention of scientists to these compounds. Zygomycete fungi are well-known as good candidate for production of essential oils

Methods : Essential oils of fungi Mucor rouxii, Mucor circinelloides and Cuninghamella echinulata were extracted and fatty acids were analyzed by GC, for the first, antimicrobial activity of the fungi essential oils against foodborne pathogenic bacteria E.coli, S.aureus, B.cereus, B.subtilis, and S.enterica was examined by disc diffusion and well diffusion methods and the minimal inhibitory concentrations (MIC) of oils were determined by microtiter plate.

Results : The fungi oils were exhibited the strong antibacterial effect against Gram-positive bacteria, B. Cereus, S. aureus and B.subtilis higher than gram-negative and commercial oleic acid and linoleic acid. The MIC of the fungi oil extracts was 0.25 mg/ml for B.cereus and B.subtilis and 0.5 mg/ml about S. aureus

Conclusion : Results indicate that microbial essential oils may be suitable for their antimicrobial properties in food. However, that combination or whole oils may be beneficial as a means of preventing the development of microbial resistance than each fatty acid alone

Keywords : Essential Fatty acid, Omega 3, 6, Pathogen, MIC

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P68-356: In vitro activity of Bacillus subtilis metabolites in the control of mucosal candidiasis in the elderly

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Background and Aim : Bacillus species as antagonistic bacteria are promising biocontrol agents of infections. This study aimed to investigate the antifungal activity of Bacillus subtilis metabolites on the growth of clinical strains of Candida isolated from the elderly.

Methods : 82 elderly patients suspected of oral candidiasis were studied. Candida species were identified and isolated by culture on CHROM agar Candida medium and API 20CAUX system. In order to isolate B. subtilis from 10 soil samples of Gorgan (North of Iran), routine and specific laboratory tests were used. Antifungal activity of B. subtilis metabolites on Candida isolates was investigated by agar diffusion method.

Results : 75.6% of the isolates were confirmed as Candida strains of three species of albicans, tropicalis and glabrata, with the highest abundance (77%) belonged to C. albicans. Bacterial metabolites had the highest inhibitory effect (66.7%) on C. glabrata (with an inhibition zone diameter of 19.1mm) and the least effect (16.7%) on C. albicans ($P<0.01$).

Conclusion : Native isolates of B. subtilis have effective anti-Candida effects, so using pure extracts of these isolates to control candidiasis may be effective in the future.

Keywords : Candida, Bacillus subtilis, Antagonism

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P69-359: the study of the prevalence of Staphylococcus aureus caused by clinical swelling and determination of antibiotic susceptibility to dairy cattle in eyvan County

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Background and Aim : Inflammation of the breast or inflammation of the mammary gland is one of the most important diseases in lactating cows, the economic losses of which are significant. There are several factors involved in the development of diseases in lactating cows, such as mastitis, the most important of which are staphylococcal agents. Due to the prevalence of diseases in lactating cows and antibiotic resistance, the aim of this study was to isolate staphylococcal disease agents, determine their susceptibility and antibiotic resistance.

Methods : For this purpose, milk samples were prepared from 100 heads of Holstein dairy cows belonging to cattle farms around Ivan city in Ilam province, and after C.M.T experiment, the infected samples were cultured bacterially and staphylococcal agents were isolated. Antiseptic and resistance factors of Staphylococcus aureus were then determined using mast antibiotic disks.

Results : The results showed that out of 100 cows, 30 had subclinical mastitis and 1 had clinical form, of which 30 were subclinical, 9 were staphylococcal (6 specimens of urea). The results of a sensitivity test for some antibiotics showed that 92% of the Staphylococcus aureus isolated from the subclinical form were sensitive to erythroloxacin, 68% to trietometopyrim, 65% to gentamicin, 61% to lincospectin and 32% to oxytocrysycin And 20% were semi-sensitive to amoxicillin. No susceptibility to penicillin and ampicillin antibiotics was observed.

Conclusion : According to the results of this study, staphylococci were the most pathogenic cause of mastitis in the samples of cow's milk tested, and the antibiotic erofluoxacin and trimethoprim had the greatest effect on inhibiting the growth of staphylococci in the study area. Therefore, it is recommended that erofloxacin and trimethoprim antibiotics be used to treat breast uremia.

Keywords : Inflammation of the breast, staphylococcus, antibiotic susceptibility

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P70-373: Prevalence of Carbapenemase and Aminoglycoside Resisrance Genes and Biofilm Formation among Clinical Isolates Acinetobacter baumannii

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Background and Aim : A. baumannii have emerged as a problematic organism in clinical setting due to resistance to carbapenems, aminoglycosides and biofilm formation ability. The aim of current research was to determine antimicrobial susceptibility pattern, carbapenems and aminoglycoside resistance genes and biofilm formation among clinical isolates of A. baumannii.

Methods : A total of 133 A. baumannii was collected in Yasuj and Bandar Abbas, Iran. Antimicrobial susceptibility was deretmined using disk diffusion. Carbapenem resistance genes, including: blaOXA-51-like, blaOXA-23-like, blaOXA-24-like, blaOXA-58-like and aminoglycoside resistance genes: aac (3)-I, aac (6 ')-Ib, aph (3 ')-I was amplified by PCR. Biofilm formation was evaluated by using microtiter plate assay.

Results : All isolates contained blaOXA-51-like and confirmed as A. baumannii. High level resistance was observed for carbapenems and aminoglysosides. The prevalence of blaOXA-23-like and blaOXA-24-like was 66.9% and 34.6% respectively. Moreover, co-occurrence of bla-OXA-23-like and bla-OXA-24-like was 7.5%. The rate of aac (3)-I and aph (3 ')-I was 54.9% and 51.9% respectively. Furthermore, coexistence of these two genes was observed in 41.4% of isolates. No blaOXA-58-like and aac (6)-Ib was found. The result demonstrated that 97% of isolated were strong, 2.3% moderate and 0.8% weak bioflim producer.

Conclusion : According to the results, bla-OXA-23-like and aac (3)-I were the most prevalent resistance genes. Since a vast majority of isolates were resistant and biofilm producer, Infection control programs and policies should be frequently reviewed to control the transmission of drug resistant A. baumannii isolates in the future.

Keywords : Acinetobacter baumannii, Carbapenem and Aminoglycoside Resistance, Biofilm

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P71-386: Pan drug-resistant Acinetobacter baumannii causing nosocomial infections among burnt children

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Background and Aim : Nosocomial infection caused by Acinetobacter baumannii has emerged as a world-wide serious problem in the emergence of multidrug-resistant (MDR). Infections caused by antibiotic-resistant strains of A. baumannii cannot be completely eliminated among the infected patients. This study aimed to monitor antibiotic resistance among A. baumannii strains isolated from burnt children.

Methods : After performing biochemical identification tests on 115 isolates, 62 were detected as A. baumannii. Minimum inhibitory concentration (MIC) was used to test susceptibility to colistin, and disk agar diffusion was used for the susceptibility of the isolates to the antibiotics Ciprofloxacin, Amikacin, Gentamicin, Cefepime, Meropenem, Imipenem, Ceftazidime, Levofloxacin and Piperacillin/Tazobactam. Bacterial species were isolated and identified as multidrug-resistant (MDR), extensively drug-resistant (XDR) and pan drug-resistant (PDR), based on the susceptibility patterns to elected antibiotics, deputing different classes of antimicrobial.

Results : The antibiotic susceptibility pattern out of a total of 62 bacterial strains used in this study. Thirty-six (58%) strains were categorized as MDR, 17 (27.5%) as XDR, and nine (14.5%) as PDR.

Conclusion : To reduce the threat of antimicrobial resistance, MDR, XDR and PDR A. baumannii strains must be evaluated by all clinical microbiology laboratories

Keywords : PDR, Acinetobacter baumannii, Burnt Children

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P72-399: Antimicrobial Resistance Pattern in Relation to Virulence Genes and Clonal Groups Among Uropathogenic Escherichia coli in Iran

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Background and Aim : Uropathogenic Escherichia coli (UPEC), is one of the most important etiologic agent of urinary tract infection (UTI). Investigating the relationship between different characteristics of UPEC strains is advantageous for epidemiological surveillance of high-risk clones.

Methods : PCR, the Kirby Bauer disk diffusion method and MLST were used to characterize and correlate among the clonal groups, virulence genes and antimicrobial resistance pattern in 101 UPEC strains.

Results : The fimH, pai, and traT genes were highly prevalent among UPEC strains isolated from patients in our region. Among 9 different Sequence-types, ST131 was the most prevalent clonal group that significantly correlated with the pai gene. 70.3% of the tested population were multidrug-resistant and the majority of the isolates were resistant to Ampicilin and trimethoprim/sulfamethoxazole.

Conclusion : Clonal groups showed no significant differences in terms of antibiotic resistance patterns. There was no significant difference between virulence genes and antibiotic resistance patterns in the studied clonal groups. These findings suggest that the relationship between virulence and antimicrobial resistance pattern can vary according to different genetic and environmental factors and Understanding these relationships requires deep molecular research and may help in the future to manage the spread of infectious diseases.

Keywords : Antimicrobial Resistance Pattren, Virulence Genes, Clonal Groups

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P73-405: Detection of bla SHV, sul2 and aadA genes among Escherichia coli clinical strains isolated from Bu-Ali and Amiralmomenin hospitals in Tehran by PCR

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2. *Farshad Hashemian*

Background and Aim : Background and Aim: E.coli is one of the most commonly pathogens isolated from urinary tract infections. Unfortunately, antibiotic resistance has become increasingly as a pressing clinical issue in many countries. The aims of this study were to determine the antimicrobial susceptibility pattern and prevalence of bla SHV, sul2 and aadA genes in E.coli strains obtained from Bu-Ali and Amiralmomenin hospitals in Tehran.

Methods : Methods: One hundred clinical Escherichia coli isolates were collected from Bu-Ali and Amiralmomenin hospitals in Tehran. After identification of Escherichia coli isolates by biochemical tests, antibiotic susceptibility was done using the Kirby-Bauer disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI, 2019). PCR were applied for detection of bla SHV, sul4 and aadA genes among the antibiotic resistant isolates.

Results : Results: The results of this study showed high antibiotic resistance among of the isolates. The highest resistance of E.coli isolates was seen to piperacillin (87%) and carbenicillin (92%). The resistant rates to various other antibiotics were as follows: ceftazidime (53%), cefotaxime (60%), ceftriaxone (57%), cotrimoxazole (55%), gentamicin (40%), nalidixic acid (67%), ciprofloxacin (73%), streptomycin (27%), and chloramphenicol (65%), respectively. Of 55 cotrimoxazole resistant isolates, 44 (80%) strains contained sul2 gene. The frequency of aminoglycosides resistance gene including aadA in streptomycin and gentamicin resistant isolates were (40%).The prevalence of blaSHV in piperacillin and carbenicillin resistance was 65.71%.

Conclusion : Conclusion: This study detected clinical E.coli isolates harboring antibiotic resistance genes. Determination of antibiotic susceptibility patterns of E.coli against antibiotic and study of related genes are necessary for elucidating molecular and epidemiological mechanisms of resistance.

Keywords : Key words: Escherichia coli, Antibiotic resistance, bla SHV, sul2, aadA.

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P74-422: Evaluation of drug resistance pattern and frequency of ipaH gene in Shigella strains isolated from patients referred to hospitals in Tabriz city in 2019

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Background and Aim : Today, one of the most important barriers to controlling shigellosis is its resistance to common types of antibiotics. Therefore, the aim of this study was to evaluate the drug resistance and frequency of ipaH genes in Shigella strains isolated from patients referred to hospitals in Tabriz city.

Methods : In this cross-sectional study, 100 Shigella specimens were identified from patients referred to Tabriz hospitals using agglutination method with specific antiserum on slides. The pattern of antibiotic resistance was evaluated by disk diffusion method. Polymerase chain reaction (PCR) was used to identify the ipaH gene.

Results : In this study, 56 cases of Shigella flexneri (56%), 37 cases of Shigella sonei (37%) and 7 cases of Shigella boydii (7%) were observed, but there was no Shigella dysenteriae. The highest resistance was seen to tetracycline and cotrimoxazole. The presence of ipaH gene was confirmed in all strains.

Conclusion : In this study, the prevalence of Shigella flexneri strains is higher than other species. The studied strains showed high sensitivity to third generation cephalosporins and aminoglycosides. The study of ipaH virulence gene showed that this gene can be used as a marker for rapid identification of Shigella species.

Keywords : Shigella, PCR, antibiotic resistance, ipaH gene

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P75-424: Plasmid mediated fluoroquinolone resistance associated with intestinal Escherichia coli isolates from healthy subjects

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Background and Aim : Quinolone/fluoroquinolone (Q/FQs) antibiotics have an effect on microbiota members such as Escherichia coli (E.coli) with reaching high concentrations in the gut. Prevalence of Q/FQ resistance E. coli in the healthy fecal carriers is a serious problem in developing countries. The aim of this study was to determine the prevalence rate of Q/FQ resistant E.coli isolates and plasmid-associated quinolone resistance genes (PMQR) in the asymptomatic fecal carriers.

Methods : A total of two hundred thirty-three community Extended-Spectrum B-Lactamase (ESBL) producing E.coli isolates were collected from healthy subjects without a history of antibiotic consumption in the last three months on Tehran in 2018. After evaluating the antibiogram pattern of E.coli isolates to nalidixic acid and ciprofloxacin, the minimum inhibitory concentrations (MIC) for ciprofloxacin were determined by E.Test.The presence of PMQR genes (qnrA, qnrB, qnrS, and qepA) was detected by PCR.

Results : Antibiotic susceptibility results showed that 121 (51.9%) and 75 (31.3%) of 233 of E.coli isolates were resistant to nalidixic acid and ciprofloxacin respectively. The MICs of ciprofloxacin for isolates ranged from 0.01 to 32 ug /ml. There were one or more PMQR genes in all the isolates with high and intermediate resistance phenotypes. The qnrS gene was the most frequent gene (40.3%) followed by the qnrB (24.5%) gene. Neither qnrA nor qep genes were detected.

Conclusion : In summary, fecal carriage of Q/FQ resistant E. coli occurs with alarming frequency among healthy people. Contact with other people or the food supply such as meat, dairy, or vegetables is the potentials explanation for the frequency of fecal carriage of resistance strains in people who not receiving antibiotics. The existence of PMQR genes confers high resistance to Q/FQ antibiotics.

Keywords : Extended-Spectrum B-Lactamase (ESBL), Plasmid-Mediated Quinolone Resistance (PMQR), E.coli, Intestinal carrier, Healthy people

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P76-425: Antibiotic resistance profiles of Pseudomonas aeruginosa strains isolated from urinary tract infections in Kerman, Iran

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Background and Aim : Treatment of Pseudomonas infections is difficult right now due to the recent decreased in antibiotic sensitivity. So, our information on antibiotic resistance patterns should be upgraded for appropriate therapy. Accordingly, the aim of this research was to evaluate the antibiotic resistance profiles of Pseudomonas aeruginosa strains related to urinary tract infections.

Methods : In this study, 15 isolates of Pseudomonas aeruginosa were isolated from 84 specimens isolated from patients with urinary tract infection in Kerman hospitals (Afzalipour and Shafa). Fifteen isolates were selected and disk diffusion susceptibility testing was performed for the antibiotics gentamicin, ciprofloxacin, imipenem, ceftazidime, tobramycin, cefepime, meropenem and cefotaxime and due to the higher sensitivity of the isolates to gentamicin Imipenem was determined by MIC micro agar dilution method.

Results : Results showed sensitivity to Gentamicin 11.25 (75%), ciprofloxacin 9 (60%), imipenem 9.75 (65%), ceftazidime 9.75 (65%), Cefepime 9 (60%), Tobramycin 11.25 (75%) and cefotaxime 0.75 (5%) and meropenem 8.25 (55%). The highest antibiotic resistance of Cefotaxime (50%) and the lowest antibiotic resistance (25%) were estimated in Gentamicin, Cefepime and Tobramycin. Two-bacterial hydrophobicity test was used to select bacteria for biofilm testing with HI below 30% (IAUK1143 and IAUK1147) and above 70%(IAUK1142 and IAUK1139). Strong hydrophobicity was selected to evaluate biofilm formation. The rate of biofilm formation in the plastic tube was higher than glass tube under both constant and conditions. In the case of isolates with strong hydrophobicity, the absorbance in the plastic tube is higher than in shaking condition and in the glass tube, the absorbance is higher in the static condition.

Conclusion : So, these data indicate that both antibiotic resistance and biofilm formation of most isolates are responsible for complicated therapy and physicians must receive the recent information about these traits of clinical strains of P.aeruginosa.

Keywords : Pseudomonas aeruginosa, MIC, biofilm, Antibiotic resistance

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P77-426: Antibiotic resistance and biofilm formation of Pseudomonas strains isolated from patients with respiratory tract infections in Kerman hospitals, Iran

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Background and Aim : Pseudomonas is one of the most common pathogenic bacteria in pulmonary infections and frequently develops resistance to different antibiotics. Accordingly, the aim of this research was to investigate antibiotic resistance and biofilm formation of Pseudomonas strains isolated from respiratory tract infections of hospitalized patients in Kerman, Iran.

Methods : In this study, 89 samples were obtained from patients and identified by biochemical methods during 2019. Antiboigram test with eight antibiotics was performed by disk diffusion method. Hydrophobicity of the bacteria was investigated by xylene for biofilm analysis. Selected bacteria with biofilm formation were examined on glass and plastic surfaces under static and shaking conditions.

Results : Twenty Pseudomonas were isolated with the highest resistance to Carbenicillin (76%) and the lowest antibiotic resistance to gentamicin (32%). Minimum inhibitory concentration of the Gentamicin was observed in concentrations of 2 to 4 micrograms/ml 5 (28%), and for the same concentrations for amikacin 1 (4%). For the biofilm test, two bacteria with hydrophobicity above 70% and two bacteria with hydrophobicity below 30% were evaluated. Accordingly, high hydrophobicity was directly related to biofilm production under shaking conditions. Resistant strains with high biofilm formation were also identified by PCR method.

Conclusion : Overuse and self-administration of drugs during recent years have caused antibiotic resistant strains of Pseudomonas with high ability in biofilm formation, which can lead to deaths in immunocompromised patients. So, by similar researches, our information about antibiotic resistance and biofilm formation patterns of Pseudomonas strains should be upgraded for appropriate therapy.

Keywords : Pseudomonas, MIC, Antibiotic resistance, Hydrophobicity, Biofilm formation

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P78-16: Assessing the knowledge and performance of nurses in selected hospitals under the auspices of Yazd University of Medical Sciences on the control of hospital infections in 2019

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Background and Aim : Hospital infections are one of the medical problems of this century. Hospital infections can lead to increased mortality and increased costs, as well as increased hospital stay. The lack of proper treatment by nurses in controlling hospital infections can cause many problems. Therefore, the present study was conducted to evaluate the knowledge and performance of nurses in selected hospitals under the auspices of Yazd University of Medical Sciences on the control of hospital infections.

Methods : This was a descriptive-analytical study that was performed cross-sectional in 2019 in selected hospitals under the auspices of Yazd University of Medical Sciences (Shahid Sadoughi Hospital, Shahid Rahnemoun Hospital and Afshar Hospital). The study population included nurses. The sample size was 270 according to the Cochran's formula. A researcher-made questionnaire was used to collect information. The questionnaire had 30 questions. The validity of the questionnaire was evaluated by content validation method and its reliability through internal consistency review and retesting method. Data analysis was performed by SPSS software and the scores obtained were classified into three levels: weak, medium and good.

Results : According to the present study, 69% of nurses were women and 31% were men. The results showed that in terms of knowledge, 18.43% of nurses were assessed at poor level, 44.71% at moderate level and 36.86% at good level. In terms of performance, 21.54% of nurses were evaluated at poor level, 27.32% at medium level and 51.14% at good level. Based on the results, the level of nurses 'knowledge in Shahid Sadoughi Hospital was higher and the level of nurses' performance in Afshar Hospital was higher.

Conclusion : According to the results of the present study, it is recommended that hospital managers increase the knowledge and improve the performance of nurses in controlling hospital infections as well as reduce additional costs, and make the necessary plans to hold training courses. Develop appropriate and appropriate policies in this area. It can also be very effective to provide educational pamphlets to nurses.

Keywords : Knowledge, Performance, Nurses, Hospital Infection Control

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P79-25: A narrative review of Injuries caused by needles and sharp objects and their dangers in medical staff

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Background and Aim : Needle injuries are a major source of nosocomial infections and the growing prevalence of communicable diseases. The growing prevalence of blood-borne diseases such as hepatitis (B and C) and AIDS raises serious concerns for health care providers. Therefore, the aim of the present study was to investigate the current situation in terms of injuries caused by needle and sharp objects and the relevant risk factors in the personnel of the health care provider to take the necessary action when necessary

Methods : The above article is an overview of articles used in databases such as Google Scholar (4 articles) and PubMed (3 articles) and SID (4 articles). Other scientific books have been used for writing

Results : The results show 33% of nursing staff in one year has been damaged by needle injuries. Accumulation these injuries are 68 injuries per 100 people per year. The injuries from he needles were abundant in the hospital's nursing staff . Due to the possibility of transmitting dangerous diseases such as hepatitis C, B and HIV As blood-borne diseases caused by these injuries It is possible to understand the importance of this study

Conclusion : Despite the infection control programs in hospitals, the rate of damage caused by needles and sharp objects in the study community is still high, and according to The presence of a variety of blood-borne infections can be a cause for concern. Inserting the needle cap is still done in a significant number of personnel that should be in Training should be considered. Applying safe devices to injections seems to be one way to reduce harm.

Keywords : Needles,sharp objects,hepatitis,nosocomial infection

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P80-37: Study of bacterial infection frequency in burn patients at a burn hospital in Iran

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Background and Aim : Wound infections are common problems in burn hospitals. Development of infections in burn wound is serious because of their effects on the course of the disease and patient outcomes. Many wound patient die as a result of infection during their hospital courses. The rate of infection in burn cases is extremely high in developing country. For this reasons we carried out study of the bacteriological profiles and a comparison of antimicrobial resistance patterns of these, over a period of one year.

Methods : : from March 2017 to April 2018, 1500 sample from Swabs and wound biopsy were included in this study. Identification of isolates was performed according to conventional bacteriological methods. The antibiotic susceptibility test was performed by disk diffusion method (Kirby – Bauer) according to Clinical Laboratory Standards Institute guidelines.

Results : 957(63.8%) of 1500 samples included of bacterial infections that were from different wards. 83.9% of isolates were gram negative and 16.1% of isolates were gram positive. the highest rate of infections were from ICU (50.2%) and the lowest were from restoration (6.6%). The commonest gram negative bacteria were Acinetobacter baumannii (34.7%) and Pseudomonas aeruginosa (29.6%). Staphylococcus aureus (10.2%) was the commonest gram positive bacteria. 50.7% of isolates were multi-drug resistant. The most resistant isolates were Acinetobacter baumannii and Pseudomonas aeruginosa. Between A.baumannii isolates the highest and the lowest antibiotic resistance were to ceftazidime (95.2%) and tobramycin (58.2%). Among P.aeruginosa the highest and the lowest antibiotic resistance were to ciprofloxacin (91.9%) and amikacin (57.9%). Among S.aureus the highest and the lowest antibiotic resistance were to Penicillin (63.2) and vancomycin (0%).

Conclusion : High prevalence of burn wound infections and presence of multidrug resistant bacteria in burn patients suggest strong surveillance of burn infections and develop strategies for antimicrobial resistance control and treatment of infectious complications.

Keywords : antibiotic resistance,burn ,infection

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P81-38: Molecular detection of extended-spectrum β-lactamases (ESBLs) in MDR Acinetobacter baumannii Strains isolated from burn wound infection in Isfahan, Iran

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Background and Aim : Acinetobacter baumannii is an opportunistic pathogen that is resistant to many antibiotics including beta-lactams. Production of β-lactamases is the main mechanism of β-lactam resistance in A.baumannii. The aim of this study was to determine the frequency of genes in clinical isolates of A. baumannii and relationship between antibiotic resistant and present ESBL genes in isolates of burn wound infection in Isfahan.

Methods : 123 A. baumannii strains were isolated from burn wound infection. After antibiotic resistance evaluation with the Kirby-Bauer disc-diffusion method .all isolates were evaluated with the Polymerase Chain Reaction (PCR) technique to detect the ESBL genes and followed by the statistical analysis in the end.

Results : Out of 123 A. baumannii isolates, 62.60% were ESBL positive according to PCR. The frequency of blaTEM and blaVEB genes were 30 (43.2%) and 13 (54.5%). there was significant relationship between the antibiotic resistance and the presence of ESBL gene (blaTEM and blaVEB) in A. baumannii.

Conclusion : The high prevalence of blaTEM and blaVEB gene in A. baumannii strains found in this study gives cause for important anxiety about burn wound infections in Isfahan and Iran because of the treatment complexity of these strains. Results this study highlight the need for infection control measures to prevent the spread of resistant isolates and ESBL, especially in burn hospitals.

Keywords : Acinetobacter baumannii, Antibiotic resistance, blaTEM and blaVEB

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P82-53: Nasal Carriage of Multidrug Resistant Staphylococcus aureus Among Health care workers in Kashan, Iran

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Background and Aim : Nasal carriage of Staphylococcus aureus is a substantial source of human infections. Detection and treatment of nasal carriage in children with methicillin-resistant and multidrug resistant S. aureus (MRSA and MDRSA, respectively) may be an important modality in prevention of infections. This study determined the prevalence, antibiotic resistance patterns and risk factors for nasal carriage of MDRSA among health care workers.

Methods : This cross-sectional study was carried out on 350 health care workers in Kashan city, Iran. From all health-care centers, four were chosen by simple random sampling. Nasal samples were cultured in blood agar medium for S. aureus and antibiotic susceptibility profile was determined by disc diffusion and E-test. Risk factors for nasal carriage of MDRSA were also determined.

Results : A total of 92 (26.3%) S. aureus isolates were obtained, of which 33 (35.9%) were MRSA and 27 (29.3%) were MDRSA. Of MRSA strains, 19 (70.4%) were MDRSA. S. aureus isolates showed 52.2% resistance to cephalothin, 33.7% to co-trimoxazole, 26.1% to clindamycin, 26.1% to ciprofloxacin, 4.3% to vancomycin, and 35.9% to oxacillin. The risk factors for nasal carriage of MDRSA were antibiotic usage during the last three months (P = 0.006) and emergency parts workers (P = 0.044).

Conclusion : MDRSA was not uncommon among health care workers in Kashan and prevention of its spread in the population is judicious.

Keywords : Staphylococcus aureus, Multidrug Resistance, Nasal, Carriers, Healthy workers

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P83-155: Association of blaPER-1 gene with quorum sensing and virulence factors in clinical Acinetobacter baumannii isolates

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Background and Aim : Acinetobacter baumannii is a gram negative opportunistic pathogen that is an important source of infections and one of the pathogens in patients hospitalized in the hospitals for a long time particularly in Intensive Care Units (ICUs).

Methods : 70 isolates from clinical different samples were collected.The antibiotic resistance pattern was evaluated based on the standard laboratory (CLSI). Analyzed the presence of blaPER-1, LuxR, LuxI, pld and ptk by polymerase chain reaction.

Results : Based on the results, all isolates had 100% resistance to ciprofoxacin, imipenem, rifampin and cefotaxime, whereas resistance to meropenem and amikacin and were 98.6% and 81.7%. The frequency of genes was Pld 100% , LuxI 85.7% , ptk 80%, LuxR 75.7% and blaPER-1 64.2%. Twenty-one isolates had coexistence of these six genes. We detected simultaneous presence of blaPER-1 gene with each of genes LuxI, LuxR, Ptk and pld in 38, 34, 36 and 45 isolates, respectively

Conclusion : There was no association between the presence of blaPER-1 gene and each of LuxI, LuxR, Ptk, and pld genes.

Keywords : Acinetobacter baumannii · quorum sensing · virulence genes

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P84-156: Investigate the association of Phenotypic and Genotypic of Biofilm Formation in Acinetobacter baumannii

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Background and Aim : Acinetobacter baumannii is an opportunistic pathogen that have persistence and survival ability in the hospital environment due to its multiple antibiotic resistance and ability to formation biofilms, and has been made as a serious problem health care worldwide.

Methods : Seventy clinical isolates of the Acinetobacter baumannii were collected and identified using biochemical tests. Biofilm formation ability was performed by crystal violet staining. Isolates were tested for the presence of biofilm related genes (bap, epsA, blaPER-1, pgaB) by PCR method.

Results : The phenotypic results of biofilm formation showed that 19 (27.14%), 30 (42.85%), 21 (30.06%) of the isolates had weak, moderate, and strong activities, respectively. The prevalence of pgaB, epsA, bap and blaPER-1 genes were 98,6%, 91.9%, 73.2% and 93.2%, respectively. All isolates had at least one gene associated with biofilm and 44.2% of isolates carried 4 biofilm related genes, simultaneously. Statistical analysis showed there was significant association between the ability to form biofilms and the presence of bap gene ($P < 0.05$).

Conclusion : Our study revealed the high prevalence of biofilm related genes and the correlation between the frequency of bap gene with the of biofilm formation.Therefore, that the prevention and treatment measures are necessary the Acinetobacter baumannii strains in our country

Keywords : Acinetobacter baumannii; biofilm formation; biofilm related gene

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P85-157: Association of molecular characterization and phenotypic in Acinetobacter baumannii

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Background and Aim : Extensive use of antimicrobials has led to the emergence of multidrug-resistant (MDR), as well as extensively -DR (XDR) and now more Pan-DR (PDR) strains. This led which A. baumannii strains is considered great and immediate threat to human lives and public health in healthcare settings in worldwide.

Methods : A total of 70 clinical isolates of Acinetobacter baumannii were collected during five months. The source of infection of these isolates included blood, urine, wound, and tracheal. The minimum inhibitory to colisitin and antimicrobial susceptibility to eight antibiotics tested and molecular typing was performed using random amplified polymorphism DNA.

Results : All of the isolates were MDR and 58.5% of them were XDR. Six of the isolates were resistant to all antibiotics used. Nine (12.8%) of the isolates were resistant to colisitin (MIC= 4 µg/mL). The random amplified polymorphism DNA patterns were clustered into five major genotypes.The results RAPD showed among the high genetic diversity isolates. According to RAPD profiles in agarose gels, the bands were in the range of 100-3000 bp.

Conclusion : The isolates had a nearly identical antibiotic resistance pattern with a high genetic variability. RAPD-PCR results showed no association between antibiotic resistance pattern and site of infection ($p < 0.05$).

Keywords : Acinetobacter baumannii, antimicrobial susceptibility, RAPD-PCR

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P86-158: Evaluation of protease activity, gelatinase production and hemolytic in Acinetobacter baumannii isolates

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Background and Aim : Acinetobacter baumannii causes a extensive range of infections that due to its adaptability to conditions and organism's survival, presence of different virulence factors and capacity to transmission in nosocomial environment, it has made treatment difficult.

Methods : 70 clinical isolates Acinetobacter baumannii were collected during January through May 2019 from three hospitals in Northwest, Iran. The isolates were identified using biochemical tests. The disk diffusion method for eight antibiotics and as well as the MIC for colistin was used. Gelatinase, protease and hemolytic activities were done by the phenotypic methods.

Results : The rate of XDR and MDR were 58.5% and 100%, respectively. Moreover, 9 (12.8%) isolates were resistant to colistin. The results showed twenty seven (38.5%) of the isolates of gelatinase activity were positive. hemolytic activity was detected in 11 isolates (15.5%), while 32 (45.7%) isolates production of protease.

Conclusion : Various virulence factors play a role in causing infections. Knowing the factors that play a role in the development of this organism is effective in preventing infection and treatment

Keywords : : Acinetobacter baumannii; Hemolytic; Gelatinases; Protease

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P87-162: Study of biofilm formation and molecular detection of antimicrobial resistance among the clinical isolates of Acinetobacter baumannii

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Background and Aim : Acinetobacter baumannii is a nonfermentative Gram-negative and non-motile rod. This bacterium is broadly found in intensive care units (ICUs) and can cause various hospital-acquired infections including urinary tract infection, bacteremia, burn wound infection, bloodstream infection, and respiratory tract infection. Unfortunately, an arising dilemma with A. baumannii is acquiring resistance to almost all regularly used antibiotics including ß-lactam agents, aminoglycosides, fluoroquinolones and Tetracyclines. This study was aimed to evaluate the presence of aminoglycosides and tetracycline resistance encoding genes and biofilm formation ability among clinical isolates of A. baumannii in intensive care units in the north

Methods : A. baumannii isolates were collected from various sources of hospitalized patients in ICUs. Antibiotic susceptibility test was per¬formed by disk-diffusion method as recommended by the (CLSI-M100-S28). The bacterial whole genome was extracted by the boiling method. we studied three major MDR A. baumannii genes, including efflux pumps (tetA), aminoglycoside-modifying enzymes (aacC1, aadB, aacC2, aphA6, aadA1, aacA4) and biofilm-related genes (csuE and ompA). The mi¬crotiter plate assay was used to determine the biofilm formation.

Results : Of 59 A. baumannii isolates, 33.9% were resistant to Doxycycline and 98.3% were resistance to gentamicin. The frequency rate of resistance genes was 76.3%, 0%, 78%, 44.1%, 28.8%,16.9%, 4.3%, 0%, 98.3% and 94.3% for tetB, tetA, aacA4, aphA6, aadB, aadA1, aacC2, aacC1, csuE and ompA respectively. All isolates were biofilm producers.

Conclusion : Our results revealed a significant diversity of resistance genes in our region. Dissimilar types of genes are carried by clinical isolates of A.baumannii in ICUs; so, it is necessary to isolate and detect precisely to reduce their severe consequences and patients mortality rate

Keywords : A.baumannii, multidrug-resistant bacteria (MDR), aminoglycoside-modifying enzymes (AMEs), tetracycline resistant, Biofilm.

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P88-164: Investigation of the effect of liposome containing clove essential oil on Pseudomonas aeruginosa and Escherichia coli as nosocomial infections

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Background and Aim : The aim of this study was to investigate the antibacterial effect of liposome containing clove essential oil. For this purpose, the lipid system containing clove essential oil has been synthesized for nosocomial infections Pseudomonas aeruginosa and Escherichia coli antibacterial methods.

Methods : The type of study is laboratory research. The nanoparticle synthesis method is Mozaffari method. Particle characterization has been performed in terms of size and charge with DLS and morphology with the Atomic Force Microscope (AFM) and the amount of loading and release with the spectrophotometer. MIC tests were then performed to evaluate the performance of nanoparticles containing clove essential oil on Pseudomonas aeruginosa and Escherichia coli.

Results : The average particle diameter was 46 nm and its zeta potential was -12.7 mV. The loading rate in nanoparticles was 63%, which was calculated by reading the absorption of light from the standard Trachyspermum Copticum curve. The minimum inhibitory concentration (MIC) of Pseudomonas aeruginosa and E.coli for nanoparticles was 15.625 and 31.25 mg / ml.

Conclusion : Nanoparticles containing clove essential oil kill nosocomial infections Pseudomonas aeruginosa and Escherichia coli and can be used as antibacterial nano-systems.

Keywords : clove, Antibacterial, Pseudomonas aeruginosa, Escherichia coli

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P89-169: Multiple-drug resistant and antimicrobial resistance pattern Enterobacteriaceae in hospitalized patients with cancer

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Background and Aim : Nosocomial infections are one of the most leading cause of morbidity and mortality in patients with cancer. The emergence of multiple-drug resistant (MDR) strains of Gram-negative bacteria causing nosocomial infection has become a serious concern in cancer patients.The present study aimed to determine the spectrum and antibiotic resistance pattern of Gram-negative bacteria related nosocomial infections among cancer patients.

Methods : This descriptive cross-sectional study was performed during the 6 months period from December 2015 to May 2016 in two tertiary care centers located in Isfahan and Arak Province. Gram-negative bacteria obtained from different clinical specimens from hospitalized patients with cancer and were identified using standard microbiological methods. Antibiotic susceptibility pattern was determined by the disk diffusion method according to the CLSI recommendation.

Results : Of totally 259 culture positive cases, E. coli showed the highest isolation rate (60.6%) followed by K. pneumoniae (26.6%), and Proteus spp. (11.2%). The rate of MDR isolates were 91.5% (237/259). Overall, the most frequent source of bacterial isolation was urinary tract infection (65.6%) followed by skin and soft tissue infection (23.6%). The antibiotic susceptibility results showed meropenem and ceftazidime as the most effective antibiotics toward E. coli, K. pneumoniae and Proteus spp. isolates. Moreover, meropenem was the most effective antibiotic against MDR isolates.

Conclusion : Our findings showed a significant distribution of MDR Gram-negative bacteria which may increase the burden of health care-associated infections in cancer patients. Although, carbapenem can be considered as effective agents toward MDR strains for empirical antibiotic therapy in our region.

Keywords : Nosocomial infection, Antibiotic resistance, Enterobacteriaceae, Cancer

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P90-172: Evaluation of drug resistance rate in Acinetobacter baumanii isolated from patients with ventilator-associated pneumonia of 2010 to 2020 in world: A systematic review and meta-analysis

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Background and Aim : The high resistance of Acinetobacter baumanii to various antibiotics and the prevalence of multidrug-resistant (MDR) strains make it difficult to control and treat. The aim of this study was of drug resistance in A. baumanii isolated from patient with ventilator-associated pneumonia (VAP).

Methods : All articles indexed in international databases (PubMed, Science Direct, Google Scholar, Biological abstracts, ISI web of knowledge and IranMedex) on drug resistance A. baumanii isolated from patient with VAP from 2010 to 2020 were reviewed. The full texts of English and Persian articles related with these subjects were included. Review articles, abstracts, articles in languages other than English and Persian, articles with unknown sample locations were excluded. Data were analyzed using meta-analysis and random effects models with the software package Meta R, Version 2.13 ($p < 0.0001$) (confidence interval: 95%).

Results : The prevalence of A. baumanii and MDR A. baumanii in VAP patients was 56.74% ($p = 0.00$) and 70.68% ($P < 0.0001$), respectively. Both of them had a significant relationship, with increasing A. baumanii and MDR A. baumanii in VAP patients, rate of A. baumanii infection was increased. The prevalence of A. baumanii in VAP had a significant relationship with the continent ($p < 0.0001$), Asia with 43.07% and Africa with 7% had the highest and lowest prevalence, respectively.

Conclusion : VAP is of particular importance in the intensive care unit of the hospital. Compliance with infection control standards is essential to prevent and, given the high prevalence of MDR A. baumanii.

Keywords : Drug Resistance, Acinetobacter baumanii, Ventilator-Associated Pneumonia

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P91-212: Clostridium difficile in patients with nosocomial diarrhea, Northwest of Iran

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Background and Aim : Clostridium difficile is an emerging healthcare problem in the world isolating from range of infections from mild diarrhea to pseudomembranous colitis. C. difficile infection is associated with administration of broad-spectrum antibiotic. Therapy. The main objective of the current study was to investigate the prevalence of C. difficile from hospitalized patients with nosocomial diarrhea in different wards of the northwest region of Iran.

Methods : In the present study, 485 stool specimens were analyzed from 384 patients referred from Imam Reza, Sina and Pediatric hospitals, during March 2015 to March 2018. Immuno-chromatographic method was used to detect of toxins A and B of C. difficile

Results : C. difficile was detected from 24 (4.7%) out of 485 specimens. Fifteen patients (62.5%) were males and 9 were females (37.5%). Twelve positive patients were from the gastrointestinal ward (50%), 5 patients (20.8%) from surgery ward, 3 patients from infectious disease ward (12.5%), 3 patients from rheumatology ward (12.5%) and 1 patient (4.1%) were collected from neurology ward. 95.3% of diarrhea samples had no signs from toxin A and B.

Conclusion : These findings show C. difficile infections were more prevalent in the gastrointestinal and surgery wards. C. difficile is a health care problem especially fallowing antibiotic usage. Developing alternatives for decrease antibiotic usage are vital for decrees frequency of C. difficile infections.

Keywords : Clostridium difficile, Incidence, Immunochromatographic test, Toxin A, Toxin B, Diarrhea

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P92-233: Chronic Nasal Infection Caused by Klebsiella Ozaenae

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Background and Aim : Klebsiella Ozanae is associated with chronic diseases of upper airway ozanae meaning stench. It is a rare progressive chronic rhinitis characterizes by a trophic changes in the nasal with resorption of the underlying bone formation of thic and greenish crust and a distinct fetid odor.

Methods : A 36 years old woman presented with a crusting rhinitis and foul greenish discharge mainly from the right nostril. She complained of bad nose smells.The nasal discharge specimens were inoculated on to sheep blood agar , chocolate agar , Mackonkey agar and thioglycolate broth and incubated at 37° in a 5% Co2 atmosphere . Identification was performed by using biochemical reactions

Results : After 24h of incubation on blood agar, chocolate agar, Mac agar revealed abundant growth of mucoid colonies . biochemical characteristics showed urease(-), indole (-) , MR (+), VP (-) , citrate (+), Lysin decarboxylase(-), motility(-). Antimicrobial susceptibility test showed resistant to Amoxicilin , Trimethoprime and Sulfamethoxazole.

Conclusion : The incidence of ozanae is little in developed countries . It is doubtless more common in developing countries . Ozanae has be reported to account for 0.3 – 7.8% of ear, nose and throat diseases in endemic areas. A low index of suspicion in non endemic areas could explain the delay in in its diagnosis and its management . This bacteria are not included in routine analyses. It was isolated because the physicians were aware of ozanae.

Keywords : Klebsiella Ozanae, Nasal infections, Greenish crus, Fetid odor

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P93-242: The Role of Ureaplasma urealyticum bacteria in infertile men

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1. *Shahed university, Tehran , Iran*

Background and Aim : Ureaplasma urealyticum bacteria is one of the most important microorganisms due to infertility. The aim of this study is to test the prevalence of U. urealyticum in infertile men. The patients that arrive to infertility clinics (Royan Institute in Tehran) with the semen culture analysis request are asked to fill in a questionnaire about infertility smear collection.

Methods : In this case control study presence of U. urealyticum were analyzed in tested men. we have compared 40 infertile males with unexplained infertility and 40 normal men with male factor as a control case group. The semen samples were sent to microbiology laboratory for culture and Selection of bacteria. The information were analyzed with SPSS software by frequency, chi-square & T-test Method .

Results : The average age in patients and control groups were 31.87+5.22 and 31.45+5.81 the value of U. urealyticum cases were 11(27.5%) and in normal men were 4(10%). (P=0.045) then we have found statistically significant differences in the U. urealyticum frequency of the patients. We have not found statistically significant relations between premature ejaculation and infertility. We have not found statistically significant relations between educational levels, ages, and marriage age, Duration of infertility, testis pain, smoking and infertility.

Conclusion : We have shown a significantly Ureaplasma urealyticum infections increase in the infertile men. The similarities between this study and the results obtained by others are limited and it may be due to different cultural and normal values in various societies. Though statistically significant due to limited number of subjects, however the difference observed in the prevalance of infection between cases and controls indicates an association between Ureaplasma urealyticum infection and infertility. So, it is suggested to check up those patient with unexplained infertility, for genital micro-organisms infections, and if positive, to control the rate of infertility with a suitable and cost effective therapy

Keywords : infertility-men- Ureaplasma urealyticum - Bacteria

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P94-243: Antibiotic resistance genes in Acinetobacter baumanii isolates from nosocomial infection

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Background and Aim : Bla-oxa enzymes are belonged to the beta-lactamase enzymes with strong penicillinase activity. Most of these enzymes can hydrolyze the carbapenems which cause resistance increasing to the carbapenems. bla-oxas, like betalactamases are exist on the naive chromosome in A.bumannii.

Methods : Presence of following bla-oxa related genes were assessed by polymerase chain reaction (PCR), for 100 clinical isolated A.baumannii samples: bla-oxa bla-oxa like, bla-oxaz like and bla-oxa4 like. Agar disk diffusion antibiotic susceptibility testing was performed for at least 10 different antibiotics. And finally using E.test. MIC measuring was evaluated for these three antibiotics ampicillin-sulbactam, gentamicin and meropenem.

Results : Present study showed that 100% of the clinical isolated A.baumannii samples have bla-oxas like gene, 38% were positive for bla-oxazı gene, 32% for bla- oxazlike and the presence of bla-oxa58 like gene was only 1%. Gentamicin and Meropenem were most effective antibiotics against A.baumannii in this study with 57% and 46% sensitivity respectively.

Conclusion : Due to the presence of bla-oxa related genes A.baumannii isolated clinical samples are highly resistance to the carbapenem in this study. Identifying of bla-oxas like gene can be a potentially reliable marker for specific diagnosis of A.baumannii

Keywords : Acinetobacter baumannii, Beta-lactamases enzymes, Bla-oxa genes

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P95-244: Mycoplasma hominis Bacterial Role in infertile women

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Background and Aim : Infertility is one of the most important problems for every family especially for women. The aim of this study is to test the prevalence of M. hominis, in infertile women. The patients that arrive to infertility clinics (Royan Institute in Tehran) with the cervical smear culture analysis request are asked to fill in a questionnaire about infertility smear collection.

Methods : In this case control study presence of M. hominis were analyzed in tested women who have been sent by gynecologists because of infertility. In this study we have compared 40 infertile females with unexplained infertility and 40 Normal pregnant women as a control case group. The samples were sent to microbiology laboratory. The information were analyzed with S.P.S.S software by frequency, chi-square, Mann-Whitney & T-test Method.

Results : The average age in patients and control groups were 28.92±6.20 and 24.97±43.37 the value of M.hominis. In infertile cases were 8. (20%) and in Normal pregnant were 3(7.5%) (x= 2.58) and (P= 0.1) then we have not found statistically significant differences in the M.hominis frequency of the patients. But we have found statistically significant relations between educational levels, the history of abdominal pains, the history of genital secretions and infertility, also we have not found statistically significant relations between marriage age, history of genital infections, history of smoking and infertility.

Conclusion : We have shown a significantly M. hominis infections increase in the infertile women. The similarities between this study and the results obtained by others are limited and it may be due to different cultural and normal values in various societies. Though statistically non-significant due to limited number of subjects. However the difference observed in the prevalence infection between cases and controls indicates an association between M. hominis infection and infertility. So, it is suggested to check up those patient with unexplained infertility, for genital micro-organisms infections, and if positive, to control the rate of infertility with a suitable and cost effective therapy.

Keywords : Mycoplasma hominis- infertility - women

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P96-245: Mycoplasma hominis bacterial Role in infertile men with abnormal Semen

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Background and Aim : Mycoplasma hominis is one of the most microorganism due to infertility. The aim is to test the prevalence of Mycoplasma hominis in infertile men. The patients that arrive to infertility clinics (Royan Institute in Tehran) with the semen culture analysis request are asked to fill in a questionnaire about infertility smear collection.

Methods : In this case control study presence of M.hominis were analyzed in tested men. we have compared 40 infertile males with unexplained infertility and 40 Normal men with Female factor as a control case group. The samples were sent to microbiology laboratory. The information were analyzed with SPSS software by frequency, chi-square & T-test Method.

Results : The average age in patients and control groups were 31.975.54 and 31.9.25.9 the value of M.hominis in infertile cases were 7(17.5%) and in Normal men were 2(5%). (X=3.13) and (P=0.077) then we have not found statistically significant differences in the M.hominis frequency of the patients. But we have found statistically significant relations between educational levels, the history of and infertility. Also we have not found statistically significant relations between history of libido, history of Impotency history of premature ejaculation, history of abdominal pain, history of testis pain history of smoking and infertility.

Conclusion : We have shown a significantly M.hominis infections increase in the infertile men. The similarities between this study and the results obtained by others are limited and it may be due to different cultural and normal values in various societies. Though statistically non-significant due to limited number of subjects, however the difference observed in the prevalence infection between cases and controls indicates an association between Mycoplasma hominis infection and infertility. So, it is suggested to check up those patient with unexplained infertility, for genital micro-organisms infections, and if positive, to control the rate of infertility with a suitable and cost effective therapy.

Keywords : Mycoplasma hominis- infertility - men

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P97-270: Raoultella Planticola as a urinary tract infection

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Background and Aim : Raoultella Planticola is a gram negative , anaerobic , nonmotile bacterium of the genus Raoultella , most frequently found in soil, water and aquatic environment.R. Planticola is quite similar in appearance to Klebsiella and so distinguished from Klebsiella by use histamine as the only source of carbon in the medium. Also, Raoultella grow at 4 °C and do not produce gas from lactose at 44.5 °C

Methods : A 35 years old man presented with UTI infection. The urine specimen was inoculated on to sheep blood agar and Mackonkey agar and incubated at 37° in a5% CO2 atmosphere. Identification was performed by using biochemical reactions.

Results : After 24h of incubation on blood agar, Mackonkey agar revealed abundant growth of mucoid colonies . biochemical characteristics showed urease(+), MR (+), VP (+), Lysin decarboxylase(+), motility(-).

Conclusion : R. planticola is an environmental bacterium that can cause serious infections in humans. Commonly, it does not cause human infections in the normal state, but human infections are in invasive medical procedures, , significant comorbidities , trauma with potential soil contamination or with the decline of immunization state. This bacteria are not included in routine analyses. It was isolated because the physicians were aware of Raoultella.

Keywords : Raoultella Planticola , urinary tract infection, klebsiella

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P98-283: Investigation on Urinary Tract Infections Following C-section and Assessment of CTX-M and TEM Genes Prevalence in Escherichia coli and Klebsiella Causing the Infections in Lamerd

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Background and Aim : : Antibiotics are usually prescribed by surgeons before and after surgery to prevent postoperative infections. Prophylaxes used for cesarean section in Lamrerd are cefazolin and cephalexin. According to studies carried out, urinary tract infections can also occur in spite of the above prescribed antibiotics. So, this research was carried out to determine those strains resistant to the mentioned antibiotics and also to identify genes causing resistance in antibiotic-resistant strains.

Methods : : 140 cases of mothers who had cesarean section (C-section) were considered in this study. The research began in April and lasted till July 2014 for case selection and sampling. It was emphasized to those women delivered via C-section to refer to laboratory 15 days after delivery. UA-UC tests were done on them. Phenotypic confirmatory test was performed for cefazolin and cephalexin antibiotic-resistant strains in the presence of ceftazidime, ceftazidime/clavulanic acid and cefotaxime, cefotaxime/clavulanic acid discs. The presence of CTX-M and TEM genes in the resistant strains were examined finally by performing PCR test.

Results : : Of 140 studied C-sections, 10 cases of urinary tract infections including 3 cases of E. coli (2.1%), 1 Klebsiella (0.7), 2 cases of Proteus (1.4%) and 4 cases of Staphylococcus (2.8%) were observed. According to phenotypic confirmatory test, Escherichia coli and Klebsiella strains were isolated as strains containing ESBL for next studies. Finally, according to PCR test for Escherichia coli and Klebsiella isolates, all of them contained CTX-M and TEM genes.

Conclusion : : It is necessary that microbial culture and antibiogram tests to be done before administering any antibiotics, in order to prevent the spread of strains containing ESBL with proper prescription of antibiotics.

Keywords : Urinary Tract Infections, C-section, CTX-M, ESBL, TEM

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P99-311: Frequency of Staphylococcus aureus adhesion genes in clinical isolates and nasal colonizer in the same patients

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Background and Aim : Staphylococcus aureus is an important human pathogen that can cause serious diseases such as septic arthritis, pneumonia, septicemia, osteomyelitis, toxic shock syndrome. The aim of this study was to evaluate the association of Staphylococcus aureus adhesion genes in clinical isolates and nasal colonizer in the same patients.

Methods : A total of 181 Staphylococcus aureus isolates (100 clinical isolates and 81 nasal colonizer isolates from the same patients) were collected from three hospitals. clfA, clfB, spa, and fnbA genes were detected by PCR. Antimicrobial susceptibility testing was carried out by disc diffusion method. Susceptibility to vancomycin was accomplished by microbroth dilution.

Results : The frequency of clfA, spa, fnbA and clfB genes in clinical isolate were 93%, 93%, 89% and 67% and in nasal colonizer in the same patients were 93.8%, 87.7%, 81.5% and 66.7%, respectively. Resistance to erythromycin, clindamycin, ciprofloxacin, cefoxitin, gentamicin, and co-trimoxazole in clinical isolates were 36%, 35%, 31%, 29%, 11%, 4% and in nasal colonizer in the same patients were 56/8%, 55/6%, 53%, 49/4, 28/4, 25/9 respectively. All isolates were susceptible to vancomycin and linezolid.

Conclusion : There is a high concordance rate between colonizing and clinical Staphylococcus aureus isolates in terms of adhesion factors. It is suggested that decolonization could be effective in preventing Staphylococcus aureus infections.

Keywords : Staphylococcus aureus, Adhesion genes, Nasal colonization

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P100-312: Frequency of superantigen genes of Staphylococcus aureus in clinical isolates and nasal colonizer in the same patients

Hamideh Rishi sharabiani[1] *, Javid Sadeghi[1] , Delara Laghousi[1] , Fatemeh yeganeh Sefidan[1]

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Background and Aim : Staphylococcus aureus is a leading cause of human infections. Nasal colonization by Staphylococcus aureus play important role in the epidemiology and pathogenesis of infection. The purpose of this study was to compare the frequency of superantigen genes of Staphylococcus aureus in clinical isolates and nasal colonizer in the same patients.

Methods : A total of 181 Staphylococcus aureus isolates (100 clinical isolates and 81 nasal colonizer isolates from the same patients) were collected from three hospitals. tst, sea, eta genes were detected by PCR method. Antimicrobial susceptibility testing was carried out by disc diffusion method. Susceptibility to vancomycin was accomplished by microbroth dilution.

Results : The frequency of sea, tst, eta genes in clinical isolates were 65%, 49%, 24% and in nasal colonizer in the same patients were 71/6%, 37%, 22/3% respectively. Resistance to erythromycin, clindamycin, ciprofloxacin, cefoxitin, gentamicin, and co-trimoxazole in clinical isolates were 36%, 35%, 31%, 29%, 11%, 4% and in nasal colonizer in the same patients were 56/8%, 55/6%, 53%, 49/4, 28/4, 25/9 respectively. All isolates were susceptible to vancomycin and linezolid.

Conclusion : There is a high concordance rate between colonizing and clinical Staphylococcus aureus isolates in terms of superantigen genes. It is suggested that decolonization could be effective in preventing Staphylococcus aureus infections.

Keywords : Staphylococcus aureus, Superantigen genes, Nasal colonization

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P101-314: Determining the frequency of the presence of two fimH, mrkD genes in ESBL-positive Colebisella pneumoniae isolates in hospitalized patients

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Background and Aim : Klebisella pneumoniae is a gram-negative bacterium that is involved in nosocomial infections, including respiratory, urinary, and blood infections. This bacterium has various pathogenic factors including fibrils, capsules, membrane transmitters, siderophores and LPS. FimH and mrkD are the sticky parts of the femur that play an important role in various infections. The aim of this study was to determine the frequency of two genes, fimH and mrkD, among the positive ESBL klebisella pneumoniae isolates in hospitalized patients in the cardiac hospital.

Methods : In a descriptive, cross-sectional study, 100 positive ESBL klebsiella pneumoniae isolates were selected. In this study, the antibiotic resistance pattern of these isolates was performed by diffusion disc method. After DNA extraction with the help of commercial kit, ESBL enzyme classes including SHV / TEM / CTX-M and frequency of FimH and mrkD genes were evaluated by PCR method.

Results : : Among the studied isolates, the most common enzyme class SHV / TEM / CTX-M, ESBL was examined which had one, two or all three. The frequency of CTX gene was 71.1% and the frequency of SHV gene was 47.1%. The frequency of the TEM gene was 64.4%. The frequency of mrkD gene was 82.8% and the frequency of fimH gene was 86.6%.

Conclusion : The mrkD and fimH genes are the most common coding genes for pathogenic factors in the positive strains of ESBL.

Keywords : Klebsiella pneumoniae, ESBL, hospitalized patients, fimH, mrkD

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P102-315: Occurrence of SCCmec types I–IV among clinical methicillin-resistant coagulase-negative staphylococci isolates in Ahvaz, Southwest Iran

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Background and Aim : Aims: The current study aimed to investigate the resistance patterns, and diversity of SCCmec types I, II, III, and IV in clinical methicillin resistant coagulase-negative staphylococci (MR-CoNS) isolates in Ahvaz, southwest of Iran

Methods : In this study, 44 clinical isolates of MR-CoNS were identified using microbiological tests, cefoxitin disc method, and polymerase chain reaction (PCR) amplification of the mecA gene. Antimicrobial susceptibility was investigated by disc diffusion. The differentiation of CoNS species was performed by d sequencing of the tuf gene. Multiplex PCR method was done for the detection of SCCmec elements.

Results : The Staphylococcus epidermidis and Staphylococcus haemolyticus were the most predominant isolates with a prevalence of 45.4%. The highest resistance was observed against erythromycin (84.1%) and clindamycin (75%). The most effective antibiotics were linezolid (77.3%) and quinupristin–dalfopristin (63.2%), respectively. The SCCmec type I was the predominant type (n = 20, 45.5%), followed by type IV (n = 4, 9.1%), type III (n = 2, 4.5%) and type II (n = 1, 2.3%). Six isolates had two types, III+ I (n = 5, 11.4%) and IV+ III (n = 1, 2.3%). Eleven (25%) isolates showed no band for types I-IV and might had other types. The presence of SCCmec elements and resistance to antibiotics was not significantly associated (p-value> 0.05).

Conclusion : Because of frequent occurrence of MR-CoNS harboring SCCmec type's genes in Ahvaz, southwest of Iran, the periodical monitoring of their drug resistance pattern should be considered in regional stewardship programs for useful antibiotic prescription strategies.

Keywords : SCCmec types , methicillin-resistant coagulase-negative staphylococci, S. epidermidis

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P103-319: The study Cell surface hydrophobicity and biofilm formation of Acinetobacter strains Isolated from Respiratory samples of the hospitals of Kerman, IRAN

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Background and Aim : Background: Acinetobacter a gram-negative, coccobacilli pathogen has emerged as causing nosocomial infections. The increased cell surface hydrophobicity caused an enhanced biofilm formation on surfaces.

Methods : Method: In this study, 53 specimens of the respiratory tract were collected in hospitals of Kerman. Biofilm formations were surveyed broth dilation and Microliter plates. Hydrophobicity was calculated using the procedure Rosenberg

Results : Results: The more hydrophobicity index was 85.31%. The ability to form biofilm on the polypropylene surface was higher than on the glass surface. Therefore determination of the most hydrophobicity index and biofilm formation of this organism can helps in treatment associated infection

Conclusion : Conclusion: The evolution of biofilm on different surfaces has an important role in decreasing the pathogenicity of Acinetobacter. Prevention and control of biofilm can affective colonization reducing of bacteria in hospital environments and medical instrument.

Keywords : Keyword: biofilm formation, hydrophobicity, Acinetobacter

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P104-387: The role of nursing in prevention and control of hospital acquired infections: a systematic review

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Background and Aim : Healthcare-associated infections (HAIs) or nosocomial infections are infections that occur while receiving health care. In hospitals, infected patients are a source of infection transmission to other patients, health care workers, and visitors. Nurses play a crucial role in preventing and controlling transmission of the infection through the application of standard precautions and maintenance of the health care environment. The aim of this study was to investigate the role of nursing in prevention and control of hospital acquired infections.

Methods : This article is a systematic review and a comprehensive search of three electronic databases, including Medline, Scopus and Web of Science was completed from 2010 until 2020. The search words was "nosocomial infection" , "HAI" , "nurses" and "health care workers" .23 articles found and 16 articles selected based on compliance with the key words and availability of the full text.

Results : Nursing professionals play an important role in the prevention and control of hospital infections since they carry out direct contact with the individual, invasive and potentially contaminated procedures, as well as the manipulation of patient equipment, instruments and medications. Nurses have many tools available to create a safe environment for patients that among others, there are five main areas of nursing practice where they can help and monitor control and prevention of HAIs which are as follows: promotion of hand hygiene, make best use of aseptic techniques, universal precautionary practices, patient's education and cleaning and disinfection practices.

Conclusion : It seems that the observance of health items by nurses has an important role in controlling and preventing nosocomial infections, so teaching these items to nurses during and after nursing education can be important in controlling and preventing nosocomial infections.

Keywords : Nosocomial infection, HAI, Nurses

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P105-400: The prevalence of Klebsiella pneumoniae isolated from patients in intensive care units (ICUs) of Firoozabadi hospital in Tehran during 2019-2020

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Background and Aim : Klebsiella pneumoniae has recently gained notoriety as an infectious agent due to a rise in the number of severe infections and the increasing scarcity of effective treatments. These bacteria are common cause of health-care associated infections including pneumonia, urinary tract infections (UTIs), and bloodstream infections. The aim of this study is to evaluate the prevalence of K.pneumoniae in intensive care units (ICUs).

Methods : 151 sputum samples were collected from intensive care of Firoozabadi hospital. Microscopic and biochemical tests were confirmed for all the samples. The collected data was analyzed by SPSS24.

Results : The frequency of Klebsiella pneumoniae in intensive care units (ICUs) of Firoozabadi Hospital was 48 (31.8%).

Conclusion : Klebsiella pneumonia is one of the main cause of infection in intensive care units. In this bacterium, resistance to antibiotics is increasing. These studies can help clinician to manage the prescribe medicine to prevent antibiotic resistance in intensive care units.

Keywords : Klebsiella pneumoniae , frequency, Intensive Care Units, Hospital infection

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P106-401: Study of the prevalence of Acinetobacter baumannii in intensive care units (ICUs) of Firoozabadi Hospital

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Background and Aim : Acinetobacter baumannii is an important opportunistic human pathogen that causes a variety of infections as ventilator-associated pneumonia, meningitis, bacteremia, wound and soft-tissue infections, peritonitis and urinary tract infections. In recent years, multidrug-resistant Acinetobacter baumannii has emerged as a major cause of health care-associated infection. The aim of this study is to evaluate the prevalence of A.baumannii strains in intensive care units (ICUs) of Firoozabadi hospital.

Methods : 151 sputum samples were collected from intensive care of Firoozabadi hospital. Microscopic and biochemical tests were confirmed for all the samples. The collected data was analyzed by SPSS24.

Results : The frequency of Acinetobacter baumannii in intensive care units (ICUs) of Firoozabadi Hospital was 67 (44.4%).

Conclusion : Examining the intensive care units of hospitals in terms of the type of bacteria and its antibiotic resistance helps physicians and treatment staff in prescribing effective antibiotics and controlling nosocomial infections. By conducting these studies, in addition to reducing costs for patients and hospitals, the mortality rate is reduced and the treatment process will be improved.

Keywords : Acinetobacter baumannii, Abundance, Intensive Care Units, Hospital infection

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P107-423: Association of pathogenicity islands and virulence factors among extended spectrum beta-lactamase producing Escherichia coli

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Background and Aim : Genes encoding virulence factors (VFs) such as toxins and adhesins are often encoded on pathogenicity islands (PAIs) which contribute in Escherichia coli (E. coli) pathogenicity and the development of urinary tract infection (UTI). Also, global increase in the extended-spectrum beta-lactamase (ESBL)-producing E. coli is an important public health concern. Molecular characterization of PAI genetic markers and its correlation with virulence traits of the ESBL producers can assist in better understanding of theirs evolution, epidemiological surveillance, and future preventive intervention. This study investigated the prevalence rate of virulence genes and PAIs in non-ESBL E. coli and ESBL producing E. coli isolates.

Methods : Current study was carried out in 2018 on 100 ESBL producing E. coli and 60 non-ESBL E. coli isolated from patients with UTI in Tehran. Sixteen genes encoding VF, and 8 PAI markers were screened by PCR method.

Results : We illustrated that 65% (n=100/155) of isolates were ESBL producers. PAI IV536 (86?%), genes of fimH (94%) and iroN (95%) were the most prevalent traits in most of isolates. PAI IJ96 marker was not detected in any isolate studied. A significant association ($p < 0.05$) in papA, hlyA, sat, and usp genes with ESBL producers, and also in afa gene with non-ESBL E. coli isolates was observed. ESBL producers had a higher number of PAI markers compared to non-ESBL E. coli. There was a significant positive association between the presences of PAI III536 in ESBL producers vs. non-ESBL isolates (57% vs. 29%). The sat gene was detected in non-ESBL and non-ESBL isolates carrying more than three and four PAI markers. Increased VFs and high resistance in ESBL producers can give a fitness advantage in the pathogenic niche and promote progression to pyelonephritis, septicemia, and septic shock, and as well as reduced the therapeutic options for UTI.

Conclusion : Our study suggests a correlation between ESBL production and some VFs. The ESBL producers associated with high virulence leads to increase in severity of UTI, and treatment failure.

Keywords : urinary tract infection, extended-spectrum beta-lactamase, virulence factors, pathogenicity islands

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P108-433: Isolation of a specific bacteriophage against antibiotic-resistant Klebsiella pneumoniae

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Background and Aim : Nosocomial infections are one of the major medical problems in the world. The members of the Enterobacteriaceae family, especially Klebsiella pneumoniae, play an important role in the development of antibiotic-resistant nosocomial infections. One way to fight antibiotic-resistant bacteria is to use bacterial viruses or bacteriophages. In this regard, the present study was aimed to isolate specific bacteriophage against K. pneumoniae.

Methods : To isolate Klebsiella specific bacteriophages,50mL of municipal wastewater sample was added to 50mL BHI broth (2X). One milliliter of an overnight culture of K. pneumoniae was then added to the mixture. After 24 h incubation at 37 ◦C, specific bacteriophage was isolated against antibiotic-resistant Klebsiella by double layered agar method. Finally, the host range of the isolated phage was determined by spot test.

Results : The findings of this study show that the isolated bacteriophage only affects some strains of K. pneumoniae and forms a clear zone of inhibition, suggesting that the virus is a virulent phage.

Conclusion : Phage therapy can be introduced as an alternative to antibiotics to fight antibiotic-resistant infections. For this purpose, virulent bacteriophages like the isolated Klebsiella phage can be used.

Keywords : -

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P109-13: Investigation phylogenetic groups distribution of commensal Escherichia coli strains of people with colorectal cancer and healthy people.

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Background and Aim : Colorectal cancer or CRC, is the third-most common cancer in the world. Escherichia coli is one of the components of gut microbiota, which approved that in comparison with healthy people, it,s population is increased in people's gut with CRC. pathogenic E. coli strains fall into phylogenetic group B2 or D which have a type of virulence factor and most E.coli strains that isolated from the patients with CRC, belonged B2 phylogenetic group, Therefore it can be considered as a risk factor for the development of CRC. The aim of this study was the distribution of phylogenetic groups distribution of E. coli strains which isolated from patients with CRC and healthy people.

Methods : In this study from 70 stool samples (50 normal and 20 patients with colorectal cancer), E. coli strains were isolated and cultured. PCR was performed with a standard protocol. In isolates related to the B2 phylogenetic group, chuA and also yja genes are positive but in D phylogenetic group yja gene is negative. In B1 and A phylogenetic groups, the chuA gene is negative; however TSEP4C2 DNA fragment in B1 exists but A phylogenetic group has not this fragment of DNA.

Results : From 20 E. coli strains of patients 11(55%), 7 (35%), 0 and 2 (10%) were related to B2, D, B1, and A phylogenetic groups respectively.

Conclusion : Phylogenetic analyses have shown that most of the E.coli strains isolated from patients fall into the B2 phylogenetic group significantly.

Keywords : Colorectal cancer, Escherichia coli, A, B1, B2, and D phylogenetic groups

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P110-14: Occurrence multidrug resistance (MDR) in commensal Escherichia coli strains in patients with colorectal cancer

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Background and Aim : Antibiotic resistance is a serious problem for health. On one hand, because E.coli is a versatile species containing both highly virulent and commensal strains and antibiotic resistance inducer genes are transferable between the Enterobacteriaceae family, It is of importance to identify factors that are responsible for pathogenicity. And the other hand E.coli as one of the components of gut microbiota, in comparison with healthy people, it,s population is increased in the gut of people with colorectal cancer or CRC. Our study aimed to investigate the antibiotic resistance and proteome profile of MDR and susceptible isolates of E. coli flora from people who have colorectal cancer.

Methods : 20 and 50 gut flora E.coli isolates from CRC patients and healthy people were cultured and antibiotic susceptibilities were determined by the disc diffusion method. The discs used in this study were Sulfamethoxazole(SXT), Tetracycline (TE), Ciprofloxacin (CP), Amoxicillin (AMX), Nalidixic acid (NA), Cotrimoxazole (CTX), Ampicillin (AM), Ceftazidime (CAZ) and Kanamycin A (K).

Results : Among the isolates of the healthy group, first place for the most sensitivity and resistance in order belonged to Ciprofloxacin (CP) and Ampicillin (AM). While in the other group, almost sensitivity and resistance were for Ceftazidime (CAZ) and Sulfamethoxazole (SXT) respectively.

Conclusion : Among these isolates in both groups of patients and control, the difference in frequency of antibiotic resistance for 7 antibiotics was significant and in both groups more than 90% of commensal E.coli strains were MDR.

Keywords : Antibiotic resistance, MDR, gut flora, Escherichia coli, colorectal cancer, CRC.

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P111-20: A Systematic Review of Gut Microbiota Roles in Irritable Bowel Syndrome

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Background and Aim : Irritable bowel syndrome (IBS) is common but difficult to treat. Altering the gut microbiota has been proposed as a strategy for treatment of IBS, but the association between the gut microbiome and IBS symptoms has not been well established. We performed a systematic review to explore evidence for this association.

Methods : We searched databases, including MEDLINE, EMBASE, Cochrane CDSR, and CENTRAL, through January, 2018 for case–control studies comparing the fecal or colon microbiomes of adult or pediatric patients with IBS with microbiomes of healthy individuals (controls). The primary outcome was differences in specific gut microbes between patients with IBS and controls.

Results : The search identified 2631 citations; 24 studies from 22 articles were included. Most studies evaluated adults presenting with various IBS subtypes. Family Enterobacteriaceae (phylum Proteobacteria), family Lactobacillaceae, and genus Bacteroides were increased in patients with IBS compared with controls, whereas uncultured Clostridiales I, genus Faecalibacterium (including Faecalibacterium prausnitzii), and genus Bifidobacterium were decreased in patients with IBS. The diversity of the microbiota was either decreased or not different in IBS patients compared with controls. More than 40% of included studies did not state whether cases and controls were comparable (did not describe sex and/or age characteristics).

Conclusion : In a systematic review, we identified specific bacteria associated with microbiomes of patients with IBS vs controls. Studies are needed to determine whether these microbes are a product or cause of IBS.

Keywords : Inflammation; Intestine; Comparison; Infection.

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P112-22: The Gastric Microbiota in Health and Disease: A Systematic Review

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Background and Aim : Helicobacter pylori is the most infamous constituent of the gastric microbiota and its presence is the strongest risk factor for gastric cancer and other gastroduodenal diseases. Although historically the healthy stomach was considered a sterile organ, we now know it is colonised with a complex microbiota. However, its role in health and disease is not well understood. The aim of study was to systematically explore the literature on the gastric microbiota in health and disease as well as the gut microbiota after bariatric surgery.

Methods : A systematic search of online bibliographic databases MEDLINE/EMBASE was performed between 1966 and February 2019 with screening in accordance with Preferred Reporting Items for Systematic Reviews and Meta-Analyses guidelines. Randomized controlled trials, cohort studies and observational studies were included if they reported next-generation sequencing derived microbiota analysis on gastric aspirate/tissue or stool samples (bariatric surgical outcomes).

Results : Sixty-five papers were eligible for inclusion. With the exception of H pyloriinduced conditions, overarching gastric microbiota signatures of health or disease could not be determined. Gastric carcinogenesis induces a progressively altered microbiota with an enrichment of oral and intestinal taxa as well as significant changes in host gastric mucin expression. Proton pump inhibitors usage increases gastric microbiota richness. Bariatric surgery is associated with an increase in potentially pathogenic proteobacterial species in patient stool samples.

Conclusion : While H pylori remains the single most important risk factor for gastric disease, its capacity to shape the collective gastric microbiota remains to be fully elucidated. Further studies are needed to explore the intricate host/microbial and microbial/microbial interplay.

Keywords : microbiota, Gastric Microbiota, Helicobacter pylori, gastric disease

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P113-175: Intestinal carriage of extended-spectrum beta-lactamase-producing Escherichia coli among a mental disability children's under the age of ten

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Background and Aim : Beta-lactam antibiotics are the most important drugs used to treat Enterobacteriaceae infections. The increase in asymptomatic carriers of ESBL-producing bacteria is a concern in the community. Thus this study aims to assess the prevalence of intestinal carriage of extended-spectrum β-lactamases(ESBLs) producing E.coli in children with mental disabilities under 10 years.

Methods : cefotaxime and ceftazidime discs were used to screen the ESBLs producing E.coli. The production of ESBLs was confirmed by double-disc synergy assay with amoxiclav, cefotaxime, and ceftazidime discs. TEM and CTX-M-1 genes were identified by PCR. Antimicrobial susceptibility was performed by disk-diffusion method.

Results : a total of 71 ESBLs producing E.coli were isolated from 110 volunteers. The highest prevalence was observed among children under 4 years (75%). 19.7% of isolates carried blaCTX-M-1 and blaTEM simultaneously. 84.5% of isolates showed a multi-drug resistance phenotype. All isolates were resistant to cefotaxime. The most resistance rate was found to ceftazidime (95.6%) and aztreonam (90.1%) and the least resistance was observed in imipenem (1.4%). 81.7% showed resistance to trimethoprim/sulfamethoxazole,49.3% to tetracycline,87.3% to ciprofloxacin and amoxicillin/clavulanate,14.1% to gentamicin and 4.2% to meropenem.

Conclusion : Our study shows evidence of a significant prevalence of carriers of ESBL-producing E.coli in children under the age of ten with a mental disability, especially under the age of four years. Efforts can be made to reduce ESBL carriers by modifying the infection control policy, banning the sale of over-the-counter antibiotics, and guiding people about the dangers of overuse of antibiotics.

Keywords : Escherichia coli, ESBLs, Intestinal carriage, CTX-M-1

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P114-176: Intestinal carriage of extended-spectrum beta-lactamases producing klebsiella among children under 10 years in Tehran

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Background and Aim : Multidrug-resistant gram-negative bacteria are a serious threat to public health. In recent years, the production of extended-spectrum beta-lactamases (ESBLs) in the Enterobacteriaceae has increased significantly. Reports of carriers of ESBL-producing bacteria are significant in healthy individuals, especially children. This article aims to assess the prevalence of ESBL-producing Klebsiella carriers.

Methods : Two cefotaxime and ceftazidime antibiotics were used to screen of ESBls producing bacteria. The production of ESBLs was confirmed by double-disc assay with amoxiclav, cefotaxime, and ceftazidime discs. TEM and CTX-M-1 genes were identified by PCR. Antimicrobial susceptibility was performed by disk-diffusion method.

Results : a total of 24 ESBls-producing Klebsiella were isolated from 332 volunteers. The highest prevalence was observed among children 4 to 6 years (41.7%). CTX-M-1 was the most common ESBL gene (66.7%). 1.6% of isolates carried blaCTX-M-1 and blaTEM simultaneously. 8.3% isolates carried only the blaTEM. The highest antibiotic resistance was observed in cefotaxime (87.5%) and ceftazidime (87.5%) and the lowest in gentamicin (4.2%). Resistance to trimethoprim/sulfamethoxazole, tetracycline, ciprofloxacin, aztreonam and amoxicillin/clavulanate antibiotics were 79.2%, 62.5%, 13%, 54.2% and 54.2%, respectively. 91.7% and 70.8% of isolates were susceptible to imipenem and meropenem, respectively. 95% of isolates exhibited multidrug resistance.

Conclusion : This prevalence of ESBls-producing Klebsiella in healthy children under 10 years is significant and poses a serious threat to community health. Carrying ESBL-producing organisms is a potential risk factor for transmission and spread of infection and requiring substantial monitoring and control over antibiotic use in agriculture and animal husbandry as well as against nosocomial infections.

Keywords : Klebsiella, broad-spectrum beta-lactamases, intestinal carriers, CTX-M-1

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P115-184: The importance of major butyrate producer bacteria, Faecalibacterium prausnitzii , in inflammatory conditions

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Background and Aim : Faecalibacterium prausnitzii (F. prausnitzii) seems to be about 5% of the fecal microbiota in healthy adults which is one of the amplest bacteria in the human intestinal microbiota of healthy adults. If F. prausnitzii is less in the gut, several disorders would be implicated, such as inflammatory bowel disease (IBD), irritable bowel syndrome (IBS), Colorectal cancer (CRC), obesity, coeliac disease, and diabetes it is still not vivid whether this is a cause or a consequence of these disorders. Most information links plentitude of F. prausnitzii to health in which comes from 16S rRNA based on profiling of microbiota in inflammation. the interaction of this bacterium with inflammation has been studied for several years. inflammation is the main key in initiation and development of cancers and has a crucial role in commencing majority of diseases specially cancer.

Methods : About 60 articles were gathered around the world and have been studied carefully. some of the important details were extracted and written in 2 tables.one is for in vivo experiments and the other table is about in vitro.

Results : In in vivo and in vitro conditions, F. prausnitzii could alleviate IL-12, IFN-**λ**, IL-8, IL-17, TNF-α, IL-6, and IL-17 levels and on the other hand could increase IL-10 secretion, IL-12p70, TGF-β, surface expression CD83, CD86 and CD40

Conclusion : F. prausnitzii and its supernatant have a great anti-inflammatory role and by these anti-inflammatory properties, this bacterium contributes to immune homeostasis in the intestine. Thus, F. prausnitzii can be introduced as next-generation probiotics and treat for inflammatory diseases.

Keywords : Faecalibacterium prausnitzii, inflammation, gut microbiota, anti-inflammatory

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P116-196: The Evaluation of Intestinal Carriage ESBL-Producing Escherichia coli among Dialysis Patients in Tehran

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Background and Aim : Gastrointestinal colonization of ESBL-producing bacteria is a worldwide concern nowadays, especially among high-risk patients. This study aimed to assess the prevalence of fecal carriage of extended-spectrum B-lactamase (ESBL)-producing Escherichia coli in dialysis patients.

Methods : From January 2018 to May 2019, 150 fecal samples were collected in the dialyze ward of a hospital in Tehran. Fecal samples were diluted in saline and cultured on MacConkey agar plates including cefotaxime(30µg) and ceftazidime(30µ) disks. Colonies growing in the inhibition zone of each disk were screened for the presence of ESBLs. Antibiotic susceptibility testing was done by the disk diffusion method. PCR was used for detecting the presence of blaCTX-M-1, blaTEM, and blaSHV genes.

Results : The total prevalence of ESBLs carriage was 50% (75/150). The most frequent gene was blaCTX-M-1 (81.4%). Seventeen isolates co-harbored blaCTX-M-1 and blaTEM, one isolates co-harbored blaTEM and blaSHV and two isolates co-harbored blaCTX-M-1, blaTEM and blaSHV. Fifty-three isolates carried a single gene, including blaCTX-M-1 in 43 isolates, blaTEM in 6 isolates, and blaSHV in 4 isolates. 7 isolates did not harbor any of the 3 genes. The highest rates of resistance belonged to cefalotin (98.9%), cefotaxime (94.7%), aztreonam (83.1%), ceftazidime (78.9%). The lowest rates were seen for fosfomycin (3.15%), meropenem and imipenem (1.05%). 96.8% of isolates were multidrug-resistant.

Conclusion : These results demonstrate highly carriage rate of ESBLs in dialysis patients. Therefore, active surveillance will be useful for reducing the transmission of antimicrobial-resistant bacteria and preventing infection.

Keywords : Escherichia coli, ESBLs, Intestinal carriage, CTX-M-1

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P117-294: Antagonistic effect of Endophytic bacteria against Erwinia amylovora

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Background and Aim : Recently, potential role of endophytic bacteria in control of phytopathogens has been demonstrated. In our country, Iran, few studies has been done about the role of these bacteria in controlling plant bacterial pathogens. Therefore, the aim of this study was to isolate and identify endophytic bacteria with antagonistic activity against Erwinia amylovora.

Methods : Soil, root and leaf samples of apple and pear trees were collected from gardens located in vicinity of Gorgan, Golestan, Iran. The samples were disinfected by ethanol and sodium hypochlorite, rinsed three times with sterile distilled water (SDW). After cutting roots and leaves into small fragments in SDW, a loopful of the resulting suspension was streaked on nutrient agar and incubated at 26°C for 3 days. All colonies were distinguished based on their morphology and purified. Finally, the ability of the isolates to produce diffusible metabolites was tested according to the agar well diffusion assay.

Results : Bacterial strains isolated from the samples were identified as follow: Bacillus spp., Brevibacillus spp., Paenibacillus spp. The inhibitory effect of these isolates was evaluated against E. amylovora and revealed that Bacillus spp. were able to inhibit E. amylovora growth in agar well diffusion assay.

Conclusion : Based on the result of this study, Bacillus spp. are promising organisms for the control of plant diseases caused by Erwinia amylovora. However, further studies required to determine accurately the biochemical and molecular characteristics used to distinguish a given species and their potential application in biological control.

Keywords : Antagonistic effect, Erwinia amylovora, Endophyte, Soil, Leaves, Root

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P118-308: Antifungal effects of cellulose-degrading bacteria isolated from bovine excrement against phytopathogenic fungi

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Background and Aim : Bovine excrement is a rich source for screening cellulolytic bacteria. The present study was conducted to isolate and identify cellulose degrading bacteria from bovine excrement and their screening for potential antifungal activity.

Methods : The cellulolytic bacteria were screened out and isolated from the collected samples by serial dilution method on modified Czapeck (CMC) agar medium and subsequent Congo red assay. Seventeen isolates were selected on the basis of cellulose degrading activity through Congo red assay. The antifungal activity of these isolates was also determined against different phytopathogenic fungi including Alternaria, Cladosporium, Verticillium, Fusarium, Mucor and Rhizopus.

Results : The isolates were identified according to standard biochemical tests in Bergey's manual. Among the 17 isolates, 10 to Bacillus spp., 2 to Pseudomonas spp., 1 to Citrobacter spp., 3 to Staphylococcus spp. and one belonged to Penibacillus. The antifungal activity against the target phytopathogens was shown by the isolates of some Bacillus species. Isolate Bacillus spp. R7 showed high activity against Alternaria by giving a zone of inhibition of 16mm while isolate R1 showed good antifungal activity against Fusarium by giving a clear zone of 13 mm.

Conclusion : The results of the present study is promising for biocontrol of phythopathogens and it is possible to use biological control as an effective strategy to manage plant diseases, increase yield and protect the environment.

Keywords : Cellulolytic bacteria, Antifungal Activity, Phytopathogen, bovine excrement

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P119-389: The Role of the gut microbiota in immune system

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Background and Aim : Recent advances in microbiome research showed that the gut microbiome is not just a passive bystander, but actively impacts multiple host functions, including circadian rhythmicity, nutritional responses, metabolism and immunity. The aim of this study is to investigate the role of the gut microbiota in immune system.

Methods : This article is a systematic review and a comprehensive search of three electronic databases, including Medline, Scopus and Web of Science was completed from 2005 until 2020. The search words was "gut microbiota" , "immune system" , "immunity" and "microbiome" .29 articles found and 17 articles selected based on compliance with the key words and availability of the full text.

Results : The gut microbiota is important for the development and functional maturation of the gut immune system, including gut-associated lymphoid tissue, T helper 17 cells, inducible regulatory T cells, IgA-producing B cells and innate lymphoid cells. The gut microbiota regulates susceptibility to extra-intestinal autoimmune diseases, such as multiple sclerosis, type 1 diabetes, arthritis and allergy. The gut microbiota prevents exogenous pathogen infection through direct (for example, competition for common nutrients and niches) and indirect (for example, enhancement of host defence) mechanisms. Understanding the interaction of the microbiota with pathogens and the host might provide new insights into the pathogenesis of disease, as well as novel avenues for preventing and treating intestinal and systemic disorders.

Conclusion : It seems that the intestinal microbiome plays an important role in regulating and organizing various immune systems, so it is necessary to protect this microbiome. Due to the relationship between the intestinal microbiome and the immune system, further studies can be performed to determine the relationship between this microbiome and autoimmune diseases.

Keywords : Intestinal microbiome, Immune system, immunity

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P120-214: SWOT analysis of Brucella abortus (IRIBA) vaccine production in Iran

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Background and Aim : The Brucella abortus (IRIBA) vaccine is currently used for calves brucellosis in Iran. Currently, the production of the vaccine is by traditional cultivation on a solid medium in RVSRI, but the fermentation production using a liquid culture medium is under development. An ideal live vaccine should have long-term protection period against infection and abortion at any age of cattle. However, the main barriers to improving quality and increasing production capacity are traditional production process as well as supplying necessary raw materials for vaccine production and lack of standard reference seed preparation from OIE centers. In order to obtain better performance of the production of brucellosis vaccines in cattle to enable the improvement of disease surveillance and reporting in Iran, a SWOT analysis was carried out for the current vaccine production to identify weaknesses and areas that could be improved to enhance disease surveillance and reporting structures.

Methods : A systematic review was carried out to obtain data on the strengths, the weaknesses, the opportunities and threats to IRIBA vaccine production, using a Matrix Preparation (SWOT) of internal and external influence factors. The identified factors were then allocated to each parameter as they were determined, and discussed.

Results : The results of the SWOT analysis a based on the situational assessment of the IRIBA vaccine production, the following gaps and challenges have been identified: Persons with experience are available for training to new generations of vaccine and build capacity for improved the vaccine production and management. The infrastructure required for implementing production line and programs for IRIBA vaccine is weak, especially during times of production and deployment. Greater involvement of expert people is needed in the creation of activities and renovation of the IRIBA vaccine production line.

Conclusion : The factors identified in this study could be effective and improvement through capacity building training, survey development and the use of this training in the production of the brucellosis vaccine in Iran. However, this concept provides a sustained groundbreaking platform for a real change in the vaccine production paradigm towards the development of successful measures to contain the Brucella vaccine dilemma.

Keywords : SWOT analysis, Brucella abortus, IRIBA Vaccine, Razi Vaccine and Serum Research Institute (RVSRI)

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P121-226: SWOT analysis of sheep and goats brucellosis vaccine Rev.1 production in Iran

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Background and Aim : Brucella melitensis is the most common species of Brucella in human illnesses. The Rev.1 vaccine is currently used for sheep and goat brucellosis. The production of Rev.1 vaccine is by traditional cultivation in RVSRI, but the production of vaccine fermentation using a liquid culture medium is under development. The production vaccine is by manual cultivation on a solid medium in RVSRI. However, the main barriers to improving quality and increasing production capacity are traditional production process as well as supplying necessary raw materials for vaccine production. In order to obtain better performance of the production of brucellosis vaccines in cattle to enable the improvement of disease surveillance and reporting, a SWOT analysis was carried out for the current vaccine production to identify weaknesses and areas that could be improved to enhance disease surveillance and reporting structures in Iran.

Methods : In this study, a systematic review was carried out to obtain data on the strengths, the weaknesses, the opportunities and threats to Rev.1 production, using a Matrix Preparation of internal and external Influence Factors. The identified factors were then allocated to each parameter as they were determined, and discussed.

Results : The SWOT analysis a based on the situational assessment of the Brucella production, the following gaps and challenges have been identified: Existence of Technology knowledge of vaccine production. Staff are available for training to build capacity for improved Rev.1 production and management. The infrastructure required for implementing Production line and programs for Rev.1 weak, especially during times of production and deployment. Management and coordination of programs and policies are weak. Relative instability and susceptibility of the vaccine. Greater involvement of expert people are needed in the creation of activities and renovation of the Rev.1 production line.

Conclusion : The factors identified in this study could be effective and improvement through capacity building training, survey development and the use of this training in the production of the brucellosis vaccine. However, this concept provides a sustained groundbreaking platform for a real change in the vaccine production paradigm towards the development of successful measures to contain the Brucella vaccine dilemma.

Keywords : SWOT analysis, B. melitensis Rev.1 Vaccine, Razi Vaccine &Serum Research Institute (RVSRI)

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P122-230: Effect of culture media and their ingredients on Poly ribosyl ribitol phosphate (PRP) production by Haemophilus influenzae

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Background and Aim : Haemophilus influenzae type b (Hib) is a gram-negative encapsulated bacterium responsible for severe diseases, including epiglottitis, pneumonia, sepsis, and meningitis almost exclusively in children aged less than 5 years. The widespread use of Hib conjugate vaccines in infancy has led to a dramatic decline in the incidence of invasive Hib disease in children. Capsular polysaccharide, Poly ribosyl ribitol phosphate (PRP) of Haemophilus influenzae type b (Hib), is important for the production of the conjugate vaccine, the production of PRP is directly related to the culture media and their ingredients. Capsular polysaccharide, Poly ribosyl ribitol phosphate (PRP) of Haemophilus influenzae type b (Hib), is important for the production of the conjugate vaccine and its production directly related to the culture media. The industrial production of the PRP capsular polysaccharide requires the cultivation of Hib in a modified medium, which impacts process costs and product purification. The present study aims to investigate the effect of the growth factor medium component on PRP production by Hib.

Methods : The industrial production of the poly ribosyl ribitol phosphate (PRP) capsular polysaccharide requires the cultivation of Hib in a modified medium, which impacts process costs and product purification. In this study, a central composite experimental design strategy was used to access the influence of key components of culture medium (percentage of dissolved oxygen, and glucose concentration) on biomass formation and polysaccharide production in 5-liter shake-flasks.

Results : The optimized medium condition, containing dissolved oxygen (30-10%) and glucose concentrations(10-15g/l) was further validated in fed-batch bioreactor cultivations. Maximum PRP production (~ 900µg /ml) was obtained in this production process for use in Hib vaccine production.

Conclusion : In this study, we were able to get a higher rate of PRP in a simpler culture media by replacing Cas amino acid with Soy peptone which is in line with the World Health Organization goal to reduce the production costs. therefore we decided to improve culture media and produce more PRP as one of the components of the Pentavalent vaccine to reduce the production costs.

Keywords : Haemophilus influenzae type b,Poly ribosyl ribitol phosphate, vaccine, culture medium

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P123-246: Economic Analysis of Seasonal Influenza Inactive Vaccine Injection in Pregnant Women of Iran

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Background and Aim : Pregnant women are considered as one of the high-risk groups for influenza. The best way to protect influenza in pregnant women and infants less than 6 months of age is to vaccinate pregnant women. Given the importance of vaccination against seasonal influenza in pregnant women and the cost of preventing influenza in pregnant women, can vaccination in pregnant women be considered as a cost-effective intervention?

Methods : The present economic evaluation study was conducted from a social perspective. The decision tree model was used for economic analysis of influenza vaccine injection in pregnant women compared with no vaccine in the same control group. Clinical efficacy and side effects of the vaccine were obtained using a systematic review study. In order to calculate the costs of treatment of patients or other unintended consequences of the disease, the records of patients admitted to Imam Reza Hospital in Tabriz were studied. Cost-effectiveness ratios were compared with cost-effectiveness thresholds to decide on vaccine effectiveness. One-way sensitivity analysis was used to investigate the effect of uncertainty on decision making.

Results : The efficacy rate of the influenza vaccine in reducing laboratory-confirmed cases of influenza was 47 %(0.22-0.64) by a meta-analysis of international studies. Vaccination of pregnant women against non-vaccination had incremental cost-effectiveness (ICER) of 14292671 Rials per QALY. The results of the study were not sensitive to key changes.

Conclusion : Influenza vaccination in pregnant women reduces laboratory-confirmed influenza in them and infants under 6 months of age who are not eligible for influenza vaccine. This is a cost-effectiveness intervention.

Keywords : Seasonal influenza vaccine, pregnant women, Effectiveness, Cost-effectiveness, Adverse effects

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P124-250: Modified purification method for Polyribosyl-ribitol Phosphate

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Background and Aim : Haemophilus influenzae is a Gram-negative, coccobacillary, the facultatively anaerobic capnophilic pathogenic bacterium of the family Pasteurellaceae. The six structurally recognized types of encapsulated H. influenzae are: a, b, c, d, e, and f. The classification of encapsulated strains was based on their distinct capsular antigens. Haemophilus influenzae type b (Hib) arrived at several invasive infections such as meningitis, septic arthritis, and pneumonia. Approximately two-thirds of children with type B haemophilia infection develop meningitis, between 15 and 30% of recovering people with hearing loss, permanent deafness or neurological disorders and about 4 percent of all patients die. That's about three million crucial infected cases in the world and cause more than 370,000 death under 5-year-old children.Capsular polysaccharide produced by Hib is the main virulent agent and used as the antigen in the vaccine formulation. Hib vaccines are commonly based on the capsular polysaccharide polyribosyl-ribitol phosphate (PRP). Traditionally purification of PRP for vaccine production is performed by phenol extractions. This purification strategy is time-consuming with environmental and health risks. Also, this method is difficult to scale to meet market demands. In this work, we propose an alternative strategy for purification of PRP.

Methods : In our strategy, the phenol extraction is replaced with increasing concentrations of formaldehyde and dialysis to remove the proteins, followed by salt precipitation and centrifugation to eliminate endotoxin.

Results : PRP was obtained from PRP crude solution by formaldehyde precipitation. After filtration and salt precipitation, the yield pure PRP with acceptable impurities level of nucleic acid and protein as recommended by WHO was obtained.

Conclusion : Here, we describe the purification of Hib PRP in an easily scalable process based on formaldehyde gradient. Using the described process, similar results, meeting the quality requirements vaccine production, were achieved. Eliminating the need for multi-step phenol extractions, the suggested process allowed PRP to be successfully purified with high recovery in a way that benefits the environment and operator health.

Keywords : Vaccine, Haemophilus influenzae type b, Poly ribosyl ribitol phosphate purification, formaldehyde extraction.

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P125-259: Effect of the levels of dissolve oxygen on the recombinant polyribosyl ribitol phosphate production

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Background and Aim : Haemophilus influenzae type b (Hib), a major cause of meningitis in young children leading to death and other neurological sequelae. The disease leaves 15 to 35% of the survivors with permanent disabilities, such as, mental retardation or deafness. Despite the availability of new and more powerful antibiotics, children with Hib meningitis still suffer from high mortality or morbidity. The emergence of multiresistant Hib strains causes increasing difficulties in selecting proper antibiotics for the treatment. Since 1970, the capsular polysaccharide polyribosyl ribitol phosphate (PRP) in H. influenzae b has been the target for vaccine development. PRP is isolated from the fermentation broth of H. influenzae type b. An important technological step in obtaining PRP is the cultivation of the producer strain under conditions that allow obtaining the maximum amount of the target product. The aim of this study is development of an optimization strategy to improve large-scale PRP production by Hib.

Methods : To improve the PRP production, the many variable that influence the expression of PRP were evaluated, using experimental design. As such fractional factorial design was used for the variables related to dissolve oxygen.

Results : The biomass of cultivated strains under constant aerobic condition was higher than that under anaerobic condition. The optimal dissolved oxygen concentration for the maximum PRP production was obtained at 28.4%.

Conclusion : The results of this work will be taken into account in carrying out the researches for optimization of H. influenzae type b production conditions.

Keywords : Vaccine, Haemophilus influenzae type b, Poly ribosyl ribitol phosphate, dissolve oxygen.

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P126-274: Extraction and isolation of Polyribosyl-ribitol Phosphate by modified salt precipitation method

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Background and Aim : Haemophilus influenza type b (Hib), an encapsulated, Gram-negative, cocco-bacillus bacterium, is one of the most common agents of meningitis in infants and immune-deficient adults worldwide. The capsular polysaccharide of H. influenza type b, a repeating polymer of ribosyl ribitol phosphate (PRP), is the most important cause of its virulence. The PRP vaccine with an immunogenic carrier protein produces T-cell dependent protection and promotes long-term immunological memory in the infant population. The traditional PRP downstream process is based on several ethanol precipitations, treatment with anionic detergents, centrifugation and salt precipitation. High production costs of Hib vaccine production, highlighted the necessity to develop an alternative less expensive purification method. This study is investigate to develop an effective-cost purification method for PRP from Haemophilus influenza type b.

Methods : The downstream process of PRP purification was carried out based on tangential flow ultrafiltration following formaldehyde precipitation. Protein contaminations of the samples were determined spectrophotometrically and the endotoxin elimination were assayed by modified salt precipitation method.

Results : The obtained yield of the extracted PRP is higher than amount of purified PRP obtained from current purification methods. The protein contamination of the samples were also low and the observed variation was not statistically significant.

Conclusion : The production of Hib vaccines is a cost-effective intervention which involved several production downstream process. Therefore, any improvement in one of these steps would contribute to enhancing the cost-benefit ratio, the quality, and purity for vaccine production. In this study, we established a process for the purification of PRP that is effective and economically suitable for scaling up.

Keywords : Vaccine, Haemophilus influenzae type b, Poly ribosyl ribitol phosphate purification, modified salt precipitation.

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P127-323: Bacterial extracellular vesicles: A novel platform for vaccine development

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Background and Aim : Bacterial extracellular vesicles (BEVs) have been attracted much attention in recent years due to their potential applications, including vaccine delivery and drug delivery (delivery of various therapeutic cargoes such as enzymes and anti-tumor drugs). In this review, we focus on the use of BEVs as a platform for vaccine development.

Methods : Scopus, PubMed, Google Scholar, and ClinicalTrials.gov were searched using the following keywords: "Extracellular vesicle", "membrane bleb", "outer membrane bleb", "outer membrane vesicle", "membrane vesicle", "Outer-membrane vesicle", "outer-inner membrane vesicle", "explosive outer-membrane vesicle", "cytoplasmic membrane vesicle", "tube-shaped membranous structure", "drug delivery", and "Bacterial Vaccine", until June 30, 2020.

Results : BEVs offer significant advantages, including natural immunogenicity and self-adjuvanticity, which can induce both humoral and cell-mediated immunity in vaccine design. Furthermore, the production of BEVs is scalable and cost-effective, and BEVs can be easily manipulated to display foreign antigens or desired properties. However, there are safety concerns for excessive secretion of proinflammatory cytokines caused by endotoxic LPS. At the time of writing this review, 46 studies about vaccination using outer membrane vesicles (OMVs) have been registered within ClinicalTrials.gov.

Conclusion : BEVs can be a promising platform for vaccine development. However, more study is required to resolve safety concerns for clinical use.

Keywords : bacteria, membrane vesicle, bacterial vaccine

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P128-346: Immunoinformatic Approach to Explore H. Pylori NapA Protein to Identify Epitopes for Vaccine Design

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Background and Aim : Helicobacter pylori can infect about 50% of the population in the world and is the etiologic agent for gastric and duodenal ulcers. Its colonization is correlated to adenocarcinoma and MALT lymphoma. Due to increasing antimicrobial-resistant rates and treatment failure, development of an effective vaccine is critical. Neutrophil-activating protein (NAP) is a virulence factor and protective antigen. It can cause mucosal inflammation by immune cell attraction and Th1 cytokine response polarization.

Methods : In this study, multiple bioinformatics approaches were used to analyze the different properties of NapA protein, including the physicochemical properties, transmembrane domain, subcellular localization, antigenicity and allergenicity, B, and T-cell potential epitopes.

Results : The findings showed that the secondary structure of NapA protein comprises 81.94% alpha-helix and 18.06% random coil. Likewise, no transmembrane domain was recognized for this protein. TMHMM posterior probabilities showed that this protein locates outside cells. It is conserved in H. pylori strains. The instability index is computed to be 27.18, so This classifies the protein as stable. Predicted scaled solubility is 0.752, and pI is 5.770. Antigenicity and allergenicity evaluation showed that this protein is immunogenic and non-allergenic. Potential B and T-cell epitopes were predicted for NapA. Based on the antigenicity and allergenicity of each epitope, VQLGHHPLVTLSE is selected for the B cell binding epitope. KEGDKVTVTY and HLQADAIVLF as MHC Class I binding epitopes and also KHLQADAIVLFMKVH and HLQADAIVLFMKVHN as MHC Class II binding epitope were selected.

Conclusion : This research provides a foundation for vaccine design using NapA protein. More studies are needed in vivo experiments using NapA complete sequence or epitope base vaccine design in the future.

Keywords : Helicobacter pylori, NapA, vaccine.

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P129-6: Antimicrobial and antibiofilm effects of Satureja hortensis L. essential oil against Salmonella isolated from poultry

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Background and Aim : Salmonella spp. cause various acute or chronic diseases in poultry. Infected poultry are considered as important reservoir of Salmonella to enter the human food chain Salmonella are isolated from poultry and its products more than any other animal sources. Antimicrobial resistance (AMR) is a global phenomenon leading to emergence of pathogens with resistance to clinically important antibacterial agents. AMR bacteria cause life-threatening illness in humans and pose a significant threat to health and well-being of humans. In United States, almost two million illnesses, 23,000 deaths/year, healthcare cost of $20 billion and a productivity loss of $35 billion to the U.S. economy are reported annually. The efficacy of medicating with antibiotics to prevent or treat Salmonella infections in poultry is matter of debate for many years. Prophylactic or therapeutic activity against salmonellae in poultry have been shown. However, due to inconsistent performance and microbial resistance concern, current protocols for poultry salmonellosis does not regularly rely on antibiotics. Using herbal ingredients such as summer savory may be effective in reducing the problem of bacterial resistance. Satureja hortensis L (Summer savory) lacks synthetic chemicals and has no side effects associated with antibiotic use. Summer savory essential oils prevent biofilm formation and do not completely eliminate bacteria; hence, the immune system remains active. The purpose of this study was to investigate the antibacterial and anti-biofilm activity of Summer savory essential oil against Salmonella isolated from poultry.

Methods : The essential oil was extracted using a Clevenger apparatus and subsequently its compounds were determined using GC-MS. Antibacterial properties of essential oil were determined by disc diffusion method, MIC and MBC. To evaluate the anti-biofilm properties the Microtiter plate test was used.

Results : The inhibition zone diameter in the disc diffusion test were 38±4 mm which was confirmed by MIC and MBC values. Regarding anti-biofilm activity, the MIC/2 and MIC/4 concentration of S. hortensis significantly inhibited biofilm formation of Salmonella.

Conclusion : Based on our results, S. hortensis essential oil showed the growth inhibition and bactericidal activity against Salmonella. Moreover, this study demonstrated anti-biofilm activity of S. hortensis essential against Salmonella.

Keywords : Satureja hortensis L., Essential oil, Salmonella, Biofilm

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P130-7: Antimicrobial and antibiofilm effects of Satureja hortensis L. essential oil against Escherichia coli isolated from poultry

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Background and Aim : Escherichia coli causes a range of local or systemic infections in poultry leading to significant economic losses. The widespread and imprudent use of antibacterial agents against E. coli infections in poultry flocks has reduced the efficacy of these agents. Moreover, the increased resistant of E. coli to many commonly used antibacterial agents in the field has become a major public health concern. Using herbal ingredients such as summer savory may be effective in reducing the problem of bacterial resistance. Satureja hortensis L (Summer savory) lacks synthetic chemicals and has no side effects associated with antibiotic use. Summer savory essential oils prevent biofilm formation and do not completely eliminate bacteria; hence, the immune system remains active. The purpose of this study was to investigate the antibacterial and anti-biofilm activity of Summer savory essential oil against E. coli isolated from poultry.

Methods : The essential oil was extracted using a Clevenger apparatus and subsequently its compounds were determined using GC-MS. Antibacterial properties of essential oil were determined by disc diffusion method, MIC and MBC. To evaluate the anti-biofilm properties the Microtiter plate test was used.

Results : The inhibition zone diameter in the disc diffusion test were 32±3 mm which was confirmed by MIC and MBC values. Regarded to anti-biofilm activity, the MIC/2 concentration of S. hortensis significantly inhibited biofilm formation of E. coli.

Conclusion : Based on our results, S. hortensis essential oil showed the growth inhibition and bactericidal activity against E. coli. Moreover, this study demonstrated anti-biofilm activity of S. hortensis essential against E. coli.

Keywords : Satureja hortensis L., Essential oil, Escherichia coli, Biofilm

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P131-24: Anti-biofilm effect of crude bacteriocin derived from Lactobacillus brevis DF01 on Escherichia coli and Salmonella Typhimurium

Alireza Jahany[1] *, moslem jahany[2]

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2. *phd*

Background and Aim : Biofilm is a community of microorganisms that adhere to abiotic or biotic surfaces, and is problematic in a wide range of food industries, as well as to human health. Although bacteriocin from lactic acid bacteria is well known as a natural antimicrobial agent in food preservation, it has been poorly investigated that bacteriocin inhibits the biofilm formation of foodborne pathogens. In this study, we demonstrated that bacteriocin produced by Lactobacillus brevis DF01 was partially purified and investigated whether the bacteriocin inhibited the biofilm formation of Escherichia coli and Salmonella Typhimurium. Assessment by the microtiter plate method, as well as by fluorescence and scanning electron microscopy, showed that the biofilm formation of E. coli and S. Typhimurium was reduced when the bacteria was co-incubated with crude bacteriocin of L. brevis DF01 (DF01 bacteriocin). Although pre-treated DF01 bacteriocin also significantly inhibited the biofilm formation of E. coli and S. Typhimurium (P=0.0035 and P=0.0003, respectively) post-treatment with DF01 bacteriocin did not significantly inhibit the biofilm formation (P=0.1314 for E. coli and P=0.2939 for S. Typhimurium), suggesting that DF01 bacteriocin interfered with biofilm formation, but did not disrupt the established biofilm of E. coli and S. Typhimurium. In addition, biofilms of both E. coli and S. Typhimuriun on the surface of stainless steel coupons were decreased in the presence of DF01 bacteriocin. Taken together, these results suggest that DF01 bacteriocin may be applied to control the biofilm formation of E. coli

Methods : 0

Results : 0

Conclusion : 0

Keywords : Bacteriocin; Lactobacillus brevis; Biofilm; Antimicrobial activity; Foodborne pathogens

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P132-50: Antibacterial effects of gold nano particles

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Background and Aim : Background and purpose: Improper use of chemical drugs to treat diseases has led to the emergence of resistant microbial isolates, and bacterial resistance to antibiotics is one of the most common problems in medical and veterinary sciences. Gold nanoparticles are targeted thermal agents that have many applications in medical and pharmaceutical treatments and have a high accuracy of thermal effects in subcellular dimensions. In this study, the antibacterial effect of gold nanoparticles on seven pathogenic bacteria Escherichia coli, Klebsiella Oxy Toka, Citrobacter Frondy, Enterobacteriaceae, Staphylococcus aureus, Bacillus cereus, and Streptococcus agalactia was evaluated in laboratory conditions.

Methods : Materials and Methods: In this study, gold nanoparticles in different concentrations were applied to the bacterium using agar diffusion method and tetracycline and gentamicin antibiotics as positive control and from DMF negative control. The minimum inhibitory concentration and the minimum lethal concentration were determined

Results : Results: In this study, the results showed antibacterial effects of gold nanoparticles on 7 bacteria, and the most sensitive was showed in Escherichia coli with the highest diameter of non-growth zone (25 mm) and MIC was(100 mg-mg / m)l. And the Staphylococcus aureus bacterium was(22 mm) and the MIC was (200 mm).

Conclusion : Conclusion: The results of this study showed that gold nanoparticles have a growth inhibitory effect on all seven bacteria and have the greatest inhibitory effect on Escherichia coli and Staphylococcus aureus bacteria.

Keywords : Keywords: Gold nanoparticles, antibacterial effect

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P133-52: Interference of Lactobacillus plantarum with the quorum-sensing controlled pathogenic properties of Pseudomonas aeruginosa

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Background and Aim : Researchers have turned to the use of microorganisms against those that are pathogenic, given the growing prevalence of antibiotic resistance in today's society and slow pace of the discovery of new antibiotics. Probiotics are promising options that can target quorum sensing (QS) systems of resistant bacteria. Production of virulence factors in these bacteria is under control of QS system. QS is a highly attractive target for the development of novel therapeutics. The present study investigated whether Lactobacillus plantarum might interfere with the pathogenic properties of Pseudomonas aeruginosa, in vitro.

Methods : The minimum inhibitory concentration (MIC) of L. plantarum culture filtrate (acid filtrate) was determined against P. aeruginosa ATCC 27853, P. aeruginosa PAO1 and two clinical isolates. L. plantarum filtrates were tested for their effects on the production of P. aeruginosa virulence factors controlled by QS system (biofilm formation, pyocyanin and rhamnolipid production, swarming, swimming and twitching motility).

Results : The MIC against P. aeruginosa ATCC 27853 and P. aeruginosa PAO1 was 6.25 mg/ml, and against clinical isolates was 12.5 mg/ml. Sub-MIC concentrations demonstrated statistically significant reduction of virulence factors including pyocyanin and rhamnolipid production. Biofilm formation, swarming, swimming and twitching motility were also reduced after L. plantarum culture filtrate treatment.

Conclusion : These results indicate that by-products of L. plantarum as potent QS inhibitors and anti-biofilm agents would be an effective therapeutic strategy for combating P. aeruginosa infections.

Keywords : Psedomonas aeruginosa, antibiotic resistance, QS system, Lactobacillus plantarum

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P134-81: Eugenol: a potent quorum sensing inhibitor to restrict Pseudomonas aeruginosa pathogenicity

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Background and Aim : Pseudomonas aeruginosa is an opportunistic human pathogen. This is one of the most important causes for nosocomial infections in immunocompromised patients. It produces a wide range of virulence factors and is highly resistant to lots of usual antibiotics. Production of virulence factors in this bacterium is under control of quorum sensing (QS) system. QS is a highly attractive target for the development of novel therapeutics. Eugenol is a major component of clove oil. Previous studies have shown its antibacterial activities. This study aimed to determine the in vitro anti-QS activity of eugenol on QS-regulated biofilm formation and virulence factors production in P. aeruginosa.

Methods : The minimum inhibitory concentration (MIC) of eugenol was determined against P. aeruginosa ATCC 27853, P. aeruginosa PAO1 and three clinical isolates. The effect of eugenol on bacterial proliferation was also determined by monitoring the growth curve. The biofilm formation, exopolysaccharide (EPS), pyocyanin and rhamnolipid production, swimming, swarming and twitching motility were evaluated after eugenol treatment.

Results : The MICs against P. aeruginosa ATCC 27853 and P. aeruginosa PAO1 were 0.3% v/v and 0.6% v/v, respectively. Different concentrations of eugenol (≤0.15%) demonstrated statistically significant reduction of virulence factors including pyocyanin and rhamnolipid production. Biofilm formation, EPS production, swarming, swimming and twitching motility were also reduced after eugenol treatment.

Conclusion : These results indicate that the use of eugenol as a potent QS inhibitor and anti-biofilm agent would be an effective therapeutic strategy for combating P. aeruginosa infections.

Keywords : Eugenol,Pseudomonas aeruginosa,Quorum sensing

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P135-100: Production of egg yolk immunoglobulin (IgY) against recombinant LTB of Enterotoxigenic Escherichia coli (ETEC) and evaluation of its protective effect in animal model

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Background and Aim : Enterotoxigenic Escherichia coli is one of the most common bacterial causes of diarrhea worldwide. One of the most important ETEC colonization factors is B subunit of the Heat Labile Enterotoxin, which forms the connecting part of the toxin. In the present study, egg yolk immunoglobulin (IgY) was produced and its effectiveness against recombinant LTB protein was tested on the animal model.

Methods : Hens were injected intramuscularly with 100 µg of recombinant LTB protein. The antibody titer was estimated and the eggs were collected. The water soluble part of the yolk was separated and the antibody titer was subsequently estimated by ELISA.Effecacy of different concentrations of IgY on nutralising the effect of LT toxin on Y1 cells was also studied. In order to investigate the effect of IgY-treated bacteria on intestinal epithelial cells, the standard Ileal loop technique was used.

Results : Protein expression led to the production of recombinant LTB showing molecular weight of 11 kDa on SDS PAGE. Immunization of hens induced serum antibody rise. The purified antibody was 144 mg per 12 ml of egg yolk. Purified IgY exhibited significant effect against recombinant LTB proteinAt the concentration of 125 ?g per ml, the IgY could prevent the effects of Heat Labile Enterotoxin on Y1 cells. In the Ileal loop test, 1.5 mg / ml IgY neutralized the toxin effect of LTB on the intestine. The accumulation of fluid in the test loops decreased by 74.8% compared to the untreated control loops.

Conclusion : The results showed that specific egg yolk immunoglobulin was effective against recombinant LTB protein and can be used as a preventive antibody to inhibit the Heat Labile Enterotoxin function of ETEC bacteria

Keywords : Heat Labile Enterotoxin , Enterotoxigenic Escherichia coli ,Passive Immunity,Colonization Factor , egg yolk immunoglobulin

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P136-118: Phage therapy; renewed method for multi drug resistant Staphylococcus aureus

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Background and Aim : Introduction and objective: Bacteriophages are group of viruses that infect and replicate inside host bacteria and finally lyse the host cells. Phages require a specific receptor for penetrating to the host bacterial cells. The therapeutic use of phage to treat bacterial infections (pahge therapy) was conceived by Felix d'Herelee nearly a century ago. Due to the discovery of antibiotics that provide greater breadth and potency, phage therapy lagged behind. The widespread resistance to antibiotics push microbiologists to find alternative therapeutic methods to replace with common methods for therapy of bacterial infection, phage therapy is used again and is known as an effective method.

Methods : Method : in this study 103 samples of Staphylococcus aureus were isolated from Isfahan hospital, Iran. The resistance to methicillin, clindamycin, erythromycin, cefoxitin, tetracycline, ciprofloxacin and gentamycin were measured and determined by disk diffusion method. Staphylophages were isolated from urban swage then purification of it. To indicate the effect of Staphylophages was used double layer agar method.

Results : Result: out of 103 samples, 33% were clindamycin resistant, 85% were methicillin resistant, 31.5% were erythromycin resistant, 46.6% were cefoxitin resistant, 43.6% were tetracyclin resistant, 51.1% were ciprofloxacin resisrant and 25.5% were gentamycin resistant. Fifty samples were formed plaque which indicated they were lysed by isolated staphylophage.

Conclusion : Conclusion: anti bacterial drug resistante is important problem, to deal with this problem ,alternative method must be replaced. In this study, staphylophages had lytic effect on Staphylococcus aureus multi drug resistance. Phage therapy could be effective method that replaced with chemical tehrapy.

Keywords : phage therapy, bacteriophage, staphylococcus aureus, antibiotical resistant

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P137-138: Investigation of the antibacterial function of liposome containing aloe vera extract by Mozaffari method

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Background and Aim : The aim of this study was to investigate the antibacterial function of liposomes containing aloe vera extract. For this purpose, liposomes containing aloe vera extract have been synthesized for optimal use against Staphylococcus aureus and Escherichia coli.

Methods : The type of study is laboratory research. The nanoparticle synthesis method is Mozaffari method. Particle characterization has been performed in terms of size and charge with a DLS device and morphology with an atomic energy microscope (AFM) and the amount of loading and release with a spectrophotometer. MIC tests were then performed to evaluate the performance of nanoparticles containing aloe vera extract on Staphylococcus aureus and Escherichia coli.

Results : The mean particle diameter was 69 nm and its zeta potential was 16 mV. The loading rate in nanoparticles was 54%, which was calculated by reading the absorption of light from the standard Zanian curve. The minimum inhibitory concentration (MIC) of Staphylococcus aureus and Escherichia coli for nanoparticles was 62.5 and 125 mg / ml.

Conclusion : Nanoparticles containing aloe vera extract kill the bacterial bacteria Staphylococcus aureus and Escherichia coli and can be used as antibacterial nanosystems.

Keywords : Aloe Vera, Antibacterial, Staphylococcus aureus, Escherichia coli

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P138-139: Protective effects of egg yolk immunoglobulins (IgYs) against recombinant immunogens Ctxb, OmpW and TcpA on infant mice infected with Vibrio cholerae

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Background and Aim : Vibrio Cholerae causes Cholera and other infections, especially in children under five years of age. Cholera toxin (CT), toxin-coregulated pilus (TCP) and outer membrane protein W (OmpW) are three major virulence factor of this bacterium. The emergence of antimicrobial-resistant (AMR) strains and the absence of a comprehensive and flawless vaccine, has prompted other treatments. So in this study, IgYs against recombinant proteins Ctxb (responsible for the CT binding to eukaryotic cells), TcpA (enhances bacterial attachment to enterocytes) and OmpW, in single, coupled or combined forms, were produced and their protectivity were evaluated

Methods : IgYs titer were analyzed by protein and whole cell ELISA and their neutralizing effects on CT and heat-labile enterotoxin (LT) of Escherichia Coli were evaluated in Y1 cell culture. IgY titers were gavage administered to different groups of infant mice infected with V. cholerae.

Results : Based on the results, Anti-CtxB IgY showed the highest titer and had the most neutralization effects on the toxins, while the most protectivity of the infant mice were obtained by Anti-TcpA IgY. No considerable difference was observed in protectivity or antibodies titer produced against single or combined proteins.

Conclusion : The results of ELISA, cell culture, and animal challenge indicated a higher antibody titer and a higher protection achieved using the IgYs based on single antigen. Among them Anti-TcpA IgY selected as the best antibody due to more protection in infant mice model.

Keywords : Vibrio Cholerae, Cholera, IgY, CtxB, TcpA, OmpW

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P139-148: Comparison of the effect of liposomes of red pepper extracts (Capsicum frutescens) and Allium cepa onion against Staphylococcus aureus with beta-lactamase gene isolated from packaged minced meat in Yazd

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Background and Aim : Background: Staphylococcus aureus is one of the most important pathogenic microorganisms in meat products, especially those that come into contact with the hand during repeated production. Beta-lactamase drugs, especially the new generation of Cephalosporins, is used to treat most infections caused by Staphylococcus aureus, but the production of beta-lactamase by some strains has failed to treat infections associated with the organism. Objective: The aim of this study was to evaluate the degree of contamination and compare the antimicrobial effect of liposomes of red pepper extracts and red onion on Staphylococcus aureus with beta-lactamase gene isolated from minced meat in Yazd.

Methods : Methods: For this purpose, sampling of 35 packaged meat distribution and supply centers in Yazd city was performed under hygienic conditions and all samples were tested for the presence of Staphylococcus aureus with beta-lactamase gene tested by biochemical methods and molecular confirmation with PCR test. Were placed. The antibacterial effect of the liposomes of red pepper extracts and red onion on the mentioned isolates was evaluated with the tests of minimum inhibitory effect (MIC), minimum lethal effect (MBC), well release and bacterial growth curve.

Results : Results: The results showed that 18% of the samples were infected with Staphylococcus aureus bacteria with the beta-lactamase gene. The liposomes of red pepper extracts and red onion showed a good antibacterial effect against these isolates, and in all tests, the liposomes of red pepper extract was more effective than green onion.

Conclusion : Conclusion: By proving the stronger antimicrobial effect of red pepper extract liposomes, it is recommended that in dishes such as grilled types of meat prepared from minced meat, be sure to use the liposomes extract system in addition to onions.

Keywords : Staphylococcus aureus, liposomes, red pepper, red onion, minced meat

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P140-171: Production of egg yolk immunoglobulin (IgY) against recombinant chimeric protein CfaB-EtpA-LtB (CEL), and evaluation of its specificity and neutralization efficacy against Enterotoxigenic Escherichia coli (ETEC)

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Background and Aim : Enterotoxigenic Escherichia coli (ETEC) strains are the most common cause of diarrhea among children and travelers in developing countries. Colonization factors (CFs) and enterotoxins are the major virulence factors in ETEC pathogenesis and hence can be considered as vaccine candidates. Passive immunotherapy through oral administration of chicken egg yolk antibodies (IgY) is applied as a new alternative strategy for the prophylaxis and treatment of diarrhea caused by ETEC. In the present study, we evaluated the protective efficacy of specific egg yolk antibody (IgY) produced against recombinant chimeric protein CfaB-EtpA-LtB (CEL).

Methods : Recombinant chimeric protein (CEL) was expressed in E. coli BL21 (DE3) after IPTG induction, purified through a Ni-NTA affinity chromatography column, and confirmed through SDS-PAGE and western blotting. Hens were immunized intramuscularly with purified recombinant protein thrice with two-week intervals. IgY was purified through a water dilution method, using NaCl precipitation and its purity was analyzed by SDS-PAGE. The activity and specificity of the produced IgY antibody were examined by indirect ELISA. The protective effect of produced IgY against LT toxin was also investigated on the Y-1 cell line.

Results : The produced IgY showed specific binding activity to the chimeric protein in indirect ELISA, and a significant difference was observed between test and control IgY groups. Anti-chimeric CEL IgY in a concentration of 700 µg/mL was able to reduce LtB cytotoxic effects on Y-1 cells.

Conclusion : The obtained immunoglobulin could effectively act in passive immunotherapy against ETEC-induced diarrhea infection.

Keywords : ETEC, Diarrhea, Enterotoxin, Egg yolk immunoglobulins (IgY), Recombinant protein.

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P141-178: The anti-bacterial effect of Eucalyptus and Medlar extracts against Klebsiella pneumonia from Rasht hospitals

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Background and Aim : Using plant based drugs against drug resistant bacterial infections is gaining special importance. The aim of this study was to evaluate the prevalence of extended spectrum beta lactamase producing clinical isolates of Klebsiella pneumonia and the antibacterial effects of aquatic and ethanol extracts of Eucalyptus and Medlar against these bacteria.

Methods : In this study, a total of 45 isolates of K. Pneumonia were collected from urinary tract infections. ESBL production was determined by the double disk diffusion and disk diffusion tested and specific primers PCR method was used to detect TEM and SHV genes. To investigate inhibitory effect of Eucalyptus and Medlar leaf extracts against ESBLs harboring ESBL isolates, well diffusion method and broth macro dilution method was used to determine the minimum inhibitory concentration and minimum bactericidal concentration.

Results : 26 Out of 45 isolates, 57 % phenotypically recognized as ESBL producing and based on the results of PCR, the prevalence of SHV genes among ESBLs-positive isolates was 42% SHV and 11% TEM positive isolates were detected. MIC of Eucalyptus extracts ranged between 17/5 - 31mg/ml and Medlar extracts ranged between 165-250 mg/ml. MBC of Eucalyptus extracts ranged between 600-1000mg/ml and Medlar extracts ranged between 500-1000mg/ml.

Conclusion : The obtained results showed Eucalyptus and Medlar extracts possess significant antibacterial activity against resistant bacteria. So these plant extracts may be used as an accomplishment in Klebsiella infection treatment, particularly in topical treatment of urinary tract infections.

Keywords : Klebsiella pneumonia, ESBLS, Eucalyptus, Medlar, TEM, SHV

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P142-194: Antibacterial effects of extract of Pistacia khinjuk on Streptococcus pyogenes in laboratory condition

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Background and Aim : Pistacia khinjuk (P. khinjuk) is a species of plants in the family Anacardiaceae and mostly native to Iran, Afghanistan, Egypt and India. Increasing antibiotic resistance and sensitivity reactions to chemical compounds are the main reasons that researchers are trying to find alternative antimicrobial herbal compounds. Extract of P. khinjuk is recently effective as an antimicrobial compound against some microorganisms. The purpose of this investigation is to determine the effects of the extract of P. khinjuk on Streptococcus pyogenes. St. pyogenes causes both invasive and noninvasive diseases such as Pharyngitis, Acute Rheumatic fever, Impetigo, etc.

Methods : This research is performed in the laboratory by antibiogram testing method and measuring the inhibitory aura's diameter. In this way, first of all the three parts of P. khinjuk (outer membrane, inner membrane and seed) are separated and sterilized by UV-ray. Then three Erlenmeyer flasks containing 200 ml of sterile distilled water and three Erlenmeyer flasks containing 200 ml of 75% ethanol are separated and 30gr of the samples are added separately to the Erlenmeyer flasks. Subsequently, 1000 λ of the extract are diluted with DMSO and transferred to blank disks. Finally, the disks are transferred to the Blood agar culture medium containing St. pyogenes.

Results : The results showed that among the six extracts, the ethanolic liquid extract of the inner membrane of P. khinjuk is the only extract that showed inhibitory aura after 24h incubation. The aura's diameter is about 9±0/5 mm.

Conclusion : The ethanolic liquid extract of the inner membrane of P. khinjuk fruit on St. pyogenes in laboratory condition has a few inhibitory property. The development of herbal antibiotics is an alternative way to reduce consumption of chemical antibiotics.

Keywords : Pistacia khinjuk, Streptococcus pyogenes, antibiotic, bacteria, antibiogram

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P143-210: Antibacterial effect of Datura stramoniums ethanolic extraction on the Bacillus subtilis

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Background and Aim : Bacillus subtilis is associated with bacteremia/septicemia, endocarditis, meningitis, and infections of wounds, ears, eyes, respiratory, urinary and gastrointestinal tract. The purpose of the present study was to determine of antibacterial effect of Datura stramoniums alcoholic extract on the Bacillus subtilis.

Methods : Leaves and bark of the stem of the Datura stramoniums were collected from Behshahr city (Mazandaran province, 2015 summer). Ethanolic extraction was performed by rotary evaporator. Bacillus subtilis ATCC 6633 was applied. Antimicrobial effects by tubes in the concentrations of 0.78, 1.56, 3.12, 6.25, 12.5, 25, 50 and 100 mg/ml of extract were used. Then disk diffusion, MIC (Minimum Inhibitory Concentration) and MBC (Minimum Bactericidal Concentration) of extracts were determined (Positive control; Gentamicin 30 µg, Negative control: dimethyl sulfoxide). For statistical analysis, SPSS 16 software and two-way analysis of variance were used ($p \leq 0.05$).

Results : In the disk diffusion, maximum diameter of the halo was 11.8 mm at the 20 µl of 100 mg/ml of extract. MIC and MBC also were in the 25 mg/ml and 50 mg/ml, respectively. Statistical results showed that increasing the concentration increased antimicrobial effects. It was directly related to the high concentrations of the extract (p?0.05).

Conclusion : The extracts studied have antibacterial effects on Bacillus subtilis. It can be hoped that in the future, by replacing these extracts with antimicrobial drugs. Chemistry drugs, which have always many side effects, so instead of it, herbal medicines can be used in the pharmaceutical industry for infection treatments.

Keywords : Antibacterial effect, Datura stramoniums, alcoholic extract, Bacillus subtilis

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P144-215: Antimicrobial activities of isolated bacterial endophytes from Cichorium intybus L, Pelargonium hortorum and Portulaca olevacea on bacterial pathogens

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Background and Aim : Background: A variety of microorganisms, mainly bacteria and fungi, inhabit plants and are, therefore, known as endophyte.Endophytes are sources of potentially important secondary metabolites for applications in the pharmaceutical and food industries.

Methods : Methods: Random samples from asymptomatic leaves and branches of three medicinal plants namely: Cichorium intybus L, Pelargonium hortorum and Portulaca olevacea were collected. For isolation of endophytic bacteria, the disinfected portions of the plants were distributed onto the isolation media. To examine endophytic bacterial contents, the bioassays were conducted using growing colonies in PA and YEA inactivating them by chloroform.

Results : Results: A total of 24 phenotypically distinguishable bacterial endophytes were isolated in pure form 3 medicinal plants. In part of chloroform inactivated colonies of all 24 isolated endophytes the most effective herb was C. intybus L leaves followed by branches of Po. Olevacea.

Conclusion : Conclusions: Endophytic microorganisms reside in Cichorium intybus L, Portulaca olevacea and Pelargonium hortorum, are a very promising source for production of bioactive compounds at least against some field isolates of pathogenic bacteria.

Keywords : Keywords: Medicinal plants, Endophytes, antibacterial activity, Iran

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P145-235: Antibacterial effect of Gleditschia caspica ethanolic extraction on the Escherichia coli

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Background and Aim : Escherichia coli (E. coli) strains live harmlessly in the colon and seldom cause disease in healthy individuals, a number of pathogenic strains can cause intestinal and extraintestinal diseases both in healthy and immunocompromised individuals. According to researches, Gleditschia caspica plant extracts showed activity against bacteria. In recent years, resistance to a variety of drugs has emerged in humans due to excessive use of antimicrobial drugs. The drug resistance created use of herbal medicines. The aim of this study was to determine of antibacterial effect of Gleditschia caspica alcoholic extract on the E. coli.

Methods : Gleditschia Caspica plant from areas around Behshahr city (Mazandaran province, 2015 summer). was collected and identified in Herbalist Farabi (Tehran-Iran). Ethanolic extraction was performed by rotary evaporator. Antimicrobial effects by tubes in the concentrations of 0.78, 1.56, 3.12, 6.25, 12.5, 25, 50 and 100 mg/ml of ethanolic extract were used on the Escherichia coli ATCC 25922. Then disk diffusion, MIC (Minimum Inhibitory Concentration) and MBC (Minimum Bactericidal Concentration) of extracts were determined (Positive control; Gentamicin 30 µg, Negative control: dimethyl sulfoxide). For statistical analysis, SPSS 16 software and two-way analysis of variance were used ($p \leq 0.05$).

Results : The halo diameter was not higher than that gentamicin antibiotic (15.3 mm). Maximum diameter of the halo was 11.5 mm at the 20 µl of 100 mg/ml of concentration. MIC and MBC were in the 25 mg/ml and 100 mg/ml, respectively. According to the statistical results, with increasing the concentration of plant extract, its antibacterial effect is more ($p \leq 0.05$).

Conclusion : This study is a scientific basis for using herbal extracts to treat infections that caused by strains of bacterial organisms. Due to the low price, ease of access and significant antibacterial effects of Gleditschia caspica plant extract on the E.coli, it can be considered as a plant product and natural medicine by researchers and users.

Keywords : Gleditschia caspica, Antibacterial effect, Escherichia coli, alcoholic extract

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P146-236: The effect of Nano-Curcumin on biofilm regulatory genes of Pseudomonas aeruginosa

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Background and Aim : Pseudomonas aeruginosa is a pathogen that causes nosocomial infections, especially in immunodeficient patients. The biofilm has an important role in the virulence of P. aeruginosa and is under the regulation of the Quorum sensing of bacteria. Curcumin, an active phenolic extract of turmeric has shown an inhibitory effect on the biofilm formation of some pathogenic bacteria. Thus, this study aims to evaluate the effect of Nano-Curcumin on the expression of biofilm regulatory genes of P. aeruginosa.

Methods : The biofilm formation of P. aeruginosa ATCC 10145 was assessed in the presence of 15, 20, and 25 µg/ml concentrations of Nano-Curcumin using the microplate titer method. The effect of Nano-Curcumin on the expression of evaluated genes was determined by relative Real-time PCR.

Results : In the absence of Nano-Curcumin, P. aeruginosa strain ATCC 10145 strongly produced biofilm (3+) and in the presence of 15 and 20 µg/ml, biofilm formation was reduced to moderate (2+) and weak biofilm producer (1+), respectively. Nano-Curcumin at a concentration of 25µg/ml inhibited biofilm formation in P. aeruginosa. The expression of regulatory genes was not affected by biofilm inhibitory concentrations of Nano-Curcumin.

Conclusion : The antibiofilm mechanism of Curcumin is not related to the exchange of genes involved in biofilm formation of P. aeruginosa and probably it inhibits the biofilm intact structure.

Keywords : Pseudomonas aeruginosa, Biofilm formation, Nano-Curcumin

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P147-263: Effect of increasing positive charge on antimicrobial activity of aurein 1.2

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Background and Aim : Antimicrobial peptides are promising drugs against microbial infections with a low probability to develop antimicrobial resistance. In this study, the effect of increasing positive charge on antimicrobial activity of aurein 1.2 was investigated against Gram-positive bacteria.

Methods : The aurein 1.2 sequence (GLFDIIKKIAESF) was derived from the APD3 database. A modified peptide was designed in which aspartic and glutamic acids were substituted with lysines. Their physicochemical properties and antimicrobial activities were predicted by ProtParam and CAMPR3, respectively. The aurein 1.2 and modified peptide were synthesized with C-terminal amidation. The minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) of the peptides were determined by standard methods against Enterococcus faecalis and Staphylococcus aureus in the range of 200 to 0.39 µg/ml of the peptides.

Results : Amino acid substitutions increased the positive charge of the aurein 1.2 from +1 to +5, without changing its hydrophobicity (53%). The results of bioinformatics prediction showed that the substitutions improved the antimicrobial property of the peptide. The MIC and MBC of the modified peptide were equal and they were 12.5 and 25 µg/ml for S. aureus and E. faecalis, respectively. However, the MIC and MBC values of aurein 1.2 were 25 and 50 µg/ml for S. aureus and E. faecalis, respectively.

Conclusion : The beneficial effect of increasing positive charge on the antibacterial activity of peptides has been reported on several researches. Here, the studied substitutions decreased the MIC and MBC values for Gram-positive bacteria. The modified peptide can be used as a new drug candidate.

Keywords : Aurein 1.2, Cationic peptide ,Rational design

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P148-265: Carvacrol Improves antifungal activity of voriconazole against drug – resistant Candida species

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Background and Aim : Terpenoid phenolsnare components of plant essential oils that exhibit potent antifungal activity against a wide range of pathogens, including Candida species. The purpose of this study was to determine the interaction activity of carvacrol in combination with voriconazole against Candida albicans (C. albicans), C. glabrata and C. krusei isolates

Methods : The minimum inhibitory and fungicidal concentrations (MICs and MFCs) of carvacrol and voriconazole were determined against various Candida species isolated from patients with candidiasis using the Clinical Laboratory Standards Institute (CLSI) M27-A2 broth microdilution method. The nature of the interaction was studied from fractional inhibitory concentration indices (FICIs) for carvacrol plus voriconazole combination calculated from checkerboard microdilution assay

Results : Carvacrol presented an antifungal effect, with mean MICs of 66.87 mg/mL for C. albicans, 75 mg/mL for C. glabrata and 95 mg/mL for C. krusei isolates. The mean MICs of voriconazole against C. albicans, C. glabrata and C. krusei isolates were 0.087, 1.25 and 0.35 mg/mL, respectively. Carvacrol in combination with voriconazole exhibited the synergistic anti-Candida effects against all species of Candida tested. FICI values for carvacrol plus voriconazole combination ranged from 0.370 to 0.853 for C. albicans isolates, 0.412 to 0.625 for C. glabrata isolates, and 0.474 to 0.748 for C. krusei isolates. No antagonistic activity was seen in the strains tested.

Conclusion : From these results we suggest that carvacrol has great potential as antifungal, and that voriconazole can be supplemented with carvacrol to inhibit clinical Candida isolates.

Keywords : carvacrol, voriconazole,antifungal effect, Candida albicans

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P149-266: a study on the antifungal properties of cationic peptides derived from Rana ridibunda on Candida albicans and Candida glabrata

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Background and Aim : Antimicrobial peptides with relative length (2-100 amino acids) and positive charge (pure charge (+9)-(+2)) are amphiphilic that isolated from a wide range of animals. Recently, these peptides have been known as a part of innate immune response. Nowadays, more than 500 antimicrobial peptides from animals have been reported. Objectives: The aim of this study was to evaluate the anti-Candida effects of cationic peptides derived from Rana ridibunda skin.

Methods : In this study, using alcohol-acid technique, peptides of frog's skin were isolated and purified by Sep-Pack and Sephadex column. Then the anti-Candida activity (Fluconazole Resistance C. albicans, Fluconazole Sensitive C. albicans, and C. glabrata) of the peptides in different concentrations were evaluated.

Results : Regarding to statistical analysis, peptides in concentration ranging from 25 to 100 µg/ml had the most anti-Candida activities. In respect to different understudy Candida species, these agents had the less effect on the Fluconazole Resistance C. albicans ($p<0.05$).

Conclusion : The anti-Candida effects of cationic peptide obtained from frog skin are approved in this study.

Keywords : cationic peptides, Rana ridibunda, Candida albicans, Candida glabrata, fluconazole

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P150-268: Improvement of the antimicrobial activity of aurein 1.2 by introduction of lysine and tryptophan residues

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Background and Aim : The development of antibiotic-resistant of bacteria is an important reason to find an appropriate alternative to the traditional antibiotics. Antimicrobial peptides seem to be promising candidates in this field. Here, the simultaneous effect of increasing positive charge and the introduction of tryptophan residue on aurein 1.2 activity was studied.

Methods : The aurein 1.2 peptide was used as a template and its sequence was derived from APD3 database (GLFDIIKKIAESF). Three substitutions including D4K, A10W, and E11K were introduced in the sequence and the antimicrobial property and secondary structure of the peptides were predicted by iAMPpred and NetWheels, respectively. The minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) of the modified peptide and aurein 1.2 were evaluated by standard methods against Staphylococcus aureus and Enterococcus faecalis. MIC and MBC were determined in the range of 200 to 0.39 µg/ml.

Results : According to the iAMPpred result, the altered peptide was an antimicrobial peptide and its structure was alpha-helical similar to aurein1.2. The results of MIC and MBC of aurein 1.2 for E. faecalis and S. aureus were 50 and 25 µg/ml, respectively. The MIC and MBC of the altered peptide for E. faecalis and S. aureus were reduced to 25 and 6.25 µg/ml, respectively.

Conclusion : Increasing positive charge usually enhances the interaction between antimicrobial peptides and the bacterial membrane. Tryptophan residue by membrane-anchoring ability can also improve the antimicrobial activity of some peptides. The designed modified peptide showed that three substitutions have positive effect on the improvement of aurein 1.2 peptide.

Keywords : Antimicrobial peptide - aurein 1.2 - relation design

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P151-292: The Effect of propolis Nanoemulsion on Wounds Contaminated with Pseudomonas aeruginosa in rabbit: An Experimental Study

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Background and Aim : Objective: The microorganisms have been usually noted as the major cause of delayed wound healing. Pseudomonas aeruginosa is the most common pathogen causing these infections. The aim of the present study is to evaluate, the effect of Propolis, Nanoemulsion alone and in combination with ciprofloxacin on bacterial load reduction of the wound infection with Pseudomonas aeruginosa in rabbit.

Methods : High-energy propolis Nanoemulsion was prepared using ultrasound waves.Then Broth microdilution method was used to determine MIC. Afterwards,Twenty eight rabbit anesthetized and full-thickness skin wounds created on back of them and the bacterial suspension added to each wound bed. Wound infection assessed using total count of bacterial load and also wound healing monitored, macroscopically. In all groups treatments applied topically in the wound bed: control(CO), Tween 20(T), Ethanolic extract of propolis(P), Nanoemulsion of Propolis(NP),Ciprofloxacin(C),Ciprofloxacin+Ethanolicextractof propolis(C+P),Ciprofloxacin+propolis Nanoemulsion(C+NP).

Results : The Ciprofloxacin along with propolis Nanoemulsion achieved 100% wound closure on day 14. In the propolis Nanoemulsion group, the percentage of wound contraction has close figures compared to Ciprofloxacin and normal saline as 83.2, 74 and 54.8 percent, respectively. By day 14, all of the treated groups showed decreases in surface bacterial concentration compared with Tween 20 and control groups.

Conclusion : It seems that propolis nanoemulsion accompanied with ciprofloxacin have a synergistic antimicrobial effect on Pseudomonas aeruginosa in vitro and invivo. Therefore by using of propolis nanoemulsion, the dose of ciprofloxacin can be decreased and resistance to drugs can be reduced. Propolis nanoemulsion also be used as an antimicrobial compound in various industries.

Keywords : Wound infection; Pseudomonas aeroginosa; Propolis EthanolicExtract; Nanoemulsion

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P152-295: Anti-Novel Coronaviral Herbal Extract As Supportive Medication Strategy

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Background and Aim : The novel Coronavirus disease, in comparison with SARS and MERS, has spread more quickly, due to the adaptation of the virus in every environment. Although various drugs are being developed, treatments perform as supportive care which depends on the severity of the illness. Accordingly, limiting the SARS-CoV-2- severely infected patients will significantly diminish the strain on the healthcare system of the country.

Methods : In this plan, we have provided a list of 10 effective herbal compounds against coronavirus, and their chemical construction was achieved using the PubChem database. The compounds were configuration by ChemSketch software. Accordingly, the crystal construction of the Coronavirus virus spike protein S2 receptor was achieved from the PDB protein database (7BZ5). Energy level optimization was Also done using SPDBV software. The protein-ligand docking procedure was defined by PyRx software and the designed algorithm was executed with Cygwin software. Eventually, the information obtained from the file was investigated.

Results : A review of 10 anti-nCornonaviral compounds revealed positive and inconclusive results about the efficacy of treatment, using herbal medicine as an adjuvant. Amid examined compounds, Triterpenoid was selected as the most suitable compound with a binding energy of about 11 KJ / mol with an active site and binding energy of -5 / 94 of total protein blind docking.

Conclusion : Through this study, we advise medicinal plants as possible effective and alternative therapeutic procedures by exclusively targeting SARS-CoV-2 and its pathways.

Keywords : ACE2, SARS-CoV-2, Herbal Extract, Spike Protein.

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P153-306: Study of fosfomycin, colistin resistant in accordance to ESBL production among E. coli isolates from UTI after kidney transplantation

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Background and Aim : The aim of this study was phenotypic and molecular evaluation of fosfomycin and colistin resistant in accordance to ESBL production among E. coli isolates from UTI after kiney transplantation

Methods : 60 E. coli isolates from urine samples of kidney transplant patients with UTIs from 3 different Kidney transplant centers in Tehran were collected during 2018-19. Antimicrobial susceptibility test(AST) was done by disk diffusion method based on the CLSI 2018. Minimum inhibitory concentration (MIC) of fosfomycin was performed by E-test. Further ESBL phenotypic screening by double disk synergy test(DDST) were evaluated. Molecular survey of ESBL genes (including; CTX-M, TEM, SHV), some of fosfomycin resistance (uhpT, murA) genes and mcr-1 gene as plasmidic colistin were detected by PCR after DNA extraction. As control, K. pneumonia ATCC 700603, a fosfomycin resistant and a colistin reistant E.coli isolates which were bestow from Dr.C. Giske (Karolinska, Sweden) were evaluated simultanously. Sequencing was done by Bioneer Korean company and further analysis and blasting was done in data bank/NCBI.

Results : Based on AST, highest susceptibility was to: doripenem, ertapenem (100%) and Imipenem 95%, and the highest resistant rate was to: ampicillin (86%), cefotaxime (80%), cefazolin and cefpodoxime (77%). Of 60 E. coli isolates, 27(45%) were associated with multidrug resistance (MDR) phenotype. Only (3.3%) of E. coli isolates showed intermediate resistant (MIC 128µg/ml) to fosfomycin based on the E- test. By DDST, 46% of isolates were identified as ESBLs producer. The frequency of ESBL genes were: blaTEM (54%), blaCTX-M (51%) and blaSHV (40%) and mcr-1 (3.3%) respectively by PCR. Mutation in different points of uhpT and murA genes were detected after sequencing analysis

Conclusion : : Fequency of fosfomycin resistant was not high in this study, but, coexistence of ESBL and fosfomycin plasmidic resistance genes in E. coli isolates among kidney transplant patients, show the importance of awareness among infection-control practitioners and physicians during prescription. Also, colistin is not a recommended antibiotic for treatment and during AST for E. coli isolates based on CLSI. But detection of mcr-1 gene among 3.3% of isolates is alarming because it can be exchange between different bacteria and may increase globally soon

Keywords : colistin, ESBL, Fosfomycin, E. coli

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P154-328: Pseudomonas aeruginosa isolated from patients with cystic fibrosis: A systematic review and meta-analysis

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Background and Aim : Pseudomonas aeruginosa is an opportunistic pathogen that can form biofilms in the lungs and airways of cystic fibrosis (CF) patients. Increasing rates of resistant and multidrug-resistant (MDR) P. aeruginosa in hospitalized patients constitute a major public health threat.

Methods : Data sources of this study were 52 original articles (2000-2019) that were published in the literatures in several databases including PubMed, Science Direct, Google Scholar, Biological abstracts and ISI web of knowledge. Data were analyzed using meta-analysis and random effects models with the software package Meta R, Version 2.13 ($P < 0.10$) (confidence interval: 95%).

Results : Out of 110 searched articles, 52 were selected. The most common definition of MDR was resistance to more than one agent in three or more categories of antibiotics. Finally, out of 2340486 samples, 23.83% of the strains were present in 52 studies of MDR. The highest prevalence of cystic fibrosis due to Pseudomonas was higher in men than in women and 40,130. Most of the searched articles were related to the continent and the United States with 26 and 21 items, respectively. Most of the tests used were MIC and PCR. Also, the most searched type of cross-sectional study was with 27 cases.

Conclusion : Hospitalized patients with resistant and MDR P. aeruginosa infections appear to have increased all-cause mortality and LOS. The initial empirical treatment of these patients remains challenging because of the strikingly high prevalence of antimicrobial resistance.

Keywords : Cystic fibrosis; Pseudomonas aeruginosa; Multidrug-resistant (MDR)

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P155-335: Analyzing the antimicrobial effects of herbal extracts to improve burns infections

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Background and Aim : The repair of skin lesions depends largely on the regenerative role of fibroblast cells in the regeneration of the extracellular environment, which contains large amounts of collagen. One of the leading causes of death and disability in the world is skin burns and the resulting lesions. Burn injuries are more prevalent in developing countries, leading to long-term disability and hospitalization, and even death. Today, due to the increasing growth of microbes resistant to common antibiotics on the one hand and the lack of antimicrobial compounds, on the other hand, it is necessary to continue research on the identification of new antimicrobial compounds. For many years, natural remedies, especially herbs, have been the basis and in some cases, the only treatment. Many of the plants used in traditional medicine are indigenous and studies on the effectiveness of medicinal plants on Staphylococcus aureus And Escherichia Coli have occurred all over the world.

Methods : After confirming the antimicrobial effect of fennel, black cumin, thyme, and white tea to prepare the burn ointment, the glycerin is poured into a sterile beaker and placed in a bain-marie (direct heat using water vapor) and then melted. When it cools down a bit (before it closes), add thyme extracts, fennel, black cumin, white tea, zinc oxide, and vitamin E to it.

Results : Because bacterial resistance is increasing and transmission of resistance from resistant bacteria to susceptible bacteria is easily done in various ways and causes resistance to common antibiotics, the extract of medicinal plants with antibacterial properties can be used as an alternative or complementary compound in the treatment of bacterial infections. Overall, the results of this study show that the medicinal plant can be used as a quick and effective healer to heal skin wounds and has faster and better effectiveness than antibiotics.

Conclusion : With these interpretations, it can be said that plant extracts alone or in combination with other antimicrobial agents can be useful in treating bacterial infections. However, additional and in vivo tests are needed to assess the possible toxicity of the extract, to study its properties and effects, and to obtain appropriate concentrations for use in living organisms.

Keywords : Medicinal plants, Antimicrobial ointment, Plant extract, Burn infection

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P156-337: Analyzing the antimicrobial effects of herbal extracts to improve burns infections

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Background and Aim : The repair of skin lesions depends largely on the regenerative role of fibroblast cells in the regeneration of the extracellular environment, which contains large amounts of collagen. One of the leading causes of death and disability in the world is skin burns and the resulting lesions. Burn injuries are more prevalent in developing countries, leading to long-term disability and hospitalization, and even death. Today, due to the increasing growth of microbes resistant to common antibiotics on the one hand and the lack of antimicrobial compounds, on the other hand, it is necessary to continue research on the identification of new antimicrobial compounds. For many years, natural remedies, especially herbs, have been the basis and in some cases, the only treatment. Many of the plants used in traditional medicine are indigenous and studies on the effectiveness of medicinal plants on Staphylococcus aureus And Escherichia Coli have occurred all over the world.

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P157-357: Investigation of the Inhibitory Effect of the Proposed Chemical Composition on the Activity of Streptococcal Sortase A in Control of Dental Caries Invitro

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Background and Aim : One of the most common childhood problems is tooth decay, and viridans group streptococci are the most common bacteria that cause the infection. The purpose of the study was to investigate the inhibitory effect of triclosan on the activity of streptococcal sortase A enzyme in controlling dental caries in vitro condition.

Methods : This study was done on specimens isolated from teeth of pupils (n =150) in Golestan province in 2019. After identifying Streptococcus viridans strains using specific tests, The SrtA gene was identified using polymerase chain reaction (PCR) with specific primers. Broth microdilution test was used according to CLSI M100-S25(2015) criteria to determine the minimum inhibitory concentration(MIC) of triclosan.

Results : The frequency of S. viridans isolates containing Srt A was 87 %. There was a significant difference between the frequency of tooth decay and presence of srt A ($P<0.05$). Determining MIC of triclosan showed that 61% isolates of S.viridans tested were susceptible (MIC, 16?g/ml) and 39% (MIC, 64?g/ml) of isolates were resistant to triclosan respectively. The concentration of triclosan that inhibited 90% of isolates (MIC90) was 256 ?g/mL.

Conclusion : The results demonstrated that there is a relationship between the presence of sortase A and dental caries caused by isolates and triclosan showed a good antibacterial effect in vitro condition.

Keywords : Streptococcus viridans, Sortase A, Triclosan, Antibacterial effect

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P158-358: Invitro study of human amniotic fluid in the control of Impetigo common pathogen

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Background and Aim : Impetigo is an infective dermatitis and a common skin disorder. It can be very difficult to control in some cases and might be life-threatening if not treated, especially in children. The aim of this study was to investigate the antibacterial effect of amniotic fluid of pregnant women on drug-resistant Staphylococcus aureus isolates from children with impetigo.

Methods : S. aureus isolates were collected from children suspected of having impetigo. The isolates were identified using microbiological and biochemical tests. Antibiotic susceptibility was evaluated using the Kirby-Bauer method according to the M100-S25 (2015) guidelines. The antibacterial effect of different concentrations of amniotic fluid on drug-resistant S. aureus isolates was investigated by the disk diffusion method.

Results : Of 35% S. aureus isolates, 88% were sensitive to teicoplanin and vancomycin, while 65% of the isolates were resistant to penicillin, which is conventionally used for treatment of impetigo. Based on the results, 64% of drug-resistant isolates were sensitive to amniotic fluid. There was a significant relationship between the concentration of amniotic fluid and the diameter of bacterial growth inhibition zone ($P<0.01$).

Conclusion : The amniotic fluid of pregnant women has favorable antibiotic effects against antibiotic-resistant S. aureus isolates from children with impetigo. Therefore, it can be potentially used for natural biocontrol of this common infection.

Keywords : Amniotic fluid, impetigo, Drug resistance, Staphylococcus aureus

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P159-393: Use of Cinnamon and Garlic Essential Oils as an Alternative to Antibiotics in the Treatment of Aeromonasis in Fish

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Background and Aim : In the aquaculture industry, one of the important problems is bacterial infectious diseases. Accordingly, farms fish of Kerman province was the aim of the present research and Aeromonas hydrophila isolation and identification of infection from coldwater

Methods : . Samples were from the skin and kidney of 90 infected fish with signs of hemorrhagic septicemia in gill and skin, exophthalmia and dropsy, as well as 36 water samples, were also taken from fish farms aseptically and subculture on TSA. From 126 isolates of the fish and water samples, 24 isolates of gram-negative bacteria were identified as Aeromonas at genus level by biochemical characteristics. After isolating the bacteria and PCR, different concentrations of cinnamon and garlic essential oil (50, 100, 150 and 200 ppm) were tested on the bacteria and the best antimicrobial concentrations of essential oils were determined.

Results : The result showed 50 ppm concentration essential oil of Garlic and 100 ppm concentration essential oil of Cinnamon is the best of level bactericide. The combined effect of different treatments of essential oil and its different concentrations also caused a significant difference ($P < 0.05$) in the growth of bacteria in the experimental culture medium.

Conclusion : It can be concluded that the plant essential oils used in this study have antibacterial properties with varying degrees and effectiveness.

Keywords : Aeromonas hydrophila, Garlic, Cinnamon, Antibacterial.

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P160-402: Investigation of Antimicrobial Effect of Ziziphus jujube on nosocomial bacterial infections

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Background and Aim : The Incidence of drug resistance against chemical antimicrobial drugs has led to attention to the use of medicinal plants in the treatment of infections. The aim of this study was to evaluate the antimicrobial activity of extracts of Ziziphus jujube against pathogenic bacteria especially nosocomial infections.

Methods : In this experimental study, aqueous and alcoholic extracts of, Ziziphus jujube were extracted. Inhibitory effects of plant extracts against Pathogenic bacteria (Staphylococcus saprophyticus, Escherichia coli, Salmonella typhimurium and Proteus mirabilis) and Pathogenic nosocomial (Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter and Pseudomonas aeruginosa) Through Disk diffusion methods, well diffusion method, and microdilution were investigated. Serial dilutions of the extracts were prepared in the range of 50 to 1000 mg / ml to determine the minimum inhibitory concentration.

Results : The aqueous extract of the plant showed higher inhibitory effects against microbial strains than the alcoholic extract. The two strains of Staphylococcus saprophyticus and Staphylococcus aureus showed greater sensitivity than extracts (aqueous, methanol, ethanol). Statistically, there was a significant difference in the minimum inhibitory concentration of aqueous extract growth compared to alcoholic extracts The aqueous extract on gram-positive bacteria of Staphylococcus saprophyticus and Staphylococcus aureus had a minimum inhibitory concentration of 133 mg / ml and a minimum bacteriocidal concentration of 200 mg / ml.

Conclusion : The study found that Ziziphus jujube extract had significant effects on microorganisms, inhibitory zone of two gram positive bacteria including , Staphylococcus saprophyticus, 57 mm in diameter, Staphylococcus aureus, 55 mm in diameter, And the bacterium Pseudomonas aeruginosa showed the highest resistance between gram-negatives bacteria. The extracts also showed significant effects compared to the antibiotics as contorol. Although further research is needed in this regard, Ziziphus jujube extract can be suggested as a new antimicrobial agent in medicine resarch.

Keywords : Medicinal plant extract, Pathogenic bacteria, MIC Minimum Inhibitory Concentration, Digestive and skin diseases.

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P161-28: Species diversity, molecular characterization and antimicrobial susceptibility of opportunistic actinomycetes isolated from immunocompromised and healthy patient of Markazi province of Iran

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Background and Aim : Abstract Introduction Actinomycetes are widely exist in nature and these species caused infections in immunocompromised and healthy patients although frequently found as members of the normal microbiota of human and animal. These subsequent infections are often misdiagnosed with malignancy and tuberculosis. Due to this issue in the present study, we aimed to determine the presence and diversity of actinomycetes species causing infections in Iranian patients.

Methods : Materials and methods A total of 79 clinical samples collected from 5 hospitals in Markazi province were analyzed for the existence of actinomycetes using standard protocols for isolation and characterization of the isolates. The conventional tests were used for preliminary identification, the PCR amplification of hsp65 gene, the specific region of the 16S rRNA and sequence analyses of 16S rRNA were applied for the genus and species identification. MICs of the antimicrobial agent were determined by the broth microdilution method and interpreted according to the NCCLS guidelines.

Results : Result A total of 17 (21.51 %) actinomycetes isolates were recovered from clinical samples. In other analyzed samples 8 (10.12%) gram-positive, 12 (15.18) gram-negative bacteria and 6 (7.6) fungi isolates were recovered. The most prevalent actinomycetes species were M. fortuitum 17.64%, N. Mexicana and S.heliomycini 11.76% each and 10 species, i.e., N. farcinica, M. lehmanii, M. flavescens, Arthrobacter crystalopoetis, N. neocaledoniensis, M. phocaicum, M. abscessus, M. arupense M. setense and N.cyriacigeorgica consisted the single isolates. Results of DST illustrated that all of the isolates were susceptible to Amikacin, Levofloxacin, Ofloxacin and Ciprofloxacin, whereas all of them were resistant to Rifampicin and Doxycycline.

Conclusion : In conclusion, increasing isolation of actinomycetes found in various clinical case merits special attention by health authorities in developing countries. In health centers, action should be taken to increase awareness of appropriate diagnostic criteria and management guidelines for actinomycetes diseases. Furthermore, an increase in the number as well as the quality of national and regional reference laboratories may facilitate more accurate diagnosis of actinomycetes diseases.

Keywords : actinomycetes; 16SrRNA; Drug susceptibility pattern; immunocompromized

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P162-39: The Novel Corona Virus Disease-2019 (COVID-19); Mechanism of Action, Detection and Recent Therapeutic Strategies

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Background and Aim : Novel coronavirus SARS-CoV-2 designate as COVID-19 by the WHO on the 11th of February 2020, is one of the highly pathogenic β-coronavirus which infect human. Early diagnosis of COVID-19 is the most important step for the illness treatment. Recently CRISPR-based method has been investigated to diagnosis and treatment of Coronaviruses. Because the 2019-nCoV pneumonia have been emerged during the influenza season, orally and intravenously antibiotics and neuraminidase enzyme inhibitors including oseltamivir has been extensively applied. Nowadays, antiviral drugs including Griffithsin, as an inhibitor of SARS and MERS spike, Remdesivir, favipiravir and ribavirin, lopinavir/ritonavir, oseltamivir, anti-inflammatory drugs and EK1 peptide, Umifenovir, ShuFeng JieDu and Lianhua qingwen capsules used as only available treatment options for SARS-CoV-2 infected individuals. Also, Chloroquine previously used for malarial and autoimmune disease, clinically has efficiency for treatment of the 2019-nCoV infection. Western-type antiviral therapies with antibiotics, α-interferon and lopinavir as well as support therapies including oxygen and mechanical ventilation have also been administered to the treatment of patients infected by COVID-19, according to the severity of hypoxaemia. This therapeutic strategy will help patients worldwide to protect themselves against deadly and serious viruses that have the potential to evolve and develop drug resistance, also reduce mortality rates.

Methods : Review paper

Results : Using accumulated knowledge of the innate immune response system, will make it possible to propose the potent antiviral drugs with its effective therapeutic measures for detection and prevention of viral infection.

Conclusion : The clinical virology of COVID-19 is obviously in its beginning, and there is much to be learned about the behavior of the coronavirus pathogen in the human host.

Keywords : Coronavirus; Immune response; Respiratory syndrome; Treatment; Pathogen.

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P163-88: Coronavirus (COVID-19) in Pregnant Women

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Background and Aim : Coronavirus is a common pathogen between humans and animals. In late 2019, in Wuhan China was recognized by the World Health Organization (WHO) as the causative agent of pneumonia. The main clinical symptoms of COVID-19 were patients with fever, cough, myalgia, or fatigue, and shortness of breath. Laboratory findings include more common lymphocytopenia, increased CRP, increased LDH, and leukocytopenia.

Methods : The material is from scientific articles on gynecology, midwifery, infectious diseases, as well as searching the valid scientific databases.

Results : Our findings from studies conducted in Iran and other countries involved in the virus make it clear that more studies are needed on the behavior of this virus. Due to the fact that the virus has certain basic symptoms, these symptoms can be used for primary screening, but new serological and molecular kits must be made to be accurate and sensitive, as well as a rapid diagnosis for primary screening in adults and It can be used in both pregnant and fetal mothers.

Conclusion : Studies on pregnant mothers and the pathological effects of the virus on mothers, as well as the effects that the virus can have on the placenta and fetus, should be investigated by midwifery associations and gynecological associations to determine exactly what effects the virus has on the mother and the fetus. Affect the fetus and determine whether the virus can be complications in infants born to infected mothers give birth or not.

Keywords : COVID-19, Pregnant, Coronavirus

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P164-114: A review on medicines used for treatment of SARS-CoV-2

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Background and Aim : SARS-CoV-2 or CoVid19 pandemic caused a huge mortality and fear all over the world for so long. Finding a cure or prophylaxis is necessary to reduce global panic as well as mortality.on the other side the approach for finding an effective vaccine seems to be not successful so far.

Methods : Over 20 articles have been studied and medicines which were recently used to cure and cause relief were extracted. some of them were clinical and mostly were used in vitro in which the effect of the would be discussed carefully an addition to the role of each drug.

Results : It seems that the following drugs could be kind of effective; Chloroquine and hydroxychloroquine, remdesivir, favipiravir, Ritonavir, Tocilizumab, Depo-medrol, Arbidol, Nitazoxanide, Ivermectin, Glucocorticoid and JAK inhibitors.

Conclusion : Despite all the efforts and large use of antiviral and anti-inflammatory medicines, there is no promising and proven treatment. Most of the drugs above are studied in vitro and there is no evidence of being successful in clinical trials. so more studying and investigation on other drugs or probable vaccine is essential.

Keywords : SARS-CoV-2 , treatment , antiviral drugs , RNA virus , infectious genome ,

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P165-115: Biochemical, Hematological and Immunological elements changing in non-hospitalized people in Tehran through Covid-2019

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Background and Aim : COVID-19 as a novel strain of Coronaviruses family that are known to cause colds and more serious diseases was discovered in 2019 and has never been found in humans before. Respiratory symptoms, fever, cough, shortness of breath, and dyspnea in infected person with COVID-19 observed. There is currently no specific treatment for COVID-19, therefore infection can cause pneumonia, severe acute respiratory syndrome, kidney failure, and even death. Thereby, there is need rapid and accurate diagnostic tests for screening of suspected persons. This study is aimed to evaluate the clinical significance of Biochemical, Hematological, Serological and antibodies for the highly suspected COVID-19 infection persons.

Methods : 235 samples of suspected person collected from 3 labratories in Tehran and clinical tests done with Pars Azmon Kit and Hematological parameters assayed with Mindray BC-3000and CRP were detected by Generic Assay kit. COVID-19 IgG and IgM were detected with Pishtaz Teb Kit (ELISA). Data analyzed by SPSS software v.19.

Results : Among 235 persons who detected for Covid-19 antibodies and clinical tests, 16 persons had positive and 3 ones had borderline result. 14 ones were positive for IgG and 1 ones were IgM positive. 2 ones were positive for IgM+IgG together and 3 ones were borderline for IgM. 5 ones of these persons had history of cough, fever and Shortness of breath (asthma). 22 persons had N/L ratio under 1.3 those 5 ones were antibodies positive that 1person was IgG+IgM positive, 3 ones were IgG positive and 1person was IgM positive. Significance association between N/L ratio with antibodies observed (P value for IgG <03 and for IgM<05 with CI:95).

Conclusion : Regards to this study, CRP and other biochemical tests cannot be reliable for screening of suspected persons but CBC test as a first line of diagnostic test can be reliable for screening and also can confirm immunological results for suspected patients.

Keywords : Covid-19, Coronavirus, IgG,IgM, Biochemical, Hematological

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P166-153: Molecular survey and hematological changes of Ehrlichia canis in Cats by the first time in Tehran, Iran

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Background and Aim : Ehrlichiosis is a worldwide distributed disease caused by microorganisms of the Ehrlichia genus that is transmitted by arthropod vector Rhipicephalus sanguineous. However, little information we have about the occurrence of Canine monocytic ehrlichiosis (CME) in Tehran province in Iran.

Methods : The current study was carried out to evaluate the presence of E. canis in blood samples of one hundred domestic and stray cats in Tehran, Iran using the Polymerase Chain Reaction technique. Cats are infected to this rickettsia by dog's brown tick or Rhipicephalus sanguineous bite. The tick has a horizontal transmission, and tick Maternal vertical transmission of the parasite is not approved yet. One hundred blood samples of Domestic and Stray cats, different races (DSH, Persian and Scottish) From Different districts of Tehran, Iran referred to veterinary hospitals, with the average age of 1 year old were selected and examined. Out of one hundred Domestic and stray Cats whose blood samples were examined using PCR.

Results : nine samples were positive (9%). The positive samples consist of five (55.55%) male and four female Cats (44.44%). There was a significant difference between Cats races, seasons, and infestation rates. Hematologic changes in infected samples consist of the shift to the left, Leukocytosis, and three cytoplasmic inclusion bodies have been found. The prevalence values based on breeds and season compared by Fisher's exact test had a significant difference between season (P=0.032) and breeds (P=0.026). This study is the first molecular detection of E. canis in cats in Iran.

Conclusion : The prevalence values based on breeds and season compared by Fisher's exact test had a significant difference between season (P=0.032) and breeds (P=0.026). This study is the first molecular detection of E. canis in cats in Iran.

Keywords : Ehrlichiosis, Feline, PCR, Iran

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P167-154: Molecular survey and hematological changes of Ehrlichia canis in a tick infested dogs by the first time in Isfahan province, Iran

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Background and Aim : Ehrlichia canis has a worldwide geographic distribution, but little is known about the occurrence of Canine monocytic ehrlichiosis in Isfahan province, Iran. The current study was carried out to evaluate the presence of E. canis in blood samples of two hundred and fourteen guard and sheepdogs in Isfahan, using the PCR technique. Dogs are infected to this rickettsia by dog's brown tick or Rhipicephalus sanguineous bite. The tick has a horizontal transmission, and tick Maternal vertical transmission of the parasite is not approved yet.

Methods : two hundred and fourteen blood samples of guard and sheepdogs in districts of Isfahan, Iran, with an average age of 3.5 years were selected randomly and examined. PCR was applied to analyze the extracted DNA from blood samples. Out of two hundred and fourteen guards and sheepdogs whose blood samples were examined using PCR.

Results : 26 samples were positive (12.14%). The positive samples consist of fourteen (53.84%) male and twelve female dogs (46.15%). Hematologic changes in infected samples were not recognizable. The prevalence values based on gender compared by chi-square and ages were compared by Fischer exact test.

Conclusion : There was a significant difference between age groups older than three years (P=0.041). This study also demonstrated the importance of dogs as chief host and the ways of transmission of this rickettsia. The results demonstrate that the prevalence of E. canis is relatively high in dogs from the Isfahan province, Iran and the molecular study of E. canis prevalence in fifty-five blood samples of owners were negative.

Keywords : Ehrlichia canis, Infected Dogs, PCR, Isfahan, Iran

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P168-187: Molecular mimicry causes the autoimmune phenomenon shown in Covid-19

Maedeh Raei[1] *

1. *Maedeh raei*

Background and Aim : Every day near 100000 people become infected with novel coronavirus so It is necessary to better understand the immunology of COVID-19, to restrain the pandemic by developing medicines and vaccines for the treatment of patients.

Methods : In this systematic review, we use data that were collected by performing searches using a specified set of Medical Subject Heading (MeSH) and search engines: MEDLINE and ISI Web of Science, Data were extracted directly from full-length articles.

Results : Molecular mimicry has been proposed as a cause of the autoimmune phenomena in COVID-19. Evidence has recently shown that COVID-19 in addition to respiratory infections also causes thrombosis and disseminated intravascular coagulation (DIC) in COVID-19 patients. Reflecting on what induces thrombosis and DIC, we suggest molecular mimicry against endothelial cells as the cause of the multi-organ failure. In fact, antibodies elicited against viral proteins could very well cross?react with vascular endothelial proteins if they shared antigenic epitopes. recently researchers reported three human proteins (namely DAB1, AIFM, and SURF1), that are present in neurons of the respiratory pacemaker in the brainstem that share potentially antigenic epitopes with SARS-CoV-2. Particularly, they postulated that damage to the brainstem pacemaker may contribute to respiratory failure in COVID-19 as a consequence of molecular mimicry between neuronal and viral proteins.

Conclusion : Some cases show Guillain-Barré syndrome(GBS), immune thrombocytopenia(ITP) and rheumatoid arthritis(RA) associated with COVID-19 infection. That molecular mimicry plays an important role in creating them.

Keywords : SARS-CoV-2, COVID-19, molecular mimicry

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P169-209: T-cell and B-cell epitopes vaccine design on S-Ag of 2019 novel coronavirus (SARS-CoV-2) using Immunoinformatics approach

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Background and Aim : Coronaviruses are a large group of viruses that can infect animals and humans and has caused a large number of deaths with thousands of confirmed cases worldwide. These discomforts can be range from mild to severe. People of all ages can be infected by the new coronavirus (2019-nCoV). Older people, and people with pre-existing medical conditions (such as asthma, diabetes, heart disease) appear to be more vulnerable to becoming severely ill with the virus. As regards, there is no drug for treatment, it seems to be the most effective way to prevent and treat vaccinations. The aim of this study was T-cell and B-cell epitopes vaccine design against SARS-CoV-2 in based on In silico analysis to determine the most conserved B and T-cell epitopes of S protein that could be able to stimulate a remarkable immune response.

Methods : Sequence of S protein was collected from protein databases (NCBI & Uniprot) and analyzed by In silico tools (IEDB – ABCpred) for recognizing the most conserved immunogenic epitopes to trigger the T and B cell immune response. These suitable epitopes were evaluated in terms of toxicity and allergenicity and immunogenicity with used of Toxinpred and AllerTop and Vaxigen servers, respectively. Finally, the chimeric protein as a novel epitope-based vaccine was designed and assayed in terms of 2D and 3D structures by Prabi garland & Swiss-model servers, respectively.

Results : T-cell and B-cell epitopes vaccine design study was predicted the most immunogenic epitopes (LPLVSSQCV) and (FLVLLPLVS) to stimulate TCD8 and TCD4 respectively, by IEDB server, also was predicted a suitable epitope (YGFQPTNGVGYQ) by ABCpred server, to motivate B cells. These peptides were bound to the largest number of alleles. Also they weren't toxigenic and allergenic epitopes that were investigated by Toxinpred and AllerTop servers. Designed chimeric protein was suitable in terms of physicochemical properties and stability.

Conclusion : Epitopes vaccine design study showed that, predicted epitopes were with high efficiency and stability that can be used as a therapeutic peptide vaccine to be selected for prevention of SARS-CoV-2 infection.

Keywords : SARS-CoV-2 - Immunoinformatics - Vaccine

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P170-216: The prevalence of hybrid enteroaggregative/uropathogenic E. Coli (EAEC/UPEC) genotypes and detection of some virulence genes isolated from patients referred to Al-Zahra and Imam Hossein hospitals in Isfahan, Iran

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Background and Aim : Virulence genes from special Escherichia coli pathotypes are combined in hybrid strains. E. Coli with hybrid enteroaggregative/uropathogenic (EAEC/UPEC) genotypes have sporadically emerged causing outbreaks of extraintestinal infections, but their association with recurring infections is but underappreciated.

Methods : In this sectional-descriptive study which was performed in 2019, clinical isolates of E. coli were collected from patients referred to 2 hospitals of Isfahan. Extensive virulence genotyping was carried out to detect 7 virulence genes, including molecular predictors of EAEC and UPEC strains. The presence of the genes was screened by PCR using specific primers for pap, aatA, aggR, Aap, chuA, fyuA and fimH in extracted plasmid DNA.

Results : The frequency of Hybrid EAEC/UPEC strains virulence genes was aatA (19.23%), pap (57.69%), aggR (69.23%), Aap (69.23%), chuA (76.92%), , fyuA (80.77%), and fimH (92.31%).

Conclusion : Our study showed that the fimH, fyuA and chuA virulence genes were highly prevalent among hybrid strains isolated from hospitalized patients in our region; therefore, these genes could be studied as targets for medical interventions.

Keywords : Uropathogenic Escherichia coli, Enteroaggregative Escherichia coli, Virulence genes, Hybrid strain

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P171-225: SWOT analysis of Brucella abortus antigens (S99) production in Iran

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Background and Aim : Brucellosis is an important disease between humans and animals, which is widespread throughout the country and causes economic complications and risks to public health. The diagnosis of human brucellosis is usually based on the isolation of Brucella spp. from blood, tissue and organs, the serological tests such as RBT and etc. Poor diagnosis and treatment may result in complications such as neurologic disorders and etc. The production of brucella antigen is by manual cultivation on a solid medium in RVSRI, using S99 strain. However, the main barriers to improving quality and increasing production capacity are traditional production process as well as supplying necessary raw materials for antigen production .In order to obtain better performance of the production of brucella antigen to enable the improvement of diagnostic tests surveillance and reporting, a SWOT analysis was carried out for S99 production to identify weaknesses and areas that could be improved to enhance disease surveillance.

Methods : In this study, a systematic review was carried out to obtain data on the strengths, the weaknesses, the opportunities and threats to S99 production, using a Matrix Preparation (SWOT) of internal and external influence factors. The identified factors were then allocated to each parameter as they were determined, and discussed.

Results : The results of the SWOT analysis a based on the situational assessment of the brucella antigen production, the following gaps and challenges have been identified: Persons with experience are available for training to build capacity for improved S99 antigen production and management. International Standard or references are not available to standardize antigens. Lack of extensive field studies to determine the sensitivity and specificity of production S99 antigen. The infrastructure required for implementing production line for S99 antigen is weak.

Conclusion : The factors identified in this study could be effective and improvement through capacity building training, survey development and the use of this training in the production of S99 antigen. However, this concept provides a sustained groundbreaking platform for a real change in the vaccine production paradigm towards the development of successful measures to contain the brucella diagnostic dilemma.

Keywords : SWOT analysis, S99 Antigen, Razi Vaccine &Serum Research Institute (RVSRI)

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P172-282: The COVID-19 and Immune Response

Maedeh Raei[1] *

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2. *Mina Owrang*

Background and Aim : In December 2019, an outbreak of COVID-19, an acute respiratory illness caused by the novel coronavirus, was detected in China. Every day near 100000 people infected with COVID-19. So in this systemic review, we explain the immune response of COVID-19 to find the best treatment for patients.

Methods : We use data that were collected by performing searches using a specified set of PubMed Central (PMC) and search engines: MEDLINE and Science Direct. Data were extracted directly from full-length articles.

Results : COVID-19 can evade from an immune response by distracting the way of IFN-I and cytotoxic T cell production. Afterward immune cells produce more IFN-I to compensate. Therefore, a cytokine storm that can cause tissue damage occurs. Also, T cells lose their function during exposure to the virus and lose the ability to produce molecules such as Perforin and Granzyme, which play an important role in killing cells. These T cells express a molecule on their surface called PDL-1, which is increases in people with COVID-19, especially those in need of intensive care.

Conclusion : Studies have shown that neutrophilia and lymphopenia are directly related to the severity of the COVID-19 disease. The cause of lymphopenia in these patients is unknown. Since there is no COVID-19 receptor to enter the cell at the lymphocyte surface, It can be concluded that the cause of lymphopenia is not due to direct infection of virus and can be attributed to increased cytokine levels during inflammation.

Keywords : SARS-CoV-2, COVID-19, immune response

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P173-347: COVID19: Interaction between virus spikes and cell receptor

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Background and Aim : Understanding and recognition the viral structure of COVID-19 can help us to design vaccines and drugs for controlling and preventing this new acute respiratory syndrome. The attachment step in viral life cycle occurs when virus enters to body and penetrate into target cells. In this systematic review we want to explain how it will be occurred.

Methods : In this systematic review we collected all data information by searching in NCBI and PubMed Central (PMC) and we use search engines like as: Science Direct, MEDLINE and ISI Web of Science. These Data were gathered from full- length articles.

Results : SARS-CoV-2 infects the host using the angiotensin converting enzyme (ACE2) receptor, which is expressed in several organs, including the lung, heart, kidney, Corona virus entry into target cells by its surface spike named "S" Protein. S protein is a type 1 glycoprotein that consists of S1 and S2 subunits and is present on the virion surface as a trimer. The S1 region is involved in receptor binding and contains N and C-terminal domains(S1-NTD and S1-CTD)respectively that may both act as receptor-binding domain (RBD),with the major determinants of cell tropism residing in S1-CTD. . the COVID-19 also might interact with some of the previously known host targets like as: CD26, Ezrin, Cyclophilins.

Conclusion : Our knowledge about the life cycle and pathogenicity of COVID-19 are increased. Recognition All steps in virus replication can help us to controlling of this epidemic disease.

Keywords : COVID-19, Cell receptor, ACE2.

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P174-350: 2019-nCoV enents in Qom province, Iran

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Background and Aim : Recently, a new coronavirus (2019-nCoV), has emerged in the region of Wuhan (China) as a cause of severe respiratory infection in humans. This short report investigate a virus genome analysis and symptoms of disease in Qom province.

Methods : The literature search was performed by finding related case-control articles from the PubMed, Google Scholar, Web of Science, Scopus, databases and patients referred to general hospitals in Qom Province.

Results : 2019-nCoV is closely related (with 88% identity) to two bat-derived severe acute respiratory syndrome (SARS)-like coronaviruses but were more distant from SARS-CoV (about 79%) and MERS-CoV (about 50%). The envelope spike (S) protein mediates receptor binding and membrane fusion and is crucial for determining host tropism and transmission capacity. Different symptoms were seen: Having no underlying chronic medical conditions but reported fever, Significant changes in the lung, Fever and cough, Shortness of breath or difficulty breathing, Muscle aches, Chills, Sore throat, Runny nose, Headache, Chest pain, vomiting and diarrhea, and Different pattern of Chest CT scan immagings from first day to the fifteenth day. Also, RT-PCR method and chest CT scan are the best diagnostic methods.

Conclusion : This is the first reportation in Qom province. These data along with data from our study could clarify the transmission dynamic of the 2019-nCoV supporting infection control policy during the ongoing epidemic.

Keywords : 2019-nCoV, virus genome, symptoms of disease.

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P175-410: Prevention, diagnosis and treatment for the new coronavirus, the causative agent of COVID-19

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Background and Aim : The unprecedented outbreak of new coronavirus in Wuhan, Hubei Province, China, occurred in December 2019. The International Committee on Taxonomy of Viruses (ICTV) named the virus SARS-CoV-2 because of its similarity to the SARS virus, and the World Health Organization named the disease caused by this virus, COVID-19. The virus is composed of positive sense single-stranded RNA surrounded by capsid proteins and a membrane. Large number of infected individuals exposed to live animals (bats, snakes, marmots, and pangolins) in Wuhan, China, suggested that these animals may be the source of the COVID-19. Extensive measures have been taken to reduce the person-to-person transmission of COVID-19 to control the current outbreak. Special care should be taken to protect or reduce transmission in vulnerable populations, including children, health care providers, and the elderly. The virus can have irreversible effects on human health and cause serious damage to various organs of the body, including the lungs, gastrointestinal tract, kidneys, heart and brain.

Methods : In this review study, the ways of transmission and prevention of the new coronavirus and diagnostic methods including PCR test and antibody test and the latest research in the field of treatment and results of using drugs have been discussed.

Results : The results revealed that different drugs such as ibuprofen, chloroquine, Viral protease and RNA polymerase inhibitors and plasma therapy had positive effect in recovery of patients. Hopeful results was obtained to design effective vaccine especially RNA vaccine.

Conclusion : Several strategy must be used for eradication of COVID-19. Prevention by social distancing, using face mask and herd immunity by vaccination, rapid diagnosis of patients and treatment by effective drugs such as RNA-dependent RNA polymerase (RdRp) could help us to control and eradicate COVID-19

Keywords : Coronavirus, SARS-CoV-2, COVID-19

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P176-111: role played the interleukin 17(IL-17) axis in uveitis of leptospirosis

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Background and Aim : Leptospirosis is a zoonosis caused by infection with pathogenic strains of the bacterium Leptospira . This infection has a worldwide distribution, and is an emerging/re-emerging public-health problem, particularly in large urban centres of tropical and subtropical regions. Uveitis represents the 5th leading cause of visual loss in Europe with a prevalence of approximately 35–80 per 100,0001 causing approximately 5%–20% of blindness. Interleukin (IL) 17 is a proinflammatory cytokine released by helper T cell-17 (T-helper 17) already known to play a defense role against microbes. Recently, the association of Th-17 cells or IL-17 with ocular inflammatory diseases such as uveitis, scleritis and dry eye syndrome was discovered. In this study, researchers aimed to investigate role of IL-17 in inflammation of eye by leptospirosis.

Methods : Sample of eye (aqueous humor) collected from 50 mice fall into two groups (healthy control and patient) for RNA extraction. The extracted mRNA was subjected to cDNA synthesis and the resultant cDNA was used for analysis of IL-17 using real time PCR. The IL-17 was also measured by ELISA (enzyme-linked immune-sorbent-assay).

Results : Results of the present investigation have indicated that all of leptospirosis patient exhibited elevated levels of IL-17 when compared to control. The mean level of IL-17 was 136.38±8 pg/mL and 21.07±2pg/mL in leptospirosis patients and controls, respectively.

Conclusion : According to the findings of the present study the IL-17 axes may play fundamental parts in pathogenesis of leptospirosis by recruitment of immune cells toward eye inflammation. These axes may possibly serve as therapeutic factors for therapy of leptospirosis. The demonstration of IL-17 involvement in various ocular and infectious disease is supporting evidence for recent reports (13, 19) showing that Th-17 cells are important in the pathogenesis of ocular surface diseases. We demonstrated in this study that elevated IL-17 levels.

Keywords : leptospirosis , uveitis , interleukin 17 (IL-17)

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P177-113: Roles of clusterin and IL-18 reflected kidney injury in leptospirosis

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Background and Aim : Leptospirosis is a zoonosis caused by infection with pathogenic strains of the bacterium Leptospira. Clusterin may play an important role to chronic kidney inflammation. Interleukin 18 (IL-18) is a proinflammatory cytokine. In the kidney it is induced and cleaved mainly in the proximal tubules and released into the urine under different conditions of kidney injury. Serum creatinine is not an ideal marker of renal function in patients with acute kidney injury (AKI). Previous studies demonstrated that urinary IL-18 is increased in AKI. Thus, whether urine IL-18 is an early diagnostic marker of AKI was investigated Urinary IL-18 is a useful biomarker of AKI with moderate predictive value across all clinical settings. In this study, researchers aimed to investigate roles and levels of clusterin and IL-18 reflected kidney injury in leptospirosis

Methods : Tissue damage was examined by histology, infiltrate phenotypes by flow cytometry analysis, and fibrosis-related gene expression by PCR array then we studied the renal alterations in relation with the regulation of inflammatory cytokines and chemokines, comparing two experimental models of chronic leptospirosis, the Mice that survived the infection, becoming carrier of virulent leptospires, and the OF1 mouse, a usual reservoir of the bacteria. Animals were monitored until 28 days after injection with a virulent L. borgpetersenii serogroup Ballum to assess chronic infection

Results : Mice developed morphological changes such as tubulointerstitial nephritis and fibrosis. lower expression levels of cytokins indicated a better regulation of the inflammatory response and possible resolution processes likely related to resistance mechanisms. PCR array showed the association of clusterine deficiency with up-regulation of CCL12, Col3a1, MMP9 and TIMP1 and down-regulation of EGF in kidneys.

Conclusion : : Our data suggest that clusterine deficiency worsens renal inflammation and tissue fibrosis. Urinary IL-18 is a useful biomarker of AKI with moderate predictive value across all clinical settings. Urine IL-18 levels of >100 pg/ml are associated with increased odds of AKI of 6.5 (95% confidence interval 2.1 to 20.4) in the next 24 h., urine IL-18 predict AKI in the next 24 h. The urine IL-18 values were also significantly different between survivors and nonsurvivors ($P < 0.05$), and on multivariable analysis, the urine IL-18 value on day 0 is an independent predictor of mortality.

Keywords : leptospirosis , interleukin 18 (IL-18), clusterin, kidney , AKI

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P178-179: Investigating tularemia spread during the past seven years in Iran

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Background and Aim : Introduction Tularemia known as Rabbit fever, Dee-Fly fever, and Ohara Disease is a common disease between human and animals caused by francisella tularensis, which is a gram negative bacterium. The bacteria are transmitted to the host through different forms of disease such as ulceroglandular, oropharyngeal, and pneumonia. The variety of transmission ways has made francisella tularensis a candidate for making biological weapons. Since the disease mostly spreads among northern hemisphere especially in Russia, Kazakhstan, Turkmenistan, Finland, and Sweden and to less extent in other European and Asian countries, unfortunately there is not a thorough and precise statistic for tularemia and limited studies have been done on it. This article investigates all studies having been done in Iran especially in high-risk areas during the past five years and discusses the importance of the disease and prevention methods.

Methods : Method: articles published in both English (science,medline,google scholar,pro quest,direct,embase,scopus,Cochrane library) and Persian (sid,magiran,iran medex) from 2013 to 2020,they were collected and included in this article.

Results : Results: Several articles have been found on tularemia in Iran, a limited number of which have been on the human form of infection, indicating an average prevalence of 7.38% in the country. Studies have shown that among the various forms of tularemia, the ulceroglandular form of the disease is more prevalent, especially among farmers, slaughterhouse staff, butchers, hunters, and people who have eaten wild animal meat. Although the disease is also prevalent in the east of the country, the highest prevalence of the disease is seen in the western regions (Kurdistan, Marivan, Sanandaj, Sarvabad, Ilam and Lorestan).

Conclusion : Conclusion: Only a limited number of articles have been found on human tularemia in Iran, indicating that it has been neglected in Iranian microbiological studies, so given the importance of tularemia as a new and emerging disease, it is recommended to be informed and educated. Necessary measures should be taken against this bacterium, especially in high-risk areas, continuous monitoring and more research on this bacterium.

Keywords : tularemia.francisella tularensis.infection.iran.rabbit fever

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P179-249: Identification of Brucella melitensis biovar 2 of bovine and human origin in Markazi province

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Background and Aim : Brucellosis is one of the common diseases of man and animals are caused by bacteria of the genus Brucella. The objective of this study was to identify fifteen Brucella isolates of bovine and human origin, the species causing brucellosis, from Markazi provice based on proliferating IS711 gene using PCR and sequencing.

Methods : In this study during the spring and summer of 2018, a total of 100 samples from suspected human and animals brucellosis. The identification was carried out through conventional methods such as macro and microscopic morphological descriptions, enzymatic activity, biochemical profile, substrate use and sensitivity to dyes. Complementary genotypic characterization was carried out using multiplex PCR for B. abortus, Brucella melitensis, Brucella ovis .

Results : The Fifteen isolated DNA was extracted by Salting out method and amplified based on IS711 fragment u.sing PCR, a band 731bp on 1% agarose gel, confirmed and identified all sampels are brucella melitensis. The results sequences and blasting with the data base sequences in gene bank shown high identity with Brucella melitensis biovare 2 like strain M5-90 M25, ATCC23457 with %100 similarity

Conclusion : It was concluded that the phenotypic and molecular identification of fifteen isolates as B. melitensis biovar 2 could be achieved using conventional and molecular techniques with enough resolution power. The identification of these isolates to the biovar level in epidemiological terms will allow the use of this genetic method as reference in future research. This finding constitutes the main out broke species might be brucella melitensis biovar 2 in markazi province

Keywords : Brucellosis, Identification, zoonosis, IS711,Markazi province

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P180-362: survey on carrier state of leptospirosis in dogs

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Background and Aim : Leptospirosis is an infection caused by spirochetes of the Leptospira genus that are the most common zoonosis worldwide and is endemic in tropical environments. Clinically recovered dogs frequently become asymptomatic renal carriers, and as such can be an important source of human leptospirosis. leptospirosis is now recognized as an important re-emerging disease in dogs. in this research was decided to study the incidence of leptospirosis carrier state in vaccinated and unvaccinated dogs.

Methods : For this purpose, 150 urine samples were collected from two group (urban or rural) of dogs in Ahvaz city. 5 ml of urines were centrifuged, and concentrated to 0.5 ml. Darting motility of leptospira in urine was studied by wet mount technique from concentrated urine and dark field microscope. After DNA extraction by commercial kit (RahaZist Padtan-IRAN), contamination of each sample to Leptospira genus and 4 its serogroup (Icterohaemorrhagiae, Pomona, Hardjo and Grippotyphosa) were evaluated by PCR and PCR-RFLP technique, respectively.

Results : Based on results, regardless of confirmation of leptospira genus contamination in 79 (50.67%) samples by PCR, in none of them darting motility observed. Restriction Fragment length polymorphism by HindIII وHeaIII enzymes, defined that abundant serogroup was Icterohaemorrhagiae (51.85%), and thereafter Pomona and Hardjo (24.07%). In this research not important relation between leptospira contamination with age, breed, gender, vaccination, urban or rural was observed by Chi-squared test.

Conclusion : At all, Contamination in dogs more than 2 years old, male, Shih-tzu terrier, unvaccinated and rural, was more than dogs with less than 2 years old, female, vaccinated and urban with another breed and Icterohaemorrhagiae was predominant serotype.

Keywords : Dog, Leptospirosis, PCR-RFLP

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P181-363: Effect of sub-inhibitory antibiotic concentrations on the production and structural density of biofilm by methicillin- resistant Staphylococcus aureus

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Background and Aim : The ability of Staphylococcus spp. to form biofilm is one of the virulence factors that facilitate the adhesion and colonization on the different surface, a fact that leads to recurrent or persistent infections. One of the factors of the increased resistance of biofilms is the protection by a self-produced extracellular polymeric substance (EPS), which is a matrix made up of proteins, polysaccharides, lipids, and nucleic acids. There is a subtle change of micro-organism behavior caused by antibiotics. Studies showed that low quantities of antibiotics and other pharmaceutical drugs can either induce or repress growth of micro-organisms. One of the concerns of these changes is the either induced or reduced biofilm formation by low levels of antibiotics.

Methods : In this study, effects of sub minimum inhibitory concentration of some antibiotics evaluated on reduction or induction of biofilm producing ability in 29 isolates of methicillin resistance staphylococcus aureus. Also, increase or decrease of N-acetylglucoseamine in inducted biofilm was studied. For this aim, antibiogram and biofilm producing ability of studied isolates was done by Kirby-bauer and microtitre plate crystal violet methods, respectively. Vancomycin, trimethoprim-sulfamethoxazole and clindamycin used in antibiogram. After extraction of exopolysaccharide (EPS), amount of N-acetylglucoseamine in inducted biofilm evaluated by TLC method

Results : Based on results, all the isolates were susceptible to vancomycin and biofilm producing ability in weak and average levels. Sub minimum inhibitory concentration of vancomycin increased biofilm producing ability in 38% of isolates. Increase of N-acetylglucoseamine was not demonstrated in isolates with inducted strong producing ability of biofilm.

Conclusion : Based on literature review, it could be based on absence of this compound or its changing to different composition which need to complementary studies.

Keywords : Antibiotic, Biofilm, Methicillin, Staphylococcus aureus.

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P182-366: Survey on the captive turtles roles as reservior of Yersinia ruckeri and Salmonella enterica serotype Typhimurium

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Background and Aim : Captive and wild-caught reptiles, more often present in domestic environment as pets, may harbor and excrete a large variety of zoonotic pathogens. Among them, Salmonella spp. is the most well-known agent and also numerous reports demonstrate that Y. ruckeri has a wide host range and geographical distribution, and can cause both epizootics and zoonosis diseases. Also free-ranging and captive reptiles could be involved in the epidemiology of these infections. Because of turtle's role as concern pet in different regions, the aim of this research was the epidemiologic survey on Salmonella typhimurium and Yersinia ruckeri carrier states of turtles in Pardisan wildlife rehabilitation center.

Methods : For this aim, one hundred cloacal swabs were collected from studied turtles and sent to Veterinary school microbiology lab of Shahid Chamran university of Ahvaz. Different points such as gender, age, family, species, ratio, and origin were recorded. Cultivation in pre-enrichment and selective media was done and 3-5 doubtful colonies were collected from each sample. After DNA extraction of each isolate by boiling, molecular identification of two studied bacteria, was done by PCR

Results : Based on results, infection with Salmonella typhimurium and Yersinia ruckeri was detected in 15% and 27% of turtles, respectively. Coinfection was demonstrated in 11.9% of infected turtles. The incidence of Yersinia infection was not significantly related to all of noted items. But incidence of Salmonella infection was significantly related to family, species, ratio, origin of studied turtles. Also incidence of coinfection showed significant relation between family and ratio of turtles.

Conclusion : Finally, determination of the presence of infection with proven role of turtle in zoonotic and epizootic disease, are reminder of more attention to illegal entrance of turtles to local markets as a threat for Iran wildlife and aqueous training area for prevention of significant economic losses in the fish farming industry.

Keywords : Salmonella spp., Yersinia spp., Turtle, Wildlife

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P183-408: Seroprevalence of West Nile virus in blood donors referring to Kurdistan province blood bank

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Background and Aim : West Nile virus (WNV) is an endemic infection in Africa and the Middle East that is not limited to international borders. Infected mosquito bites are the most common cause of this infection. There is no definitive treatment or vaccine for this infection. Its treatment is more supportive and based on controlling the symptoms of the disease. The aim of this study was to investigate the presence of this virus in continuos blood donors as the most important and reliable sources of blood supply for patients in medical centers and also the spread and endemicity of this virus in the Middle East and the proximity of western provinces of Iran, With endemic areas of the virus.

Methods : In a descriptive-analytical study, 259 continuos blood donors referred to the Kurdistan Blood Transfusion Organization, after obtaining their informed consent and filling out a checklist, venous blood was taken from them and after separating the blood serum, the amount of IgM and IgG antibodies against West Nile virus were measured by ELISA in them. The results were analyzed using SPSS V.20 software.

Results : IgG antibodies were positive for IgM against West Nile virus in 14 patients (5.4%) and 3 patients (1.2%). In patients over 40 years of age, seropositive IgG was observed in 11 patients (12.5%). However, only 3 patients (1.8%) of patients under 40 years of age had seropositive IgG, which was statistically significant (OR = 7.95; 95% CI: 2.16 to 29.32; p <0.01).

Conclusion : : Due to the high value of blood and blood products of continuos blood donors, for medical purposes and the significant prevalence of this virus, as well as the presence of positive IgM cases, the need for screening blood donors in blood transfusion centers, in addition to routine viral tests, is essential and it seems necessary in the western region of the country.

Keywords : West Nile virus, blood donors, Kurdistan, blood bank

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P184-318: Epidemiological study of bacterial causes of blood and urinary tract infections in patients referred to Besat Hospital in Sanandaj during the first three months of 2019

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Background and Aim : Identifying the causes of septicemia as one of the leading causes of death in hospitalized patients and urinary tract infection¬¬¬¬¬¬ (UTI) as the second most common cause of infection in the human body is essential in the management and treatment of patients. The aim of this study was to Epidemiological study of bacterial causes of blood and UTI in patients referred to Besat¬¬¬¬ Hospital in Sanandaj during the first three months of 2019.

Methods : This study was descriptive-retrospective, based on data from 3947 urine culture samples and 943 blood culture samples taken from patients referred to Besat Hospital in Kurdistan Province, Sanandaj, from March to June 2019. The samples were examined for infection-causing agents identified by culture and Biochemical methods of bacterial identification. Findings with SPSS20 software and Chi-Square test were analyzed.

Results : 7.63% of blood culture samples and 6.77% of urine culture samples were positive. Bacteria isolated from blood culture and urine culture included: Escherichia coli (5.55% and 65.17%), Staphylococcus saprophyticus (9.72% and 6%), Enterobacter (4.17% and 5.24%), Citrobacter (6.94% and 5.24%), Staphylococcus epidermidis (31.94% and 4.9%), Klebsiella (0.0% and 4.11%), Serachia (1.39% and 4.11%) , Proteus (1.39% and 2.67%), Streptococcus (1.39% and 0.37%), Acinetobacter (22.22% and 0.74%), Pseudomonas (0.0% and 1.12%) and Stenotrophomonas maltophilia (15.28% and 0.0%) respectively.

Conclusion : According to the results of the study, Staphylococcus epidermidis and Acinetobacter are the most common causes of blood infection and Escherichia coli is the most common cause of UTI. Careful diagnosis of pathogens that cause infection is essential.

Keywords : Urine culture, Blood culture, Bacterial

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P185-68: Synthesis, characterization, and activity determination of dendrimer-streptokinase conjugated and finding protein crona and Evaloation of cytotoxicity

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Background and Aim : Nowadays, dendrimer conjugation with low molecular weight drugs has been considered for improving pharmacokinetics, targeting drugs to particular sites, and helping cellular uptake. Increasing the performance of relatively great therapeutic proteins like streptokinase (SK) using dendrimers is being explored.

Methods : In this study, G2 dendrimer and dendrimer-streptokinase-conjugates were synthesized. After synthesis of dendrimer-SK conjugates, characterization of these conjugates by Fourier-transform infrared radiation (FT-IR), nuclear magnetic resonance (NMR) and high performance liquid chromatography (HPLC) showed that the conjugation reaction was successful.resulting in relatively pure SK-dendrimer conjugates and checked the cytotoxicity effect.

Results : Here, we show that dendrimer-streptokinase conjugates formed crona protein in whool blood cells.hese results emphasize the need of investigating the formation and biological importance of the protein corona in the blood as the nanoparticles are intended for or released into. Moreover, potency of dendrimer-SK conjugates was greater than streptokinase. It seems that high enzymatic activity of dendrimer-SK conjugates can be a favorable way for changing bioactive macromolecules with dendrimer. Furthermore, injection of dendrimer-streptokinase conjugatesmay be promising for treatment of many conditions.

Conclusion : Dendrimers were useful for effective attachment to various proteins. It seems that high enzymatic activity of dendrimer-SK conjugates could be a favorable way for changing bioactive macromolecules with dendrimer. Furthermore, injection of dendrimer-streptokinase conjugatesmay be promising for treatment of many conditions

Keywords : Dendrimer, streptokinase. conjugation, potency, characteristic, Protein crona

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P186-69: Evaluation of the Release of Nanoconjugate Streptokinase Using State-Ease Software Application

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Background and Aim : Controlled drug release is a process in which a nanoparticle specifically incorporated into a medicine is separated from the medicine in a predetermined and desirable manner and the retention time of the drug in the biological system is increased. Therefore, estimation of the lifespan of conjugated nanodrug relative to the retention time of the drug itself is of great importance. I

Methods : n the present study, nanoconjugate release was designed based on RSM statistical method and was tested at different temperatures, pH values, and rotation times

Results : According to the peak produced by a high-performance liquid chromatographer, the highest drug release (highest peak) is at pH = 2, t=0 and 300 rpm rotation. The 7-minute period is related to the recombinant Streptokinase drug and the 4-minute period is related to Dendrimer.According to the 2ndpeak, the lowest drug release is at pH = 2 and day 7 with a rotation of 200 rpm. The 7-minute period is related to the recombinant Streptokinase drug and at the time of 4 minutes is related to Dendrimer

Conclusion : The purpose of the design with state-ease software was to estimate the proper time, pH, and rotation to obtain conjugated nanodrug stability because this software helps to estimate the right result within the specified time with the minimal test. According to the design, this test was designed at three levels of time, pH and rotation and was exposed to different conditions based on the design of the drug and the results were analyzed by two sample absorption assay method including spectrophotometry and liquid phase chromatography. The advantage of using this method is that it can measure the release of the drug in areas where the test cannot be performed and the effect of each factor and the interactions between variables is also determined. Since the predictive power of response has three factors in different values, it is a proper way to design and obtain the release time of the drug.

Keywords : Test design; Nanodrug; RSM; HPLC

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P187-75: Evaluation of Antibacterial effect of Silver Nanoparticle on clinical Pathogenic Bacteria

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Background and Aim : Development of multidrug resistance has become a global issue with serious consequences in the management of infectious diseases caused by pathogenic bacteria. Many research studies have investigated the antimicrobial activity of silver nanoparticles. In this research, the effects of silver nanoparticle were studied on some clinical gram-positive and gram-negative bacteria.

Methods : The antibacterial effect of silver nanoparticle on clinical and standard isolates of Staphylococcus aureus (gram-positive) and Pseudomonas aeruginosa (gram-negative) was assessed by minimal inhibitory concentration (MIC). One of the clinical strains of Pseudomonas aeruginosa was drug-resistant strain.

Results : Silver nanoparticles inhibited the growth of all strains in different concentrations. The drug-resistant strain had a higher MIC than the other strains.

Conclusion : The findings suggest that the silver nanoparticles have antibacterial effect against staphylococcus aureus and pseudomonas aeruginosa strains.

Keywords : Silver Nanoparticle, Antibacterial, Staphylococcus, Pseudomonas.

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P188-193: A novel equipment for making nanocomposites for investigating the antimicrobial properties of nanotextiles

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Background and Aim : The purpose of this article is the development of up-to-date equipment for making nanocomposites for investigation of the antimicrobial properties of nanotextiles and the creation of a scientific base to choose materials of clothing with a special purpose.

Methods : Investigations are focussed on modifying the surface of textile materials by metal ions nanoparticles (AgJ, CuJ). The work of the equipment is based on the creation of metal nanocomposites in polyethyleneglycol (PEG). It is heated up to a temperature of not more than 130ºC, followed by adding the dispersion of metal in small portions to water. Nanoparticles are uniformly distributed on material surface that provides the improvement of its characteristics.

Results : It has been found that modifying natural fibrous materials by nanoparticles of metal ions (AgJ, CuJ) promotes increasing their bactericidal and fungicidal properties with a comparison with traditional cotton materials. Microbiological investigations of antimicrobial properties of the cotton fabric have been conducted according to their effects on staphylococcus bacteria, E. coli and fungi.

Conclusion : Special equipment for investigation of antimicrobial properties of nanomodified textile materials of different kinds has been engineered, and there is an opportunity to create materials with antibacterial and antifungal properties. The application of this equipment provides the receiving of new characteristics for textile materials with silver ions nanoparticles. Such properties of nanomodified materials are useful for human health and can be used in the production of various textile products.

Keywords : Textile materials, Solid nanocomposites, Antimicrobial peroperties, Silver nanoparticles, Nanomodified samples

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P189-232: Effect of Nanoparticles on the Prevention , Diagnosis and Treatment of Malaria (review of the current evidences)

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Background and Aim : Malaria is one of the mortalist parasites of the tropics and subtropics worldwide. Overcoming on benefit vaccine or proficiency of treatment malaria is not an easy task. Nanomedicine is combined modern technology with original products to improve antimalarial drug delivery and rapid detection assays for malaria diagnostics.

Methods : Databases including Science direct, PubMed and Scopus were searched using the terms "nanomedicine OR nanoparticle" AND "malaria OR plasmodium OR plasmodium falciparum ". There was no time limitation on the search strategy. A total of 58 out of 139 articles were selected under the inclusion criteria .81 articles were rejected due to lack of direct relevance.

Results : Dendrimers have been tested for drug delivery, encapsulated chloroquine, and primaquine. Also, they were able to discriminate between plasmodium-infected RBC and none-infected cells that reduced the amount of drug needed to death malaria up to four times. Solid lipid nanoparticle (SLN) proposed an intermittent encapsulation system for both hydrophobic and hydrophilic drugs. For presenting malaria antigens to the immune system was self-assembly of 60 circumsporozoite protein of Plasmodium falciparum (pfCSP) chains into spherical self-assembling protein nanoparticles to improve a vaccine against p.f. The sensibility of p.f to dsRNA against a parasite key replicating enzyme topoisomerase-2. Chitosan-based nanoparticles trapping of a long dsRNA against this gene displayed increased inhibition of p.f growth in culture.

Conclusion : Nanomedicine may have increased the therapeutic activities by enhancing their stability, prolonging their circulation and site-specific accumulation and increasing drug delivery according to various biological and external stimuli.

Keywords : Nanomedicine. Antimalarial . Malaria . Plasmodium . Nanoparticle.

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P190-376: Antibacterial activity of Cu nanoparticles against E-Coli

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Background and Aim : Antibacterial have been widely used in the textile industry, water disinfection, medicine and food packaging. Organic compounds used for disinfection have some drawbacks, including toxicity to the human body, therefore, the interest in inorganic disinfectants such as metal oxide nanoparticles (NPs) is increasing. The antibacterial mechanism of NPs depend on the applied dose and size and have been more effective for Gram-negative bacterium as compared to Gram-positive ones. In this study, synthesis of copper nanoparticles was approached by a single-precursor route via controlling the growth temperature.The current research examined the calculated inhibition of E-coli after adding various amounts of Cu-NPs to the culture medium.

Methods : 0.01 mol Cu(acac)2 was added to the three test flask, which contained 5 mL oleylamine (OA) under Ar while, the temperature kept at 200°C. This temperature kept at the selected value for 5 h. The solutions, then, were cooled at room temperature and nanoparticles were obtained by centrifugation (5 min) and washing. The as-prepared nanoparticles were dried in vacuum at 60°C for 24 h for further experiments. Growth curves of bacterial cell cultures were attained through repeated measures of the Optical Density (OD) at 600 nm. A control medium, which contained no copper nanoparticles, was also used to examine the true differences between samples and control groups.

Results : The growth curves of bacterial cells treated with Cu nanoparticles indicated that Cu could inhibit the growth and reproduction of bacterial cells. The bacterial growths of cells treated with 50, 100 and 150 µg mL-1 were inhibited. After 2 h, almost all treated bacterial cells were dead.

Conclusion : Cu-NPs showed anti bacterial activity against E. coli.

Keywords : Copper nanoparticles, E- Coli, inhibition

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P191-383: Antimicrobial activity of turmeric aqueous extract and chitosan

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Background and Aim : Turmeric and chitosan are natural-derived compounds. The present study investigates the antimicrobial and anti-biofilm potentials of turmeric extracts and chitosan against for multiple drug-resistantbacteria.

Methods : A group of isolated bacteria from clinical samples with resistance to most of antibiotics were collected by phenotypic and genotypic assays. The minimum inhibitory concentration of turmeric aqueous extract and chitosan investigate with the broth micro-dilution methods. The checkerboard assay used to investigate the synergistic effect of the combination of these natural compounds.

Results : The turmeric and chitosan showed inhibitory effect on bacteria, especially on the planktonic form of bacteria. The antibiofilm effect of turmeric and chitosan were more found in isolates.

Conclusion : The combination of turmeric and chitosan on the tested bacteria has a synergistic effect. Therefore, turmeric and chitosan can be used in pharmaceutical and disinfectants formulations. The aqueous extract and chitosan fiber will help to produce value added handicrafts.

Keywords : turmeric aqueous, chitosan, drug-resistantbacteria

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P192-397: Antibacterial property of a new metallic nanoparticles composite

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Background and Aim : Bacterial infections are increasing in all parts of the world and become a major challenge in the medicine and medical fields. Continuous and extensive use of antibiotics has led to the emergence of bacterial resistance, and the expansion of new bacterial resistance mechanisms threatens our ability to prevent and treat common infectious diseases. Therefore, the search for and development of new antimicrobial compounds that have antibacterial potential against multi-drug resistant bacteria is an important priority. Nanoparticles with their enhanced and unique physicochemical properties, such as ultra-small sizes, large surface area/mass ratio, and increased chemical reactivity, have led research toward new prospects of treating and preventing microbial infections. In our study, a new metallic nanoparticles composite was develop as a potential antibacterial agent.

Methods : The metallic nanoparticles composite prepared in this study, characterized using FTIR, XRD, SEM and the antibacterial activity of the composite nanoparticles was studies through MIC and MBC.

Results : The synthetized metallic nanoparticles composite showed high purity and uniform particle size distribution with homogeneous shape. Moreover, the metallic nanoparticles composite showed promising antibacterial activity as compared with the control.

Conclusion : Functionalized nanoparticles would provide an emerging method in the development of modern pharmaceutical science for conducting proprietary treatment processes for bacterial infection. However, the antibacterial efficacy of nanoparticles necessitate optimization of their physical, chemical, and biological characteristics.

Keywords : New antibacterial agent, metallic nanoparticles composite, high antibacterial activity

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P193-407: Study of the effect of the wound dressing Polyvinyl alcohol nanofiber containing Pomegranate Seed extract on surgical wounds infected by staphylococcus aureus in a rat model

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Background and Aim : Wound infection has become a major medical problem after the surgical operation. The use of nanotherapeutic agents engineered within the nanoscale consider as a promising tactics for overcoming the wound infection in recent years. the aim of this study was the evaluation of the effect of the wound dressing Polyvinyl alcohol(PVA) nano fiber-containing Pomegranate Seed against Staphyloccocus. areous in surgical wounds using a rat model.

Methods : 60 male Wistar rats were randomly divided into four groups of treatment by extract+PVA, PVA, Nitroforazon, and Normal saline for two weeks. A circular incision was made on the dorsal inter-scapular region of each rat. Then rats were inoculated with 10^6 CFU of S. areous (isolated from human wound infection) at the site of skin wound. Treatments and normal saline (control) were applied once every two days during the experiment. Tissue specimens were weighted and homogenized in broth on days 7 and 14. colony counts were conducted after serial dilution preparation.

Results : a load of bacteria in the control group and treated by extract+PVA on day 7 were 4.6*10^8 and 1.3*10^6 and on day 14 were 1.5*10^9 and 7.4*10^5 respectively while in Nitroforazone group was 5*10^6 and 4.1*10^5 CFU/ml.

Conclusion : according to the results of this study the wound dressing Polyvinyl alcohol nanofiber containing Pomegranate Seed extract on surgical wounds infected by staphylococcus aureus has a remarkable antimicrobial effect.. Therefore nanotherapeutic agents could be suggested as a potential alternative instead of traditional antibiotics.

Keywords : wound infection, Nanoextract, Pomegranate Seed

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P194-409: Study of the effect of the wound dressing Polyvinyl alcohol nanofiber containing Eucalyptus globules extract on surgical wounds infected by staphylococcus aureus in a rat model

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Background and Aim : : Wound infection is one of the frequent complications in patients with a surgical operation. The use of nanotherapeutic agents engineered within the nanoscale is one of the most promising strategies for overcoming the wound infection. This study aimed to investigate the effect of the wound dressing Polyvinyl alcohol(PVA) nano fiber-containing Eucalyptus globules against Staphyloccocus. areous in surgical wounds using a rat model.

Methods : 60 male Wistar rats were randomly divided into four groups of treatment by extract+PVA, PVA, Nitroforazon, and Normal saline. A circular incision was made on the dorsal inter-scapular region of each rat. Then rats were inoculated with 10^6 CFU of S. areous at the site of skin wound. Treatments and normal saline (control) were applied once every two days during the experiment. Tissue specimens were weighted and homogenized in broth on days 7 and 14. colony counts were conducted after serial dilution preparation.

Results : a load of bacteria in untreated and treated by extract+PVA groups on day 7 were 8.3*10^7 and 4*10^6 and on day 14 were 5.37*10^6 and 6.72*10^5 respectively while in Nitroforazone group was 2.8*10^6 and 3.85*10^5 CFU/ml.

Conclusion : the results of this study showed the wound dressing Polyvinyl alcohol nanofiber containing Eucalyptus globules extract on surgical wounds infected by staphylococcus aureus has an antimicrobial effect similar to standard treatment with traditional antibiotics. Therefore nanotherapeutic agents consider as a potential alternative instead of antibiotics.

Keywords : wound infection, Nanoextract, Eucalyptus globules

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P195-418: Investigation of synergistic effect of biosynthesised silver nanoparticles by chlorella vulgaris and curcumin against clinical isolates of Pseudomonas aesuginosa and Staphylococcus aureus

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Background and Aim : this study was done to evalute the synergistic effect of bio-silver nanoparticles synthesized by the chlorella algae and curcumin against clinical isolates. Pseudomonas aeruginosa and Staphylococcus aureus.

Methods : Silver nanoparticles were synthesized by the chlorella algae biologically. Then, spectrophotometers and XRDs were used to characterize the synthesis of silver nanoparticles. Then, the antimicrobial effect of silver nanoparticles and curcumin were separated and combined. The wells were examined carefully and finally their MIC and MBC were evaluated.

Results : The antibacterial effect of nano-silver Showed that it had more inhibitory effect on Pseudomonas aeruginosa isolates. These results obtained from the antibacterial effect of curcumin showed that the extract had no inhibitory effect on Pseudomonas aeruginosa isolates while ethanolic curcumin extract had more inhibitory effect than the aqueous extract on Staphylococcus aureus isolates. It had more anti bacterial effect on Staphylococcus aureus isolates than Pseudomonas aeruginosa .. The synergy of bio-nano-silver and nano-curcumin showed that this compound had more inhibitory effect on Pseudomonas aeruginosa isolates than Staphylococcus aureus.

Conclusion : The results of this study showed that bio-silver in combination with nano-curcumin had synergistic effect on growth inhibition of Pseudomonas aeruginosa and Staphylococcus aureus and had more inhibitory effect on Pseudomonas aeruginosa isolates. Combination therapy increases the effectiveness of each in treating infections caused by Pseudomonas aeruginosa and Staphylococcus aureus. Further studies are needed to elucidate the toxicity of these particles.

Keywords : Silver Nanoparticle, Antimicrobial Effect, , Curcumin, Synergy

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P196-18: Identification of common Salmonella enterica serovars isolated from national foodborne outbreaks using Multiplex PCR and determination the antimicrobial susceptibility profiles of isolates

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Background and Aim : Back ground: Salmonella enterica serovars are the most prevalent cause of foodborne outbreaks. They can cause a wide range of infections which the most common is gastroenteritis. This infection is usually self-limiting but high-risk groups require antibiotic therapy. The presence of drug-resistant Salmonella serovars has made treatment difficult. Thus identification of the common resistant serovars and polluted food types is a key role in the prevention and control of salmonellosis. The aim of this study is the identification of common Salmonella serovars and antibiotic resistance status as well as to determine the food groups responsible for the poisoning in fecal samples of poisoned individuals involved in foodborne outbreaks in Iran during 2013-2019.

Methods : Methods: A total of 83 isolates were obtained from 1,425 stool samples by conventional and serological tests. Serotyping of Senftenberg and paratyphoid serovars was performed by classical methods and, for other serovars, PCR was performed. Antibiotic susceptibility of strains was determined using the disk diffusion assay. The minimal inhibitory concentration (MIC) of the ceftriaxone and ciprofloxacin were determined by an E-test strip.

Results : Results: Among 83 Salmonella isolates, the most frequent serovars were S. Enteritidis and Senftenberg, respectively (26.3%, 21.3%) and S.Typhi, S.Enteritidis had the highest percentage of hospitalized patients (27.8%). The highest contamination was related to cooked meat (64.2%) and then fruits and vegetables (21.4%) And the most clinical symptoms were non-bloody diarrhea then nausea (93.7%, 76.2% respectively). The ciprofloxacin MIC value ranged between 0.19-0.38 µg/ml for four isolates

Conclusion : Conclusion: In general, our study provided valuable information on antibiotic resistance patterns of serovars involved in Salmonella outbreaks in Iran which can help in presenting effective treatment patterns for treating invasive salmonellosis to physicians.

Keywords : Salmonella enterica; ceftriaxone; ciprofloxacin; Multiplex PCR; serogroup

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P197-21: The effect of Cold Plasma on Microbial Contamination and Physicochemical Properties of red Meat

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Background and Aim : Mohammad ebrahim goli mehdi abadi* The present study aims to investigate the effect of cold plasma, the combination of argon and helium gases, on the reduction of microbial load and physicochemical changes in minced sheep meat.

Methods : minced sheep meat was subjected to 36 cold atmospheric plasma treatments with different time intervals (3, 9, and 12 min) and argon-helium gas ratios (1:8 and 2:7)

Results : we concluded that both parameters of time and gas composition affect microbial load reduction by cold plasma.

Conclusion : the microbial load of the minced meat significantly decreased after plasma treatments in different gas composition and duration of exposure.the argon-helium ratio of 2:7 with an exposure time of 12 min was the most effective treatment. the ratio of 2:7 argon-helium caused fewer changes in physiochemical properties of minced sheep meat. Helium and Argon are the preferred gases due to having high thermal conductivity, rich ultraviolet emission spectrum, and lower operating discharge voltage in atmospheric pressure. these two plasma gases are rich in charged particles, which cause the damage of bacterial cell surface.

Keywords : Cold plasma,microbial load,Argon,helium,sheep meat

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P198-35: Biocontrol Effect of Lactobacillus delbrueckii on Aflatoxin Expression in Aspergillus parasiticus

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Background and Aim : Background: Recent studies demonstrated that some of the lactic acid bacteria (LAB) strains have great inhibitory effects on fungal growth as well as aflatoxin production. Aspergillus (Asp.) species are pathogenic fungi caused invasive aspergillosis. Aflatoxins are extremely toxic secondary metabolites which contaminate food products. Several investigations have been performed on the removal of aflatoxin. The aim of this study was evaluation of the effect of L. delbrueckii on Asp. parasiticus growth as well as aflatoxin production.

Methods : Material and Methods: In this study assessed Lactobacillus delbrueckii subsp. Bulgaricus (PTCC 1737) in controlling the Asp. parasiticus (ATCC 15517) growth and aflR and Nor1 genes expression. Broth microdilution method (CLSI, M27-A3) was applied to identify the antifungal activity of L.bulgaricus and examined by exposing Asp. parasiticus to different amounts of L.bulgaricus. A suspension of 1.5×108 CFU/ml of L. delbrueckii was diluted to 7.5×107 CFU/ml in Potato Dextrose Broth medium. Analysis of the aflR and Nor1 genes expression was performed by measuring the genes mRNA levels with Real Time PCR assay. β-actin was used as housekeeping gene.

Results : Results: In the presence of 2 × 103 CFU/ml of L.bulgaricus, the relative expression of aflR gene significantly reduced when compared to control. There were statistically significant differences in aflR and Nor1 gene expressions after treated with L.bulgaricus (P=0.001). The aflR mRNA expression levels were down regulated by 90% whereas the Nor1 mRNA expression level was down regulated by 30% (P<0.001).

Conclusion : Conclution: According of our results, L.bulgaricus could be suitable LAB against toxigenic effects of mouldy human foods and animal feeds.

Keywords : Key words: Aspergillus (Asp.), Aflatoxin, lactic acid bacteria

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P199-61: Refrigerated storage effect on expression of shiga toxin genes in Escherichia coli O157:H7 in ground meat

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Background and Aim : Escherichia coli O157:H7, the main agent of hemorrhagic colitis, produces shiga toxins as key virulence factors. Investigation of pathogenicity of bacteria in broth or broth like modes doesn't match properly with results obtained from food matrix. So in this work we investigated stx genes expression of E. coli O157:H7 expression in ground beef matrix during 7 days.

Methods : Comparative real-time RT-PCR was used to evaluate stx1A and stx2A genes expression of E. coli O157:H7 against glyceraldehyde-3-phosphate dehydrogenase (GAPDH) as reference gene.

Results : Expression of both of the stx genes decreased during storage of ground meat. Expression reduction was progressive during storage but there were no significant differences between different days. So the highest reduction was observed on the last evaluation day (day7) that was -3.35 and -2.9 for stx1A and stx2A, respectively.

Conclusion : It seems E. coli O157:H7 possess low risk in prolonged storage in ground beef in terms of stx genes expression. However there are different reports of stx genes expression of E. coli O157:H7 in various food matrixes such as lettuce, milk, fish and fruits. So it could be concluded that several factors are influencing on growth and pathogenicity of bacteria in different mediums and generalizing of results obtained in broth media to food matrix should not be always correct. However in this study it is not obvious that is gene expression reduction is equal to reduction in toxin release?

Keywords : Escherichia coli O157:H7, Shiga toxin gene, Expression, Ground beef

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P200-71: Effect of partial substitution of nitrite in sausage formulation by Thyme essential oil and celery powder

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Background and Aim : This study was aimed to investigate substitution of nitrite in sausages formulation.

Methods : sausage samples were produced using 60 ppm nitrite combined with a mixture of celery powder and thyme essential oil in the form of four treatments including: T1 (1.5% celery + 0.02% thyme), T2 (1.5%celery + 0.04% thyme), T3 (3% celery + 0.02% thyme) and T4 (3% celery + 0.04% thyme) and control sample produced by 120 ppm nitrite (without celery powder and thyme essential oil). All samples stored in the refrigerator for 35 days and physicochemical, microbiological and sensory properties were evaluated

Results : The results showed that thiobarbituric acid and peroxide values in control sample had the highest amounts of 0.16-0.65 and 0.36-1.37, respectively, during the study, but the lowest values were related to T4 by amounts of 0.06-0.39 and 0.13-0.92, respectively ($P<0.01$). Also the highest amount of pH and a* color index were belong to T4 and the lowest values to the control sample. In microbial tests, all samples had total bacterial counts less than 3.6 log cfu/g and significant difference were not observed between control and treatments. Moreover, Clostridium perfringens was not detected in any of the treatments and coliforms was not enumerated in treatments (except control). Also, molds and yeasts were enumerated only in control, T1, and T2 samples at 28 and 35 days of storage. Sensory evaluations mostly showed no significant difference between treatments and control sample ($P>0.01$).

Conclusion : Generally, the results indicated the possibility of partial replacement of nitrite using a combination of thyme essential oil and celery powder.

Keywords : Thyme essential oil, celery powder, Nitrite substitution, Sausage

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P201-136: Contamination of Chicken Meat With Salmonella spp Distributed in Yazd City, Iran

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Background and Aim : Foodborne diseases are one of the fundamental problems in the world. Salmonella is one of the most important foodborne bacteria, which is responsible for the prevalence of foodborne diseases in humans. The aim of this study was to investigate the presence of Salmonella in distributed chicken meat in Yazd city, Iran.

Methods : In this study, 100 samples of chicken meat were selected from Yazd city and investigated for the presence of Salmonella. Each sample was cultured in selenite cystine medium and incubated at 37°C for 24 hours. Then the obtained colonies were cultured in MacConkey agar and Salmonella-Shigella agar. Finally, biochemical and antibiogram tests were performed on isolated Salmonella samples.

Results : Totally, 8 chicken samples (8%) were found to be contaminated with Salmonella. All of the isolated Salmonella samples were identified as Salmonella enteritidis. All of S. enteritidis isolates (100%) showed the highest resistance to erythromycin and ampicillin antibiotics. All of the tested isolates (100%) showed sensitivity to gentamicin.

Conclusion : Our study showed high prevalence of Salmonella in distributed chicken meat in Yazd city. Therefore, the improvement of health conditions in food preparation centers is highly recommended.

Keywords : Contamination, Chicken meat, Salmonella, Yazd

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P202-152: Effect of adding Lactobacillus casei on the reduction of permethrin in milk/carrot juice mix drink

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2. *Associate Professor, Department of Food Hygiene and Quality Control, Faculty of Veterinary Medicine, Shabestar Branch, Islamic Azad University, Shabestar, Iran*

Background and Aim : Today, studies have shown that a relationship is found between the presence of remaining pesticides in food and the health problems. Milk is one of the most widely consumed drinks in today's communities. Preparing mixed drinks by adding ingredients such as carrots to milk can encourage individuals to consume this healthy drink. Permethrin is widely used in agriculture.

Methods : In this study, we have investigated the effect of adding lactobacillus casei on the reduction of permethrin in milk/carrot juice mix drink. Milk/carrot juice mix drink was prepared by adding 7% carrots, sugar and pectin to the sterilized milk. 15 logcfu / ml of Lactobacillus casei was added to the drink and the samples were stored in the refrigerator for 21 days. The level of permethrin and the number of bacteria were determined on days 1, 7, 14 and 21 with 3 replications. The level of permethrin was determined by the high-performance liquid chromatography method.

Results : The results showed that on day 21, 33.9% reduction was observed in the level of permethrin.

Conclusion : It seems that the adding lactobacillus casei to the drink with carrot can be reduced the amount of permethrin.

Keywords : lactobacillus casei, permethrin, milk, carrot, juice

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P203-198: Molecular identification of Chlamydophila abortus in milk of Goat and Sheep of West Azarbaijan and its molecular characterization based on genes 16S-rRNA and OMP

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Background and Aim : Chlamydophila abortus is one of the pathogens which induce abortion in small ruminants; this pathogen has a trend for ruminant placenta and causes the disease commonly referred to as Ovine Enzootic Abortion (OEA).The objective of this study was carried out to investigate the prevalence and detection of Chlamydophila abortus DNA in milk samples collected from sheep and goat flocks with and without the history of abortion in west Azarbaijan by means of Nested PCR in conjunction with the polymerase chain reaction (PCR) and molecular identification of the outer membrane protein (OMP) gene by PCR.

Methods : We have developed a Nested PCR for rapid simultaneous differential detection of C. abortus in raw milk samples taken from infected animals (sheep and goat) in Northwest of Iran (West Azerbaijan Province) and compared it with other diagnostic methods.A total number of 360 milk samples were randomly collected from sheep and goat (26 flocks with abortion and ten flocks without abortion) belonged to three different geographical areas in west Azarbaijan were tested. The milk samples were collected seasonally during 2018 and the age of animals were recorded. All the milk samples were subjected to DNA extraction.

Results : The results showed that 8.61% (95% CI: 6.13%–11.96%) of the examined milk samples (11.67 % sheep and 5.56% goat samples) were positive for C.abortus. There were signification regional, seasonal, age and animal type variations in the prevalence of C.abortus in the examined milk samples. There was a signification different in chlamydophila abortus shedding in milk was highly prevalent in autumn 18.11 (95% CI: 12.38-25.71).

Conclusion : It was concluded that sheep and goats population in west Azerbaijan should be considered as an important factor in the epidemiology of Chlamydophila and consequently in public health.

Keywords : Chlamydophila abortus-PCR- Nested-PCR- Sheeps milk- Goats milk- West Azerbaijan

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P204-219: Evaluation of Antibacterial Properties of Oregano Hydroalcoholic Extract on Microorganism Pathogenic Bacteria

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Background and Aim : The use of antimicrobial properties of medicinal plants can solve the problems associated with the use of antibiotics. The aim of this study was to evaluate the antibacterial property of Oregano hydroalcoholic extract on pathogen bacteria by microplate in laboratory conditions.

Methods : After collecting oregano, they were dried in a place by sunlight and in shade for 48-48 hours, and extraction was carried out by maceration, in order to determine the amount of inhibition (dilution) inhibitor The Muller-Hinton broth was used. The turbidity rate was evaluated in the wells method (microdilution).

Results : The results of microdilution test showed that the minimum inhibitory concentration of extract on Escherichia coli in the first (lµ50), the concentration of extract on salmonella typhimurium in the first (lµ50), the concentration of Klebsiella pneumonia in the second (lµ25) , Concentrations of Pseudomonas aeruginosa in the sixth poison (lµ1.56), concentration of Bacillus cereus in the eighth grade (lµ0.39), and the minimum concentration of Staphylococcus aureus in the tenth (without growth) strain.

Conclusion : The results showed that Oregano essential oil has antibacterial properties and can be used as a cheap and available source for therapeutic applications in some bacterial infections. In other words, Oregano can be considered as an alternative to synthetic antibiotics to combat the isolates tested. Of course, all the effects of these extracts should be carefully investigated in vivo and in vitro.

Keywords : Oregano, pathogen bacteria, extract, microplate

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P205-257: Investigating bacterial sources for vitamin K2 production

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Background and Aim : Vitamin K2 is one of the three types of vitamin K, which produced by bacteria. It has an important role in bone and cardiovascular mineralization and prevents osteoporosis and cardiovascular disease that are of the major matters in public health concern. This vitamin is rare in dietary uptake. Thus, finding high vitamin production in bacterial strains can be valuable

Methods : Ten soil samples from different regions of Iran includes Golestan, Mazandaran, Markazi, and Tehran provinces were collected. These include forest, garden, farm, forest park, and red soil fields during April and May 2019. Bacillus strains were isolated and investigated for vitamin K2 production through liquid state fermentation in specific media contain soy peptone, yeast extract, glycerol, and K2HPO4. The vitamin concentration measured in 248nm UV-spectroscopy following extraction by n-hexane: 2-propanol. High vitamin producing strains were biochemically characterized.

Results : From 97 isolated strains, 20 strains have higher absorbance value in comparison with a standard calibration curve. According to the biochemical characteristics, high vitamin producer isolates were Bacillus subtilis, Bacillus cereus, and closely related bacteria.

Conclusion : Isolating high vitamin K2 producer strains is a global matter and soil is widely used as a major source of bacillus species that are candidates for high vitamin K2 producing strains.

Keywords : Vitamin K; Bacterial sources; Bacillus

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P206-272: Evaluation of the frequency of Escherichia coli pathogroups in Brassica oleracea cultivars

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Background and Aim : Pathogenic Diseases resulting from food with microbial contamination have widely distributed in many parts of the world. Diarrhea, for example, is one of the major causes of death of children in developing countries, with approximately 2 million deaths annually. Escherichia coli is one of The most important of foodborne pathogenic bacteria . The aim of the current study was to determine the frequency of diarrheagenic E. coli pathotypes such as Enteropathogenic E. coli (EPEC), Enterotoxigenic E. coli (ETEC), Enteroaggregative E. coli (EAEC) and Shiga toxin producing E. coli in Brasica oleracea cultivars in order to provide information on the assessment of diarrheagenic E. coli pathogenesis risk in this group of vegetables.

Methods : For this purpose, 100 samples of cabbage were collected in Tehran, including kale, cauliflower, broccoli, and brussels. Pathotypes were identified by PCR molecular method using specific primers of virulent genes eae, bfpA, lt, st, pCVD432, stx1 and stx2.

Results : The results showed that the prevalence of diarrheagenic E. coli strains was 7% and the prevalence of EPEC was 3%, with two isolates from leaf cabbage and one isolate from cauliflower. All EPEC isolates were atypical. The ETEC frequency was 3%, with one isolate from cabbage leaf, one isolate from cauliflower, and one isolate from broccoli.

Conclusion : The results of the present study revealed the possible role of this group of vegetables as a source of contamination with E. coli strains causing diarrhea.

Keywords : diarrheagenic Escherichia coli, PCR, raw vegetables, Brassica oleracea

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P207-278: Antimicrobial effect of saffron petal blue extract on some foodborne bacteria

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Background and Aim : Due to public concerns about the side effects of chemical preservatives, the tendency to consume products without preservatives or natural preservatives has increased. The antibacterial activity of aqueous extract of saffron petals in vitro and methods of disk diffusion Staphylococcus aureus, Salmonella typhimurium, E. coli H7: O157, Listeria monocytogenes and Bacillus cereus that the bacteria that cause poisoning, and food infection are about The survey was conducted.

Methods : The minimum inhibitory concentration (MIC) of saffron petals extract on the four bacteria studied was studied by dilution method in solid culture medium and liquid culture medium. Among the bacteria studied, Salmonella Typhoid Morium was the most susceptible bacterium and Staphylococcus aureus and Escherichia coli O157: H7 were identified as the most resistant bacteria.

Results : The results of the amount of MIC of saffron petal blue extract in microdyelolation method for all the above bacteria were calculated to be 40 mg / ml.

Conclusion : The present study showed that the aqueous extract of saffron petals can be used as a natural preservative against antibacterials - the best management services.

Keywords : Saffron Blue Extract, Foodborne Disease Bacteria

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P208-279: Study of the antimicrobial effect of cinnamomum zeylanicum in laboratory conditions against five bacteria that cause food spoilage

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Background and Aim : The chemical composition of cinnamon essential oil (Cinnamomum zeylanicum Nees) used in the food industry was evaluated using the GC-MS device and 21 compounds were identified.

Methods : Cinnamaldehyde accounted for 60.41 percent, followed by Linanol 6.46 percent, Cinnamic Aldehyde Orthometoxia 3.63 percent, Beta Caryophyllene 3.5 percent, 8-1 Cineole 3.32 percent, Ognenol 3.19 percent and other compounds. Antibacterial activity (minimum inhibition and attenuation concentration) of cinnamon skin essential oil against 5 pathogenic and corrosive bacteria in foods including Listeria monocytogenes, Escherichia coli, Pseudomonas fluorescens, Lactobacillus plantarum, Lactobacillus sakei was evaluated.

Results : The minimum inhibitory concentration of cinnamon essential oil against 250 micrograms per milliliter L. Side and minimum concentrations were observed for other bacteria at 500 µg / ml. The minimum lethal concentration for L. sakei and Pseudomonas fluorescens was 1000 micrograms per milliliter and for other bacteria above 1500 micrograms per milliliter.

Conclusion : Cinnamon essential oil has been used in combination with films and coatings used to preserve meat products to increase shelf life.

Keywords : Cinnamon Skin Essence, Cinnamomum zeylanicum

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P209-293: The effect of different concentrations of different chitosan on yogurt sensory properties and durability

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Background and Aim : The aim of this study was to investigate the effect of different concentrations from three types of chitosan on sensory and long-lasting properties of yogurt, By investigating physical-chemical properties (such as pH, acidity percentage, Syneresis, percentage of dry matter, fat and protein), Microbial(The effect of chitosan on the growth and activity of yogurt starting bacteria, mold and yeast, coliforms, Escherichia coli in yogurt.

Methods : different chitosan with different concentrations were added to yogurt, Various treatments maintained in three weeks Physical-chemical and microbial evaluations at two temperatures in the refrigerator and room were performed.

Results : The effect of different concentrations of chitosan on protein content of yogurt samples was insignificant ($0.05 < p$) and on the dry matter content of yogurt fats was significant ($0.05 > p$). The effect of temperature and shelf life on the amount of dry matter, fat and protein was not significant ($0.05 < p$), Chitosan concentration, temperature and shelf life , On pH, acidity, dry matter, fat, Syneresis as well as starting bacteria counting and yeasts, have a significant effect ($0.05 > p$).

Conclusion : The use of chitosan increases the pH and reduces the acidity and Syneresis, Especially in refrigerated samples. The use of chitosan has reduced the number of starting bacteria and yeast . The count of mold, coliforms, and Escherichia coli was zero in all samples, Yogurt samples with high concentrations of chitosan have the highest score, While samples with low concentrations of chitosan ,The highest sensory score were Allocated.

Keywords : chitosan, yogurt, durability, physical-chemical and microbial properties

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P210-309: Phenotypic and genotypic characterization of macrolide resistance among Staphylococcus aureus isolates obtained from foodstuffs products

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Background and Aim : Currently, frequently use of macrolide antibiotics for serious staphylococcal infections has led to the emergence of Staphylococcus aureus resistant to MLSB antibiotics. There were some information about the type of MLSB resistance in a healthcare setting, however, no sufficient data has been founded on MLSB prevalence among S. aureus isolated from food sources, Therefore, the aim of this was determine the prevalence of macrolide resistance among S. aureus isolates collected from various foodstuffs products.

Methods : A total of 84 bacterial samples was collected from several foodstuffs products in the city of Isfahan. Initial identification was performed based on the phenotypic and genotypic test. Double-disk diffusion tests (D-test) were performed based on CLSI guideline. In general, DNA of all isolates was extracted using boiling method. Moreover, to detect of mecA, ermA, ermB, and ermC, PCR was performed.

Results : Totally, 84 bacterial samples were collected from several foodstuffs products. Among them, 21 isolates were S. aureus (25%). Furthermore, based on antimicrobial tests, all of the S. aureus isolates (100%) were susceptible to clindamycin; whereas 20 isolates were susceptible to erythromycin (95.24%) and just 1 (4.76%) isolate was resistant phenotype to iMLSB (resistant to erythromycin and susceptible to clindamycin). Molecular analysis revealed that two (9.52%) were MRSA (mecA positive) and 19 (90.48%) were methicillin-susceptible S. aureus (MSSA). In addition, ermC, ermA and ermB gene were detected in 23.8%, 14.28% and 9.5% isolates. Two isolates harbor ermA and ermC genes and one isolates carried ermC and ermB, simustansly. Moreover, it should be noted that some isolates did not have any erm genes.

Conclusion : In conclusion, our results indicated that erythromycin-resistant and ermC were the predominant phenotypes and genes. The results revealed that the various mechanisms of erythromycin resistance are expanding among S. aureus isolates collected from several foodstuffs products.

Keywords : Staphylococcus aureus, D-test, foodstuffs products

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P211-330: In vitro antimicrobial activity of Eryngium planum extract against food borne pathogenic bacteria

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Background and Aim : Eryngium planum is a member of the Apiaceae family and sub-family of Saniculoidae that is widely distributed in the Europe, America, and southwestern Asia. E. planum exhibit a high degree of pharmacological properties including anti-inflammatory, antinociceptive, antihemolytic, and antimycotic as well as used as a food preservative. The aim of the present study was to evaluate the antimicrobial effect of ethanolic E. planum extract against Staphylococcus aureus, Bacillus subtilis, Bacillus cereus, Listeria monocytogenes, Salmonella typhimurium, and Escherichia coli O157:H7 using agar disk diffusion.

Methods : The in-vitro antibacterial properties of the ethanolic E. planum extract at concentrations of 0.5 and 0.75% against aforementioned bacteria at 7 log CFU/ml was evaluated using agar disk diffusion.

Results : Based on our findings, the diameter inhibition zone of E. planum extract against investigated bacteria was as follows: S. aureus (3.11-3.55 mm) > L. monocytogenes (2.18-2.22 mm) > E. coli O157:H7 (1.76-1.85 mm) > S. typhimurium (1.25-1.27 mm).

Conclusion : According to the results of the present study, E. planum extract could be considered as a practical potential strong antimicrobial in food products.

Keywords : antimicrobial activity, Eryngium planum extract, food borne pathogenic bacteria

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P212-331: Plants-Derived Bioactive Compounds as Food Preservative

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Background and Aim : Microbial contamination is one of the major causes of food spoilage during prolong storage. According to World Health Organization nearly 2 billion people are suffering from illnesses due to food borne microbes annually. The search of new safe substances for food preservation is being performed around the world. The excessive use of synthetic preservatives, some of which are suspected because of their toxicity, increased pressure on food manufacturers to either completely remove these agents or to adopt natural alternatives for the maintenance or extension of a product's shelf life.

Methods : Natural bioactive compounds include a broad diversity of structures and functionalities that provide an excellent pool of molecules for the production of nutraceuticals, functional foods, and food additives. Natural Bioactive Compounds (NBCs) have been studied directly in their different natural matrices such as tea, olive oil, exotic fruits, plants, algae, microalgae, bacteria, and fungi. NBCs produced by microorganism can be incorporated into foods as nutritional supplements, flavor enhancers, texturizers, preservatives, emulsifiers, acidulants, surfactants, or thickeners. It has been reported that algae are a very interesting natural source of new compounds and many of them possess antioxidant, antimicrobial, and antiviral activities.

Results : Many plant occurring bioactive compounds can be considered as good alternatives to synthetic antimicrobial and antioxidant food additives. The antimicrobial and antioxidant properties of bioactive compounds are mainly due to their redox properties, ability to chelate metals, and quenching reactive species of singlet oxygen. Medicinal plant parts (roots, leaves, branches/stems, barks, flowers, and fruits) are commonly rich in terpenes (carvacrol, citral, linalool, and geraniol) and phenolics (flavonoids and phenolic acids), and these compounds have been effective as food additives.

Conclusion : The aim of this article is understanding the role of plants-derived bioactive compounds in food preservation.

Keywords : Bioactive compounds, antimicrobial properties, antioxidant properties, food preservative.

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P213-332: Application of Plantago psyllium for retarding the microbial population of chicken fillets

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Background and Aim : The Plantago psyllium has gradually increased its importance as a crop worldwide due to its nutritional and functional characteristics. The aim of the present study was to evaluate the effect of Plantago psyllium mucilage on microbial population (total viable count, psychrotrophic bacteria, and Pseudomonas spp.) of fresh chicken fillets during refrigerated storage over a period of 7 days.

Methods : Fresh chicken fillets were purchased from supermarket and packed with Plantago psyllium mucilage 4%. The enumeration of total viable count, psychrotrophic bacteria, and Pseudomonas spp in fresh chicken fillets during refrigerated storage over a period of 7 days was conducted using appropriate microbial culture media.

Results : The initial total viable count, psychrotrophic bacteria, and Pseudomonas spp in chicken fillets were 3.45, 3.12, and 2.14 log CFU/g, respectively. Population of indigenous bacteria of coated sample with Plantago psyllium mucilage were increased over time, but at a slower significant rate in comparison with the control ($P < 0.05$). At the end of study the total viable count, psychrotrophic bacteria, and Pseudomonas spp in chicken fillets packed with mucilage were 2.15, 2.24, and 1.15 log CFU/g lower than control, respectively.

Conclusion : It can be concluded that the packaging with Plantago psyllium mucilage can be used as an appropriate active packaging material to increase shelf-life of chicken fillets.

Keywords : Plantago psyllium, microbial population, chicken fillets

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P214-336: Salmonella and Escherichia coli contamination rate in raw meat products and kebabs meat in Khorasan Razavi province during 1398

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Background and Aim : Meat and ready-to-eat meat products such as burgers, hot dogs, meat kebabs and raw meats have a special place in the diet due to their richness in ingredients such as protein. For this reason, it is very important to prepare a healthy product due to the extent contamination of such products during preparation. The aim of this study was to determine the contamination of meat and raw meat products.

Methods : In the present study, 38 samples were collected, including 12 samples of hamburgers, 8 samples of hot dogs, 7 samples of raw kebabs, 1 chicken meat and 10 samples of raw meat from the city and related factories. All samples were evaluated according to the standards introduced by the Food and Drug Administration in terms of contamination with Salmonella and Escherichia coli. The PCR method was performed in order to detect the uidA gene for confirmation of Escherichia coli. Furthermore Multiplex-PCR performed in order to detect stx1, stx2 and eae genes to determine the pathotypes of Escherichia coli. The InvA gene was also detected to identify Salmonella.

Results : The contamination rate of the studied samples to Escherichia coli in hamburgers, raw kebabs, raw meat and chicken meat was 2 (16.6%), 1 (0.1%), 10 (100%), 1 (100%). Microbial contamination was not observed in any of hot dogs products. A chicken meat sample and a sample of hamburger contaminated with Salmonella arizonae, and PCR molecular test confirming this result. Among the samples examined by using the Multiplex-PCR, a sample of raw meat was positive for enterohemorrhagic Escherichia coli (EHEC).

Conclusion : Being nutritious and specific characteristics of red meat provide suitable conditions for the growth and proliferation of various microorganisms and cause food poisoning and intestinal diseases. Adequate cooking makes it possible to reduce this contamination. However, reducing the incidence of microbial contamination in meat samples requires hygienic considerations when preparing meat products and controlling them in a timely manner.

Keywords : microbial contamination, meat, meat products

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P215-342: Evaluating microbial contamination of saffron samples in Khorasan Razavi province during 98-99

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Background and Aim : Saffron is one of the most valuable medicinal plants in the world. This plant with extensive medicinal properties as well as widespread use in the food industry, allocated great importance to itself. The way of collection and all process related to packaging, including cleaning, drying and maintaining, will have a significant impact on the amount of saffron contamination. Regarding this, assessment of quality and microbial contamination is important according to its applications. The aim of this study was to determine the degree of contamination with saffron index-contaminating bacteria, including Escherichia coli, enterococci, as well as microorganism total count and mold count by using specific and differential media cultures.

Methods : In this study, 151 samples of saffron were evaluated for contamination with Escherichia coli and enterococci bacteria, and microorganism total count as well as rate of mould due to ISO (Iranian national standards organization standard) number 5689. For this purpose, the desired dilution prepared from each sample was enriched in the lauryl sulfate broth medium, then according to turbidity and the presence of gas and finally by performing an Endol test detection of Escherichia coli was performed. In order to identify enterococci, Kenner Fecal agar (KF agar) medium used, and then index colonies were sub-cultured on the Bile Esculin Agar (BEA) medium for confirmatory testing.

Results : Of the 143 examined samples, 1 (%0.6) and 16 (%10.59) samples were infected with Escherichia coli and enterococci, respectively. The average of microorganism total count and mold growth was 20×?10?^3 Cfu/gr and 500 Cfu/gr, respectively.

Conclusion : Despite the observation of mould contamination as well as significant total count obtained from the resulted data, the rate of microbial contamination in saffron samples was low (%11.19). However, due to the nutritional and medicinal importance of saffron, more care is needed in the processes of preparation and packaging of saffron in order to reduce the rate of contamination.

Keywords : microbial contamination, saffron, medicinal plants

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P216-344: Pathogenic bacterial contamination in vegetables and salads in Khorasan Razavi province

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Background and Aim : Changing lifestyles and daily needs to fruits and vegetables, as well as new diseases, have increased the use of this part of the food pyramid. Accordingly, it is important to prepare ready-to-eat packages with minimal contamination with pathogenic bacteria, which are abundant in vegetables. Among the isolated bacteria, the rate of contamination of leafy vegetables with Escherichia coli was higher than other bacteria, as most intestinal diseases are caused by the consumption of vegetables associated with this microorganism. Therefore, in the present study, the contamination of packaged salad and vegetables with Escherichia coli, with more importance, as well as other pathogenic bacteria were assessed.

Methods : Total of 54 vegetable and salad samples were alternately collected from packaging companies. The rate of contamination was examined by using microorganism total counts, and coliform bacteria counts tests as well as identification of Escherichia coli bacteria and enterococci. In addition, molecular confirmation test was performed by PCR method in order to detect the uidA gene for initial confirmation of Escherichia coli species. stx1, stx2 and eae genes were then detected by using multiplex-PCR to determine Escherichia coli pathotypes.

Results : The obtained data showed microbial contamination with different rates in all samples. So that the average microorganism total count and coliform counts in vegetables and salads samples were 300×?10?^5 Cfu/ml and 1600×?10?^2 Cfu/ml, respectively. 8 (%14) of the samples were positive for Escherichia coli, and the PCR result confirmed this result. Enterococci bacteria were identified in 2 (%3.7) samples.

Conclusion : The results showed high rate of coliform contamination. Despite the low rate of contamination with other studied bacteria, due to the importance of pathogenicity of isolated bacteria, it is necessary to reconsider the washing and packaging processes in order to reduce this contamination.

Keywords : Pathogenic bacterial ,contamination, vegetables

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P217-349: The Effect of Kelussia odoratissima on Pathogenic Bacteria in Enterobacteriaceae Family

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Background and Aim : Kelussia odoratissima is one of the native plants of Iran and Enterobacteriaceae is a large family of Gram-negative bacteria. The aim of this study was to determine the antibacterial effect of Kelussia odoratissima extract against a number of isolated bacteria of the enterobacteriaceae family such as Escherichia coli, Shigella flexneri and Salmonella Typhi.

Methods : After culturing the three bacteria and preparing the microbial suspension, Kelussia odoratissima extract was prepared by ethanol and methanol (Dimethyl Sulfoxide). MBC (Minimum Bactericidal Concentration) and MIC (Minimum Inhibitory Concentration) tests were determined with Kelussia odoratissima extract.

Results : According to the results, the highest growth retardation halo for Shigella flexneri, Salmonella typhi and Escherichia coli was obtained by diluting the whole methanolic extract of Kelussia odoratissima.

Conclusion : Both ethanolic and methanolic extracts have a deterrent effect on the growth of Shigella flexneri, Salmonella typhi, and Escherichia coli. This study showed that the inhibitory effect of methanol extract was greater than that of ethanol extract.

Keywords : Kelussia odoratissima,Ethanol,Methanol and extract

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P218-353: Comparison of microbial contamination quality of traditional and industrial dairy products offered in Yazd province in 1398

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Background and Aim : Foodborne illness is one of the most common health problems in the public health sector. Milk is an important part of the food pyramid and can meet many of the daily human nutritional needs. Dairy products can be infected with bacteria, which are the main causes of infections and food poisoning. This study is designed to investigate the level of contamination of traditional and industrial dairy products offered in Yazd province and determine the degree of contamination of contaminant bacteria in these products.

Methods : 209 samples included 72 samples of traditional yogurt, 31 samples of traditional dough, 85 samples of traditional ice cream and 21 samples of traditional cheese and 187 samples including 63 samples of industrial yogurt, 28 samples of industrial dough, 78 samples of industrial ice cream and 18 samples of industrial cheese. From the city of Yazd, based on a simple random sampling model, it was collected and sent to the Food Microbiology Laboratory of Yazd University of Medical Sciences, and then the samples were tested for bacterial contamination according to the national dairy standard.

Results : The results showed that the samples of yogurt, dough, ice cream and traditional cheese were 18%, 6.4%, 28.2% and 52.4 % of the samples were not usable according to Escherichia coli, respectively. Also, 26.3%, 54.8%, 85.8%, 66.6% of the samples were infected with the coliform or enterobacteriaceae. The results of microbial tests on industrial dairy products showed that only 3% of the samples were contaminated with Escherichia coli and none of them were infected with the coliform. The average microbial contamination in traditional products was significantly higher than in industrial products.

Conclusion : : In general, industrial dairy products have a lower percentage of microbial contamination than traditional dairy products, and according to the findings, to prevent microbial contamination of traditional dairy products, it is necessary to observe hygienic tips during the production process supply of traditional dairy products and training

Keywords : Bacterial Contamination, Dairy Products, Food Health, Milk

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P219-354: Investigation of microbial contamination of packaged spices distributed in Yazd province in 1398

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Background and Aim : Spices are added to foods to improve the taste of food. Spices, like most post-harvest agricultural products, are exposed to other contaminants, such as bird droppings, rodents, and insects, in addition to primary contamination. Contamination of these food flavorings is important in terms of the likelihood of foodborne illness and food spoilage. This study was conducted to investigate the microbial contamination of spice packages offered in Yazd province.

Methods : In this study, the study population was 4 types of spices offered in Yazd stores in 1398.165 samples including 21 samples of sumac, 57 samples of black pepper, 36 samples of yellow wood and 51 samples of cinnamon were collected by simple random sampling method from different parts of Yazd city. In terms of the number of mold, coliform and Escherichia coli, according to the methods defined in the Iranian Institute of Standards and Industrial Research, 3677 people were tested for microbes.

Results : The results showed that 100% of the samples of sumac, black pepper, turmeric and cinnamon were allowed in terms of counting the identification of coliform and Escherichia coli in the allowed range. Also, 100%, 79%, 92% and 94% of the samples were in the allowed range in terms of mold count, respectively. The highest and lowest pollution was observed in black pepper product with 21% and sumac with 0%, respectively.

Conclusion : Given that most of the spices examined were affected by gamma rays, these results could indicate a favorable effect of gamma rays on reducing the microbial load of packaged spices. Microbial loads are likely to be higher in non-packaged spices. Therefore, it is recommended to use gamma rays to reduce microbial load, disinfect and sterilize.

Keywords : spices, microbial contamination, gamma rays, flavoring

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P220-360: bacterial contamination in vegetables and salads in Khorasan Razavi province

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1. *Food and Drug Control Laboratory, Food and Drug Administration, Mashhad University of medical science, Mashhad, Iran*

Background and Aim : Changing lifestyles and daily needs to fruits and vegetables, as well as new diseases, have increased the use of this part of the food pyramid. Accordingly, it is important to prepare ready-to-eat packages with minimal contamination with pathogenic bacteria, which are abundant in vegetables. Among the isolated bacteria, the rate of contamination of leafy vegetables with Escherichia coli was higher than other bacteria, as most intestinal diseases are caused by the consumption of vegetables associated with this microorganism. Therefore, in the present study, the contamination of packaged salad and vegetables with Escherichia coli, with more importance, as well as other pathogenic bacteria were assessed.

Methods : Total of 70 vegetable and salad samples were alternately collected from packaging companies. The rate of contamination was examined by using microorganism total counts, and coliform bacteria counts tests as well as identification of Escherichia coli bacteria and enterococci according to ISO (Iranian national standards organization standard) number 10082. In addition, molecular confirmation test was performed by PCR method due to food microbiology protocols recommended by standards organization, in order to detect the uidA gene for initial confirmation of Escherichia coli species. stx1, stx2 and eae genes were then detected by using multiplex-PCR to determine Escherichia coli pathotypes.

Results : The obtained data showed microbial contamination with different rates in all samples. So that the average microorganism total count and coliform counts in vegetables and salads samples were 300×?10?^5 Cfu/gr and 1600×?10?^2 Cfu/gr, respectively. 35 (%50) of the samples were positive for Escherichia coli, and the PCR result confirmed this result. Enterococci bacteria were identified in 14 (%20) samples.

Conclusion : The results showed high rate of coliform contamination. Despite the low rate of contamination with other studied bacteria, due to the importance of pathogenicity of isolated bacteria, it is necessary to reconsider the washing and packaging processes in order to reduce this contamination.

Keywords : Pathogenic bacterial ,contamination, vegetables

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P221-361: Contamination rate with index bacteria in raw meat products and kebabs meat in Khorasan Razavi province during 1398

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Background and Aim : Meat and ready-to-eat meat products such as burgers, hot dogs, meat kebabs and raw meats have a special place in the diet due to their richness in ingredients such as protein. For this reason, it is very important to prepare a healthy product due to the extent contamination of such products during preparation. The aim of this study was to determine the contamination of meat and raw meat products.

Methods : In the present study, 38 samples were collected, including 12 samples of hamburgers, 8 samples of hot dogs, 7 samples of raw kebabs, 1 chicken meat and 10 samples of raw meat from the city and related factories. All samples were evaluated according to the ISO numbers (Iranian national standards organization standard) in terms of contamination with Salmonella and Escherichia coli. The PCR method was performed due to food microbiology protocols recommended by standards organization in order to detect the uidA gene for confirmation of Escherichia coli. Furthermore Multiplex-PCR performed in order to detect stx1, stx2 and eae genes to determine the pathotypes of Escherichia coli. The InvA gene was also detected to identify Salmonella.

Results : The contamination rate of the studied samples to Escherichia coli in hamburgers, raw kebabs, raw meat and chicken meat was 2 (16.6%), 1 (0.1%), 10 (100%), 1 (100%). Microbial contamination was not observed in any of hot dogs products. A chicken meat sample and a sample of hamburger contaminated with Salmonella arizonae, and PCR molecular test confirming this result. Among the samples examined by using the Multiplex-PCR, a sample of raw meat was positive for enterohemorrhagic Escherichia coli (EHEC).

Conclusion : Being nutritious and specific characteristics of red meat provide suitable conditions for the growth and proliferation of various microorganisms and cause food poisoning and intestinal diseases. Adequate cooking makes it possible to reduce this contamination. However, reducing the incidence of microbial contamination in meat samples requires hygienic considerations when preparing meat products and controlling them in a timely manner.

Keywords : microbial contamination,raw meat, meat products

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P222-365: Detection of riboflavin-producing probiotic strains isolated from dairy products by 16SrRNA sequencing

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Background and Aim : The probiotic bacteria has the main effect in boosting the immunity, reducing the duration of certain diarrheal diseases, treatment of gastro intestinal disorders. Probiotic bacteria are able to synthesize B-group vitamins particularly riboflavin to obtain fermented bio-enriched food. The aim of our study was detection of riboflavin-producing probiotic strains isolated from dairy products by 16 S rRNA sequencing.

Methods : A riboflavin producing lactic acid bacterium was isolated from raw milk and traditional dairy products in Tehran. Samples were cultured on MRS.broth) for isolation of lactic acid bacteria, MRI broth (for isolation of Bifidobacterium), MRI broth (for isolation of Lactobacillus acidophilus), a broth neutrino (for yeast isolation). Diagnostic tests to identify lactic acid bacteria and the probiotic properties of this strain were examined. After DNA extraction accordance with the kit protocol, PCR amplification, and DNA sequencing of the 16S rRNA gene were done by Lactobacillus 16s rRNA Sequence Specific Primers included: 5-CTCAAAACTAAACAAAGTTTC-3 and 5-CTTGTACACACCGCCCGTCA -3. The sequence of the PCR product was compared with known 16S rRNA gene sequences in GenBank by multiple sequence alignment with the CLUSTAL W program. The riboflavin quantification was performed by High Performance Liquid Chromatography (HPLC) analysis.

Results : In the molecular study, the results of blast strains at EZ Taxon identified five isolates: L. salivarius, L. johnsonii, L. paracasei, L. xiangfangensis, L. helveticus. Also, the HPLC result of an over-the-counter solution for isolating cultures showed that one of the isolates, L. paracasei, was able to produce vitamin B2.

Conclusion : The results of the present study showed that vitamin B2-producing isolates are present in traditional milk and dairy samples, and by purifying and optimizing the amount of vitamin production by these isolates, they can be supplemented as He used a variety of foods.

Keywords : riboflavin-producing, 16SrRNA sequencing, probiotic, dairy products

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P223-371: Isolation and molecular identification of Aspergillus niger species from soybean oilseed

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1. *Master of Cellular and Molecular Biology - Microbiology*
2. -

Background and Aim : Aspergillus niger mushroom grown on nuts and oilseeds is an important source for the production of various industrial enzymes, so in this study we tried to use soybean oil seeds to purify it.

Methods : Real-Time PCR is used for molecular detection of 18srRNA.

Results : -

Conclusion : The results showed that soybean oil is a suitable substrate for the growth and purification of Aspergillus niger and this purified and isolated fungus can be used to produce useful biochemicals such as various industrial enzymes

Keywords : Aspergillus niger - PDA culture medium - Real-Time PCR - 18srRNA molecular detection

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P224-372: Enzymatic activity of lipase produced from Aspergillus niger species grown on soybean oil seed

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1. *Master of Cellular and Molecular Biology - Microbiology*
2. -

Background and Aim : Lipase is an enzyme that is able to hydrolyze esters and break down triglycerides into glycerol and fatty acids, and this enzyme is very important in organic chemistry and industry. Aspergillus niger is one of the microorganisms that produce this enzyme. In this study, screening of suspected Aspergillus niger species grown on soybean oil seeds was performed to determine lipase activity

Methods : Pure culture was prepared from the fungus to be used for molecular detection of 18srRNA. Aspergillus niger species were compared in terms of lipase activity using colorimetric method at 410 nm and with nitrofenyl palmitate substrate.

Results : -

Conclusion : From 100 fungal colonies 50 colonies belonged to Aspergillus and 5 colonies suspected to be Aspergillus niger, which were identified after molecular analysis of Aspergillus niger. And these 5 colonies also showed acceptable lipase activity.

Keywords : Aspergillus niger - Nitrophenyl palmitate substrate - Lipase enzyme - PDA culture medium

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P225-375: Antimicrobial effects of garlic

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Background and Aim : Garlic has been used as a source of food and medicine for thousands of years.Given that the garlic contains different biologically active materials and acts as an antibiotic and a fungicide, the purpose of this research was to estimate the degree of sensitivity of three different Gram-positive bacteria: Staphylococcus aureus, methicillinresistent Staphylococcus aures (MRSA) and Bacillus subtilis; two types of Gram-negative bacteria: Escherichia coli and Salmonella enteritidis; as well as the fungus Candida albicans.

Methods : The degree of sensitivity of tested microbes with regards to the agency of fresh and thermally processed local and imported garlic was determined using the disc-diffusion method.

Results : Examined antimicrobial-test substances exhibited antibacterial effect on all tested gram-positive bacteria and gram-negative bacteria, as well as the fungistatic agency upon fungus C. albicans. The strongest antimicrobial effect on all tested species was exhibited by fresh local garlic. Preparates based on A. sativum could be introduced in clinical practice for the treatment of infections caused by C. albicans.

Conclusion : Fresh domestic and imported garlic showed better antimicrobial effect compared to heat treated domestic and imported garlic. The strongest antimicrobial activity against all species tested was found in fresh homemade garlic. Fresh domestic and imported garlic showed the strongest antimicrobial activity against Candida albicans. Following these findings, particularly the intense antimicrobial effect of Allium sativum L. against Candida albicans, we believe that the preparations based on A. sativum L. could be introduced into clinical practice in the treatment of infections caused by C. albicans.

Keywords : garlic,antimicrobial,Allium sativum

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P226-379: Identification of Microbial Contamination of Traditional Sweets in Yazd, Iran

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Background and Aim : Diseases and poisonings, caused by the consumption of sweets contaminated with microorganisms, have always been considered as one of the major nutritional problems of people living in the developing countries, including Iran. Regarding this, the present study aimed to determine the prevalence of microbial contaminations of traditional sweets supplied in Yazd city, Iran.

Methods : This cross-sectional study was conducted on 303 samples of traditional sweets supplied in Yazd confectionaries, which were randomly selected. These samples were tested in terms of such microorganisms as Enterobacteriaceae, Escherichia coli, yeasts, and molds, using the microbiological tests, which were based on the Iranian national standards.

Results : According to the results, the prevalence rate of microbial contaminations was 30.8%. Furthermore, the "Pistachio Luz" and "Hajji Badam" had the highest (85.8%) and lowest (0%) prevalence rates of microbial contamination, respectively. Additionally, the prevalence rate of contamination to Enterobacteriaceae, Escherichia coli, Molds, and Yeasts were 14.3%, 6%, 22.2%, and 12.1%, respectively.

Conclusion : Given the high rate of microbial contamination in the traditional sweets, especially "Pistachio Luz", offered in Yazd, more regulatory and monitoring measures should be taken in the production and distribution of these sweets.

Keywords : Candy, Food Contamination, Traditional Sweets, Yazd

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P227-380: Effects of cold-water egg shell washing on Salmonella contamination in the shell and its contents

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Background and Aim : Washing eggshells is one of the simplest and least expensive methods and is used by many people in the community today to clean eggshells.In this study, the effect of rinsing the egg shell with 5 ° C water on its salmonella contamination during 20 days of refrigeration was evaluated.

Methods : Sixty samples of industrial eggs offered in Qazvin market were examined in terms of the degree of contamination of the eggshell and also its contents during storage in the refrigerator before and after washing with cold water at 5 ° C. Eggs were divided into control group including unwashed eggs and treatment group including washed eggs with cold water at 5 ° C.

Results : Salmonella was not isolated in any of the treatments after washing with cold water during refrigeration. Washing with cold water followed by refrigeration removed the salmonella load on the surface of the eggs. No contamination was reported in any of the contents.

Conclusion : Cold water washing method as a simple and low cost method in the community can be used to improve the hygienic quality of eggs and clean the shell.

Keywords : Salmonella, egg, Wash, Durability

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P228-398: Relationship between Helicobacter pylori infection and its severity with eating habits

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Background and Aim : Gastric cancer is the most common malignancy in Iran. Helicobacter pylori and some components of the diet are among the risk factors for this disease, but there are few studies on the relationship between these two factors in the world. The aim of this study was to investigate the relationship between Helicobacter pylori infection and its severity with diet in Yazd.

Methods : This study was a cross-sectional descriptive study. The samples were 86 people who underwent upper endoscopy in Tabriz Gastroenterology and Liver Research Center. A questionnaire containing demographic information and a food frequency questionnaire for individuals was filled out and a sample of anther was sent for pathological examination. Data analysis was performed by non-parametric tests.

Results : The rate of Helicobacter pylori infection was 42.6% based on pathological examination (hematoxylin-eosin). Positive HP infection was inversely related to weekly consumption of fish (P = 0.009), green pepper (P = 0.01) and water (P = 0.019) and weekly consumption of tuna (P = 0.013) and tea (P = 0.048) was directly related. The severity of HP infection was inversely related to weekly consumption of fish (P = 0.001), green pepper (P = 0.045) and water (P = 0.001) and with weekly consumption of tuna (P = 0.011) and sugar (P = 0.044) was directly related.

Conclusion : The results indicate the possibility of the effect of some foods such as fish (except tuna), green pepper and water on HP and the severity of this infection. Due to the limitations of this study, more comprehensive and accurate studies are necessary to prove the findings and achieve more details.

Keywords : Helicobacter pylori, Eating habits, Gastric cancer, Risk factors

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P229-417: Stydy of Yoghurt Probiotic Bacteria viability

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Background and Aim : Yogurt is a popular fermented dairy product that produce by lactic acid bacteria, including Streptococcus thermophilus and Lactobacillus bulgaricus. It has diverse nutritional and therapeutic properties can be the most suitable probiotic carrier. Viability of probiotic bacteria are important factor in quality of yoghurt.

Methods : Two kinds of probiotic yoghurts made using commercial starter culures. Viability of probiotic bacteria (lactobacillus acidophilus,Lactobacillus bulgaricus) of yoghut were assessed during 21-days at 3 days interval. statistical analysis was carreid out using T-test and ANOVA in SPSS software.

Results : At this experiments number of lactobacillus acidophilus and Lactobacillus bulgaricus were 6.22± 0.02 and 5.30 ± 0.05 log cfu/gr in MY1821 and 6.45 ± 0.11 and 6.16 in ABY3 . population of lactobacillus acidophilus andLactobacillus bulgaricus decreased by 2.1 and 0.26 log cfu/gr in MY 1521 And 0.53 and 1.13 cfu/gr in ABY3 yoghurts. Viability of lactobacillus acidophilus also reduced and by 0.55 Log cfu/gr in MY 1821 yoghurt.

Conclusion : Because of therapeutic benefits of probiotics, consumption of these products for their high population of probiotic bacteria can improve the public health.

Keywords : Probiotic bacteria , Yoghurt, Viability,lactobacillus

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P230-428: Study of some of the most important virulence gens in Acinetobacter baumannii isolated from raw milk in Karaj city

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Background and Aim : Acinetobacter baumannii is a virulent bacterium that causes nosocomial infections. The present study was performed to determine the prevalence and frequency of some virulence factors in Acinetobacter baumannii strains isolated from raw milk collected from Karaj city.

Methods : Raw milk samples were collected randomly in 90 samples from traditional dairy shop of karaj city and evaluated for Acinetobacter baumannii using microbial culture and biochemical tests. Then DNA samples were extracted from Acinetobacter baumannii isolates and the presence of some virulence factors(PAI, cnf2 and kpsMT genes) was evaluated.

Results : The prevalence of Acinetobacter baumannii in raw milk samples was 5.55%. The prevalence of Acinetobacter baumannii in raw milk samples of cattle, sheep and goats was 10, 6/ 66 and 6.66%, respectively. The frequency of PAI, cnf2 and kpsMT virulence gens in Acinetobacter baumannii isolates were 25, 25 and 25%, respectively.

Conclusion : The use of pasteurized milk and complete boiling of milk before consumption can reduce the risk of transmission of strained Acinetobacter baumannii strains in these foods. It is recommended to investigate the role of milk contaminated with the virulant Acinetobacter baumannii genes the occurrence of food intoxication.

Keywords : Acinetobacter baumannii, raw milk, virulence factors, Karaj city.

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P231-429: Study of some of the most important antibiotic resistance genes encoding in Acinetobacter baumannii isolated from raw milk in Karaj city

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Background and Aim : Acinetobacter baumannii is one of the causes of nosocomial infections resistant to antibiotic treatments. The presence of some genes encoding resistance is considered as one of the mechanisms of antibiotic resistance in Acinetobacter baumannii strains. The present study was performed to determine the frequency of some genes encoding antibiotic resistance in Acinetobacter baumannii strains isolated from raw milk collected from Karaj city-Alborz.

Methods : A total of 5 isolates of Acinetobacter baumannii were isolated from raw milk samples (that bought from traditional dairy shops in Karaj city-Alborz). Isolated strains were first confirmed by microbial culture and biochemical tests of IMVIC, urease, TSI, OF, MRVP, SIM, catalase and oxidase and growth evaluation at 37 and 42 ° C. Then DNA samples were extracted from Acinetobacter baumannii isolates and the presence of some genes encoding antibiotic resistance(tetA, aac (3) -IV, CITM, baSHV and cat1) was evaluated using PCR test.

Results : The frequency of genes encoding tetA, aac (3) -IV, CITM, baSHV and cat1 antibiotic resistance in Acinetobacter baumannii isolates was 80%, 60%, 80%, 40% and 20%, respectively.

Conclusion : Prescribing antibiotics according to international guidelines and using simple and inexpensive methods such as the release of antibiotic discs can prevent severe antibiotic resistance in Acinetobacter baumannii strains.

Keywords : Acinetobacter baumannii, raw milk, genes encoding antibiotic resistance, Karaj city.

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P232-23: Absence of Cytomegalovirus in Women with breast cancer in Tabriz

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Background and Aim : The role of human cytomegalovirus (HCMV) in breast cancer is controversial. The aim of this study was to evaluate the expression of the immediate-early antigen (IE) of HCMV in tissue blocks in a group of women with breast cancer in Tabriz.

Methods : 80 Formalin-fixed and paraffin-embedded (FFPE) tissue blocks of breast cancer and 80 non-cancerous breast tissues were obtained from the pathology laboratory in Tabriz. After the Deparaffinization and DNA extraction, the IE-antigen of HCMVgenome was used as the primer for the detection of HCMV in all samples by PCR.

Results : In our study, 66.3% of all cases and 82.8% of the controls were under 50 years of age. Fibrocystic lesions (71.3%) and grade II invasive ductal carcinoma (57.5%) were the most common in the control and case groups, respectively. All of 80 breast cancer samples and all non-cancerous samples were negative for the IE – antigen of HCMV gene.

Conclusion : No relationship was seen between breast cancer and HCMV in this study. However, the controversy on the role of HCMV in breast cancer still remains.

Keywords : Breast cancer, FFPE, Human cytomegalovirus, immediate early antigen, Tabriz.

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P233-67: Anti-cancer potential of Actinobacteria isolated from Iran

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Background and Aim : Nowadays actinobacteria were known as the source of secondary metabolites with diverse biological activities and structures. These compounds can be promising sources of novel anti-cancer drugs. According to Bacterial products reduction, actinobacteria isolation from the unique ecosystems to find novel bioactive compounds is an interesting approach. This study for assessment of production of anti-cancer compounds from native Iranian actinobacteria.

Methods : The samples were collected from different locations like Persian Gulf water, soil and plants root. Serial dilution was prepared (10-1 - 10-4), then the diluted samples were inoculated in media (isp2 and isp4) and incubated at 30°C for 10 days. After that, the isolated strains were cultured in a 200 mL broth media and incubated in 30°C with 140 rpm for 8 days. For assessment of anti-cancer products, the media were centrifuged at 10000 rpm for 10 min and the supernatant was separated. Also, the crude extract were extracted from the cell free supernatant with ethyl acetate (1:1 V/V). Finally the anticancer effects of the crude extracts and supernatant on MCF-7 tumor cell were evaluated using the MTT assay method.

Results : The isolated actinobacteria were identified by morphological and microscopic criterias. Nine strains were isolated from different samples. They were named EZ (isolated from plant root), Ga31, Ga5, Ga20, Ga18 (isolated from soil), Mar1, Man1, Sa, Red2 (isolated from Persian Gulf water). The isolates showed anti-cancer activity against the MCF-7 cell line. The Ga31 strain had the highest anti-cancer (75%-90%) activity against MCF-7 cell line.

Conclusion : The results of this study showed the products of isolated strains have the ability to inhibit tumor cells and these ecosystems can be resources of anti-cancer compounds. The Ga31 strain had the best anti-cancer effect against MCF-7 cell line. Therefore can be done further research for Purification of these compounds and used the products to in-vivo studies.

Keywords : actinobacteria, anti-cancer, MCF-7

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P234-133: Prevalence of Campylobacter spp. in patients whit colorectal cancer

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Background and Aim : Colorectal is the cancer of the colon or rectum, and its incidence is steadily rising in developing nations(1). One of the risk factors is infectious and microbial agents such as Campylobacter spp.. Campylobacter is caused many undiagnosed cases of diarrhea in developing countries, including Iran(2, 3). Recent studies have shown a relation between Campylobacter spp. infection with the risk of colon cancer(4). Due to the high prevalence of this bacterium in developing countries such as Iran and its role in infection and gastrointestinal cancer and its lack of diagnosis in clinical laboratories, in this article, we investigated the prevalence of this bacterium in colorectal cancer.

Methods : This study was performed on tissue samples from patients suspected of colorectal cancer referring to Gastroenterology and Liver Disease Research institutes in Taleghani Hospital from 2017 to 2018. In the next step, DNA was extracted by the available kit(QIAamp DNA Mini). The presence of DNA in samples was confirmed by using Nano drop. Then the presence of Campylobacter spp. was determined by polymerase chain reaction (PCR) using specific primers targeting 16srRNA gene and PCR products were run on 1.5% gel electrophoresis and results were observed using gel doc. finally, the data was analyzed by SPSS 16.0 statistical

Results : A total of 86 patients that 18 controlled and 68 were cancer patients were studied. This study included 32.6% females and 62.8% males (Mean age 56.4 years; age range 21 to 87 years). In the patient group the areas of involvement were respectively Rectum 22 case (31%), Recto sigmoid 12 cases (17%), Colon 12 cases (17%), Descending colon 9 cases (15%), And other areas related to Cecum, Duodenal, Rectal, Transverse colon, Ascending shown in Figure 1. Of 86 biopsy specimens, 14(20%) were positive for Campylobacter spp. (Figure 2) .

Conclusion : Campylobacter spp. produces toxins one of them is a cytolethal distending toxin (Cdt). This toxin causes DNA damage and secretion pro-inflammatory cytokines. Which promotes tumor progression and cancer through angiogenesis and metastasis. Thus, based on our previous studies and the achievement of our paper, Campylobacter can play a role in colon cancer.

Keywords : Campylobacter spp., colorectal cancer

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P235-186: Identification of Antibacterial, Antifungal and Anticancer Activity of Five Strains of Soil Microorganisms Isolated From Tangkuban Perahu Mountain by Fermentation

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Background and Aim : Soil microorganisms from the group of actinomycetes are well accepted to be the best producer of antibiotics. microorganisms were isolated from soil taken from Tangkuban Perahu mountain.The aim of this study was to screen the highest antimicrobial and anticancer activity of strains isolated from Tangkuban Perahu mountain.

Methods : One gram of dried soil sample was taken in 100 mL of sterile distilled water and mixed thoroughly in a shaker for 15 minutes at 120 rpm. Five strains were investigated in this study designated TP1, TP2, TP3, TP4, and TP5, respectively. Morphological, biochemical and molecular identifications were conducted for all five strains.

Results : These isolates were shown to be closely related to Nocardia sp. YIM 65630 (90%), Streptomyces galbus (99%), Aspergillus unguis (86%), Paecilomyces marquandii (100%) and Nocardia niigatensis (95%), respectively. Production of antibacterial, antifungal and anticancer metabolites was done by fermentation. Screening for bioactivity of five isolates was done by testing the fermentation broth against resistant and pathogenic bacteria, fungi and T47D breast cancer cell line. TP2 strain showed the best bioactivity; the metabolite was purified by extraction with ethyl acetate. Antibacterial, antifungal and anticancer activities from the ethyl acetate extract of TP2 strain were tested by agar diffusion, microdilution and MTT.

Conclusion : The extract was shown to be active against methicillin resistant Staphylococcus, methicillin sensitive Staphylococcus aureus, methicillin resistant coagulase negative Staphylococcus, vancomycin resistant Enterococcus, Escherichia coli, Microsforum gypseum with the minimum inhibitory concentration (mg/mL) and diameter of inhibition (mm): 150, 35; 150, 30; 300, 35; 300, 35; 300, 29; 4.7, 36, respectively. The IC50 value of the T47D cell line was 457 mg/mL.

Keywords : antibacterial, antifungal and anticancer activities, ethyl acetate extraction, fermentation, identification.

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P236-324: An investigation of the effect of nisin-loaded small extracellular vesicles on melanoma cells

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Background and Aim : Small extracellular vesicles (sEVs) have recently been attracted much attention as novel nanocarriers for drug delivery. Nisin is a 34-amino acid bacteriocin produced by Lactococcus lactis during fermentation and has been approved by the Food and Drug Administration (FDA) as a food biopreservative. It has been shown that nisin exhibits selective anticancer activities. In this study, we evaluated the effect of nisin-loaded sEVs on melanoma cells.

Methods : One group of the A375 cells cultured in 96-well plate were exposed to free nisin at 20, 40, and 80 µg/ml and the other group were exposed to nisin-loaded sEVs (Nis-sEVs) with different nisin to sEVs volume ratios (3:2, 2:1, 1:1, 1:2, 2:3) for 48 hours. Doxorubicin and PBS were used as the positive and negative control, respectively, and in the same volume with experimental interventions. MTT [3-(4, 5-dimethylthiazolyl-2)-2,5-diphenyltetrazolium bromide] assay was performed to determine the percentage of metabolic viability of the cells.

Results : Metabolic activity of the Nis-sEVs treated cells decreased more than 50 percent at the 3:2, 2:1, and 1:1 ratios, and the most decrease observed at the 3:2 ratio. Metabolic activity of free nisin treated cells reduced more than 50 at 80 and 40 µg/ml.

Conclusion : Results from this study mark that sEVs can be a potential drug delivery system for the efficient delivery of nisin to melanoma cells.

Keywords : extracellular vesicle, nisin, melanoma

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P237-351: Simultaneous detection of cytomegalovirus, varicella zoster and Epstein-Barr virus viruses isolated from women with breast cancer by Multiplex-PCR

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1. *Mojtaba Sadeh*

Background and Aim : Background:Breast Cancer is one of the chronic non-communicable diseases and the most common cancer in women at the global level. Breast cancer is a multifactor disease with genetic and epigenetic components such as environmental, physicochemical factors and contaminants caused by viruses. Viruses may affect the development of breast cancer.Most of the tumor-causing viruses are those containing DNA. Herpes viruses such as Varicella-zoster virus (VZV), Cytomegalovirus (CMV), and Epstein-Barr virus (EBV) are some of these viruses.

Methods : Materials and Methods:The current study was conducted on 60 plasma/serum samples in breast cancer patients undergoing chemotherapy. And VZV, EBV and CMV viruses were identified simultaneously using multiplex PCR . First, Multiplex PCR was performed for samples. Then samples were tested using Seprerate PCR. Positive viruses control was provided by Dr. Keyvan's virology laboratory.

Results : Results:The obtained results showed that 6 of 60 samples (10 %) were positive for VZV DNA. In addition, 5 of 60 samples (8.33 %) were positive for CMV DNA. And, finally, 7 of 60 samples (11.66%) were positive for EBV DNA. The highest and lowest percentage of detected viruses was related to EBV and CMV respectively.

Conclusion : Conclusion:It was concluded that there is a statistically significant relationship between breast cancer and these viruses. Rapid and accurate identification of viral pathogens help physicians with rapid identification, prevention of disease in human societies and proper treatment. However, more epidemiological, biological and molecular investigations are required to make clear the contribution mechanism of viruses in the process of carcinogenesis.

Keywords : Key words:Breast cancer, Cytomegalovirus, Epstein-Barrvirus, Varicella-zostervirus, Multiplex PCR

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P238-10: Investigating the effect of lavender plant extracts, oregano, Thyme and marshmallow on the growth of bacteria Lactobacillus acidophilus

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Background and Aim : People with irritable bowel syndrome suffer from a lack of microorganisms in their gut. Antibiotics have a negative effect on the growth of microorganisms in the gut. The goal of this study is to find out if plant extracts can also damage probiotics and prevent them from growing. Therefore, we investigated the effect of lavender, oregano, thyme and marshmallow plant extracts on probiotic bacteria.

Methods : This study was performed experimentally and using the culture medium prepared from MRSagar and MRSbroth, concentrations of 0.1, 0.01, 0.001 of the bacterium were prepared. To prepare the extracts, a clevenger apparatus was used using a water solvent. The variables of this study were the concentration and types of extracts.

Results : Herbal extracts had different effects on the growth of probiotic bacteria due to their different concentrations. Among the extracts, thyme had the highest antibacterial properties at a concentration of 0.01, and oregano at a concentration of 0.001 was useful and effective for the growth of probiotics.

Conclusion : All extracts had an effect on the growth of probiotics. Oregano and marshmallows in different concentrations helped the growth of probiotics and had a positive effect, but thyme had different effects in different concentrations. Lavender destroyed probiotics in all concentrations. The findings show the effect of concentration and type of bacteria on the results.

Keywords : probiotic, herbal extract, marshmallow, thyme, lavender, oregano

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P239-65: Effect of oral administration of probiotic Bacillus coagulans on blood levels of nano-calcium supplement in adult male Wistar rats

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Background and Aim : this study aimed to evaluate the simultaneous oral administration of Bacillus coagulans probiotic bacteria on the level of nano-calcium supplementation in male Wistar rats

Methods : 15 adult male rats were divided into three groups؛ The control group was dissolved daily by 1000 mg/kg calcium nanoparticles, The test group was dissolved by PBS, which was dissolved in a probiotic Bacillus coagulans bacterium with a dilution of 109 cfu per day and 1000 mg/kg calcium nanoparticles and the sham group was treated with 1000 mg/kg calcium nanoparticles dissolved in PBS every day and the results were evaluated after 48, 24 and 72 hours

Results : The results indicated that the test and control groups that received both bacteria and nanoparticles, differing only in the solvent from the sham group, showed no changes in calcium levels on day one. On the second day, the level of calcium in the test and control group was more than that, and this difference can be attributed to the absence of bacteria in the sham group (p value <0.001)

Conclusion : In general, the results of this study showed that probiotic bacteria Bacillus coagulans can contribute to elevated calcium levels and can be used as a prevention and treatment method for osteoporosis

Keywords : Bacillus coagulans, osteoporosis disease, probiotic, nano calcium

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P240-79: Are probiotics as safe as become available universally?

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Background and Aim : Widespread use of probiotics and the presence of these microorganisms in human food-chain established an argument against the safety profile of probiotics. Various case-reports, clinical trials, and experimental studies have been mentioned different types of side-effects induced by the consumption of probiotics.

Methods : This review is based on a PubMed and Clinicaltrials.gov search for studies undertaken over the past 20 years (2000–2020) using the following keywords: probiotics, safety, adverse effects, side effects

Results : Although previous studies reported beneficial impacts in alleviating the gastrointestinal (GI) problems, cardiovascular disorders, and metabolic syndromes, the most at-risk groups of populations such as pediatrics, geriatrics, critically-ill patients are at higher risks of the occurrence of some life-threatening or life-lasting adverse events. Bacteremia, fungemia, GI disorders, metabolic problems, extreme immune stimulations, seizure, Kawasaki disease and etc. have been associated with the use of probiotics. Moreover, due to the antibiotic resistance gene reservoir property of the GI tract, transference of the resistance genes among probiotics, human normal flora and pathogenic microorganisms endow probiotics to propagate antibiotic resistance genes globally.

Conclusion : With the increased tendency of probiotic consumption, several arguments have been made regarding the safety and efficacy of these products. Several clinical complications and adverse effects are reported in different studies as consequences of probiotics. Since these microorganisms might carry antibiotic resistance genes, the risk of antibiotic resistance gene transfer between available bacteria increases. The overall conclusion of this review is to take careful considerations for the utilization of probiotics.

Keywords : Probiotics, Safety, Adverse effects, Antibiotic resistance

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P241-102: Assessment of lactic acid bacteria isolated from poultry feces as potential probiotic and its in vitro competitive activity against Salmonella Typhimurium.

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Background and Aim : In intensive poultry production, there is no opportunity for newly hatched chickens to keep in touch with their mothers, which would lead to slow colonizing of microbial flora in their intestine tract. As a result, this condition makes them susceptible to infections of pathogenic microorganisms such as S. Typhimurium, E. coli and Clostridium perfringens. the application of lactic acid bacteria as decontamination of foodborne pathogens might demonstrate antagonism towards pathogenic bacteria in poultry intestinal tract. The bio-compound from LAB can synergistically would enhance the antimicrobial activity of eukaryotic peptides against Gram-negative bacteria and this would be another useful mechanism of action for LAB antimicrobial substances in the gastrointestinal tract.

Methods : Thirty-seven samples of chicken feces were collected from 7 broiler chicken farms in Northern Iran. The probiotic characteristics were detrmined such as acid and bile tolerance, antibiotic susceptibility, Antagonistic activity against pathogens, Caco2 cell cultures and adherence assay, inhibition of S. Typhimurium adhesion to Caco2 and molecular identification of LAB isolates.

Results : Among the isolates,36 isolates which showed appropriate probiotics characteristics, were selected. The 3 isolates were highly attachment. Competitive elimination of S. Typhimurium by the 3 isolates was 48, 37 and 28% (in the exclusion method), 36, 25 and 17% (in the competition method) respectively. The 16S rDNA sequence revealed that the isolates were 99% similar to Lactobacillus salivarius, Lactobacillus johnsonii and Pediococcus acidilactici, respectively

Conclusion : In the present study, three strains of native LAB (Lactobacillus salivarius, Lactobacillus johnsonii and Pediococcus acidilactici) with probiotic properties were isolated from chicken feces in Golestan province of Iran. These isolates due to having resistant to acid and bile salts and creating the high levels of organic acids have more compatible with the poultry gastrointestinal tract which leads to increase growth performance and also improving the immune system. Also, these isolates have the high ability to attachment to intestinal epithelial cells and competitive elimination of Salmonella spp. from colonization on intestinal cells. Therefore, the

isolated LAB from the present study can be used to produce native probiotic products which are suitable for usage in poultry to reduce the consumption of antibiotics and the incidence of various diseases.

Keywords : probiotic, antimicrobial activity, broiler chicken, competitive elimination

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P242-134: Lactococcus lactis expressing salivary protein SP15 of Phlebotomus papatasi as a live vaccine for cutaneous leishmaniasis

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Background and Aim : Cutaneous leishmaniasis is a debilitating parasitic disease without effective vaccine. The parasite is transmitted by sand fly blood feeding. Recently, the well-defined role of sand fly proteins has brought them into focus as vaccine candidates. The goal of this study was to evaluate the protective efficacy of a live-vectored vaccine (expressing an immunogenic sand fly protein) against L. major challenge with sand fly saliva homogenate.

Methods : Two synthetic optimized sp15-egfp and egfp genes were cloned in pNZ8121 and transferred into E. coli strain MC1061. Both genes were cloned at downstream of PrtP signal peptide to secret proteins on the cell wall. Then, each recombinant plasmids were episomally transferred into L. lactis subsp. Cremoris strain NZ9000 and generating aspNZ8121-sp15-egfp and pNZ8121-egfp recombinants. Confirmation of protein expression on the cell wall was completed by TEM, western blotting and ELISA using anti-GFP antibody. After two times immunization, we assessed the protective effects in BALB/c mice by measuring footpad swelling, parasite burden, nitric oxide, humoral and cellular immune response at one and two months post challenge with L. major plus salivary gland homogenate.

Results : Immunization with L. lactis-SP15-EGFPcwa (vaccinated group) caused a significant delay on development of footpad swelling and reduction of lymph node parasite burden in vaccinated group in comparison with control groups (L. lactis and PBS groups). In addition, these results showed that IgG2a/IgG1 ratio and nitric oxide production in immunized group were higher than control groups (L. lactis- EGFPcwa, $P< 0.05$). After stimulation of lymphocytes with L. major antigens, nitric oxide, IFN-γ and IL-17 production significantly were highest in vaccinated group comparing with control groups in both time points ($P< 0.05$). Furthermore, IL-10 and IL-5 were equal or significantly less than control groups.

Conclusion : In our study, the lower level of parasite burden and higher IFN-γ /IL-5, IFN-γ /IL-10 and also in IL-17/IL-5 and IL-17/IL-10 ratios in immunized BALB/c mice with L. lactis-PpSP15-EGFPcwa indicated that membrane associated PpSP15 on the L. lactis can induce strong Th1-immune responses and could act as live-vectored vaccine for human studies

Keywords : Vaccination, L. major, L. lactis, P. papatasi, SP15, cutaneous leishmaniasis

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P243-149: isolated of lactic acid bacteria from local dairy products with the ability to inhibit the growth of some gastrointestinal pathogens in Yazd city

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Background and Aim : : Isolation and identification of lactic acid bacteria from local products can play an important role in introducing unique types of probiotics. The aim of this study was to isolate lactic acid bacteria from local dairy products in Yazd city with the ability to inhibit the growth of some digestive pathogens.

Methods : : Isolation and identification of lactic acid bacteria from local products can play an important role in introducing unique types of probiotics. The aim of this study was to isolate lactic acid bacteria from local dairy products in Yazd city with the ability to inhibit the growth of some digestive pathogens.

Results : Out of 30 samples of doogh and local cheese and 6 industrial samples, a total of 81 isolates were identified, among which Lactobacillus casei had the highest frequency with 40.34%. Lactobacillus casei and Lactobacillus acidophilus isolated from doogh and sheep's cheese, and Lactobacillus delbrocci and lactobacillus ramenosus isolated from sheep's butter against all pathogenic bacteria studied, namely Escherichia coli, Candida, and Staphylococcus aureus. Also, lactic acid bacteria isolated from industrial samples showed less antibacterial activity compared to local sample isolates.

Conclusion : In general, due to the antagonistic activity of lactic acid bacteria isolated from local dairy products, it is recommended to evaluate their use as probiotic bacteria.

Keywords : Lactic Acid Bacteria, Local Dairy Products, Yazd, Antibacterial Activities, Digestive Diseases

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P244-151: Isolation and phenotypic and genotypic characterization of the potential probiotic strains of Lactobacillus isolated from the Guilan province population

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Background and Aim : Among different causes of inflammatory bowel disease (IBD), the imbalance of the gut microbiome (dysbiosis) is one of the main reasons in the development of the disease. Probiotics are the live microorganisms that can maintain gut microbiota and affecting its composition and activity by different mechanisms. Therefore, we aimed to isolate and characterize the potential probiotic strains of Lactobacillus from the Iranian population.

Methods : This cross-sectional study was conducted during 2019 on fecal samples of 83 volunteer individuals living in the north of Iran. The primary identification of Lactobacillus strains was performed by standard microbiological tests and confirmed by amplification of 16s rRNA specific primers. The acid and bile salt tolerance were assessed for all recovered strains. Also, the presence of 3 bacteriocins encoding genes was investigated by PCR method.

Results : Totally, 42 samples were positive for Lactobacillus species. Acid and bile resistance assay showed that 67% and 33% of strains were resistant to acid and bile salt stress, respectively. Also, 28% were able to resistance to both low pH and bile salt. PCR results revealed that the prevalence of gassericin A, plantaricin S, lactacin bacteriocin genes were 16.6%, 12%, and 9.5%, respectively. Meanwhile, 5 out of 12 Lactobacillus strains that were resistant to both low pH and bile salt stress contained one of the gassericin or plantaricin bacteriocins.

Conclusion : We isolated 42 potential probiotic strains of Lactobacillus. Of which, results of 5 strains were more promising and can be considered as potential probiotics sources for future functional products.

Keywords : Probiotic, Lactic acid bacteria, Lactobacillus, Guilan

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P245-190: Effects of Lactobacillus rhamnosus on acetaminophen-induced renal injuries in male Wistar rats

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Background and Aim : Today, the use of probiotics in the treatment and prevention of diseases is increasing. It has been shown that different species of genus Lactobacillus, as probiotic bacteria, might prevent some injuries induced by oxidative stress in laboratory animals. Oxidative stress has an important role in acetaminophen-induced renal toxicity. Therefore, the present study aimed to investigate the effects of Lactobacillus rhamnosus on acetaminophen-induced renal toxicity.

Methods : In this study, four groups of laboratory rats (6/group) were used. The negative control group received no treatment. Acetaminophen control group received a single high dose of acetaminophen (1000 mg/kg, orally). The bacterial control group received 6×109 CFU of the bacterium (orally) daily for two weeks. The experimental group, after receiving 6×109 CFU of Lactobacillus rhamnosus daily for two weeks, received a single high dose of acetaminophen (1000 mg/kg). One day after acetaminophen administration, sampling of blood serum and kidney tissues was conducted for all groups.

Results : The amount of urea and creatinine in the acetaminophen control group was significantly higher than the amount of these parameters in the negative control and bacterial control groups but not the experimental group. Renal tissue analysis showed damages such as glomerular necrosis and degeneration of tubular cells in both groups that received acetaminophen. Kidney tissue in the negative control and bacterial control groups had a normal appearance.

Conclusion : : Lactobacillus rhamnosus has no preventive effects on renal toxicity caused by acetaminophen in Wistar rats.

Keywords : Renal toxicity, Acetaminophen, Lactobacillus rhamnosus, Wistar rats, Probiotics

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P246-228: Investigating the possibility of reducing the concentration of salt in fermented salted cabbage (Sauerkraut) using Kakoti extract

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Background and Aim : Sauerkraut is a fermented food product that is nutritionally restricted due to its high salt content. The aim of this study Investigating the possibility of reducing the concentration of salt in fermented salted cabbage (Sauerkraut) using Kakoti extract

Methods : The present study to produce low-salt sucrose (with a salt content of 1 and 1.5%) with a suitable shelf life was performed by replacing the ethanolic Kakoti extract with part of the salt and the most important chemical, microbial and sensory characteristics of the samples were investigated. Four samples containing different concentrations of salt (1 and 1.5 %) and Kakoti extract (2 and 4 grams per liter) and one control sample at six intervals after preparation (0, 4, 7, 8, 14 and 21 days) Were tested and a total of 90 treatments were considered, including three iterations.

Results : At the end of the fermentation process on the seventh day, the pH value in all samples decreased but was in the standard range (3 -4), the acidity of the products also increased but corresponded to the standard value (0.045-1.60). On the seventh day, the number of lactic acid bacteria increased in all treatments without significant difference ($P < 0.05$) and there was no fungus in most treatments. The effect of Kakoti extract on sensory characteristics was not significant ($0.05 < P$) and the sample containing 1.5% salt gained more sensory score than its lower concentration (1%).

Conclusion : In order to increase the durability and reduce the amount of salt in the product and at the same time maintain the desired organoleptic, chemical and microbial characteristics of sucrose, Kakoti extract can be used with concentrations of 1 and 1.5% salt.

Keywords : Kakoti extract, sucrose, durability, salt, sensory properties

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P247-261: Investigating the variety of cultivable lactobacilli in crops of the local chickens of Mazandaran province and investigating the capabilities of their hydrolytic and probiotic enzymes.

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Background and Aim : In poultry industries, two goals are considered: Increasing the growth rate of chickens by accelerating the digestive system by consuming microorganisms that produce hydrolytic enzymes and increasing the growth rate of chickens by preventing infectious diseases by using probiotics .The term "probiotic" refers to living microorganisms that enter the body of a living organism through the digestive tract and can survive and multiply there and have beneficial effects on the health of the host.In this study, the enzymatic activity and probiotic traits in lactobacilli that can be cultivated in the crops of local chickens in Mazandaran province have been investigated.

Methods : In this study, at first, 30 local chickens were collected, separating the crops, cultivating their samples on MRS Agar, purifying the gram-positive bacteria, The ability to produce hydrolytic were studied in them. These isolates were evaluated for primary probiotic tests.

Results : In this study, 220 bacteria were isolated from 30 crop specimens of chickens, of which 72 isolates (33.02%) were negative catalase and gram-positive rod, which were considered as lactic acid bacteriat. In the study of enzymatic activity,1 isolate (1.3%) with protease activity, 1 isolate (1.3%) with amylase activity, 2 isolates (2.7%) with lipase activity were obtained. In the study of probiotic activity,10 isolates (13.88%) without beta-hemolytic activity, 4 isolates (5.55%) were able to tolerate pH=2, 7 isolates (9.72%) were able to tolerate pH=4 and 1 isolate (1.33%) was able to tolerate bile salts.

Conclusion : Lactic acid bacteria are a physiological group and include optional gram-positive-anaerobic bacteria wich includes bacteria with probiotic ability. Most of lactic acid bacteria are weak in the activity of hydrolytic enzymes. In the study of Lutluf kabir et al., Only three species of Lactobacillus acidophilus and Lactobacillus vitilinus were isolated from chickens crops by amylase activity. The four isolates of lactic acid bacteria isolated in this study, which have been able to produce the amylase, protease and lipase.

Keywords : amylase, esterase, lactic acid bacteria, probiotic, protease, crop, lipase, chicken, microflora.

P248-316: Functional Beverages

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Background and Aim : The definition of functional beverages falls under the general definition for functional foods. In the International Food Information Council (IFIC), functional foods are Foods or dietary components that may provide a health benefit beyond basic nutrition. At present, beverage are the most active functional food category because of convenience and possibility to meet concumer demand for container contents, size, shape, and appearance, as well as ease of distribution and storage for refrigerated and shelf-stable products.

Methods : A functional beverage is a drink product that is non-alcoholic and includes in its formulation ingredients such as herbs, vitamins, minerals, amino acids, antioxidants,plant extract, fiber, prebiotics, and probiotics or additional raw fruit or vegetables. Sports and performance drinks, energy drinks, ready to drink teas, dairy based beverages, enhanced fruit drinks (juice), soy beverages and enhanced water are examples of functional beverages.

Results : Functional beverage are promoted with benefits such as : heart health, improved immunity and digestion, joint health, satiety, energy-boosting.

Conclusion : This review focus on commercially available functional beverage, as well as on the potential health benefits related to their consumption.

Keywords : functional foods, functional beverages, nutritional benefits, health benefits.

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P249-329: In vitro antimicrobial activity of Lactobacillus acidophilus, Lactobacillus reuteri, and Bifidobacterium bifidum against food-borne pathogenic bacteria

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Background and Aim : The global market for probiotics has been increasingly growing in recent years guided by the rising consumers' demand for healthy diets and wellness. The aim of the present study was to evaluate the in-vitro antimicrobial properties of probiotic bacteria including Lactobacillus acidophilus, L. reuteri, and Bifidobacterium bifidum against Listeria monocytogenes, Salmonella typhimurium, Staphylococcus aureus, and Escherichia coli O157:H7.

Methods : The in-vitro antibacterial properties of the probiotic microorganisms (9 log CFU/ml) against the growth of 9 log CFU/ml Listeria monocytogenes, Salmonella typhimurium, Staphylococcus aureus, and Escherichia coli O157:H7 were evaluated using broth macrodilution method.

Results : The results of the present study showed that the probiotic bacteria effectively reduced the growth of pathogenic microorganisms as follows: L. monocytogenes (-3.86 - -5.56) > S. aureus (-2.99 - -3.45) > S. typhimurium (-2.21 - -2.09) > E. coli O157:H7 (-1.45 - -1.11). The highest and lowest antimicrobial property was found for L. reuteri and B. bifidum, respectively.

Conclusion : According to the results, addition of probiotic strains including L. acidophilus, L. reuteri, and B. bifidum could remarkably decrease the growth of S. aureus, L. monocytogenes, S. typhimurium, and E. coli O157:H7, which is an effective solution to the issue of safety in the food industry.

Keywords : Lactobacillus acidophilus, Lactobacillus reuteri, Bifidobacterium bifidum, antimicrobial property

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P250-340: Antibacterial activity of Lactobacillus rhamnosus cell-free supernatant against Staphylococcus aureus and Escherichia coli

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Background and Aim : Probiotics may be a good alternative to antibiotics in fighting pathogenic bacteria. The current study aimed to evaluate the antibacterial activity of Lactobacillus rhamnosus cell-free supernatant against Staphylococcus aureus and Escherichia coli.

Methods : L. rhamnosus ATCC 7469 was cultured in the MRS broth medium at 37˚C. The medium was transferred to the tube after 48 h and centrifuged at 8000 rpm for 20 minutes. The supernatant was passed through a filter with 0.2 µm pores under sterile conditions. The antibacterial activity of the filtered supernatant was determined against S. aureus ATCC 25923 and E. coli ATCC 8739 by minimum inhibitory concentration (MIC) method.

Results : The minimum inhibitory concentration of L. rhamnosus cell-free supernatant against S. aureus and E. coli was 25 and 12.5 microliter/ml, respectively.

Conclusion : The cell-free supernatant of L. rhamnosus had a good antibacterial effect on S. aureus and E. coli.

Keywords : Lactobacillus rhamnosus, Escherichia coli, Staphylococcus aureus, Antibacterial activity

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P251-391: Probiotic bacteria induces apoptosis of Gastric cancer through signaling pathways in H. pylori

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Background and Aim : Gastric cancer (GC) is considered as the second prevalent agent that leads to death a high population of humans around the world. This type of cancer is generally induced by Helicobacter pylori which could be colonized the gastric mucosa of at least half of the population worldwide. Today, triple antibiotic therapy is routinely utilized for controlling the H. pylori-induced infection. However, this strategy is unsuccessful because of some obstacles such as occurring point mutations in the H. pylori genome resulting in resistance to the antibiotics. Recently, it is showed that different probiotics have strong anti-cancer effects in which they are capable of inhibiting H. pylori by both immunological and non-immunological mechanisms. Here we tried to find some anti-cancer impacts of the probiotic bacterium L. plantarum on the gastric cells (AGS cell line).

Methods : The anti-cancer effects of the conditioned media of the locally isolated L. plantarum on the AGS cells were evaluated by different analyses such as flow cytometry, DNA ladder assay, DAPI staining and, RT-PCR.

Results : our results showed that the conditioned media of L. plantarum can inhibit both H. pylori and AGS cells through up/down regulation of PTEN, Bax, TRL4, and AKT genes.

Conclusion : Different reports confirmed the anti-cancer effects of several strains of probiotics especially lactobacilli. Accordingly, it seems the probiotics could be considered as at least an assistant treatment for the many types of cancers.

Keywords : Gastric cancer, Helicobacter pylori, Lactobacillus plantarum, Apoptosis, PTEN, AKT.

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P252-403: Production of selenium enriched biomass of Lactobacillus bulgaricus as a potential food supplement: optimization of culture conditions using response surface methodology

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Background and Aim : Selenium is an important trace element which plays vital roles in human health. Probiotic strain of Lactobacillus bulgaricus, which can store in its bulk, can reduce the effects of selenium deficiency in addition to being able to produce products with probiotic benefits.

Methods : By designing the one factor at the time tests, the ranges of possible effective factors on selenium absorption in bacterial mass and effective factors were selected. Optimization of selenium entrapment in biomass of bacteria was performed using response surface methodology via Box-Behnken design. The qualitative analysis of Se-enriched L. bulgaricus was performed by FT-IR spectra.

Results : Among the parameters affecting selenium entrapment, three factors including optimum initial pH, inoculum doses and incubation temperature, were most effective. The optimal points were obtained at selenium concentration of 6.82%, initial pH of 5.86 and incubation temperature of 33.5 °C. Under the optimal conditions, the maximum ratios of selenium enrichment reached 88.52% which was consistent with the proposed statistical model.

Conclusion : The optimization of culture parameters can improve the viable counts of L.bulgaricus in fermenter which are beneficial from its application in industrial production. The full compliance between the observed and predicted values by the equation confirms the statistical significance of the model and the model's adequate precision in predicting optimum conditions.

Keywords : Lactobacillus bulgaricus, Response Surface Methodology, Box-Behnken design.

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P253-84: Genotyping of environmental Helicobacter pylori strains in Kurdistan water sources

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Background and Aim : Epidemiological studies have shown an association between the prevalence of H. pylori infection and water hygiene levels. In developing countries such as Iran, contaminated Water is considered to be one of the main sources of human pollution to H. pylori. The aim of this study was to determine the frequency of H. pylori and its virulence genes in Sanandaj and Marivan water sources samples.

Methods : In this study, 100 samples of water collected from different areas of Sanandaj and Marivan were studied. After filtration of water samples, the genome of potential organisms in the samples was extracted using PowerSoil® DNA Isolation Kit (Qiagen). H. pylori contamination was determined by using PCR and specific primers for 16S rDNA gene.

Results : In this study, two samples were positive for H. pylori. In these two samples, oipA (100%), sabA(50%) genes were determined.

Conclusion : In this study, the similarity of the isolated genotypes with the genotype of the clinical strains suggests that these strains may be cloned in the human stomach if hygiene is not observed. Both strains lacked the pathogenic and important gene cagA. Therefore, it can be concluded that these suspensions were less pathogenic.

Keywords : Helicobacter pylori, Water sources, Genotyping, Virulence genes

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P254-129: Laccase enzymatic decolorization and degradation of Azo dyes

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Background and Aim : Among all dyes used in textile and related industries, azo dyes are favorite ones and water pollution after discharging the effluents to water bodies is a major problem of using them. Halotolerant bacteria, Bacillus sp. strain WT. is known for thermostable laccase production. Also there is enough data on reduction on toxicity of azo dyes solutions after treatment with Bacillus sp. This work describes activity of the laccase from Bacillus sp. strain WT.

Methods : Bacillus sp. WT was cultured in a solid medium containing 3% NaCl salt, for 72 hours to check its tolerability and ensure that the strain was tolerable to the salt. In order to ensure that the desired strain contains the laccase enzyme, it was cultured in nutrient agar (containing Manganese) and incubated for 72 hours. A microbial suspension was prepared at 50 mM Tris and tested with a specific Laccase enzyme (ABTS) substrate, which was positive. decolorization was checked at pH 5 to 8 (37 °C for 2 hours), for three azo dyes (Solphenyle blue, Remazol belack, Solphenyle green).

Results : The highest percentage of decolorization was observed at pH 5 for all three dyes, Solphenyle blue about 43.75%, Rimazole Black about 85.85%, Solphenyle green about 96.96%.

Conclusion : According to the results, the highest percentage of decolorization was observed in the three azo dyes used in acidic conditions, pH 5 to 7.

Keywords : Laccase,Halotolerant bacteria,Bacillus sp. strain WT,azo dyes

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P255-159: Study of Escherichia Coli removal from polluted water by solar disinfection (SODIS)

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Background and Aim : Microbial pollution in water resources is an important issue in the world because of high risks to humans and animals. So, the removal of microbial contaminations is necessary for access of water quality standard. Today, due to environmental friendly, have led researchers to focus on water disinfection using natural sunlight for water disinfection. This study was conducted to investigate the effect of solar radiation disinfection to treatment of polluted water for the purpose of domestic water supply.

Methods : In this study, the performance of E. coli removal efficiency was evaluated using different containers (PET and Glass) and atmospheric temperature as experimental study. The disinfection rate of E. coli (k) of SODIS was calculated from the ratio of the start (C0) and end (Ct) concentrations of E. coli, and the contact time (t), assuming first order disinfection kinetics.

Results : Results of this study show that both PET and Glass bottles are capable to decrease of 300 E.coli per milliliter to zero at 60 min contact time. Experimental results showed that SODIS was an effective method to remove E. coli in water. No significant difference was observed in between glass and PET bottles for 60 min contact time.

Conclusion : The use of solar radiation technology is suitable for drinking water disinfection both at household level and at remote communities even for water with high turbidity and high organic matter concentrations.

Keywords : Solar disinfection, E. coli, Water Sources, Water treatment

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P256-160: Contamination rate of surface waters in ilam province with pathogenic speacum of Enterobacteriacea.

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Background and Aim : As the province of Ilam is a mountainous area with rivers that are used by rivers in many rural and nomadic areas even as drinking water. It is possible to contaminate this water with different pathogens and bacteria and to transfer water to other areas. Therefore, this study investigated the rate of bacterial contamination of surface waters of Ilam province with various Enterobacteriaceae and.

Methods : In this study, sampling from 23 ILAM surface pollen stations and their biochemical tests showed the infection rate of different Enterobacteriaceae bacteria in winter and summer and compared their prediction and infection.

Results : The population of Enterobacteriaceae at different stations in summer and winter is different population of Enterobacteriaceae is the most polluted in summer and winter. So that the Kemer Meymeh Dam and pavzanstation and chaviz stationare are the most polluted.also, the population of Enterobacteriaceae is the minimum polluted in summerand winter at ilam dam station

Conclusion : The more suitable the temperature and the higher the discharge of municipal wastewater into the river water has been the cause of increased pollution. In addition, the lower the precipitation in these seasons, and the higher the pollution load.

Keywords : Pollution, surface water, Enterobacteriaceae

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P257-161: Contamination rate of surface waters in ilam province with pathogenic speacum of Enterococci.

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Background and Aim : Water is a vital fluid that is contaminated by a variety of biological factors.Enterococcus species are the most important indicator of surface water pollution.surface water can be contaminated with enterococcus species and transmitted to other area.therefore,in this study,the frequency of bacterial contamination of surface waters of ilam province with enterococcus species was measured.

Methods : In this study, sampling from 23 ILAM surface pollen stations and their biochemical tests showed the infection rate of different Enterococcus bacteria in winter and summer and compared their prediction and infection.

Results : The population of Enterococci at different stations in summer and winter is different so that the population of Enterococci in Mehran saffron station in summer and in Chenguleh station in winter are the most polluted.

Conclusion : The more suitable the temperature and the higher the discharge of municipal wastewater into the river water has been the cause of increased pollution. In addition, the lower the precipitation in these seasons, and the higher the pollution load.

Keywords : Pollution, surface water, Enterococcus

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P258-181: Isolation of petroleum hydrocarbon-degrading bacteria from Gwadar Bay

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Background and Aim : Marine oil pollution is one of the most important environmental problems. These compounds tend to bio accumulate and threaten human health, as a result, development of efficient techniques for treating contaminants is necessary. Due to the large passage of tankers from the Oman Sea, the region is at risk of oil spills.The aims of the present study was to isolation of petroleum hydrocarbon-degrading bacterium from costal sediments of Gwadar Bay.

Methods : Surface sediment and water from different regions of the Gwadar Bay were collected and stored in the refrigerator until the bacteria were isolated. Samples were enriched in mineral salt medium with crude oil (1%) as the only source of carbon and energy. Crude oil degrading bacteria were isolated by serial dilutions of bacterial consortium. Isolated strains then identified by molecular (16S rDNA) and biochemical analysis.

Results : A Gram-negative bacterium strain was isolated from enrichment consortium and named GW1. Isolated strain has been identified by 16S rDNA sequence analysis and revealed most homology with Bacillus sp. The ability of the isolated strain to degradation of crude oil has shown that it is able to decompose more than 85% of crude oil in a week.

Conclusion : In general, the results show the ability of the isolated strain to degradation crude oil. In addition, to increase the efficiency of GW1, it is necessary to optimize bacterial growth conditions in the presence of crude oil.

Keywords : Gwadar Bay. oil pollution . Bioremediation

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P259-224: Sequencing of the L-glutaminase gene isolated from Streptomyces of sea water and cloning in Escherichia coli origami for clinical and industrial usage

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Background and Aim : Streptomyces are a gram-positive bacteria and have a unique role in the production of secondary metabolites and biological active substances.L-glutaminase is an enzyme is used for industrial applications such as pharmaceutical and food industries for increasing the flavor and taste of food. Because of the importance of using of this enzyme,the aim of this study is sequencing of the L-glutaminase gene isolated from Streptomyces of sea water and cloning in Escherichia coli origami bacteria for clinical, industrial and food utilization .

Methods : After sampling from the Persian Gulf waters,Streptomyces were isolated and DNA was extracted.Then by the PCR test the strains of Streptomyces which had a L-glutaminase gene were identified.The L-glutaminase gene positive strains were cloned through the vector into the E.coli and cloned by TA cloning technique.Finally,with the Real Time PCR technique measured the expression of these genes in E.coli origami.

Results : After screening of sea water samples,12 isolates of Streptomyces were isolated totally, of these, 7 isolates had the L-glutaminase gene.In order to confirm the cloning results,the DNA was extracted from the suspected colonies and were evaluated with the PCR and finally,the Real time PCR product confirmed the expression of L-glutaminase gene in E.coli origami.

Conclusion : The results of this study showed that this procedure can be a suitable candidates for design and manufacture of drugs and antimicrobial compounds. In the present study, the production of glutaminase enzyme was performed by recombinant plasmid and TA cloning,but subsequent studies could be used to optimize different conditions for producing this enzyme.

Keywords : Sea Streptomyces, L-glutaminase, Cloning

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P260-227: Isolation and Identification of Native Decolourizative Microorganisms from Isfahan Textile Industrial Effluent

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Background and Aim : Azo disperse dying are the most widely used among dying in the textile industry. Due to the xenobiotic is one of the most important reasons for water pollution and the environment. They destroy the ecosystem of microorganisms. In addition, it increases the COD of water. In this study, it has been attempted to remove these compounds by native microorganisms isolated from Isfahan textile industrial effluent and the COD parameter is reduced.

Methods : In order to isolation of native industrial effluent microorganisms, sampling of textile effluent was done from Sepahan factory in Isfahan city. Accordingly, 18 strains of bacteria were isolated. To decolorization assay was done by UV-Visible spectrophotometry was evaluated along 144 h and potent strains were selected. Identification of macroscopic and microscopic was studied followed by biochemical tests. molecular identification done by 16SrRNA primer and the optimization of different concentrations of dying, temperatures and pH were done.

Results : Evaluation of the results of blast sequencing revealed 99% similarity to Bacillus cereus. Decolorization assay showed that the green color of the effluent is deleted about 56.12% in 48 hours. The orange color of the effluent was removed at 41.82% along 48 hours. Results of optimizations determined isolated strain have best effect at 30°C and pH 7. It could reduce 80% COD.

Conclusion : Textile industries use several colors that increase the toxicity of these wastewaters, this project's try to use microorganisms to reduce pollution factors (CODs) is a cost-effective investment that will deliver high returns.

Keywords : Bioremediation, Decolorization, COD, Textile industrial effluent.

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P261-251: Isolation of selenate resistant Enterobacter from Khouzestan industrial wastewaters

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Background and Aim : Nowadays, pollutants cause increasing contamination of the most valuable source of the earth planet, waters. Among this, heavy metals have been attracted high attention because toxicity and inability to biodeterioration which make problems for all organism. With the regard of high costs of physicochemical treatments, bioremediation get attention as an alternative process which use natural materials such as bacteria. Microbial activity is responsible for transformations of at least one-third of periodic table elements. Selenium is a trace essential element which play important roles in many cellular processes; however, it is toxic at micro-molar concentrations.

Methods : With this regard, isolation of efficient selenate resistant bacteria was performed from industrial wastewaters, Ahvaz, Khouzestan province using modified Luria-Bertani (mLBA) medium supplemented with 32.5-1200mM selenate. Study of resistance threshold of one promising isolate and toxicity effect of selenate on it, were investigated using MIC, MBC and disc diffusion methods. Finally, biochemical characterization was done based on Bergey's manual. Further studies (molecular confirmation and the selenate removal mechanisms) are be doing.

Results : Among the 73 gathered isolates, AM2-W9a strain showed high resistance ability with MIC/MBC equal to 600mM and low inhibition zone diameter was selected for following studies. The results of biochemical identification showed that this isolate was belonged to Enterobacter genus.

Conclusion : Therefore, the only solution for recovery of environmental health is designing efficient process such as bioremediation. With the ability of introduced strain, it is necessary to study further its properties to becoming as a suitable candidate for bioremediation purposes.

Keywords : Enterobacter; selenate; Khouzestan; wastewater

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P262-253: Investigation on genetic origin of heavy-metal resistance genes of a native selenate-resistant bacteria

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Background and Aim : Wastewaters loaded with metals harbor microorganisms with inherent resistance to survive in such habitats. They may contain genetic determinants contributing to the resistance (natural or acquired through plasmids) against heavy metals. These plasmids from these strains may therefore be used for the genetic transformation of the lower resistant strain to boost up its metal resistance. In this regard, this study was designed for use of safe resistance strain for bioremediation purposes.

Methods : Plasmid extraction was done and transformed to E. coli DH5α. The cultivation of transformed bacteria was done on modified-Luria Bertani (mLBA) medium supplemented with selenate oxyanion and compared with growth pattern of wild-type strain. On the other hand, the plasmid curing was done to eliminate plasmid and investigate the survive of resistance ability in presence of selenate.

Results : With compared to wild strain of E. coli DH5α, transformed strain acquired resistance ability to selenate. Moreover, curing studies showed that with plasmid removal, the resistance ability became lowered. With reference to these results it could be said that heavy-metal resistance of test strain has mainly plasmid origin.

Conclusion : Metals in higher concentrations displace the essential nutritional minerals in the living systems and prove deleterious effects. Existing methods for metal remediation have certain limitations. Hence, there is an imperative need to explore new and effective remediation techniques. Genetic engineering technology is an alternate method to develop novel biosorbents which have the potential to improve or redesign microorganisms pertaining to their selectivity and accumulating properties of the organisms.

Keywords : Genetic origin, multi metal resistance, heavy metal, bacteria

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P263-262: Prevalence and molecular charachterization of Gram negative pathogenic bacteria in rainbow trout from fish farm in Mazandaran province

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Background and Aim : The aquaculture industry has evolved dramatically over the last few decades but various infectious diseases threaten aquatic life. Due to increased consumption of marine products, the health of aquatic animals needs constant monitoring. Fishes viscous skin cover is a good place to grow a variety of pathogenic bacteria. The purpose of this study was to isolate and survey the prevalence of Gram-negative bacteria in trout in Mazandaran province.

Methods : . Clinical samples of trout in some fish farms of Mazandaran province were collected during year 2019 (from winter to autumn). These farms were selected based on the previous occurrence of bacterial disease. After disinfection of fish body surface with ethanol, samples were taken from the kidneys, liver and spleen of fish. The clinical specimens were inoculated in nutrient agar and incubated at 25 °C for 48 to 72 hours. Colony characteristics, cell morphology, gram staining, biochemical tests and PCR test were performed to identify bacteria.

Results : The results were demonstrated that the most contamination with gram-negative bacteria in Mazandaran trout farms, related to Aeromonas hydrophiliae and Yersinia ruckeri (among the identified isolates in the province for Y. ruckeri and A. hydrophiliae) were 40.9% and 31.8%, respectively. In addition the high prevalence of bacterial disease was Flavobacterium psychrophilum with 20.4%. In the clinical samples collected from trout farms in Babol city, F. psychrophilum had the highest prevalence, compared to the clinical fish samples of other cities

Conclusion : Therefore, serious measures to prevent and observe health issues, including reducing environmental stress such as food storage health, environmental temperature and transportation conditions in fish farms are important.

Keywords : Pathogenic bacteria, rainbow trout, fish farm, Mazandaran province

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P264-284: counting and determining the quantiti of naphthalene degrading bacteria in the persian golf

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Background and Aim : Persian Gulf has about 2/3 of world's oil reserves. and its marine ecosystem is Seriously in danger because of oil pollution, THERE FORE studying about the statues of Hydrocarbons pollutions so necessary. increase in world oil production consumption caused Environmental pollution And made many serious problems for ecosystem. Asphaltenes, Heterocyclic, Aliphatics and Aromatics are four oil components which are regarded as main chemical pollutants. Aromatic compounds are very toxic and also have carcinogenic and mutagenic effects. So concerns about these compounds are not deniable.

Methods : Material and Methods: For isolation of naphthalene-degrading bacteria, marine environmental samples were collected from polluted sites in the Persian Gulf. And with consecutive passage, Naphthalene-degrading bacteria were isolated in ONR7a medium supplemented with 200 ppm of naphthalene .and In order to determine the bacteria growth curve in different concentrations of naphthalene ONR7a medium was supplemented with various concentrations of naphthalene from200 ppm to 2000 ppm. Only one strain could tolerate 2000ppm concentration of naphthalene which is identified Biochemically and molecularly. The naphthalene removal assay was carried out using calibration curve of naphthalene at 276 nm by spectrophotometer. Growth curves of the isolates were routinely assessed indirectly by turbidity measurement as (O.D. at 600 nm).

Results : 23 different strains of Naphthalene-degrading were isolated from marine samples. Most of these strains were gram negative . All selected bacterial strains were grown in 200 ppm of naphthalene but by increasing the concentration of naphthalene to 1500 ppm the count falls to 3 strains. And in 2000ppm only one strain could degrade naphthalene which is chosen as top strain. Molecular identification showed that it's a Bacillus.

Conclusion : This study showed that there are high potent Naphthalene-degrading bacteria in Persian Golf region that can be used in Biological regeneration processes in contaminated areas.

Keywords : concentration_naphthalene_Persian Golf degrade _Bacterias

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P265-287: Comparison of the metal removal capability of somecyanobacterial strains separated from the salt waters of Golestan province

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Background and Aim : Cyanobacteria are find in any ecological environment, from salt water to dry metal-contaminated environments. The negative charge of extracellular polymeric materials (EPS) of Cyanobacteria is widely used to isolate low-concentration metal cations in the cell environment. The aim of this study was to compare the ability of some cyanobacterial strains to remove heavy metals.

Methods : Twenty-five cyanobacteria isolated from salt waters of Golestan province were cultivated with a concentration of 10 mg/l nickel, copper and chromium cultivation. After twenty-four hours, the amount of metal removed from the solution was measured. Analysis of the results of three replications was performed using SPSS and Excel software.

Results : The results of statistical analysis showed that all twenty-five salinity-resistant cyanobacteria were easily able to remove heavy metals, which is an indication of the ability of their habitat. However, strain N3 (dry weight 513 mg), which belongs to the order Nostocales had a significant difference in the ability to remove nickel, chromium and copper metals compared to other strains.

Conclusion : The results of this study could be an important step in introducing salt-resistant Cyanobacterial strains in the removal of heavy metals.

Keywords : Cyanobacteria, removal of heavy metals

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P266-289: Production of biosurfactant by heavy-metal resistant native isolate:

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Background and Aim : Petroleum-based fuels are prominent pollutants in the most countries. While surfactants enhance recovery of crude oil, their toxicity and carcinogenicity are problematic. Besides, attention to microbial surfactants is increasing. Biosurfactants (BS) or bioemulsifiers are pioneer groups of valuable natural microbial compounds with unique features. However, studies typically using isolated microorganisms from different sites for biodegradation of oil pollutions but there is possibility to presence of bacteria with high biodegradation ability from uncontaminated environments.

Methods : With attention to increasing demand for microbial biosurfactants, this study aimed to screening of biosurfactant-producing bacteria from previous heavy-metal resistant isolates. For this, at the first stage, some qualitative assay such as haemolytic activity (HA) was used for screening. Other assays which were applied including oil-displacement test (for efficiency of produced biosurfactant); emulsification index (EI) (for BS stability) and cellular surface hydrophobicity (BATH). The identification and further studies are being doing.

Results : The screening results showed that one isolate (CBS-8C) has the potential of HA as an indicative for biosurfactant production. In the following step, CBS-8C isolate showed EI equal to 60 in minimal salt medium (MSM) with crude oil.

Conclusion : In recent years, with attention to biosurfactants applications in different industries, their production has been studied. Biosurfactant-producing microorganisms are ubiquitous in waters, land and extreme environments. With reference to gathered results, it could be said that with further studies for produced biosufractant characterization and with enhancement of its production, this strain could be used especially with its heavy-metal resistant ability.

Keywords : biosurfactant, heavy metal, native, petroleum

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P267-321: Biodegradation of different concentrations of crude oil by the bacterial consortium isolated from mangrove sediments

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Background and Aim : Mangrove forests are one of the most valuable ecosystems in the world. Since the importance of mangrove forests as a valuable ecosystem in southern Iran, it is necessary to investigate the bacterial potential of mangrove forests in the biodegradation of oil pollutants. The aim of this study was to investigate the biodegradation of various concentrations of crude oil by the bacterial consortium enriched from Minab Mangrove forest sediments.

Methods : Sediment and water collected from the Minab Mangrove forest were added to the mineral salt medium with crude oil as the only source of carbon and energy and crude oil-degrading bacteria were enriched by successive cultivation. The bacterial consortium was then cultured in a nutrient broth and after 24 hours the bacterial consortium were precipitated and inoculated to the mediums containing different concentrations of crude oil (0.5, 1, 2 and 3) with a final OD of 0.15

Results : The results showed that the enriched bacterial consortium was able to consume crude oil. At the end of the experimental period, almost all crude oil degraded in treatments containing 0.5% and 1% crude oil. In the treatment containing 2% crude oil, 78.5% of the crude oil was consumed and the lowest crude oil biodegradation was measured in the 3% crude oil treatment.

Conclusion : In general, the bacterial consortium had a significant ability to degradation different concentrations of crude oil. As crude oil concentrations increased, the rate of biodegradation decreased significantly, indicating a decrease in bacterial growth at high concentrations of oil. It is also recommended to determine the optimal biodegradation conditions to increase the biodegradability efficiency.

Keywords : biodegradation, mangrove, oil pollution

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P268-322: Investigation of the quantity of Phenol degrading bacteria in oil-contaminated areas in Persian Gulf

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Background and Aim : Fossil fuels, especially petroleum products, are used as the primary source of energy for industry and routine life around the world. Petroleum products such as gasoline, diesel and oils have caused serious ecological concerns in modern society compared to other chemicals. However, through accidents, industrial and urban activities, sewage emissions, oil industry activities in the sea and coasts, and leaks that occur during exploration, production, transportation and fuel storage, petroleum products and derivatives release into the environment and cause petroleum hydro carbonic pollution. The degradation of petroleum hydrocarbons, especially phenols, by native microbial activity is a significantly economic approach to rehabilitating phenol-contaminated sites.

Methods : In this study, sampling of 7 oil-contaminated areas in the Persian Gulf was performed. After determining the bacterial population, isolation and identification of bacteria were performed by MPN and CFU methods. After two weeks and during two stages of screening, E strain, which belongs to the Mango Forest area of Bushehr, and D strain, which belongs to the Qashka region, were identified and approved as the top and final Phenol degrading bacteria's by biochemical and molecular methods.

Results : These bacteria showed a high ability in removing phenol. The high ability of these strains in mixed cultures and with the help of nutrients makes it possible to use these strains at field level to rehabilitate phenol-infected sites. After constantly treatments, the top degrading colonies reduced the degradation time from ten days to two days, demonstrating the potential of bacteria's to clear and remove phenol.

Conclusion : Isolated bacteria showed high phenol removal ability. The abundance of bacteria in infected areas is high, and by identifying the genes and enzymes involved in the degradation, there is capability of genetic manipulation of these strains and the transition of active genes to other native bacteria in the region to facilitate and accelerate degradation.

Keywords : Phenol degrading bacteria, biodegradation, oil pollution, Phenol

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P269-377: Antibiotic resistance genes (ARGs) as environmental emerging contaminants

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Background and Aim : Improper use of antibiotics has led to their entry into the environment and the development of antibiotic-resistant genes in many bacteria. Many of these resistant genes are found in microorganisms distributed in a variety of environments, such as soil, water, and wastewater. The aim of this review study was to investigate environmentally resistant genes and drugs that have developed resistance in the body of microorganisms

Methods : In this review study, articles entitled "Drug Resistance" and "Environmental Microorganisms" were used and then information from 30 appropriate articles was extracted.

Results : Environmental ARGs are chiefly developed by the following mechanisms; Target bypass (like dfrA1, A5, A7, A12, A15, A17), which demonstrates mutation changes or loss on the enzymes has led to the unreachability of antibiotics for the target enzyme, Efflux pumps (such as cmlA1 and A5), which affects structural cellular membrane and consequently decreases intracellular concentration of antibiotics,Target modification (like ermA, B,C, E, F, T, V, and X;mecA;penA) which exhibits the alternation of antibiotics activation sites and finally Antibiotic inactivation (such as blaOXA-1,blaOXA-2,blaOXA-10,blaOXA-30,andblaPSE-1) which inactivate antibiotic molecules directly. beta-lactams, sulfonamides and tetracycline were dominant ARGs detected in the environment.

Conclusion : ARGs are found in all media and it is very difficult to remove them from the environment so they are called 'easy-to-get, hard-to-lose'pollutants. Since they can be exchanged among environmental micro-organisms of different genera their possible human health risk should be considered.

Keywords : Antibiotic resistance gene, Environment, microorganisms

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P270-385: Isolation and identification of oil enhancing recovery bactery frome Oil-contaminated effluents and oil sludge in desalination tanks.

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Background and Aim : Oil leakage and oil crude products lead to lots of damages throughout exploitative process in the sea and the land .Therefore, world environmental protection agency and non-governmental organization supporting environment in the most of industrial countries attempted to solve this problem.Recently, it is increasingly considered to biological technology in industrial scope and these days most of industries use high potential of the organisms including petroleum although they did not used to apply biological systems This issue provides the most studies and researches in the biological industry

Methods : Sampling.culture.Isolation. Gas chromatography.Surface tension measurement

Results : In order to identify several samples of effluents and oil sludge from the desalination tanks of the National Company for Southern Oilfields, 10 isolates were isolated using conventional selective enrichment (msm medium with crude oil). The measured surface tension and degraded hydrocarbons showed that the efficiency of theses two isolates (w1,s6)were better than the others. The isolates s6 ,w1 were observed negative by using biochemistry tests. The two isolates reproduced and sequenced 16s rRNA gene to identify these isolates accurately. According to BLAST application in NCBI database and Ez taxone software ,w1 isolate was most similar to pseudomonas alcaliphila bacteria and s6 was most similar to pseudomonas mendocina. The supernatants of the isolate treatment in recovered culture analyzed through gas chromatography to study and to degrade aromatic and saturated compounds . Chromatic results of s6, w1 showed that heavy hydrocarbons degrade to light compound ,shortening chains and decreasing their peak and also degradation of n-alkane and it can call alkane degrading bacteria .Therefore, the degradation of high-weight compounds and changing them into low-weight compounds as a substrateto determine Carbone source and biosurfactant production are the most important mechanism for bacteria

Conclusion : Two isolated native bacteria have high efficiencies in biosurfactant production and decomposition of petroleum hydrocarbons and growth in salt-containing medium.Therefore, it can be said that these bacteria can be used in bioremediation of oil-contaminated environments and other environmental applications and biotechnology.Also, due to the isolation of bacteria from samples containing high concentrations of salt, they are likely to show resistance to salinity stress

Keywords : biosurfactant ,oil hydrocarbon , Bioremediation

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P271-291: Investigation of biogas production by bacteria using pistachio skin waste in Sirjan-Kerman city

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Background and Aim : Waste and agricultural waste can be used as substrates for microorganisms to produce energy and biofuels. Currently, biogas is one of the world's sources of energy supply, both directly from thermal and lighting energy and as a viable option for use in internal generators, microturbines and fuel cells to generate electricity.

Methods : In the course of these studies, the prediction of biogas production process from waste was first designed and manufactured in an anaerobic fermentation device and after sampling the total solid mass (TS) and solid volatile rate (VS) for analysis. Methane was used in gas chromatography (GC) and the reduction of COD and BOD in measured samples was also investigated.

Results : Studies showed that biogas production per kilogram of VS removed was 200 liters and pH changes were observed from 6.7 to 7.8. The COD removal rate was 43.4 and the BOD reduction was 55%, and the TS removal percentage was 44.19% and the VS removal percentage was 54.14%.

Conclusion : Methane fermentation and biogas production are microbial products in which methanogens play the most important role and it is a very complex process that is influenced by many factors. In this study, high rates of substrate solution as well as high biogas production were observed in the mesophilic temperature range. The biogas produced in the production of electricity and the feasibility study of the power plant can be used.

Keywords : electricity, biogas, pistachio skin, Sirjan city

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P272-3: bacterias

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2. *author*

Background and Aim : This article explains the bacteria and bacteria that cause the disease and how to treat and prevent it. The bacteria have a simple cellular structure and rapidly multiply.

Methods : These properties make them very suitable for laboratory research. The bacteria are used in the study of cells and how they act, as well as diseases. Some bacteria are used to produce important drugs. Some antibiotics are used.

Results : They also make different vaccines with the help of weakened or dead bacteria. Tooth Decay Symptoms of the disease: color changes in the color of the tooth (yellow, gray, black, ...) 2-swelling and lips 3. Gingival infection

Conclusion : An explanation about the disease: Although there is a toughness on the tooth surface called the enamel, the bacteria rubbing the acid on the enamel, it rubs it and penetrates into the teeth, and at the very least improves its penetration and reaches the root and it Worn and loose and cause tooth decay. Why tooth decay is more common in the mouth and on the teeth in Asia? As bacteria enter the mouth more with food and we feed more food with Asian teeth, bacteria affect the teeth of Asia more. Prevention methods: 1-Brushing 2-Use of toothpick 2-Use of dental floss 4-Use of fluoride Rhode-work: surface decay, toothbrushes and refills through the doctor In the event of a general tooth decay: drain through the doctor

Keywords : Bacteria, Reproduction, Diarrhea, Black scars, Black cough, Brucellosis, Diphtheria, Plague, Tesba

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P273-9: Pseudomonas aeruginosa isolates and their antimicrobial susceptibility pattern to SXT and IPM between hospitalized patients at Urmia University Teaching Hospital, Iran

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Background and Aim : Pseudomonas aeruginosa considered as prevalent bacterial pathogen with high distribution in health care settings. Regardless of progress in medical cares, Pseudomonas aeruginosa remains a cause of infection. Therefore, this study aims to isolate and determine antimicrobial susceptibility patterns of Pseudomonas aeruginosa from Patients admitted to educational hospitals at the Urmia University of Medical Sciences, Iran.

Methods : Body fluids and aspirate specimens hospitalized patients were collected. The samples were inoculated on MaConckey and blood agar plates, and incubated at 37 °C for 24 h. The isolates were recognized with conventional microbiological tests. Antimicrobial susceptibility pattern was detected by modified Kirby-Bauer disk diffusion test.

Results : From total examined cases, 100 specimens have Pseudomonas aeruginosa positive cultures. The high rate of collected Pseudomonas aeruginosa was isolated from urine samples (62 %) followed by sputum, wound and tracheal aspirates respectively. Major Pseudomonas aeruginosa isolates were found to be susceptible to IPM and most isolates were resistant to SXT.

Conclusion : The result shows higher prevalence of Pseudomonas aeruginosa isolates among urine samples. the isolates were more susceptible to the IPM in compared to SXT. While the susceptibility of the isolates to the two examined antibiotics is a valuable data for the their future usage in infection management strategies.

Keywords : urine, antibioyic,Body fluids, antibiotic resistance pattern

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P274-15: Prevalence of the 18 virulence genes in uropathogenic Escherichia coli (UPEC) clinical isolates.

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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, such as adhesins, invasins, toxins, siderophores and genes required for capsular biosynthesis. This study aimed to investigate some virulence factors of Uropathogenic Escherichia coli.

Methods : One hundred thirty-eight (138) uropathogenic E. coli (UPEC) clinical isolates were investigated in this study. Besides, 30 E.coli(samples) as control were collected from the feces of healthy humans. multiplex PCR assays were performed for investigating 18 genes encoding virulence genes finally Chi-square test or Fisher's exact test was used to compare the occurrence of virulence markers in cases and controls. Results were considered statistically significant at $P < 0.05$.

Results : From 138 (UPEC), 22 (15.9%), 6 (4.3%), 0 (0%), 2 (1.4%), 2 (1.4%), 17 (12.3%), 0 (0%), 83 (60.1%), 81 (58.6%), 45 (32.6%), 20 (14.4%), 11 (7.9%), 18 (13%), 1 (0.7%), 8 (5.7%), 6 (4.3%), 58 (42%) and 45 (32.6%) isolates presented afa/draBC, bmaE, gafD, nfaE, hlyA, cnf1, cdtB, fyuA, iutA, kpsMT II, kpsMT III , kpsMT k1, kpsMT k5, rfc, ibeA, cvaC, traT and PAI genes.

Conclusion : Among 18 VFs, the only statistical difference between abundance the UPEC and commensal isolates was significant for 3 VFs (fyuA, PAI, and traT). Therefore, confidently it can be said that the frequency of these factors in UPEC isolates is higher than that of commensal isolates.

Keywords : Escherichia coli, Uropathogenic E.coli (UPEC), virulence factors

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P275-60: Assessment of Demodex folliculorum density in seborrheic dermatitis patients

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Background and Aim : The Demodex folliculorum is a saprophytic ectoparasite microorganism on human skin. Their food source is sebum, concentrating mainly on the facial skin and scalp. The density in normal skin is less than five per cm2. Demodex can intensify some clinical complications such as seborrheic and perioral dermatitis, rosacea, acne, and hair loss. Seborrheic dermatitis (SD) is a chronic inflammatory skin disease. The D. folliculorum is one of the most important factors that their concentration raised in the skin with SD implication.

Methods : Patients, 100 case with average 34.9 years old, presents SD on the facial skin, accompanied by intense itching and scaling. Control group were consist of 186 case without dermatitis symptoms. We took five sample of facial skin sebum for soaking with clear oil. The direct microscopic examination, allows the observation and numeration of D. folliculorum.

Results : D. folliculorum sampling was positive in 71 patients (71%) and 16 controls (16%). The average of Demodex mite density in patient with SD was 49.16. Demodex test was positive in 19 men (70.3%) and in 115 women (72.3%) in SD group.

Conclusion : The number of DF mites was significantly higher in patients with SD. This suggests that DF can introduced as an important factor in aetiological cause of SD. The observation of fungal spores within Demodex mites has led to the suggestion that the mites may act as vectors for Malassezia spp. as an important intensifying factor in SD.

Keywords : Demodex folliculorum, Seborrheic dermatitis (SD), Ectoparasite

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P276-70: The importance of Demodex mites density in rosacea.

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Background and Aim : Demodex mites are microscopic obligate parasite of the human pilosebaceous follicle. Demodex mites are associated with bacteria, both in their gut and on their exoskeleton. Demodex folliculorum and Demodex brevis are known as a microorganism's vector and maybe have pathological role in some skin disorders like rosacea. Bacillus oleronius and Staphylococcus epidermidis have been isolated from rosacea patients. Rosacea is a chronic disorder affecting the facial convexities, characterized by frequent flushing, persistent erythema and telangiectasia. The aim of present study was assessment of Demodex mites density in rosacea patients and comparing with normal group without rosacea.

Methods : According to clinical symptoms, rosacea was diagnosed in 186 patients by dermatologist. Control group were consist of 186 case without rosacea symptoms. Direct microscopic examination was done from 1 cm2 of facial skin sebum. Some references consider the density of more than five mites per cm2 as a pathogenic criterion.

Results : Demodex mites sampling was positive in 134 patients (72%) and 26 controls (13.1%). The average of age in rosacea and control groups were 37.5 and 34 years old respectively. The average of Demodex density in rosacea group was 39.1 mites per cm2.

Conclusion : Demodex mites may play an important role in the etiology of rosacea, since Demodex was significantly higher in the rosacea group. It seems high density of Demodex feed on epithelial cells and destroyed skin barrier then triggered a localised pro-inflammatory response.

Keywords : Demodex folliculorum, Demodex brevis, Rosacea

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P277-74: Study on correlation between demodex folliculorum density and androgenic alopecia

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Background and Aim : Demodex folliculorum is an obligate parasite of the human hair follicles. D. folliculorum can mechanically block follicles. Androgenetic alopecia (AGA) is a kind of hair loss that affected by testosterone hormone. Inflammatory activators such as Demodex infestation may play a role in the pathogenesis of some cases of androgenetic alopecia. The goal of this study is to assess the relationship between Demodex density and AGA.

Methods : The study comprised 100 patients with AGA and 100 controls without alopecia symptoms. We take sebum smear from hairless areas, examined under a microscope, and counted Demodex mites/cm2. Based on references positive Demodex test means five or more mites/cm2.

Results : In our study, positive Demodex tests were seen in 36 patients with AGA (36%) and in 4 controls (4%). Among 36 patients with positive test, 28 cases of them were women (34.5%) and 8 cases of them were men (42.1%). The average of Demodex density in AGA cases was 3.85 mites/cm2

Conclusion : There are some mechanisms that seem intensify hair loss by Demodex. The Demodex use the chelicerae to cut the epithelial cells of the host skin, feeding nutrients and bacteria from the hair roots. Demodex may be one of second factor (co factor) in hair loss and one of main factor in resistant to cure alopecia and the other disorder that lead to hairless.

Keywords : Androgenetic alopecia, Demodex folliculorum, Hair less

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P278-82: PCR Detection of Herpes Simplex Virus II in Idiopathic Abortions

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Background and Aim : Herpes simplex virus type 2 (HSV-2) is one of the most important human pathogenic viruses. The virus causes genital herpes and can cause miscarriage, pregnancy complications, and infertility in women. The aim of this study was to evaluate the role of HSV-2 in idiopathic abortion by PCR.

Methods : Fifty blood serum samples of women with idiopathic miscarriages were collected and transferred to the laboratory. The PCR test was performed using standard HSV-2 strain DNA and then the limit of detection (LOD) and specificity of the test were determined using different strain of DNA. Standard test was performed using positive and negative controls on the samples and the results were analyzed by agarose gel electrophoresis.

Results : PCR test optimized and 231 bp amplicon were observed in agarose gel. In specificity test only with DNA HSV-2 achieved positive results as well as a limit of detection 10 Copy / Reaction. Of the 50 samples studied, 9 (4.5%) were positive.

Conclusion : Idiopathic miscarriages are miscarriages that do not seem to have a definite cause. But clearly, several factors, including infectious agents that are difficult to identify, can cause miscarriage. One of these factors could be HSV-2. The results of this study showed that HSV-2 is one of the most important factors in this type of miscarriage and that HSV-2 can be quickly identified by tests such as PCR.

Keywords : Herpes simplex virus 2 , polymerase chain reaction , diagnosis , idiopathic abortion

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P279-99: Evaluation of Cytomegalovirus in leukemia by PCR molecular method

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Background and Aim : Introduction: Leukemia begins with the destruction of hematopoietic bone marrow cells and with the turmoil in the blood appears (Immature blood cell proliferation, homeostasis disorder, degrees of inflammation, mutation, immunodeficiency, antioxidant deficiency and infectious agents), Due to its high numbers in Iran, we decided to measure in Leukemia by PCR method, to quantify the prevalence of cytomegalovirus (CMV) as the largest member of the herpes family that can cause latent infections for a lifetime,

Methods : Methods: 100 leukemic blood samples and 100 healthy blood samples were collected from Tehran hospitals and DNA extraction was performed by phenol-chloroform method. CMV PCR test was optimized and evaluated for specificity and limit of detection (LOD). Optimized test was performed on all patient and healthy samples along with positive and negative controls. The PCR product was identified by agarose gel electrophoresis

Results : Results: PCR test was optimized, and 257 bp product was observed in agarose gel electrophoresis. In specificity test, No product other than the CMV sample was observed. LOD was 100 Copy/reaction, and all healthy controls were negative and 33 of the samples were CMV positive.

Conclusion : Conclusions: Cancer has many causes, including leukemia. The role of infectious agents in cancers is increasing every day. This study shows that CMV can be considered as an infectious and influencing factor in leukemia.

Keywords : : Detection, leukemia, Cytomegalovirus, infections, PCR

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P280-116: An Overview of Noroviruses as gastroenteritis viruses in people in all ages.

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Background and Aim : Noroviruses(NoVs) are recognized as the leading cause of viral acute gastroenteritis in people of all ages worldwide.NoVs are classified within the Caliciviridae family with RNA genome.The genome is organized into 3 open reading frames (ORFs).ORF1 encodes a polyprotein,ORF2 encodes VP1 and ORF3 encodes VP2.Based on sequence differences of the VP1 protein,NoVs are classified into 10 genogroups(GI-GX) and subclassified into 49 genotypes.The emergence of new recombinant strains are high and these recombinations most frequently occurs between the junction of ORF1 and ORF2.The symptoms includes: diarrhea, vomiting, nausea, stomach pain, fever and headache.NoVs are highly infectious and can be spread from person to person through fecal-oral transmission,contaminated food,water,and environmental surfaces.There are no vaccines to prevent norovirus infection,although several candidate vaccines are in clinical and pre-clinical trials.However,WHO highlighted NoVs as a priority for vaccine development,few studies have been conducted in Iran on genetic characteristics and circulating genogroups and genotypes.

Methods : In this review,we summarized over 35 different studies on NoVs from 2015 to 2020 in Iran and the rest of the world.The overall protocol is to extract the RNA of virus with special kits and amplify the genome with real-time quantitative RT-PCR, followed by nucleotide sequencing and phylogenetic analysis.

Results : According to these studies, 24 of the 35 articles,were included for a norovirus prevalence and genotyping data.The infection causes by norovirus GII is more prevalent than GI.There was a significantly higher proportion of GII.4 in samples of NoVs.Although in recent years, non-GII.4 strains such as:GII.17,GII.3,GII.6 and GII.2 have replaced GII.4 strains in several countries.The prevalence in cases of acute gastroenteritis was estimated at about 18% worldwide.

Conclusion : The rapidly expanding infection causes by NoVs shows its contribution with global burden across all settings and age groups. In agreement with previous reports, most infections in these studies, were caused by GII viruses. The prevalence of NoV in European and American countries, because of different feeding patterns may be different with Middle Eastern countries. Although the prevalence of NoV in Iran is lower than other developing countries, promoting public health education and preparation of health care setting for controlling the Norovirus sporadic cases and outbreaks are strongly recommended.

Keywords : Norovirus – Infection – Acute Gastroenteritis - Recombination

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P281-117: Microbial diversity as an index in monitoring of desert soil quality

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Background and Aim : Microorganisms have vital roles in soil processes such as geochemical cycles of elements and maintenance of the soil structure. However, information on the soil diversity especially in arid and semiarid areas, which cover %40 of the Earth and more than %70 of Iran areas, is very limited. The aim of this study was to determine the effect of disturbance (grazed or not grazed) on soil chemical properties and bacterial diversity in a semiarid area.

Methods : Two plots were selected in the cold and warm sites of Khabr National Park and Ruchun Wildlife Refuge, Kerman province. The soil samples were taken from the disturbed (grazed and undisturbed (not grazed) areas. The soil chemical properties and microbial diversity was determined via standard methods and the next generation sequencing (Illumina platform), respectively.

Results : According to the results, the sensitivity of the soil chemical properties was less than the microbial diversity to grazing. Although there was no significant difference in chemical properties between grazed and not grazed area, the bacterial diversity differed qualitative and quantitative between the grazed and not grazed areas. The frequency of the diverse groups of bacteria differed as a result of disturbance. In addition, there were special taxonomic groups of bacteria under disturbance effect. The differences among microbial community compositions were more in the lower ranks of classification (family and genus) with more unknown phylotpes, showing challenges in microbial ecology in the soil complex environment.

Conclusion : In conclusion, changes in the microbial community compositions at semiarid sites estimated by next generation sequencing, precede detectable changes in the soil chemical properties, thereby it can be used in the soil quality assessment or the soil destruction.

Keywords : Dessert, Diversity, Illumina, Next Generation Sequencing, Quality, Soil,

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P282-163: Inhibitory properties of enzymes involved in the Quorum Sensing process in Pseudomonas aeruginosa by molecular modeling

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Background and Aim : Quorum Sensing is a bacterial communication mechanism that regulates the production of many pathogenic factors, including the formation of pigments and the ability to form biofilms that are essential for chronic infections.

Methods : The molecular modeling was done using the Glide software in Schrödinger drug discovery suite. More than 700 drugs downloaded from PubChem were prepared with Ligprep software; proteins were obtained from a protein data bank (PDB). The Qikprop application was used to obtain the Lipinski formula for the compounds.

Results : The results of molecular modeling showed that compounds with PubChem ID 118732850 and 122187653 showed the highest docking score -12.019 and -8.009 Kcal.mol-1 had the highest inhibitory activity on triphenyl-LasR complex receptor and AHL synthase protein, respectively.

Conclusion : Regarding the importance of biofilm formation in the survival and continuation of bacterial infection and antibiotic resistance in most bacteria, in this study, the inhibitory activity of selected compounds against Triphenyl-LasR and AHL Synthesis Lasl enzymes involved in the Quorum Sensing system and biofilm formation of Pseudomonas aeruginosa investigated by molecular docking.

Keywords : Molecular docking, Quorum Sensing, biofilm formation

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P283-177: Screening of tyrosinase enzyme producing Actinobacterial isolates from soil samples of Iran

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Background and Aim : Tyrosinases are one of the most important enzymes in biotechnology and play a special role in various industries, including bioremediation industries. Although various natural sources are considered to find tyrosinase, the enzymes derived from microbial sources, in particular bacterial sources, have practical applications and more studied. Actinobacteria are potent bacteria in biotechnology and are used to produce various metabolites with therapeutic, industrial and environmental applications.

Methods : . In this research, 20 soil samples were obtained from different regions of Iran, cultured in ISP2 agar and 58 actinobacterial strains were isolated. The isolates were cultured in tyrosine agar plates and 17 strains with transparent halo were considered as tyrosinase producers. These isolates were cultured in tyrosine broth and the tyrosinase activity was confirmed in 11 strains.

Results : The results of the quantitative evaluation of tyrosinase activity on the top 4 strains showed that the two strains designated 3165 and 3233 had more tyrosinase activity. According molecular identification, these isolates are 9/99% similarity in16 SrRNA gene sequencing to Streptomyces thermocarboxydus and Streptomyces tendae.

Conclusion : The results of this study indicated the prevalence of tyrosinase producing actinobacteria in the soils of Iran.

Keywords : tyrosinase enzyme, actinobacteria, Streptomyces, primary screening, secondary screening, molecular identification

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P284-192: Evaluation of two factors on hyaluronic acid production by mutant strain of Streptococcus equisimilis by response surface methodology

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Background and Aim : Hyaluronic acid (HA) as a biodegradable, biocompatible, non-immunogenic linear polysaccharide has been used in many applications such as pharmaceutical, clinical and cosmetics. Currently, commercial HA for human use is mainly produced by fermentation, specifically using Streptococcus sp. In present study we improved HA production by mutant strain of Streptococcus equisimilis as one of the best strains producing hyaluronic acid capsule.Two of the most important factors in medium culture are pH and temperature.The most frequently used optimization strategy is "one-at-a-time"strategy. This approach is not only time consuming, but also ignores the combined interactions between physiochemical parameters, so in this study we optimized this two factors in medium culture conditions by response surface method. RSM combines statistical experimental designs and empirical model developing by regression with a purpose of process or product optimization.

Methods : In first step we used the Minitab17 software to design of experiment in RSM by Central composite design(CCD) method. Maximum and minimum values were also considered according to recent studies. Minimum level for temperature was determined 30°C and maximum level 37°C, as well as minimum level for pH was determined 5.5 and maximum level 8.0. Finally, experiment was carried out with 14 run, 2 block and 6 center points. In the next step the primary seed of Streptococcus equisimilis were cultured in Todd Hewitt Broth for 16 h. The production medium containing Na2HPO4·12H2O, KH2PO4·5H2O, MgSO4·7H2O, yeast extract, and glucose was inoculated by 10% of seed at OD600nm 1, and incubation for 6 h of HA production (in 180 RPM, 37°C) . Then, HA was precipitated by A special method. The amount of proteins and nucleic acids was assayed at OD280nm and OD260nm. The HA concentration was determined by complexometery method using carbazole assay at 550 nm. Finally, HA values was evaluated by the MINITAB 17 software.

Results : Finding showed that the yield of HA extracted from Streptococcus equisimilis in medium culture with pH:8.0 and temperature 37°C is 3.27 mg/ml and its yield was more than other values of pH and temperature.

Conclusion : This suggested that we optimized temperature and pH in medium components with central composite design (CCD) method for high production of HA.

Keywords : Hyaluronic acid, Streptococcus equisimilis, Carbazole, response surface methodology, central composite design

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P285-201: Investigation of Toll-like receptor related genes in co-infection of IBV and APEC in the chicken trachea using RNA-Seq

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Background and Aim : Infection with Infectious bronchitis virus (IBV) and avian pathogenic E.coli (APEC) is an important respiratory infection in Worldwide. Dendritic cells (DCs), macrophages, lymphocytes, endothelial cells, and fibroblasts present PRRs such as Toll-like receptors (TLRs) that can recognize infectious agents through them that the identification of them is important for controlling programs. The aim of this study was to investigate on Toll-like receptor related genes in the trachea tissue of infected (IBV variant 2, and with APEC serotype O78: K80) SPF chickens group compare to the control group.

Methods : A number of Forty SPF chickens were divided into two treatment and control groups. Differential transcriptional profile in the trachea tissue of infected SPF chickens group compares to the control group in the early stage of infection by Illumina RNA-seq technique paired-end and strand-specific sequencing. DEGs of transcriptome profiling of the trachea from the infected group were identified. Gene ontology category, KEGG pathway, and STRING analysis were used to identify relationships among differentially expressed genes.

Results : All Toll-like receptor genes in our study were up-regulated. The number of twenty-three Toll-like receptor genes was identified consist of CD80, FADD, IFNAR1, IFNAR2, IL8L1, LY96, MAP3K7, MAPK1, MAPK14, MYD88, NFKB1, PIK3CA, PIK3CB, PIK3CD, PIK3R2, RIPK1, STAT1, TLR2-2, TLR3, TLR4, TLR7, TOLLIP, TRAF6.

Conclusion : Among them, the most important factors in identifying bacterial and viral products such as TLR2, TLR4 (recognize peptidoglycan and LPS), TLR3 and TLR7 (recognize viral products) was observed.

Keywords : TLRs, IBV, APEC, RNA-seq

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P286-217: Expression of metalloproteinase inhibitors of Hemiscorpius lepturus scorpion venom in bacterial host

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Background and Aim : One of the most dangerous endemic scorpions of Iran is Hemiscorpius lepturus that its venom is very toxic and known as responsible of most of scorpion sting dependent deaths in Iran. There are four Metalloproteinase inhibitors in the venom gland transcriptome of this scorpion. Metalloproteinase inhibitors are involved in some of the critical cells activity including the stability and surviving of ECM. This study aimed to investigate the structure and functions of a pair of these molecules and subsequently their cloning and expression for the first time.

Methods : bioinformatics analysis and molecular docking on sequences of HLMetInhibit1 and HLMetInhibit2 performed (with the MG764541 and MG764542 NCBI accession numbers). The recombinant plasmids (pET-22b- HLMetInhibit 1,2) designed and synthesized, then transformed into the E. coli BL21 bacterial host. The colony-PCR and electrophoresis on one percent agarose gel performed and protein expression induced by different concentrations of IPTG at different times. Then SDS-PAGE and staining by coomassie brilliant blue and western blotting performed.

Results : The highest binding affinity predicted for HLMetInhibit1 by molecular docking results. Gene cloning performed. Highest protein expression detected after 5 hours and with 1 mM concentration of IPTG. SDS-PAGE and western blotting confirmed the protein expression correctness for HLMetInhibit1 and HLMetInhibit2 with 26 and 17 KD of molecular weights.

Conclusion : Gene cloning and protein expression of Hemiscorpius lepturus metalloproteinase inhibitors1 and 2 as the novel proteins that have not been studied so far, is approachable and it is hoped that after further in vitro and in vivo investigations, they will be the suitable candidates for research in the Various therapeutic fields.

Keywords : Cloning and Expression; Hemiscorpius lepturus; Metalloproteinase inhibitors

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P287-218: Cytotoxicity of Hemiscorpius lepturus scorpion venom on breast cancer

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Background and Aim : Breast cancer is one of the most related cancer deaths among women. The scorpion venom consists of various peptides and proteins with cytotoxic, apoptotic and growth inhibitory effects on various cancers. Studying the Cytotoxic effect Hemiscorpius lepturus scorpion venom on T47D breast cancer cell line was the main aim of the current study.

Methods : The T47D cells were cultured as monolayer in RPMI1640 medium. The toxicity of the scorpion venom on T47D cell line was evaluated by MTT assay and the IC50 was calculated. The HEK293 cell line was used as control cell line.

Results : The MTT assay results showed the time and dose-dependent inhibitory effect of H. lepturus venom on T47D cell line. However, such effect was not observed on HEK293 cell line in identical dose.

Conclusion : The achieved results indicate the anticancer effect of H. lepturus venom on T47D breast cancer cell line.

Keywords : Hemiscorpius lepturus; Breast cancer; T47D; Cytotoxic effect

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P288-221: Human Papilloma Virus Type 16 in Epithelial Ovarian Cancer

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Background and Aim : Background: Ovarian carcinoma is the most common malignancy of women and the cancer with a 15–50% in the world. Human Papilloma Virus (HPV) is considered factors in cervical and ovarian cancer (OCa) and are related with squamous cell carcinoma in cervical region. The effect of fixed infection maybe causing to chronic inflammation, in the cancer of ovaries has received very rare attention, although a background of pelvic inflammatory disease (PID) is in a case-control study associate to higher risk for ovarian carcinoma. HPV-16 is one types of HPV and its the most common and important cause of cervical carcinoma in the developed world. Objectives: The aim of this investigate was evaluate incidence of HPV-16 in patients with OCa who referred to Imam Hossein Hospital of Shahid Beheshti University of Medical Sciences, Tehran-Iran.

Methods : Materials and Methods: In this case-control study that was conducted from May 2015 to October 2015 in Tehran, 140 samples were studied which obtained from patients with OCa. After obtaining samples from OCa tissue by the pathologist, for extraction DNA, samples were transferred to the laboratory of university. DNA was extracted with Kit (intron Biotechnology Co. Korea) according to manufacturer instructions. To confirm the presence of HPV-16 in samples of OCa, specific primers for the L1 gene of HPV, were designed and used standard PCR method for detection of HPV. PCR product was sequenced to confirm the presence of HPV-16.

Results : Results: Out of 140 samples of OCa,70 (50%) samples were malignant cancer and 70 (50%) were benign cancer as control group. From 70 malignant samples 25(36.0%) were HPV-16 positive. 2.8% of the tissue samples of control group were positive for HPV-16.

Conclusion : Conclusion: This results shows a feasible role of HPV-16 in the carcinogenesis of OCa. According to this results infection with HPV may play a relative role in the spread of OCa or it could comfort its development.

Keywords : HPV, Ovarian Cancer, Malignancy, PCR

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P289-222: Investigation of correlation of the Helicobacter pylori infection prevalence with serum ferritin and iron levels

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Background and Aim : Helicobacter pylori is one of the most common bacteria responsible for chronic infection in human. This bacteria causes a wide range of gastrointestinal diseases, including chronic gastritis, peptic ulcer and gastric adenocarcinoma. Due to the decrease in gastric acid secretion in this condition, some studies have pointed to the effect of Helicobacter pylori outbreak on iron deficiency anemia. The aim of this study was to investigate the association of Helicobacter pylori infection with serum iron and ferritin levels.

Methods : In this study, the serum of 180 patients referred to a medical diagnostic laboratory with clinical symptoms was collected. Then the IgG antibody titer of Helicobacter pylori and the levels of ferritin and iron in the serum were examined. The results were analyzed using statistical test and SPSS software.

Results : Of the 180 samples performed, 45 samples (25%) were positive for Helicobacter pylori titer IgG. 17 (37%) of IgG-positive people had low serum iron levels and 11 samples (24.4%) of IgG-positive had serum ferritin deficiency. In the group of people with a negative IgG antibody titer, 43 (31.8%) had serum iron deficiency and 47 samples (34.8%) had low serum ferritin levels. There were no significant correlation between ferritin levels, serum iron, and IgG titer of Helicobacter pylori by using chi-square test ($p = 1.43$).

Conclusion : According to the results presented in this paper, which points to the high prevalence of iron deficiency anemia, further studies are needed. Also, in order to reduce the prevalence of Helicobacter pylori infection due to the high percentage of positive IgG antibody titer of Helicobacter pylori infection, it is necessary to use codified educational and health programs to reduce the prevalence of this bacteria.

Keywords : Helicobacter pylori -ferritin- serum iron -IgG

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P290-229: Investigating the effect of antifungal properties of Kakoti and Cumin extracts on Aspergillus niger and Rhodotorula rubra

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Background and Aim : In recent years, the use of essential oils and extracts of medicinal plants for their broad-spectrum antimicrobial properties and value compared to chemical preservatives has been considered.

Methods : In this study, the antifungal properties of Kakoti and cumin methanolic extracts compared to two common fungi of food products including Aspergillus niger (PTCC5154) and Rhodotorula rubra (PTCC5076) have been investigated. The effect of antifungal properties of these extracts was investigated using agar diffusion methods to determine the inhibition zone diameter of the extract and dilution to determine the MIC and MFC of the extracts.

Results : The results of the extract tests showed that the disks containing of each extract of Kakoti and cumin in a concentration concentration of 10 (mg/ml) had the highest inhibitory zone with diameter 12 and 10 (mm) respectively against Aspergillus niger and, 8 and 14 (mm) against Rhodotorula rubra yeast. MIC of Kakoti and cumin extracts were 3.66 and 3.05 (mg/ml) against mold and 1.14 and 9.76 (mg/ml) against yeast respectively. Also their MFC was equal to 11.71 and 9.76 (mg /ml) and 3.66 and 31.25 (mg /ml) respectively.

Conclusion : Both Kakoti and Cumin extracts have effective antifungal result on Aspergillus niger and Rhodotorula rubra

Keywords : Sauerkraut, cumin, Kakoti, anti-fungal

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P291-240: Antibiotic resistance and prevalence of imp-2,vim-2, sim and ndm genes in Escherichia coli strains isolated of cause urinary tract infections

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Background and Aim : Urinary tract infection (UTI) is the second most common human infection, especially among women, caused by the genus of Enterobacteriaceae family, especially Escherichia coli. Metallobalactamase (MBL) with ability to hydrolyze beta-lactam antibiotics especially carbapenems, are one of the main enzymes that cause antibiotic resistance. The aim of the present study is evaluation of the antibiotic resistance and the frequency of imp-2, vim-2, sim and ndm genes among E. coli strains isolated of urinary tract infections in Ahvaz city.

Methods : The two hundred samples collected from people with UTI were examined after culture and isolation. The resistance pattern related to ampicillin, kanamycin, cefotaxime, streptomycin, ciprofloxacin, imipenem and meropenem was investigated according to CLSI 2018. To determine MBL-producing isolates, imipenem and meropenem resistant strains were evaluated by PCR method for the presence of imp-2, vim-2, sim and ndm genes.

Results : The highest resistance was observed against ampicillin (87.5%). The percent of resistance related to kanamycin, cefotaxime, streptomycin, ciprofloxacin, imipenem and meropenem was as follow: 28%, 63%, 46%, 50%, 4.5% and 5% respectively. The gene of ndm was found in 8 isolates; while none of isolates harbored imp-2, vim-2 and sim genes.

Conclusion : The detection of ndm gene in these isolates indicates the spread of this type of resistance among pathogenic isolates. MBL resistance leads to the ineffectiveness of the last line of antibiotics. Therefore, it is need countermeasures against this type of antibiotic resistance.

Keywords : Escherichia coli, UTI, antibiotic resistance, MBL, disc diffusion method.

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P292-247: The Global Prevalence and Distribution of Chlamydia pneumoniae, Helicobacter pylori, Cytomegalovirus and Herpes simplex virus in Patients with Coronary Artery Disease in Molecular and Serological Studies; A Systematic Review and Meta-analysis

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Background and Aim : Coronary Artery Disease (CAD) is one of the most important causes of death worldwide. The aim of this study was to determine the prevalence of C. pneumoniae, H. pylori, Cytomegalovirus (CMV) and Herpes simplex virus (HSV) in CAD patients based on published serological and molecular studies.

Methods : A systematic literature search was conducted in Medline (via PubMed), Embase, Scopus and Web of Science databases (1996-2019). Both molecular and serological studies were analyzed using STATA software (Version 14).

Results : 145 studies were included for final analysis. We gathered and investigated the prevalence of C. pneumoniae (25.1% [95% confidence interval (CI) 21.5-28.8%]), H. pylori (12.8% [(95% CI) 4.0-22.0%]), CMV (64.4% [(95% CI) 57.7-73.0%]) and HSV (31.8% [(95% CI) 21.5-42.2%]) in CAD patients from the analysis of molecular studies. Additionally, in serological studies, the prevalence of mentioned pathogens were 72.7% [(95% CI) 67.8-77.6%], 63.3% [(95% CI) 60.0-66.5%], 62.2% [(95% CI) 58.0-66.3%] and 34.3% [(95% CI) 23.6-45.1%] respectively.

Conclusion : Interestingly, there was only a significant increase in the prevalence of C. pneumoniae and H. pylori in serological studies compared to the reported data from molecular studies, while the prevalence of CMV and HSV were the same in both types of studies.

Keywords : Chlamydia pneumoniae, Helicobacter pylori, Cytomegalovirus, Herpes simplex virus

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P293-252: Investigation on protease production ability among native heavy-metal resistant gram-negative bacteria

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Background and Aim : Metabolic products such as enzymes (green chemicals) are produced using inhabitant microorganisms in extreme environments. Enzymes have application in various industries such as pharmaceuticals, detergent, dairy etc. Extracellular protease production is prominent characteristic of many bacterial species. Despite the high attention and high potential of bacilluses, finding enzymes with special features is always special attention of scientists which give rise to search new protease resources with various functionality. In this regard, the aim of the present study is to introduce new bacterial strain which could tolerate harsh environmental conditions by process optimization.

Methods : The 10 gram-negative heavy-metal resistant bacterial isolates which had been isolated from industrial wastewaters from Khouzestan province, investigated for protease production ability. These bacteria were selected by qualitative screening tests using various medium such as skim milk agar, minimal medium with various proteinaceous resources. After incubation, all plates were studied in presence of indicator solution based on halo zone production. Quantitative protease assay was done using modified protease activity assay using casein as substrate.

Results : The results of qualitative assay showed that one isolate showed halo zone around colony. Moreover, the results of protease assay experiments showed that selected isolate has the enzyme activity equal to 27.313U/ml. Further studied are be doing to determine comprehensive features of produced protease.

Conclusion : Conversion of wastes to useful biomass by microorganisms and their enzymes is new trend and novel protease-producing microbes. According to this, the presented isolate could be a promising candidate for reach to this aim.

Keywords : protease; heavy-metal; gram negative

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P294-255: Optimization of protease production conditions with gram-positive bacteria Bacillus cereus

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Background and Aim : Extracellular protease production is the prominent feature of many bacterial isolates. A large amount of alkaline proteases which are available commercially are produced by some strains of Bacillus for their high stability at various temperatures and pH. Protease production is impressed by environmental and nutritional conditions; therefore, enhancement of its production is possible by culture condition manipulation. In this regard, the optimization process of protease production of a heavy-metal resistant isolate was done to reach to high enzyme activity and become to a possible candidate for industrial applications.

Methods : In previous works, the ability of Bacillus cereus FWP2 isolate (with lead-resistance ability) was confirmed by quantitative and qualitative assays. Since the growth amount of valuable enzyme-producing microbes in culture media is the limiting factor for enhancement of production yields, therefore it is necessary to optimize of fermentation conditions. In present study, the role of various culture condition parameters (e.g. nutritional resources, temperature, pH) were investigated to enhancement of protease production based on one-factor at the time method.

Results : The results showed that by growth condition optimization, enzyme activity of the selected isolate, was increased gradually from 1.877U/ml to nearly 19-fold during step-by step optimization process.

Conclusion : Optimization of nutritional factors (i.e carbon, nitrogen, metallic ions) is an essential work for enhancement of enzyme production and convert it to a cost-effective industrial processes. With parameter optimization it could be ensure that enzyme action has the most effect.

Keywords : protease; Bacillus cereus; optimization; industrial importance

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P295-258: Prevalence of three siderophore outer membrane receptor genes (iroN, iutA, fyuA) among mastitis causing Escherichia coli

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Background and Aim : Escherichia coli is a gram negative bacteria which is responsible for different enteric and extraintestinal infections in animals and humans. Iron is an essential nutrient for growth of E. coli and other bacteria, and therefore most pathogenic bacteria developed various systems like siderophores to gain iron in competitive environments in the host. Since the ability to acquire iron is related to pathogenicity, genetic profiling of iron acquisition systems can be a valuable asset to screen pathogenic E. coli strains. The aim of the present study was to determine the prevalence of the most well-known siderophore outer membrane receptor genes: iroN (salmochelin outer membrane receptor), iutA (aerobactin outer membrane receptor) and fyuA (yersiniabactin outer membrane receptor) in mastitis causing E. coli strains.

Methods : A total of 124 E. coli isolates recovered from bovine clinical mastitis were investigated through PCR assays for the presence of the genes iroN, iutA and fyuA.

Results : Only 19 (15.32%), 16 (12.9%) and 20 (16.12%) isolates possessed iroN, iutA and fyuA, respectively. Moreover, simultaneous presence of the three genes was observed in four isolates. Besides, 13 isolates were detected positive for two of these genes at the same time.

Conclusion : According to the relatively low prevalence of siderophores obtained in this study, the role of other iron acquisition strategies like: gaining iron through haem, membrane transporters for metal ions, etc., should be taken into consideration. Especially, for mastitis causing E. coli strains which survive and multiply in poor iron milieu.

Keywords : Escherichia coli, bovine mastitis, siderophore, iroN, iutA, fyuA.

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P296-271: A Comparison of phylogenetic groups between mastitis causing strains of Escherichia coli and fecal isolates

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Background and Aim : Worldwide phylogenetic analyses have demonstrated that virulent extra intestinal pathogenic Escherichia coli (ExPEC) strains belong mainly to group B2 and, to a lesser extent, to group D. On the contrary, most of the commensal strains are associated with group A or group B1. The most important members of ExPEC group are avian pathogenic E. coli (APEC), Uropathogenic E. coli (UPEC), and Mammary pathogenic E. coli (MPEC) which are responsible for extra intestinal diseases in animals or humans. This study tries to elucidate the status of mastitis causing E. coli strains as a member of ExPEC group and their relation to commensal E. coli isolates in terms of their phylogenetic groups.

Methods : Methods: A total of 64 Escherichia coli isolates (mastitis causing isolates= 32, fecal isolates from the same cows= 32) were examined for determination of phylogroups using quadruplex PCR described by Clermont et al., 2013.

Results : Results: Most of the mastitis causing isolates belonged to the phylogroups A (43.75%) and B1 (40.62%), while 62.5% of fecal isolates were categorized as B1. The group C had the least members of both mastitis causing isolates (6.25%) and fecal isolates (3.12%). No members of the phylogroups D and E were detected among mastitis causing isolates and fecal isolates, respectively. Furthermore, among 32 paired samples, the phylogenetic groups of 12 paired samples (12 milk and 12 fecal samples from the same cows) were the same.

Conclusion : Conclusion: The high prevalence of MPEC members in groups A and B1 may represent the commensal nature of these isolates.

Keywords : Escherichia coli, phylogenetic groups, bovine mastitis, ExPEC, commensal strain

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P297-273: Investigation on the impact of pesticides on microbial flora of saline soils using the next generation sequencing

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Background and Aim : Pesticides and insecticides are the chemicals widely used in the agricultural industry, but their ecotoxicological effects on the environment is not still well understood. In this study, the impact of a pesticide, chlorpyrifos (CP) and an insecticide, deltamethrin (DM) as the organophosphorus and pyrethroid compounds on soil microbial diversity was investigated .

Methods : four different soils samples under the various salinity (0, 1%, 2% and 4%) were contaminated by these compounds. Then, the destructive effects of CP and DM on the soil microbial composition were studied by next generation sequencing (NGS).

Results : The results indicated that soil salinity had significant impact on the sample's resistance to the toxins and some of the dominant species in the blank sample were completely destroyed by CP and DM.At the phylum level ,Firmicutes and Proteobacteria were not be destroyed by DM and CP, but their population also were considerably raised by degrading the contaminants

Conclusion : The present results provided a momentous insight into the environmental impacts of chlorpyrifos and deltamethrin contaminants and their natural attenuation.

Keywords : Pesticides, deltamethrin, chlorpyrifos, next generation sequencing, Soil Salinity

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P298-297: Effect of lipopolysaccharide on MMP-2 activity in THP1 monocytic cells in vitro

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Background and Aim : Lypopolysaccharid (LPS) is an endotoxin and major component of outer membrane of gram negative bacteria. Moreover LPS has an important role in inflammation. Matrix metalloproteinases (MMPs) are a large group of enzymes that break down the extracellular matrix result in tissue remodeling and have a main role in inflammation. In this study the effect of LPS on MMP-2 activity in a monocytic cell line has been assessed in vitro.

Methods : Human THP1 monocytic cells were cultured in complete RPMI medium. Then the cells at the exponential growth phase were incubated with different concentrations of LPS for 24 hours. After that the MMP-2 activity in the cell culture supernatants was evaluated by gelatin zymography.

Results : LPS significantly increased the MMP-2 activity in the THP1 monocytic cells dose-dependently compared with untreated control cells in vitro.

Conclusion : The results of this study show that LPS up-regulates the MMP-2 activity in monocytic cells. Therefore it seems that LPS is a potent inducer/enhancer of MMP-2 activity in monocytic cells. So LPS effect on inflammation may be in part due to its stimulatory effects on MMPs.

Keywords : Lypopolysaccharid, MMP-2, monocytes

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P299-301: different effects of subinhibitory concentrations of gentamicin on expression of alginate and biofilm genes of Pseudomonas aeruginosa clinical isolates

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Background and Aim : P. aeruginosa is an important opportunistic pathogen and major cause of nosocomial infections. Alginate production and biofilm formation have important roles in pathogenesis of P. aeruginosa infections. Antibiotics at subinhibitory concentrations (sub-MIC) may affect P. aeruginosa virulence factors. The purpose of this study was to investigate the effects of gentamicin at sub-MIC concentrations on alginate production, biofilm formation and expression of their specific genes in P. aeruginosa standard strains and clinical isolates.

Methods : The minimum inhibitory concentration of gentamicin was determined by microdilution broth method against 3 clinical isolates of P. aeruginosa (P1-P3) and standard strains (PAO1 & 8821M). In each of P. aeruginosa clinical isolates and standard strains, the effects of gentamicin at 1/2MIC and 1/4MIC concentrations on expression level of alginate genes (algD, algU) and biofilm genes (pelA , pslA) were determined using Real-Time PCR method. The effects of these concentrations on alginate production and biofilm formation were evaluated using microtiter plate and carbazole assay, respectively.

Results : Gentamicin at sub-MIC concentrations reduced expression of algD, algU, pelA and pslA genes, biofilm formation and alginate production in P. aeruginosa clinical isolate P1. This inhibitory effect was also observed on alginate production and biofilm formation of standard strains 8821M and PAO1, respectively. However, exposure with sub-MIC concentrations of gentamicin increased alginate production, biofilm formation and expression of their specific genes in P. aeruginosa clinical isolatesP2 and P3.

Conclusion : This study showed that Gentamicin at sub-MIC concentrations affect the expression of alginate and biofilm specific genes and subsequently causes different changes in alginate production and biofilm formation of P. aeruginosa clinical isolates and standard strains. Further studies should be conducted to understand the regulation of virulence genes expression in the presence of sub-MIC concentrations of antibiotics.

Keywords : Alginate, Biofilm, Gentamicin, Pseudomonas aeruginosa

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P300-302: Evaluation of the effects of subinhibitory concentrations of gentamicin on alginate production of Pseudomonas aeruginosa clinical isolates

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Background and Aim : Pseudomonas aeruginosa is one of the most common human opportunistic pathogen which is considerable due to cause acute and chronic infections. Alginate is an important virulence factor of this organism which has essential role in establishment of chronic infections. This study aimed to investigate the effect of subinhibitory (sub-MIC) concentrations of gentamicin on alginate production of P. aeruginosa clinical isolates and standard strain 8821M.

Methods : In this study, a total of 83 P. aeruginosa clinical isolates were isolated from different clinical specimens. P. aeruginosa clinical isolates were identified by standard bacteriological and biochemical tests. The effects of sub-MIC concentrations (1/2 × 1/4MIC) of gentamicin on alginate production of P. aeruginosa clinical isolates and standard strain 8821M were assesed by carbazole method. The presence of alginate in clinical isolates was confirmed by detection of alginate genes (algD, algU) by PCR method.

Results : All the isolates had the ability of alginate production and were positive for algD and algU genes. sub-MIC concentrations of gentamicin significantly increased alginate production of 49 isolates (59%). On other hand, in 34 isolates (41%) and standard strain 8821M, alginate production decreased significantly in the presence of sub-MIC concentrations of gentamicin.

Conclusion : This study showed different effects of sub-MIC concentrations of gentamicin on alginate production of P. aeruginosa clinical isolates. It seems that bacterial reaction to sub-MIC concentrations of antibiotics depends on isolates type. Further studies are required to understand the mechanism of different responses of P. aeruginosa clinical isolates to sub-MIC concentrations of an antibiotic.

Keywords : Alginate, Gentamicin, Pseudomonas aeruginosa

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P301-303: Survey of heterotrophic Halophilic bacteria in saline sediments from hypersaline wetland in south of Halghe Dare hills, Alborz province

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Background and Aim : Halophilic bacteria live in many extreme enviroments under high-salt stress. Identification of novel halophilic bacteria can be very important in biotechnological and ecological studies. In This study, we survey heterotrophic bacterial diversity in sediments from saline wetland in south of Halghe Dare hills as one of the hypersaline region in Alborz province.

Methods : The sampling was performed from 0-25 cm depth. Isolation of heterotrophic bacteria was conducted using R2A agar medium. After differentiation of isolates based on morphological and biochemical characteristics, identification and phylogenetic relationships analysis of selected isolates were performed by 16S rRNA gene sequencing and analysis using NCBI databases and bioinformatics softwares.

Results : From the 102 purificated isolates, 16 strains were selected for 16S rRNA gene sequencing which included 15 species into 9 genera including Bacillus (32.2%), Halomonas 25%, Virgibacillus (6.2%), Gracilibacillus (6.2%), Streptomyces (6.2%), Aminobacter (6.2%), staphylococcus (6.2%) , Brevibacterium (6.2%) and Planococcus (6.2%). The number of 6 isolates due to the similarity of less than 98.7% in 16S rRNA gene sequence to the standard species can present novel bacterial species.

Conclusion : Presence of various types of bacterial genera and some novel taxonomic groups in saline wetland in south of Halghe Dare hills as one of the extreme ecosystem in central regions of Iran presents a new genetic and microbial source.

Keywords : Halophilic bacteria, bacterial diversity, hypersaline environment

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P302-304: A systematic Review about Clinical features and computed tomography findings of COVID-19 Positive Patients

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Background and Aim : Novel coronavirus is pandemic public health that it has begun from December 2019 in city Wuhan, China. The aim of this study was to determine the most common clinical features and Computed tomography findings among patients infected by COVID-19.

Methods : We have used different databases such as ISC, science direct, Embase (Elsevier), Web of Science, Scopus and Medline via PubMed. Searches were performed by key words including: 2019-nCoV, SARS-CoV-2, 2019 novel coronavirus, COVID-19 virus, coronavirus disease 2019 virus, Wuhan coronavirus, clinical presentation, clinical syndromes, clinical characterization, clinical symptoms, clinical signs, clinical feature, imaging finding, computed tomography (CT) feature, lung CT scan, pulmonary CT scan and chest CT scan.

Results : A total number of 1047 articles were found collectively amongst the databases. As the title screening was performed, 492 articles were removed. Abstract screening resulted in 306 more studies to be omitted during the search. Finally, after full text screening, 42 articles remained (See figure1). 42 articles reported clinical feature, 5 of publications were abstract because full texts written in Chinese among them 25 articles reported chest CT finding of COVID 19 patient. The most frequent signs COVID-19 disease were pointed fever and cough in all of studies. Among 42 studies were used: 34 (80.9%), 29 (69.04%), 24(57.1%) and 19(45.2%) were reported fatigue, diarrhea, headache, dyspnea and expectoration as common symptoms respectively. Other sign included: sore throat, shortness of breath, nasal discharge, hemoptysis and chill. In chest CT scan finding, 20(80%) of studies were introduced ground glass opacity and 19(76%) bilateral involvement as the most common patterns. Then 14(56%) and 11(44%) of publication were mentioned consolidation and unilateral pneumonia respectively. Chest CT morphology were crazy paving, halo sing, vascular enlargement, reticulation, tree in bud, plural effusion, air broncho gram and nodule.

Conclusion : Know of common clinical feature and chest CT scan due to early identification of COVID-19 positive patients and prevention of transmission among humans is very important.

Keywords : COVID-19, Clinical Characteristics, Cough, Fever, CT Finding, Ground Glass Opacity

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P303-325: Molecular identification of ultraviolet-resistant bacteria indigenous to desert areas of Iran

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Background and Aim : Hot and drouthy deserts have limitative factors as high temperature, drought, high solar radiation and salinity, but there are various microorganisms which lives in these extreme environments and they are adapted to harmful factors. UVB resistant bacteria can be used in medical and biotechnological industries due to their secondary metabolites which may be used as antioxidants and anticancer, and also, used in skincare products.

Methods : Eight soil samples were collected from desert areas in Qazvin and Qom, cities with high levels of radiation in Iran. Soil samples were cultured on Tryptone Soy Agar and Luria Bertani Agar medium and 112 colonies, with different shape and color, were isolated. Pure colonies were in exposure to UVB lamp (Philips/20w) with wavelength of 312 nm, from 30 centimeters distance for 20 to 90 minutes. Then to avoid photoreactivation they were wrapped in foils and incubated at 30◦ C. Also, photo reactivation was tested by incubating UVB irradiated colonies under photo-active radiation lamps at 30◦ C. All of experiments were repeated three times.

Results : Finally, four bacteria were highly resistant to UVB radiation which include: 1. A coccoid, gram positive, catalase and oxidase positive and nonmotile bacterium with yellow pigmentation 2. A coccoid, gram positive, catalase positive, oxidase negative and nonmotile bacterium with orange pigmentation, 3. A coccoid, gram positive, catalase positive, oxidase negative and nonmotile bacterium with orange pigmentation, that were isolated from Qazvin's soil samples, 4. A rod shaped, gram positive, spore forming, catalase and oxidase positive and nonmotile bacterium which were isolated from Qom's soil samples and they could tolerate 50, 60, 50 and 80 minutes of UVB radiation, respectively.

Conclusion : UVB resistant bacteria were isolated from desert area of Iran. These bacteria may have secondary metabolites that have anticancer and antioxidant properties and can be used as skincare products like sunscreen.

Keywords : ultra violet, antioxidant, UVB, resistant bacteria

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P304-327: Investigation of ultraviolet radiation resistance bacteria indigenous to south of Iran isolated from near-water soils.

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Background and Aim : Areas with high ultraviolet radiation which are known as extreme environments are harmful for living organisms. Although there are variety of microorganisms existing in these environments and they are adapted to chemical and physical stresses such as UVB radiation. UVB resistant microorganisms are great source of beneficial metabolites which may be used to improve skin drugs and skincare products. Also, they can be used as anticancer and antioxidants.

Methods : Eighty-two pure colonies with different shapes and colors were isolated from seven samples of soil which were collected from the Hormoz island, Qeshm island and Bandar Abbas city which are in south of Iran and they have high levels of solar radiations. To study UVB resistant bacteria soil samples were cultured on Luria Bertani Agar and Tryptone Soy Agar medium and colonies were exposure to UVB lamp (Phillips/20w/312nm) in distance of thirty centimeters. After UVB treatment to prevent photoreactivation they wrapped in foils and incubated at 30◦ C. Also, photo reactivation was tested by incubating UVB irradiated colonies under photo-active radiation lamps at 30◦ C.

Results : There were four bacteria that they showed high resistance to UVB radiation which include a rod shaped, gram positive, spore forming, catalase and oxidase positive and nonmotile bacterium with pink pigmentation and a coccoid gram positive, catalase positive, oxidase negative and nonmotile bacterium with pink pigmentation which are isolated from Hormoz island's red soil samples, a coccoid, gram positive, catalase and oxidase positive and motile bacterium with orange pigmentation which was isolated from soil sample of Qeshm island, a coccoid, gram positive, catalase positive, oxidase negative and nonmotile bacterium with pink pigmentation that was isolated from Bandar Abbas's soil sample. They were able to tolerate 80, 60, 50 and 60 minutes of UVB radiation respectively.

Conclusion : UVB resistant bacteria were isolated from the Hormoz island, Qeshm island and Bandar Abbas city which are in south of Iran. These bacteria may have secondary metabolites that have anticancer and antioxidant properties.

Keywords : ultra violet, antioxidant, UVB resistant bacteria

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P305-352: Antimicrobial Effects of Phenoxy Ethanol and Caprolyl Glycol (Verstatil pc) as Preservatives in Cosmetic Products

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Background and Aim : Background: 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 : Materials and Methods In this study, the bacterial and fungal contamination of cosmetic products produced by Pars Azma M e dical 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 : 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 : 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 : Key words: Logarithmic Reduction, Verstatil pc, PTCC, ATCC, Concentration inhibition, Preservatives

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P306-378: Evaluation of phenotypic and molecular analysis of biofilm production in streptococcus mutants producing dental plaque

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Background and Aim : Tooth decay is one of the most important problems facing general health in different societies, the activity of acid-producing bacteria, especially streptococcus mutants, is the main cause of this complication. The creation of the biofilms of the bacterium is subject to the presence of a specific enzyme called glucan sucrase or glucosyltransferase, coded by gtf gene. The aim of this study was to evaluate the genes of GtfB and GtfC of streptococcus mutants in the formation of dental plaque biofilm.

Methods : Blood agar was used to isolate streptococcus mutants.,. In this study, the biofilm was formed on a polystyrene surface using a microtiter plate and stained with a crystal violet through an ELISA reader at a wavelength of 550 nm. for confirm streptococcus mutants colonies, checked biochemical and fermentative tests. the samples were transferred to 1% agarose gel and examined after dye gel staining.

Results : Blood agar was used to isolate streptococcus mutants.,. In this study, the biofilm was formed on a polystyrene surface using a microtiter plate and stained with a crystal violet through an ELISA reader at a wavelength of 550 nm. for confirm streptococcus mutants colonies, checked biochemical and fermentative tests. the samples were transferred to 1% agarose gel and examined after dye gel staining.

Conclusion : Therefore, sucrose sugar, which is commonly found in the diet, causes the growth of streptococcus mutants, which is the main cause of dental caries

Keywords : streptococcus mutants, Biofilm, PCR, Tooth Decay

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P307-384: Analysis of the relative frequency of rotavirus detected in acute diarrhea cases in children under 5 years of age at Imam Sajjad Hospital, Yasuj City

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Background and Aim : Worldwide, rotavirus is one of the most prevalent causes of severe diarrhea among infants and other children under 5 years of age. The diarrhea induced by the virus results in loss of water and electrolytes which in return leads to dehydration and even death. The objective of the present research is to determine the frequency of rotavirus among children under 5 years of age with acute diarrhea at Yasuj City's Imam Sajjad Hospital.

Methods : In the span of one year (2018), stool samples were taken from children under 5 years with acute gastroenteritis who were hospitalized at Imam Sajjad Hospital of Yasuj City. The patients' medical data were registered in the form of a questionnaire. This was a descriptive-analytical study. Chromatographic immunoassay was used to detect any rotavirus group A in the samples. The resultant data were then analyzed using SPSS research software and chi-square test.

Results : Out of a total of 164 samples, 83 samples (relative frequency of 50.6 percent) were positively identified as infected with the rotavirus group A. The highest frequency of 49.5 percent was found in the 7-12 months age group where male infants had the maximum frequency of 61.45 within this group. The peak season of rotavirus incidence among the target population was in winter with a frequency of 41 percent, and the lowest seasonal incidence was in spring with a frequency of 8.4 percent. The frequency of rotavirus among breast feeding infants was significantly lower than infants who were on formula (33.7 percent vs. 55.4 percent); $p<0.05$.

Conclusion : Results we obtained in our research indicates a high incidence rate of acute rotavirus diarrhea among the target population. Thus, it is recommended that similar studies are conducted in various regions of Iran to detect rotavirus and prevent misusing of antibiotics for treating rotavirus diarrhea infections and take preventative measures (the need for incorporating inoculation in the national public vaccination program).

Keywords : acute gastroenteritis, rotavirus, infants, children, frequency

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P308-388: Evaluation of alginate production by native strains of Azotobacter isolated from soil by carbazole reagent by Nutson-Jeans method.

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Background and Aim : production of alginate through microbial biotechnology has become important due to the reduction of production time and costs and also the damage to the marine ecosystem due to the uncontrolled extraction of alginate from marine kelps. Azotobacter are a better choice for producing alginate than pathogenic Pseudomonas. we have tried to evaluate the ability of alginate to produce native isolates of Azotobacter from the soil by the Nutson-Jeans method and finally spectrophotometry.

Methods : Azotobacter strains were monitored and purified through differential cultures. Each strain was inoculated into mannit broth and incubated at 37 ° C for 48 hours. Alginate production was evaluated by carbsol reagent test using Nutson-Jane method at two temperatures of 55 ° C and 100 ° C in borate and non-borate conditions. Finally, by spectrophotometry at 520 nm with two repetitions of positive and negative control of culture tubes were examined.

Results : The culture tubes of the carbazol reagent test stage had a pink to purple color spectrum that indicated the presence of alginate produced by native Azotobacter. Increasing the color spectrum from pink to red and finally purple indicated an increase in alginate production.

Conclusion : This study showed that native Azotobacter isolated from soil have the ability to produce alginate, which carbazol reagent test along with spectrophotometry was able to prove their ability to produce alginate.

Keywords : Azotobacter, Alginate, Carbazole reagent test, Nutson-Jeans method

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P309-390: An outlook on covid-19 detection methods

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Background and Aim : On 30 January 2020, the World Health Organization (WHO) declared a global public health emergency over the outbreak of the new coronavirus, called the 2019 novel Coronavirus (2019-nCoV), which originated in Wuhan City, in the Hubei Province of China. Since then, COVID-19 has continuously spread to more than 200 countries; the number of confirmed infections reached 13,952,406 on 17 July 2020 and the death has risen to 585,727. The manifestation of the COVID-19 infection is highly nonspecific, including respiratory symptoms, fever, cough, dyspnea, and viral pneumonia. Since any treatment or vaccine is not yet discovered for the covid-19 virus, early diagnosis of the disease and rapid quarantine of the carriers of the disease by separating them from healthy people is the most important method recommended by the WHO. Late diagnosis of Coronavirus disease in patients is one of the main obstacles to controlling the disease, which results in serious health, economic and social repercussions. With the aim of improving diagnosis tools, this research was conducted to providing an outlook on available methods for COVID-19 virus detection.

Methods : Research articles published concerning diagnosis of coronavirus disease, were analyzed and discussed to develop new clinical diagnosis tools.

Results : Use of detection methods based on the reproduction of the virus's genomic material and based on identification of the virus-specific antibodies, to identify and diagnose the coronavirus disease in suspicious cases, has been approved by regulatory organizations and by health systems in different countries. The challenges related to the use of any of the confirmed diagnostic methods limit the use of any of the available methods for timely diagnosis of the disease in suspicious cases. Hence, development of new diagnostic methods has become an important goal for reducing the growth rate of the disease and helping to accelerate the process of combating the disease. Accessible, inexpensive and specific diagnostic tests for COVID-19 infection are urgently required to confirm suspected cases, screen patients, and conduct virus surveillance.

Conclusion : There has been a rapid surge in research in response to the outbreak of COVID-19. Although the studies are conducted relevant to control the current public emergency, more high-quality research is needed to provide valid and reliable ways to manage this kind of public health emergency in both the short- and long-term.

Keywords : COVID-19, coronavirus disease detection methods, review

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P310-392: Molecular and clinical characterization of hypervirulent Extended-spectrum beta-lactamases producer Klebsiella pneumoniae among urinary tract infections; the first report from Iran

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Background and Aim : New hypervirulent variants of K. pneumoniae (hvKp) with antimicrobial susceptibility are emerging globally.This study was conducted to identify the hypermucoviscosity, iron acquisition, and capsule serotypes of K. pneumoniae strains isolated from UTI among community patients and assess the frequency of Plasmid-mediated quinolone resistance and Extended-spectrum beta-lactamases genes between classic and hypervirulent strains

Methods : 105 UTI K. pneumoniae were isolated from community patients. Demographic data related to the underlying diseases and clinical manifestations were further collected. Antibiotic resistance pattern and molecular characterization were respectively compared among ESBL-positive, ESBL-negative, hvKp, and Classic isolates.

Results : Among 105 K. pneumoniae from UTI, 11 (10.5%) were considered as hvKp. Diabetes mellitus was the most prevalent underlying disease. Cefotaxime, cefixim, trimethoprim–sulfamethoxazole, and ciprofloxacin were the most inactive antibiotics in hvKp with a resistance rate of 54.5%. Molecular characterization revealed that 7.6% of all isolates carried k1 and 66.6% carried K2 genes. The most common qnr gene was qnrB 61 (84.7%), followed by qnrS 47 (65.2%) and qnrA 16 (22.2%). At least one ESBL genes were detected in all hvKps, and blaSHV was observed in 90.9% of hvKp group and 60.6% of CKp group (P value= .048)

Conclusion : This study showed a high frequency of antimicrobial and multi drug resistant among hvKp isolates. Therefore, hvKp isolates are turning to a growing comprehensive problem in community-UTIs Coexistence of PMQR and ESBL genes in hvkp indicates that urgent need is required to enhance the clinical knowledge and management of hvKp infections.

Keywords : hypervirulent Klebsiella. Pneumoniae, urinary tract infections, capsular group, ESBL, qnr

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P311-394: Evaluation of frequency of Enterococcus faecalis in urinary tract infections in old patients living in nursing homes referred to hospital.

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Background and Aim : Urinary tract infection is one of the most common infections diagnosed in nursing home residents. This infection is an inflammatory response of the urinary tract to the invasion of pathogenic microorganisms that can affect the upper or lower parts of the urinary tract. Enterococcus faecalis is a member of the normal human intestinal flora which can cause urinary infection. The aim of this study is to evaluate of frequency of Enterococcus faecalis in urinary tract infections in old patients living in nursing homes referred to hospital.

Methods : 236 urine samples of patients living in nursing homes referred to the emergency department of Rasoul Akram and Firoozgar hospitals were collected and transferred to the Microbial Resistance Laboratory of the Institute of Immunology and Infectious Diseases. The samples were cultured on enriched media and identified by y microscopic methods and biochemical methods. The collected was analyzed by SPSS24

Results : The frequency of Enterococcus faecalis in urinary tract infections in old patients living in nursing homes referred to hospital was 43 (14.5%).

Conclusion : Urinary tract infections are more common in the old patients and increase with age 65 and older. Early diagnosis and effective treatment are essential for this people. Due to increase the number of old people in our country, identification of bacteria and their frequency in urinary infection are very important and necessary for who live in nursing homes.

Keywords : urinary tract infections, Frequency, Elderly, Enterococcus faecalis

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P312-395: Evaluation of frequency of Staphylococcus aureus in urinary tract infections in patients living in nursing homes referred to hospital.

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2. *2-Emergency Department, Iran University of Medical Sciences*

Background and Aim : Urinary tract infection is one of the most common acquired communities and acquired hospital infections in patients. Diseases of the elderly impose significant costs on the health care system. Patients resident in nursing homes are often extensively colonized with potential pathogens such as Staphylococcus aureus. Nowadays, gram-positive cocci play an important role in human infection with various diseases, and among them, staphylococci are of special importance due to their resistance to antibiotics. The aim of this study is to Evaluation of frequency of Staphylococcus aureus in urinary tract infections in patients living in nursing homes referred to hospital.

Methods : 236 urine samples of patients living in nursing homes referred to the emergency department of Rasoul Akram and Firoozgar hospitals were collected and transferred to the Microbial Resistance Laboratory of the Institute of Immunology and Infectious Diseases. The samples were cultured on enriched media and identified by microscopic methods and biochemical methods. The collected was analyzed by SPSS24

Results : The frequency of Staphylococcus aureus in urinary tract infections in old patients living in nursing homes referred to hospital was 82 (27.6%).

Conclusion : Urinary tract infection is known as the most common infection in nursing homes and hospitals. according to statistics, the number of elderly people is increasing. Therefore, the number of elderly who lives in nursing homes increases. It is very important to study the prevalence and their antibiotic resistance pattern.

Keywords : Urinary tract infections, Frequency, Elderly, Staphylococcus aureus

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P313-404: Optimization of growth conditions of native alginate-producing Azotobacter strains isolated from kerman soil through carbon and nitrogen sources of culture medium

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Background and Aim : Optimization of alginate production during microbial biotechnology process through native productive strains of Azotobacter can have an important impact on microbial production of this important product. In this research, the effect of carbon and nitrogen source parameters of the culture medium on the optimization of alginate production by native Azotobacter isolates from the soil has been investigated.

Methods : Azotobacter isolates were inoculated in mannite broth culture medium without carbon source (without mannitol) and fructose, mannitol, glucose and sucrose carbon sources were added separately in 2% medium and finally incubated. Also for evaluation. Nitrogen source was optimized by 1% separately nitrogen sources including: peptone, yeast extract, malt extract and casein were added to the culture medium and incubated. Finally, the amount of alginate production from each of the optimized culture media was evaluated by testing the carbazol reagent of the Nutson-Jeans method.

Results : The highest alginate production was as follows - In the medium containing carbon source from high to low, respectively: sucrose, glucose, fructose and finally mannitol. - In the medium containing nitrogen source from high to low, respectively: Peptone, malt extract, yeast extract and finally casein.

Conclusion : Under equal growth conditions, carbon glucose source and peptone nitrogen source showed the highest efficiency in optimizing alginate production by native Aztobacter strains.

Keywords : Azotobacter - Optimization of alginate production - Carbazole reagent test- Alginate

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P314-414: Investigating the effects of ethanolic extract of saffron petals (Crocus Satious L) on apoptosis and alteration of BAX and BCL2 gene expression in MCF_7 breast cancer cell line

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Background and Aim : : One of the most common cancers in women is breast cancer, which has been on the rise in recent years. Therefore, in this study, we evaluated the effects of ethanolic extract of saffron petals on apoptosis and altered expression of BAX and BCL2 genes in MCF-7 breast cancer cell line.

Methods : In this laboratory study, the effect of ethanolic extract of saffron petals on survival and expression of BAX and BCL2 genes in MCF-7 breast cancer cells were investigated. For this purpose, MCF-7 breast cancer cells were cultured and treated with 24, 48 and 72 hours by ethanolic extract of saffron plant with different concentrations. The effect of the extract on cell viability was assessed by MTT. RNA extraction was performed and cDNA was performed to measure the expression of BAX and BCL2 genes Real Time PCR.

Results : This study showed that with increasing concentration and time, cell viability decreased significantly and significantly compared to control samples. Also, the results of Real-Time PCR showed that the expression of BAX and BCL2 genes at 48 and 72 hours increased and decreased significantly compared to the control sample.

Conclusion : The results of this study show that ethanolic saffron extract affects the expression of BAX and BCL2 genes in human breast cancer cells, which is associated with inhibiting the growth of cancer cells.

Keywords : saffron petals, Breast Cancer, BAX and BCL2 genes

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P315-416: Evaluation of the effect of ethanolic extract of Reum Lribes on the expression of Caspase3 gene in MCF_7 breast cancer cell line

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Background and Aim : : Problems such as drug resistance, high cost of treatment, and some problems with cancer treatment have led many researchers to turn to medicinal plants in relation to cancer, because medicinal plants have fewer side effects compared to chemical drugs. They are also relatively inexpensive to treat with herbs. Studies have shown that black seed has anti-cancer effects, but the molecular mechanism of its effect on cell death in cancer cells is unclear. Therefore, in the present study, the effect of ethanolic extract of Reum Lribes plant on cell survival rate of MCF7 and expression of Caspase 3 gene was investigated.

Methods : In this laboratory study, the effect of ethanolic extract of Reum Lribes plant on survival and expression of Caspase 3 gene in breast cancer cells MCF_7 was investigated. For this purpose, MFC-7 breast cancer cells were cultured and treated with ethanolic extract of Reum Lribes plant with different concentrations for 24, 48 and 72 hours. The effect of the extract on cell viability was assessed by MTT. RNA extraction was performed and cDNA was performed to measure the expression of Caspase 3 gene Real Time PCR.

Results : This study showed that with increasing concentration and time, cell viability decreased significantly and significantly compared to control samples. Also, the results of Real-Time PCR showed that the expression of Caspase 3 gene at 48 and 72 hours increased significantly compared to the control sample.

Conclusion : It seems that using the medicinal plant Reum Lribes, the expression of Caspase 3 gene is also increased, which causes the death of cancer cells.

Keywords : Breast cancer, Reum Lribes, Caspase3 gene

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P316-419: Quantitative analysis of mRNA expression of protease genes among different Helicobacter pylori strains by Reverse transcriptase-PCR

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Background and Aim : Helicobacter pylori is the main cause of several gastroduodenal diseases in Humans. Among various virulence factors of H. pylori, proteases may also be involved in its pathogenicity. More than 20 putative proteases were described in H. pylori strains. To show any possible role for these proteases, this study aimed to evaluate mRNA expression of seven protease genes, including htrA (hp1019), clpP (hp0794), collagenase (hp0169), pqqE (hp1012), metalloprotease (hp0382), PspA (hp1435), and protease 1350 (hp1350) among different H. pylori strains by reverse transcriptase PCR (RT-PCR).

Methods : This study was conducted on 19 H. pylori strains isolated from patients with gastrointestinal disorders referred to Taleghani hospital in Tehran, Iran. The presence of seven protease genes in all strains was identified using PCR. To determine mRNA gene expression, each strain was inoculated with 2 McFarland concentrations on BHI broth supplemented with horse serum and iron chloride and were incubated at 37 °C for 3 days under microaerophilic atmosphere. Total RNA was extracted using the RNeasy Plus Mini Kit and then was reverse transcribed into DNA using a cDNA synthesis kit. Prepared cDNA was used as a template in PCR using the specific primers of proteases. Finally, to evaluate the quantitative mRNA expression of protease genes, the gel images were analyzed using UVIgeltec software.

Results : While mRNA expression was not observed in 10.52%, 5.26%, and 5.26% of the pqqE, collagenase, and clpP encoding strains, respectively, in the cases of other proteases, including htrA, metalloprotease, pspA and protease 1350, there was a complete link between the expression of protease genes and their positive genotype. Besides, what was seen about the expression of protease genes was their high expression diversity among different strains.

Conclusion : Our results showed a great variety in the mRNA expression of protease genes. Since not all strains encoding protease genes showed the levels of the mRNA expression, the association between positive protease genotypes and their expression was not confirmed.

Keywords : Keywords: Helicobacter pylori, protease, mRNA expression, RT-PCR

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P317-432: Frequency of positive blood cultures, isolated microorganisms and their antimicrobial susceptibility profile by Bact /Alert and Vitec 2 systems in Peyvand clinical and special laboratory, a retrospective study

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Background and Aim : The aim of this study was evaluation the frequency of positive blood cultures, isolated microorganisms and their antimicrobial susceptibility profile in Payvand clinical and special laboratory.

Methods : in this retrospective study, all blood cultures from Apr to Sep 2019 were included in this survey. From each patient, 10 ml of blood sample was collected and inoculated in to blood bottles and incubated in Bact/ Alert system, immediately. All positive cultures were passaged on usual microbiologic cultures for pure colonies. Bacterial identification and antimicrobial susceptibility test (AST) was done based on direct gram stain and automated Vitec 2 system protocol.

Results : of 34 enrolled patients in this study, 32% were blood culture positive. The frequency of isolated bacteriawas: (46%) gram positive cocci, (36%) gram negative bacilli and (18%) candida spp. The most frequent gram negative bacillus was Klebsiella pneumonia and all of gram positive cocci were coagulase negative staphylococcus (CoNS). Two candida isolates were: C. tropicalis and C. parapsillosis. All gram positive cocci were resistant to erythromycin. All of gram negative isolates were resistant(R) to tested antibiotics except 3 isolates which were susceptible(S) to amikacin. Only C. parapsillosis showed intermediate susceptibility to caspofungin and micafungin.

Conclusion : the predominance of gram positive cocci vs. gram negative bacilli in this study was in accordance other studies. The high resistance rate to common tested antibiotics in gram negative isolates is alarming.

Keywords : blood culture, antimicrobial susceptibility test, gram negative, gram positive

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P318-434: Molecular typing for Neisseria meningitidis based on porA typing

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Background and Aim : Neisseria meningitidis as the cause of meningitis have different serogroups. The purpose of this study was to investigate the molecular properties of N. meningitidis strains among Iranian cases. In the present study, 450 samples were collected from children under 5 years of age. Detection of Neisseria genus was done by phenotypic and genotypic methods. Multiplex PCR was used to identify the serogroups of N. meningitides. The sequencing of variable regions of porA gene was performed for detection of the subserogroups.In the present study, 137 (30.44%) of Neisseria was isolated that 4 (0.88%) isolates have belonged to N. meningitidis and 133 (29.55%) to other species. Multiplex PCR results showed that one isolate was belonged to serogroup A and 3 to serogroup B. The analysis of amplified VR1 and VR2 variable regions of porA showed 100% similarity for the serogroup A strain with BZ83N strain and for the serogroup B strains with N. meningitidis strain 528.In accordance with other findings in Asia, serogroups A and B were the most serogroups of N. meningitides. Sequencing of variable regions of porA could identify the subserogroups of isolates.Thus, sequencing of porA could be a valuable method for identification of N. meningitides strains in epidemiological studies.

Keywords : Neisseria meningitides, PorA, Sequencing, PCR, typing