بیست‌وسومین کنگره بین‌المللی میکروب‌شناسی ایران

دارای امتیاز بازآموزی

Tehran University of Medical Sciences

دانشکده پزشکی
دانشگاه علوم پزشکی تهران

۸ تا ۱۰ شهریور

۱۴۰۱

با حضور :


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محور های اصلی

کنترل عفونت های بیمارستانی			فاژتراپی و اهمیت آن در درمان
مقاومت داروئی و روش های جدید تعیین آن	میکروبیوتا	تازه های بروسلوز	کارآفرینی و دستاوردهای تشخیصی
عفونت های ادراری و روش های نوین درمانی	پروبیوتیک و ارتباط آن با بیماری ها	اهمیت باکتری ها در آلودگی مواد غذایی	وضعیت، درمان، واکسیناسیون و کنترل بیماری کووید 19
روش های نوین تشخیصی	بیماری های مشترک انسان و دام	بیماریهای نوپدید و بازپدید	وضعیت بیماری سل در ایران و جهان و اهمیت سل مقاوم به درمان

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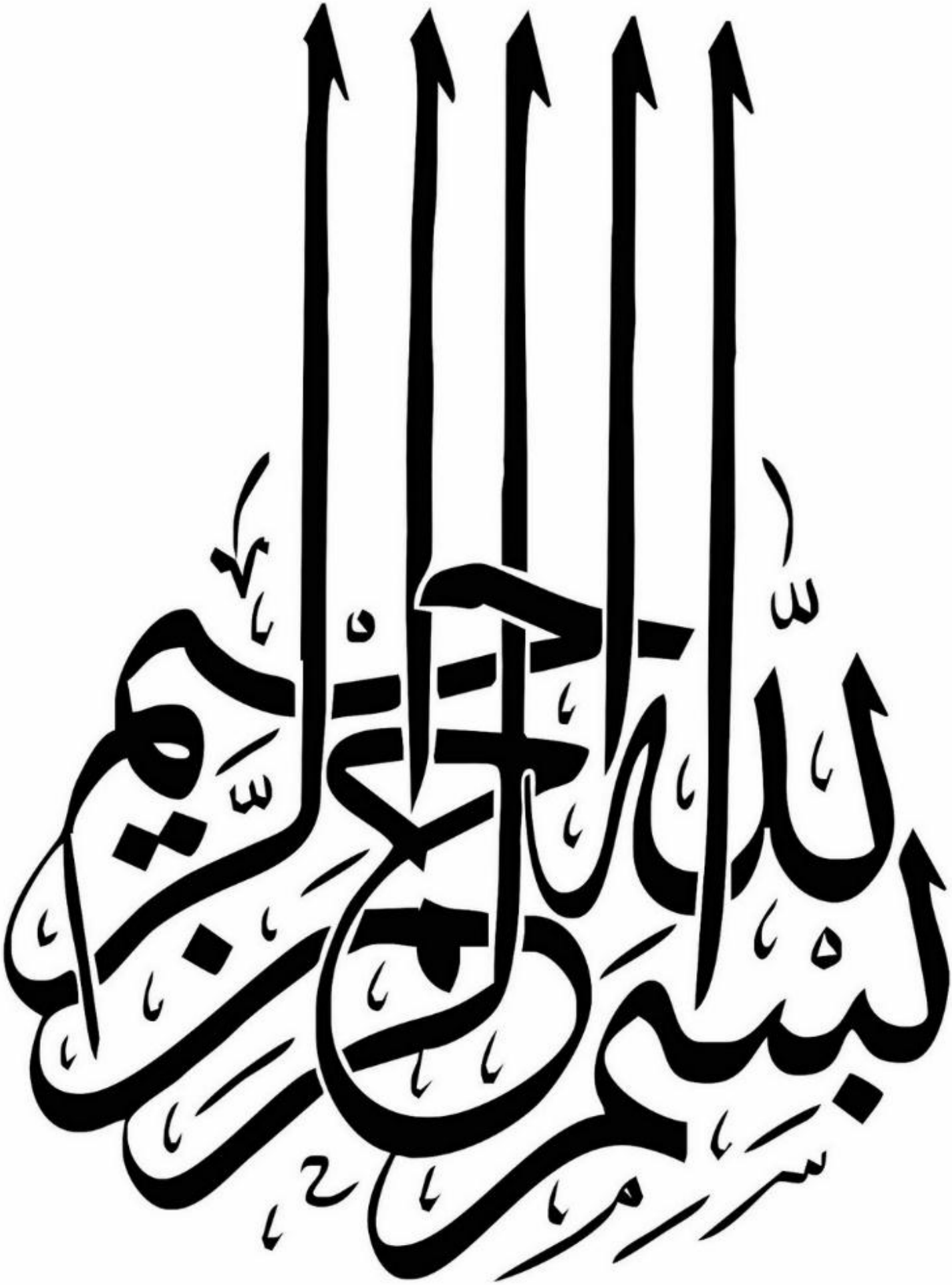
بسم الله الرحمن الرحيم

فهرست مطالب

ارکان کنگره :

دکتر محمدتقی بیگ محمدی

رئیس دانشکده پزشکی و رئیس کنگره

دکتر محمد مهدی فیض آبادی

رئیس انجمن علمی میکروب شناسی ایران

دکتر مژده حاکمی والا

دبیر علمی کنگره

دکتر مریم پورحاجی باقر

دبیر اجرایی کنگره

پیام رئیس کنگره

Message President of Congress

In the name of God, the most merciful, the creator of the sciences

Microorganisms are one of the wonders of creation in their activities and both beneficial and harmful effects can be found. The effects of microorganisms are studied by microbiologist. The field of microbiology extends from medicine to industry, food and pharmaceutical sciences. Indeed, it can be said that life is not possible without microorganisms. Recent occurrence, the COVID-19 pandemic, has shown that universe has an intelligent system that can be used well only with comprehensive dynamic knowledge of microbiology. Therefore, in order to have a world with peace and quiet we need to empower ourselves by sciences, including microbiology more than ever.

Ladies and Gentlemen,
I appreciate your participation in the 23rd International Congress of Microbiology of Iran. I hope you have a good time and enjoy during the congress due to significant and valuable scientific topics.
Wish health and happy days for all.

Professor Mohammad Taghi Beigmohammadi, MD

Dean, Tehran School of Medicine

President of Congress

پیام دبیر علمی کنگره

Message scientific secretary

In the name of God

After leaving behind the events caused by the Corona Pandemic and holding two virtual international congresses by the Iranian Association of Microbiology, we are approaching the 23rd International Congress of Microbiology to be held with the participation of valuable Iranian and foreign scientists.

The corona pandemic has taught us that humans still need to work harder to fight microorganisms and therefore need to continue to improve their knowledge. The 23rd International Congress of Iran, will provide the possibility of exchanging new information.

We hereby invite all of you, esteemed and hard-working professors, colleagues and students, to support us in the best possible performance of this congress by participating and submitting your valuable articles.

Sincerely

Mojdeh Hakemi Vala

Scientific secretory

پیام رئیس انجمن

Message President of Iranian Society of Microbiology

After 3 years combating with COVID-19, the 23rd congress has been organized to gather the colleagues in Tehran. ISM was able to hold two virtual congress in the last two years. However, it was necessary for the colleagues, students to meet face to face and share their knowledge and experiences in our annual meeting. This is part of ISM duty to organize such event and we are happy for doing the task. On behalf of the ISM board I would like to welcome you to our meeting and thank your contribution. We hope you could benefit the most from the scientific program and wish you a pleasant stay in Tehran during the congress.

Professor Mohammad Mehdi Feizabadi

President of Iranian Society of Microbiology

اعضای کمیته علمی

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اعضای کمیته اجرایی

بر اساس ترتیب حروف الفبای فارسی

۱ آزاده احمدی
۲ آرزو اسدی
۳ زهرا اسماعیل پور
۴ کیمیا اسماعیلی
۵ زهرا الهی
۶ سارا باهنر
۷ معصومه بیگ
۸ سمانه تیموری
۹ فاطمه ثامنی
۱۰ زهرا جوانمرد
۱۱ سپیده حق نظری
۱۲ منصور خالدی
۱۳ کیمیا خالق پور
۱۴ نیلوفر خدائی
۱۵ لیلا دادگر
۱۶ عطیه دربندی
۱۷ زهرا رحمانی
۱۸ پریسا رحیمی
۱۹ بهمن رحیمی اسبوئی
۲۰ نیلوفر رضایی
۲۱ فریبا رفیعی دولت آبادی
۲۲ فاطمه روزبهانی
۲۳ مریم زمانی علویچه
۲۴ بیتا زندی
۲۵ سمیرا سبزی
۲۶ پیروز شادباش
۲۷ شهلا شهبازی
۲۸ زهرا شهریاری
۲۹ علی شیوایی
۳۰ حدیث صدری
۳۱ زهرا صمدی
۳۲ مرضیه طاهری
۳۳ پریسا عابدی ایلخچی
۳۴ محمد عبدی
۳۵ امیرحسین فیاضی
۳۶ یاسر فصیحی
۳۷ حسین قهرمان پور
۳۸ نرگس گلاب
۳۹ رضوان گودرزی
۴۰ زینب محسنی پور
۴۱ سمانه محمد جواد
۴۲ مریم مسکینی
۴۳ مریم میرشکار
۴۴ زهرا نجفی اولیا
۴۵ نوشین نظری نژاد
۴۶ مهدیه نقابی حاجی آقا
۴۷ فاطمه نواب مقدم
۴۸ نگار نوروزی مطلق تهرانی
۴۹ فائزه وفائی
۵۰ سعید همتی

حامیان کنگره

۱. دانشگاه علوم پزشکی تهران
۲. وزارت بهداشت، درمان و آموزش پزشکی
۳. موسسه تحقیقات واکسن و سرم سازی رازی
۴. انستیتو پاستور ایران
۵. مرکز تحقیقات قارچ شناسی و باکتری شناسی پزشکی دانشگاه علوم پزشکی کرمان
۶. دانشگاه علوم پزشکی شهید بهشتی
۷. سازمان نظام دامپزشکی جمهوری اسلامی ایران
۸. شرکت صنایع شیر ایران (پگاه)

حامیان مالی کنگره

۱. شرکت پیشتاز طب
۲. شرکت آریوژن
۳. شرکت مصون دارو
۴. شرکت سیناژن
۵. شرکت شتاب دهنده نوآوری تشخیصی سیناپس

شرکت های پشتیبان

۱. انجمن تولیدکنندگان آب های معدنی و آشامیدنی ایران
۲. صنایع لبنیات گلا آمل
۳. صنایع لبنیات میهن
۴. شرکت دومینو
۵. گروه صنایع غذایی درنا
۶. شرکت پگاه تهران
۷. تلاونگ

برنامه روزانه کنگره

23th Iran's International Congress in Microbiology
Main Hall Ibne Sina

Tuesday August 30			
Subject	**Presentor**	**Specialty**	**Time**
Openning ceremony and welcome			**8:00-8:10**
Welcome by Scientific secretary	Dr. Mojdeh Hakemi Vala	Professor in Medical Bacteriology, Shahid Beheshti University of Medical Sciences	**8:10-8:20**
Speach	Dr.Mohammad Taghi Beikmohammadi	Anesthesiologist, Head of school of medicine, Tehran University of Medical Sciences	**8:20-8:35**
Speach	Dr. Mohammad Mehdi Feizabadi	Profesor in Medical Microbiology, Head of Iranian Society of Microbiology	**8:35-8:45**
Speach	Dr. Hossein Ghanaati	Imaging specialist, Head of Tehran University of Medical Sciences	**8:45-9:00**
Appreciation of Eminent Microbiologists			**9:00-10:00**
Break & Visit posters			**10:00-10:30**
Panel of emerging and re-emerging diseases			**10:30-12:15**
Panel President: Prof. Ehsan Mostafavi (PhD in Epidemiology, Director of the research centre for emerging and reemerging infectious diseases of Pasteur Institute of Iran) **Panel Members:** Dr Ali maleki (PhD in Medical Virology, Pasteur Institute of Iran), Prof. Max Maurin (University of Grenoble Alpes, CNRS, Grenoble INP, CHU Grenoble Alpes, Grenoble, France), Dr Saber Esmaili (PhD in Medical bacteriology, Academic staff of the department of epidemiology and biostatistics, national reference laboratory for plague, tularemia and Q fever of Pasteur Institute Iran), Prof. Seyed Mohsen Zahraei (Infectious disease specialist, head of vaccine-preventable diseases department, Iran CDC), Prof. Mohammad Reza Pourmand (PhD in Medical bacteriology, Tehran University of Medical Sciences)			
Monkeypox Outbreak – August 2022		Dr Ali maleki	**10:30-10:45**
Prediction of emerging and re-emerging diseases in the future with the ability to cause a pandemic		Prof. Ehsan Mostafavi	**10:45-11:00**
Francisella tularensis and waterborne infections		Prof. Max Maurin	**11:00-11:15**
An overview of the reservoirs, vectors and human cases of Rickettsia in Iran		Dr Saber Esmaili	**11:15-11:30**
The latest status of measles in Iran		Prof. Seyed Mohsen Zahraei	**11:30-11:45**
An overview of neglected microbial infections: (strategies and tactics)		Prof Mohammad Reza Pourmand	**11:45-12:00**
Disscussion			**12:00-12:15**
Lunch & prayer			**12:15-13:30**

Oral presentation of selected papers **Subject: Microbial Drug resistance**		**13:30-14:00**
Panel of Microbial Drug resistance: prevalence and new detection methods		**14:00-15:45**
Panel president: Dr. Freshteh Shahcheraghi(Professor in Medical bacteriology, Pasteur Institute of Iran) **Panel members:** Dr. Behnam Sobouti(Professor of pediatric Infectious diseases, Iran University of Medical Sciences), Dr. Davood Yadegarniya (Infectious diseases specialist, Shahid Beheshti University of Medical Sciences), Dr. Christian Giske (Professor/Chief consultant physician, Chairman of EUCAST and Karolinska Institutet, Stockholm-Sweden), Dr. Ali Pormohammad(Post-doctoral research fellow,University of Calgary, Alberta, Canada), Dr. Fereshteh Jabal Ameli(Medical Bacteriology, Tehran University of Medical Sciences), Dr. Seyed Sajad Khoramrooz (Medical bacteriologist, Yasuj University of Medical Sciences)		
Antibacterial resistance in pediatric burn patients	Dr. Behnam Sobouti	**14:00-14:15**
Drug resistant among gram negative bacteria during Covid-19	Dr. Davood Yadegarniya	**14:15-14:30**
Novel antimicrobial with activity against MDR gram negative bacteria	Dr. C.Giske	**14:30-14:55**
Discovering novel metal (LOID) based and plant based antibacterial compositions and uses there of against bacterial biofilm	Dr. Ali pormohammad	**14:55-15:10**
Combination therapy against multidrug resistant bacteria and biofilm	Dr. Fereshteh Jabal Ameli	**15:10-15:20**
The current status of antibiotic resistance in *Staphylococcus aureus*	Dr. Seyed Sajad Khoramrooz	**15:20-15:30**
Disscussion		**15:30-15:45**
Break & Visit posters		**15:45-16:15**
Oral presentation of selected papers **Subject: zoonosis**		**16:15-16:45**
Panel of Zoonosis		**17:00-18:30**
Panel Priciple : Dr. Nader mosavari(Head of Tuberculosis and Glanders Department, Razi Vaccine and Serum Research Institute, IRAN) **Panel Members:** Dr. Mehdi Mir Saeedi(Division of pulmonary, critical care and sleep medicine, College of Medicine, University of Florida, Jacksonville, FL, USA), Dr. Harisankar Singha(Senior Scientist), Dr. Behzad Amiri(Head of the Department of Zoonotic disease of center for communicable disease control and prevantion, Ministry of Health, IRAN) , Dr. Mohammad reza Shirzadi(Associate Professor of Infectious Disease National Zoonoses Expert of Center for Communicable Disease Control,IRAN (MOH), Dr. Mohammad Zeinali(Assistant Professor of Medical Parasitology, National zoonoses Expert of Center for Communicable Disease Control,IRAN (MOH), Dr. Darab Abdollahi (Head of Mycobacterial Diseases Control Group Iran Veterinary Organization)		
Mycobacterium-Bronchial Epithelial Cells Cross-Talk Through Type I Interferon Signaling	Dr.Mehdi Mirsaidi	**17:00-17:15**
Zoonotic aspects of *Burkholderia mallei* infection (Glanders)	Dr. Harisankar Singha	**17:15-17:30**
Epidemiology of animal bite and Rabies in Iran	Dr. Behzad Amiri	**17:30-17:40**

Prevention and control of Rabies in Iran	Dr. Mohammad reza Shirzadi	**17:40-17:50**
Epidemiology and surveillance of Brucellosis with One-Health approach in Iran	Dr. Mohammad Zeinali	**17:50-18:00**
Assessing the trend of bovine tuberculosis in Iran, challenges and approaches.	Dr. Darab Abdollahi	**18:00-18:10**
Situation of Glanders and isolation and identification of *Burkhulderia mallei* from suspect horses in Iran in last year	Dr. Nader Mosavari	**18:10-18:20**
Discussion		**18:20-18:30**

Wednesday
31August
Ibne Sina Hall

Subject	Presentor	Specialty	Time
Oral presentation of selected papers **Subject: Microbiota and their relation to diseases**			**8:00-8:30**
Panel of Metagenomics and new advances			**8:30-10:00**
Panel President: Professor.Mohammad Reza Zali (Gasterologist, Head of Research for Gastroenterology and Liver, Shahid Beheshti University of Medical Sciences) **Panel Members:** Dr.Maria Gauzoli(Greece), Dr. André Gessner(Germany), Dr.Azadeh Safarchi(Australia), Dr.Leonardo AntonioSechi (Italy)			
The role of microbiota in liver diseases		Dr. MR Zali	**8:30-8:45**
The paradigm of Inflammatory Bowel Disease		Dr.Maria Gauzoli	**8:45-9:00**
Microbiome Analytics in the 21st century: Perspectives and Caveats		Dr. André Gessner	**9:00-9:15**
Human gut microbiom, opportunities and challenges		Dr.Azadeh Safarchi	**9:15-9:30**
Mycobacterium paratuberculosis, Human Endogenous Retroviruses and Type 1 Diabetes		Dr.Leonardo Antonio Sechi	**9:30-9:45**
Microbial genomics analysis at the Italian Refernce centre		Dr. Nicholas Radomski	**9:45-10:00**
Disscussion			**۱۰:۱۵–۱۰:۰۰**
Break & Visit posters			**10:15-10:45**

Oral presentation of selected papers **Subject: Infectious diseases in cancer and transplanted patients**		**10:45-11:00**
Panel of Infectious diseases in immunocompromised patients		**11:00-12:30**
Panel President: Dr. Sara Abolghasemi (Specialist Infectious diseases, fellowship in infectious diseases in immune compromised patients, Shahid Beheshti University of Medical Sciences) **Panel members:** Dr. Rozita Khodashahi(Specialist Infectious diseases, fellowship in infectious diseases in immune compromised patients, Mashahd University of Medical Sciences),Dr. Zahra Abtahian(Specialist Infectious diseases, fellowship in infectious diseases in immune compromised patients,National Research Institute of Tuberclusis and lung, Shahid Beheshti University of Medical Sciences), Dr. Zahra Ahmadinejhad (Specialist Infectious diseases, Tehran University of Medical Sciences),Dr. Sadegh Khodaveisi(Medical Mycology, Tehran University of Medical Sciences)		
Infectious diseases in SOT Patients: Case Presentation	Dr. Rozita Khodashahi	**11:00-11:15**
Case presentation of infectious and non-infectious problem in a patient with bone marrow transplantation	Dr. Sara Abolghasemi	**11:15-11:30**
Infectious diseases in hematologic and HSCT patients: Case presentation	Dr. Zahra Abtahian	**11:30-11:45**
Presentation of a case with SBP infection before liver transplantation	Dr. Zahra Ahmadinejhad	**11:45-12:00**
New methods in diagnosis of invasive fungal infections in immunocompromised patients	Dr. Sadegh Khodaveisi	**12:00-12:15**
Disscussion		**12:15-12:30**
Lunch & prayer		**12:30-14:00**
Oral presentation of selected papers **Subject: probiotics and microbiota**		**14:00-14:30**
Probiotics, Microbiota and their importance in infectious diseases		**14:30-16:00**
Panel President: Dr. Parvaneh Jafari (PhD in Microbiology, Science Faculty, Arak Branch) **Panel Members:** Dr. Ghamartaj Khanbabaei(Pediatric pulmonarySpecialist, Shahid Beheshti University of Medical Sciences), Dr. Masoud Aleboueh(Medical bacteriology, Research Institute for Children's Health, Shahid Beheshti University of Medical Sciences), Dr. Shahriyar Dabiriyan (PhD in control and food health, Iranian Dairy products Industries Association), Dr. Maryam Hashemi (Professor in food Bioprocess, Agricultural Biotechnology Research Institute Iran)		
The effects of Microbiota in immune system	Dr. Khanbabaei	**14:30-14:45**
How probiotics can help us for treatment of chronic inflammatory	Dr. Aleboueh	**14:45-15:00**
Reviewing the potential role of probiotic yoghurt in weight management and glycemic control in type2 diabetes	Dr. Dabiryan	**15:00-15:15**
Comprehensive approach for assaying the safety of probiotic bacteria	Dr. Hashemi	**15:15-15:30**
New wound dressing products based on probiotic and postbiotic	Dr. Jafari	**15:30-15:45**

Discussion	**15:45-16:00**
Break & Visit posters	**16:00-16:30**

Thursday
September 1
Ibnesina Hall

Oral presentation of selected papers **Subject: COVID-19 and other related viral**		**10:30-11:00**
Panel of recent findings in diagnosis, treatment and vaccination of Covid-19 disease		**11:00-12:30**
Panel president: Dr. Payam Tabarsi (Infectious diseases specialist, Masih Daneshvari hospital, Shahid Beheshti University of Mediccal Sciences) Panel members: Dr. Asghar Abdoli(Medical Virology, Pasteur Institute of Iran), Dr. Salehi Vaziri (Medical Virology, Pasteur Institute of Iran), Dr. MohammadReza Salehi (Infectious diseases Specialist, Tehran University of Medical Sciences), Dr. Masoud Parsania(Medical Virology,Tehran Medical Sciences, Islamic Azad University Tehran)		
Covid-19 vaccine challenges	Dr. Asghar Abdoli	**11:00-11:15**
Covid-19 variants and their impact on vaccination	Dr. Salehi Vaziri	**11:15-11:30**
Antiviral therapy in COVID-19 patients	Dr. MohammadReza Salehi	**11:30-11:45**
Covid-19 inimmunocomprimised patients	Dr. Payam Tabarsi	**11:45-12:00**
Laboratory diagnosis challenges of COVID-19	Dr. Masoud Parsania	**12:00-12:15**
Discussion		**12:15-12:30**
Report of Dr. Maryam PorHaj Bagher (executive secretary) of 23th Iran's congress of Microbiology	**Closing ceremony**	**12:30-13:00**

Class4
Wednesday
31 August

Panel of new methods for detection of microbes		**10:30-12:15**
Panel principal: Dr. Bizhan Nomanpour (Medical Microbiology, Kermanshah University of Medical sciences) **Panel members:** Dr.Medi Razzaghi-Abyaneh(Medical Mycology,Head of department of Mycology, Pasteur Institute of Iran), Dr. Ahmad Nejati (Medical Virology, School of Public Health, Tehran University of Medical Sciences), Dr. Mahdi Rohan i(Medical Microbiology, Head of Department of Microbiology, Pasteur Institute of Iran, Invited speaker from Italy, Dr. Jamil Zaidan		
Subject	**Presenter**	**Time**
Rapid methods for carbapenemases detection at the patient's bedside (POCT) and their comparison with molecular methods and CIM	Dr. Bizhan Nomanpour	**10:30-10:45**
Microbial Whole genome sequencing at the Italian National Refernce Centre	Dr. Cesare Camma	**10:45-11:00**
Recent advances and forthcoming challenges in early diagnosis of invasive fungal infections	Prof. Mehdi Razzaghi-Abyane	**11:00-11:15**
New methods for detecting viruses	Dr. Ahmad Nejati	**11:15-11:30**
Will declare soon	Dr. Jamil Zeidan	**11:30-11:45**
Discussion		**11:45-12:00**

Class4
Thursday
1 September

Subject	**Presenter**	**Time**
Oral presentation of selected papers **Subject: Urinary tract infections**		10:30-11:00
Panel of Epidemiology, virulence, diagnosis, IPC and antimicrobial stewardship in Urinary tract infections		11:00-12:45
Panel Principle: Dr. Amir Hossein Kashi (Deputy of research, Urology and Nephrology Research Center, Labbafinejad hospital, Shahid Beheshti University of Medical Sciences) **Panel Members:** Dr. Kurt Naber (Urologist, Munich technical University, Germany), Dr. Meher Rizvi (Medical Microbiology, Sultan Qaboos University, Oman), Dr. Jyotsna Agarwal (Medical Microbiology, Department of Microbiology, Dr. R M L Institute of Medical Sciences, Lucknow, India), Dr. Sarita Mohapatra (Medical microbiology, Department of Microbiology, New Delhi, India), Dr. Saeid Bouzari (Department of molecular biology, Pasteur Institute of Iran)		
Urinary catheters and UTI	Dr. Amir Hossein Kashi	۱۱:۱۵-۱۱:۰۰
Alternative treatment of uncomplicated urinary tract infection	Dr. Kurt Naber	۱۱:۳۰-۱۱:۱۵
An Overview of Urinary Tract Infection: Different therapeutic strategies	Dr. Saeid Bouzari	۱۱:۴۵-۱۱:۳۰
Antimicrobial prescribing etiquettes in simple and complicated UTI	Dr Meher Rizvi	۱۲:۰۰-۱۱:۴۵
Are recurrent UTI associated with more virulent *E. coli*?	Dr. Jyotsna Agarwal	12:00-12:15
Molecular insights into Uncomplicated UTI from community settings	Dr. Sarita Mohapatra	12:15-12:30
Discussion		۱۲:۳۰-:12:45

Class6
Tuesday
30August

Panel of Prevention and control of nosocomial infections		11:00-12:30
Panel principle: Dr. Arash Seifi (Infectious Diseases Specialist and IPC Fellowship, Head of control of nosocomial infections, Imam Khomaini hospital, Tehran University of Medical Sciences) **Panel members**: Dr. Esmaeil Mohammadnejad (PhD in nursing, Imam Khomaini hospital, Tehran University of Medical Sciences), Dr. Fatemeh Fallah (PhD in Medical Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences), Dr. Marjan Rahnamaye Farzami (Clinical and anatomical Pathologist, Head of reference Lab of Ministry of health and education, Iran)		
Statics of nosocomial infections and microbial drug resistance in Iran	Dr. Esmaeil Mohammadnejad	۱۱:۱۵-۱۱:۰۰
Infection Control of Multi-drug Resistant Gram-negative Bacteria (MDR-GNB)	Dr. Arash Seifi	۱۱:۳۰-۱۱:۱۵
The effect of effective factors in taking samples from infectious samples and creating false positive and negative answers	Prof. Fatemeh Fallah	۱۱:۴۵-۱۱:۳۰
Medical laboratory Roles and Challenges in detection and reporting antimicrobial resistance	Dr. Marjan Rahnamaye Farzami	۱۲:۰۰-۱۱:۴۵
Discussion		۱۲:۳۰-۱۲:۰۰

Class6
Wednesday
31 August

Panel of Technology-based accelerators is held by Pishtaz-Teb Zaman company		10:30-12:00
Panel principal: Dr. Vahid Younes (Ph.D of Immunology) **Panel members:** Dr. Behrooz Tehrani, Post-DBA, Dr. Mehdi Boutorabi (Ph.D of Medical Microbiology, DCLS), Dr. Dorsa Jalaei (Pharm.D/MBA), Dr. Amirhossein Abdi (Pharm.D)		
Future of Diagnostics	Dr. Behrooz Tehrani	۱۱:۰۰-۱۰:۳۰
In Vitro Diagnostics Market, products, technologies	Dr. Vahid Younesi	۱۱:۱۵-۱۱:۰۰
From Idea to Commercialization	Dr. Mehdi Boutorabi	۱۱:۳۰-۱۱:۱۵
Entrepreneurship, soft skills and personal development	Dr. Dorsa Jalaei	۱۱:۴۵-۱۱:۳۰
Synapse accelerator; past, present and future	Dr. Amirhossein Abdi	۱۲:۰۰-۱۱:۴۵
Discussion		۱۲:۳۰-۱۲:۰۰

Class6
Thursday
1September

Panel of phage therapy		10:00-11:30
Panel principal: Dr. Noor Amir Mozaffari (Medical Microbiology, Iran University of Medical Sciences) **Panel members:** Dr.Jean-Paul Pirnay(Belgium), Ruby CY Lin(Australia) ,Dr. Raheleh Majdani (University of Maraghe)		
Clostridium difficile specific bacteriophages and the outlook for phage therapy in intestinal infections	Dr. Noor Amir Mozaffari	10:00-10:20
Phage therapy-The Australian experience	Ruby CY Lin (Australia)	10:20-10:40
Phage therapy in Belgium	Dr. Jean-Paul Pirnay (Belgium)	10:40-11:00
Phage therapy: a new therapeutic solution for infected wounds	Dr. Raheleh Majdani	11:00 – 11:20
Discussion		11:20-11:30

Teb Tajrobi Hall
Tuesday
30 August

Panel of food microbiology		17:00-18:15
Panel president: Dr. Nahid Rahimifard (Rahimifard health consultancies, Dubai, UAE , CEO, Owner and Director of Sarv Saadat laboratory Medical Diagnostic Center, Private, Tehran, IRAN) **Panel members:** Dr. Seyed Reza Mohebbi (Medical Virology, Research Institute for gastroenterology and liver diseases, Shahid Beheshti University of Medical Sciences), Prof. Keith Warriner, (Ph.D., Department of Food Science, University of Guelph, Guelph, Ontario, Canada), Dr. Omid Pajand (Medical Microbiology, Semnan University of Medical Sciences)		
Stability of foodborne viruses and inactivation methods	Dr. Seyed Reza Mohebbi	۱۷:۱۵-۱۷:۰۰
The food safety relevance of dormancy in foodborne pathogens	Prof. Keith Warriner	۱۷:۳۰-۱۷:۱۵
Emergence of methicillin resistance predates the clinical use of antibiotics	Dr. Omid Pajand Semnan University of	۱۷:۴۵-۱۷:۳۰
Most common microbial food borne diseases analysis	Prof. Nahid Rahimifard	۱۸:۰۰-۱۷:۴۵
Discussion		۱۸:۱۵-۱۸:۰۰

Wednesday
31 August
Teb Tajrobi

Panel of Brucellosis		10:00-11:30
Panel President: Dr. Masoud Mardani (Infectious diseases and tropical Medicine, Loghman Hakim Hospital, Shahid Beheshti University of Medical Sciences) **Panel Members:** Dr. Mohammad Yousef Alikhani (Medical Microbiology, Hamedan University of Medical Sciences), Dr. Sirus Jafari(Specialty in Infectious diseases, Tehran University of Medical Sciences), Dr. Fatemeh Torkaman Asadi(Specialty in Infectious diseases, Hamedan University of Medical Sciences), Dr. Maryam Adabi(Medical bacteriology, Hamedan University of Medical Sciences)		
Epidemiology of Brucellosis in Iran and the world	Dr. Masoud Mardani	10:00-10:15
Diversity of clinical symptoms in Brucellosis in Iran	Dr. Sirus Jafari	10:15-10:30
Brucellosis Diagnostic Approaches	Dr. Mohammad Yousef Alikhani	10:30-10:45
Brucellosis treatments	Dr. Fatemeh Torkaman Asadi	10:45-11:00
Brucellosis in livestock: Seroepidemiology, risk factors and preventive strategies to manage the disease in Famenin, Iran	Dr. Maryan Adabi	۱۱:۱۵ -۱۱:۰۰
Discussion		11:15-11:30

فهرست سخنرانی های اعضاء پنل

Row	Title	Submission Author	Session
1	ALTERNATIVE TREATMENT OF UNCOMPLICATED URINARY TRACT INFECTION	Kurt G Naber	- Other related topics
2	Case presentation of infectious and non-infectious problem in a patient with bone marrow transplantation	Sara Abolghasemi	سرطان، پیوند و بیماری های عفونی
3	Presentation of a case with SBP infection before liver transplantation	Zahra Ahmadinejad	سرطان، پیوند و بیماری های عفونی
4	Infection Control of Multi-drug Resistant Gram-negative Bacteria (MDR-GNB)	Arash Seifi	کنترل عفونت های بیمارستانی
5	TRENDS IN THE EPIDEMIOLOGY OF BRUCELLOSIS CASES IN IRAN DURING THE LAST DECADE	Mohammad Zeinali	بیماریهای زئونوز
6	ASSESSING THE TREND OF BOVINE TUBERCULOSIS IN IRAN, CHALLENGES AND APPROACHES	Darab Abdollahi	بیماریهای زئونوز
7	ZOONOTIC ASPECTS OF BURKHOLDERIA MALLEI INFECTION (GLANDERS)	Harisankar Singha	بیماریهای زئونوز
8	SIGNIFICANCE OF BACTERIAL DORMANCY IN FOODBORNE PATHOGENS	Keith Warriner	اهمیت باکتریهای در الودگی مواد غذائی
9	ARE RECURRENT UTI ASSOCIATED WITH MORE VIRULENT E. COLI?	Agarwal Jyotsna	عفونت های ادراری و روش های نوین درمانی
10	Investigation of microbiological characteristics of canned tomato paste product in IRAN	Masomeh Atharinia	اهمیت باکتریهای در الودگی مواد غذائی

11	Neglected Microbial Infections at a Glance: (Strategies and Tactics)	Mohammad Reza Pourmand	بیماریهای نوظهور و نوپدید
12	Most common microbial foodborne diseases analysis	Nahid Rahimi Fard	اهمیت باکتریهای در الودگی مواد غذائی
13	MICROBIOME ANALYTICS IN THE 21ST CENTURY: PERSPECTIVES AND CAVEATS	André Gessner	- Other related topics
14	MICROBIOTA COMPOSITION, HOST GENE-EXPRESSION AND INFLAMMATORY BOWEL DISEASES	MARIA GAZOULI	- Other related topics
15	Laboratory diagnosis challenges of COVID-19	Masoud Parsania	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید -۱۹
16	ANTIBACTERIAL RESISTANCE IN PEDIATRIC BURN PATIENTS	Behnam Sobouti	مقاومت داروئی و روش های جدید تعیین آن
17	Situation of Glanders and isolation and identification of Burkhulderia mallei from suspect horses in Iran in last year	Nader Mosavari	بیماریهای زئونوز
18	Reviewing the potential role of probiotic yoghurt in weight management and glycemic control in type2 diabetes	Shahriar Dabirian	- Other related topics
19	COMBINATORIAL EFFECTS OF ANTIBIOTICS AND ENZYMES AGAINST BACTERIAL BIOFILMS	Fereshteh Jabalemeli	مقاومت داروئی و روش های جدید تعیین آن
20	THE CURRENT STATUS OF ANTIBIOTIC RESISTANCE IN STAPHYLOCOCCUS AUREUS	Seyed Sajjad Khoramrooz	مقاومت داروئی و روش های جدید تعیین آن
21	Urinary Tract Infection: Different Therapeutic Strategies	Saeid Bouzari	عفونت های ادراری و روش های نوین درمانی
22	Advances in diagnosis approaches of invasive fungal infections in haematological malignancy patients	Sadegh Khodavaisy	- Other related topics

23	New methods in the diagnosis of viral infections	Ahmad Nejati	روش های جدید تشخیص میکروبها
24	THE POSSIBLE ROLE OF MAP AND HERVS IN THE TYPE 1 DIABETES ONSET.	Leonardo Sechi	کنترل عفونت های بیمارستانی
25	NOVEL ANTIMICROBIAL WITH ACTIVITY AGAINST MDR GRAM NEGATIVE BACTERIA	Christian G. Giske	مقاومت داروئی و روش های جدید تعیین آن
26	Medical laboratory Roles and Challenges in detection and reporting antimicrobial resistance	Marjan RahnamayeFarzami	کنترل عفونت های بیمارستانی
27	The effects of Microbiota in immune system	Ghamartaj Khanbabaee	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
28	MOLECULAR INSIGHTS INTO UNCOMPLICATED UTI FROM COMMUNITY SETTINGS	Sarita Mahapatra	عفونت های ادراری و روش های نوین درمانی
29	Brucellosis Diagnostic Approaches	Mohammad Yousef Alikhani	تازه های بروسلوز
30	Phage therapy: a new therapeutic solution for infected wounds	Raheleh Majdani	فاژ تراپی
31	UTI AND URINARY CATHETERS	Amir H Kashi	عفونت های ادراری و روش های نوین درمانی
32	ANTIMICROBIAL PRESCRIBING ETIQUETTES IN SIMPLE AND COMPLICATED UTI	Meher Rizvi	عفونت های ادراری و روش های نوین درمانی
33	Brucellosis treatments	Fatemeh Torkaman Asadi	- Other related topics

34	Disseminated invasive aspergillosis after liver transplantation despite good graft function	Rozita Khodashahi	سرطان، پیوند و بیماری های عفونی
35	Prevention and control of human rabies in Iran	Mohammad Reza Shirzadi	بیماریهای زئونوز
36	Brucellosis in livestock: Seroepidemiology, risk factors and preventive strategies to manage the disease in Famenin, Iran	Maryam Adabi	تازه های بروسلوز
37	Clostridioides difficile specific bacteriophages and the outlook for phage therapy in intestinal infections	Nour Amirmozafari	فاژ تراپی
38	Delamanid-containing regimens and multidrug-resistant tuberculosis	MohamamdJavad Nasiri	وضعیت بیماری سل در ایران و جهان واهمیت سل مقاوم به درمان
39	MYCOBACTERIA-BRONCHIAL EPITHELIAL CELLS CROSSTALK THROUGH TYPE I INTERFERON SIGNALING	Darab Abdollahi	وضعیت بیماری سل در ایران و جهان واهمیت سل مقاوم به درمان
40	NOVEL METAL(LOID)-BASED AND PLANT-BASED ANTIBACTERIAL COMPOSITIONS AND USES THEREOF AGAINST BACTERIAL BIOFILMS	Ali Pormohammad	- Other related topics
41	Gut-Liver Axis	Mohammad Reza Zali	- Other related topics

فهرست سخنرانی ها

Row	Absract ID	Title	Submission Author	Session
O 1	137	Emergence of colistin resistant K.pnenomonia isolates in Payvand clinical and specialty laboratory ; a 6 month survey	Sepideh Ghasemshahi	مقاومت داروئی و روش های جدید تعیین آن
O 2	152	Enhanced anti-biofilm activity of the minocycline-and-gallium-nitrate-containing niosomes against Acinetobacter baumannii in the mouse pneumonia model	Farnaz Shamkani	مقاومت داروئی و روش های جدید تعیین آن
O 3	273	Evaluation of the effect of probiotics pichia kudriavzevii on NBT test of IL-17 secretion in mice with Candida systemic infection	Delaram Safaeian	مقاومت داروئی و روش های جدید تعیین آن
O 4	319	First report of poxtA, cfr, and optrA genes related to linezolid resistance from human clinical Enterococcus spp. isolates in Iran	Farkhondeh Poursina	مقاومت داروئی و روش های جدید تعیین آن
O 5	323	The synergic effect of Levilactobacillus brevis IBRC-M10790 and vitamin D on Helicobacter pylori-induced inflammation	Ali Nabavi-Rad	مقاومت داروئی و روش های جدید تعیین آن
O 6	374	Phenotypic and genotypic characterization of carbapenem-resistant Pseudomonas aeruginosa isolates from Hamadan, Iran	Masoumeh Beig	مقاومت داروئی و روش های جدید تعیین آن
O 7	564	The effect of ampicillin/sulbactam-colistin-eluting noisome nanoparticles against the expression of biofilm-associated genes (pgaA, pglL) of Acinetobacter baumannii isolates	Fatemeh Amohammadshirazi	مقاومت داروئی و روش های جدید تعیین آن
O 8	632	Fabrication and optimization of amoxicillin-loaded niosomes: An appropriate strategy to increase antimicrobial and anti-biofilm effects against multidrug-resistant strains of Staphylococcus aureus	Pardis Shadvar	مقاومت داروئی و روش های جدید تعیین آن
O 9	737	Molecular characterization of virulence and antibiotic drug resistance pattern of Acinetobacter baumannii and distribution of intrasplasmid replicase genes and sequence types	Alka Hasani	مقاومت داروئی و روش های جدید تعیین آن
O 10	738	Genetic characterization of Klebsiella pneumoniae: Five year experience in ICU admitted patients	Alka Hasani	مقاومت داروئی و روش های جدید تعیین آن
O 11	90	Detection Of virulence factor genes in isolated Legionella pneumophila isolates from hospital water sources	Shiva Mirkalantari	کنترل عفونت های بیمارستانی
O 12	142	Bdellovibrio bacteriovorus as living antibiotic against some Enterobacteriaceae members and extensively drug-resistant (XDR) clinical pathogens	Salman Odooli	کنترل عفونت های بیمارستانی

O 13	209	Promising antibacterial effect of impregnated nanofiber mats with a green nanogel against clinical and standard strains of Pseudomonas aeruginosa and Staphylococcus aureus	Hajar Qasemi shiri	کنترل عفونت های بیمارستانی
O 14	327	New endolysin against Acinetobacter baumannii: antibacterial effect	Homa Noura	کنترل عفونت های بیمارستانی
O 15	349	FliC Protein from Enterobacteriaceae Family revealed a Promising Epitope-Delivery Platform	Amin Sepehr	کنترل عفونت های بیمارستانی
O 16	478	Mycoplasma pneumonia and Chlamydia pneumonia infection in patients admitted to Beheshti hospital in Kashan with community-acquired pneumonia	Hadis Fathizadeh	کنترل عفونت های بیمارستانی
O 17	502	A survey on ESBL, MBL Enzymes, and AcrAB-TolC Efflux Pump Frequency Correlation with MDR in Clinical Enterobacter spp.	Mohammad Taheri	کنترل عفونت های بیمارستانی
O 18	508	New treatment of bacterial infections caused by Escherichia coli based on exosomes secreted from stem cells	Bita Zandi	کنترل عفونت های بیمارستانی
O 19	661	Investigation of the relationship between the presence of genes involved in type II toxin-antitoxin systems in Acinetobacter baumannii and resistance to specific antibiotics	Shahla Shahbazi	کنترل عفونت های بیمارستانی
O 20	114	Comparison of reduced graphene oxide and Multi-Walled Carbon Nanotubes modifications on glassy carbon electrode for Escherichia coli detection	Fatemeh Behoftadeh	روش های جدید تشخیص میکروبها
O 21	111	Urinary tract infection in diabetes: Uropathogens, related factors, and antimicrobial sensitivity at Sari, Iran	Mohammad Ahanjan	عفونت های ادراری و روش های نوین درمانی
O 22	526	Evaluation of immunogenic efficacy of Hma.FdeC.UpaB.CTB recombinant protein in associated with chitosan against Uropathogenic Escherichia coli	Maryam Rezaei	عفونت های ادراری و روش های نوین درمانی
O 23	393	Prevalence , Molecular identification and Antifungal susceptibility pattern of Candida species from the Oral cavity of hospitalized patients with kidney transplantation in Iran	Maryam Roudbary	سرطان، پیوند و بیماری های عفونی
O 24	304	DNA-aptamer-nanographene oxide as a targeted bio-theragnostic system in antimicrobial photodynamic therapy against *Porphyromonas gingivalis*	Maryam Pourhajibagher	باکتریهای سخت رشد وبیهوازی ها
O 25	55	Diversity of the gastric microbiota in the Helicobacter pylori infected and non-infected patients and its link to transcriptional changes of gene mediators in the NF-κB inflammatory pathway among patients with chronic gastritis	SeyedehZohre Mirbagheri	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
O 26	695	Changes in the microbial genomic pattern of the blood of patients with Crohn's disease in	Fatemeh Ghasemi	میکروبیوتا و اهمیت آن در

		the flare and remission phases		بیماریها ی عفونی
O 27	117	Isolation and Molecular Identification of Mycobacterium from Milk Samples of Tehran Province's dairy Farms	Tayebeh Hassansoltansolghani	بیماریهای زئونوز
O 28	639	Evaluation of transgenic Leishmania major expressing mLLO-BAX- EndoG -SMAC in the apoptosis of itself parasite and the infected macrophages in vitro and in vivo.	Maryam Aghaei	بیماریهای زئونوز
O 29	97	Safety and immunogenicity of live attenuated IRIBA vaccine in a mouse model	Saeed Alamian	تازه های بروسلوز
O 30	187	Effect of eliminating hdcA gene of Staphylococcus epidermidis TYH1 on Histamine production	Majid Majlesi	اهمیت باکتریهای در الودگی مواد غذائی
O 31	558	Applications of Cold Plasma and UV Radiation Technologies in Disinfection and Increasing the Shelf-Life of Food and Agricultural Products	Alireza Ganjovi	اهمیت باکتریهای در الودگی مواد غذائی
O 32	681	Are molecular methods a suitable alternative to gold standard methods in Salmonella detection?	Maryam Meskini	اهمیت باکتریهای در الودگی مواد غذائی
O 33	439	Isolation of lytic bacteriophage ECP-ST against Antibiotic Resistant Escherichia coli strains isolated from urinary tract infection	Sadrodin Tahani	فاژ تراپی
O 34	521	Phage cocktail as wonderful bio-nanoparticles for the prophylaxis and treatment of burn wound infection caused by multidrug-resistant bacteria in a mouse model.	Masoume Hallajzadeh	فاژ تراپی
O 35	668	Use of specific Lytic nano-phage (combination of bacteriophage and nanotechnology) in the treatment of drug-resistant tuberculosis in vitro	Mohammadreza EsmaeilZadeh	فاژ تراپی
O 36	140	The assessment of antibiotic resistance changes in the Covid-19 pandemic during 2020-2022: An epidemiological study	MAHDIS GHAVIDEL	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
O 37	285	CORROBORATE A NEW SURROGATE VIRUS NEUTRALIZATION TEST FOR THE DIAGNOSTIC PURPOSES OF HUMORAL IMMUNITY AGAINST SARS-COV-2	Mehdi Razazian	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
O 38	330	Evaluation of lncRNA EGOT and ISG15 expression in SARS-CoV-2 infection	Zahra Sefatjoo	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
O 39	504	The autophagy-related Beclin-1 expression as a potential diagnostic biomarker for COVID-19.	Shahrzad Shoraka	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
O 40	153	Targeted Gene inactivation in Salmonella typhi by CRISPR/Cas9	Yosof Tarverdizadeh	-Other related topics

O 41	205	Screening of antioxidant activity of cyanobacteria species isolated from Khoor-e-Khooran mangrove forest, Persian Gulf, Iran	Ahmad Zaheri	-Other related topics
O 42	248	Effects of dietary Enterococcus faecium supplement on the gut microbiota and growth performance in Sander lucioperca	Monireh Faeed	-Other related topics
O 43	425	Antibacterial Effects of Bacteriocin secreted by Lactobacillus reuteri against pathogenic Helicobacter pylori	Fatemeh Bakhshi	-Other related topics
O 44	433	Molecular epidemiology and genetic background of PVL-positive S. aureus clinical strains isolated from Iranian patients using a combination of multilocus sequence typing (MLST) analysis	Zahra Najafiolya	-Other related topics
O 45	663	Detection of Panton-valentine Leukocidin (PVL) Gene Isoforms of Staphylococcus aureus Isolates from different hospitals in Tehran, Iran	Zahra Najafiolya	-Other related topics
O 46	667	Fabrication of a label-free electrochemical biosensor based on reduced graphene oxide-sodium diethyldithiocarbamate-polypyrrole nanocomposite for herpes simplex type 1 detection	Arastoo Vojdani	-Other related topics
O 47	688	Mathematical Modeling of Prediction of Antibacterial Properties of the Combination Honey with Alcoholic Extracts of Black Cardamom, and Zataria multiflora	Sajjad Jafari	-Other related topics
O 48	746	Recombinant CD137-Fc, applications for modulation inflammation induced by some bacteria and viruses, such as novel coronavirus.	Maryam Ajami	-Other related topics

فهرست مقالات پوستر

Row	Absract ID	Title	Submission Author	Session
P1	23	Antibacterial effect of Zingiber officcinalis extract on salmonella isolated from patients referred to health centers in East Azerbaijan province in 1400	Amir Rafiniya	مقاومت داروئی و روش های جدید تعیین آن
P2	32	The prevalence of flouroqinolon resistance and presence of qnrA and qnrS gens in Escherichia coli isolated from Tabriz, Sina and Alzahra hospitals»	Haleh Babaeipour	مقاومت داروئی و روش های جدید تعیین آن
P3	35	Molecular evaluation of vancomycin-resistant genes in Enterococcus faecalis isolated from clinical specimens	Mahshad Khalilian	مقاومت داروئی و روش های جدید تعیین آن
P4	40	In vitro activities of cellulase and ceftazidime, alone and in combination against Pseudomonas aeruginosa biofilms	Ahdieh Izanloo	مقاومت داروئی و روش های جدید تعیین آن
P5	41	Prevalence of Staphylococcus aureus nasal carriage and methicillin- resistant S. aureus among medical students of Shahid Sadoughi University of Medical Sciences in Yazd, Iran (2020-2021)	Maryam Sadeh	مقاومت داروئی و روش های جدید تعیین آن
P6	50	Chemical and Judgmental Examination of Niosomes or Vesicles of Non-Ionic Surfactants	MORAD SOURILAKI	مقاومت داروئی و روش های جدید تعیین آن
P7	51	Co-delivery of doxycycline and hydroxychloroquine to treat brucellosis: an animal study	Seyedmostafa Hosseini	مقاومت داروئی و روش های جدید تعیین آن
P8	54	The effect of vancomycin-loaded niosomes on MRSA strains of Staphylococcus aureus and expression of mecA, hla, and hlb genes	MORAD SOURILAKI	مقاومت داروئی و روش های جدید تعیین آن
P9	57	Multidrug-resistant Pseudomonas aeruginosa from sputum of patients	Zakieh Rostamzadeh	مقاومت داروئی و روش های جدید تعیین آن
P10	68	Screening and Assessment of Two Potential Bacterial Samples for Antimicrobial Activity	Bita Rahmani	مقاومت داروئی و روش های جدید تعیین آن
P11	70	Stevia rebaudiana leaf extract mediated green synthesis of cerium oxide nanoparticles for antibacterial activity and photocatalytic degradation of Tetracycline	Nastaran Asadzadeh	مقاومت داروئی و روش های جدید تعیین آن
P12	76	Evaluation of Biofilm Formation in Methicillin Resistant Staphylococcus aureus isolated from human	Zahra Hosseinzadeh	مقاومت داروئی و روش های جدید تعیین آن
P13	110	Genetic diversity, Distribution of Carbapenem Resistance Genes and Evaluation of the biofilm production in Uropathogenic Escherichia coli isolates from patients with urinary catheter in North of Iran	Sina Nasrollahian	مقاومت داروئی و روش های جدید تعیین آن

P14	118	Antibiotic Resistance of Staphylococcus aureus Isolated from Nasal Cavity of Patients Hospitalized in IMAM HOSSEIN Hospital, Hashtrud	Lida Eftekharivash	مقاومت دارویی و روش های جدید تعیین آن
P15	119	Knowledge and attitudes towards antibiotic usage: a cross-sectional survey of Zabol population in 2017	Hosniye Heydari	مقاومت دارویی و روش های جدید تعیین آن
P16	129	The prevalence of plasmid-mediated quinolone resistance genes among Escherichia coli strains isolated from urinary tract infections in southwest Iran	Nabi Jomezadeh	مقاومت دارویی و روش های جدید تعیین آن
P17	131	RAPD-genotyping of carbapenem-resistant Acinetobacter baumannii isolated from burn wound infections	Farzaneh Firoozeh	مقاومت دارویی و روش های جدید تعیین آن
P18	132	Antimicrobial Resistance Frequency in Carbapenemase Producing and Biofilm Forming Clinical Klebsiella pneumoniae Isolates in Northwest of Iran	Shima Keshavarzi	مقاومت دارویی و روش های جدید تعیین آن
P19	133	ANTIMICROBIAL RESISTANCE DURING COVID -19 PANDEMIC	Aysar AlJebur	مقاومت دارویی و روش های جدید تعیین آن
P20	143	Investigating in-vitro antimicrobial activity, biosynthesis, and characterization of silver nanoparticles, zinc oxide nanoparticles, and silver-zinc oxide nanocomposites using Pistacia Atlantica Resin	Nabi Jomezadeh	مقاومت دارویی و روش های جدید تعیین آن
P21	145	Inhibitory effect of clove plant extract on Staphylococcus aureus bacteria in vitro and its comparison with selected antibiotics	Asra Fadaeipour	مقاومت دارویی و روش های جدید تعیین آن
P22	156	Evaluation of antifungal effects of Zinc oxide nanoparticles (ZnO-NPs) and Amphotericin B (AMB) on different Candida spp in vitro condition	Sanaz Hadizadeh	مقاومت دارویی و روش های جدید تعیین آن
P23	157	Evaluation of Apoptosis effect of Amphotericin B (AmB) on different Candida spp.	Sanaz Hadizadeh	مقاومت دارویی و روش های جدید تعیین آن
P24	160	Evaloation of antimicrobial resistance of bacteria isolated from cutaneous, soft tissue and visceral abscesses	Shahram AbdoliOskouie	مقاومت دارویی و روش های جدید تعیین آن
P25	182	Phenotypic Identifcation and Genotypic Characterization of Plasmid-Mediated AmpC β-Lactamase-Producing Escherichia coli and Klebsiella pneumoniae Isolates in Iran	Saeedeh Robatjazi	مقاومت دارویی و روش های جدید تعیین آن
P26	191	Evaluation of the role of efflux pumps in multidrug-resistant Escherichia coli ST131 isolated from blood samples in hospitalized patients in Tehran, Iran	Mohsen Nazari	مقاومت دارویی و روش های جدید تعیین آن
P27	197	Evaluation of the emergence of Acinetobacter baumannii isolates containing VIM and SIM and drug resistant MDR genes isolated from	MOJTABA SADEH	مقاومت دارویی و روش های جدید تعیین آن

		surfaces and equipment of Tehran medical centers by PCR		
P28	201	Antibacterial activity of propolis nanoparticles against Enterococcus faecalis biofilm	Fariba Asgharpour	مقاومت داروئی و روش های جدید تعیین آن
P29	208	Determination of the efflux pump-mediated resistance prevalence in Pseudomonas aeruginosa strains isolated from clinical samples in shiraz	Mehdi RahimiHezarvand	مقاومت داروئی و روش های جدید تعیین آن
P30	210	Investigation of Antifungal susceptibility test against Aspergillus flavus species isolated from patients with pulmonary aspergillosis	Zahra Salehi	مقاومت داروئی و روش های جدید تعیین آن
P31	224	In Vitro evaluation of susceptibility of Trichomonas vaginalis isolates to MetronidazoleI in Alborz province	Zohreh Momeni	مقاومت داروئی و روش های جدید تعیین آن
P32	230	Evaluation of the simultaneous exposure to diclofenac and gentamicin on some virulence factors of Pseudomonas aeruginosa	Fatemeh Dadkhah	مقاومت داروئی و روش های جدید تعیین آن
P33	231	Antiparasitic activity of pyocyanin pigment produced by Pseudomonas aeroginosa against Trichomonas vaginalis	Sara Abdizadehjavazm	مقاومت داروئی و روش های جدید تعیین آن
P34	243	Susceptibility of clinically isolated strains of methicillin resistant Staphylococcus aureus to vancomycin in Tehran	Maedeh Dadzadi	مقاومت داروئی و روش های جدید تعیین آن
P35	246	Inhibitory effect of prodigiosin pigment produced by Serratia marsecsenes on Trichomonas vaginalis	Elahe Mohammadi	مقاومت داروئی و روش های جدید تعیین آن
P36	260	Prevalence of Streptococcus anginosus group in outpatients population	Zahra Mottaghiyan	مقاومت داروئی و روش های جدید تعیین آن
P37	268	Diclofenac increases the susceptibility of Pseudomonas aeruginosa to gentamicin through the inhibition of bacterial efflux pumps	Fatemeh Moniri	مقاومت داروئی و روش های جدید تعیین آن
P38	272	Evaluating the Frequency of blaIMI Gene in of Klebsiella pneumoniae Isolated from Patients in Isfahan Hospitals and Determining their Antibiotic Resistance Pattern	Maryam MohammadyariBalaki	مقاومت داروئی و روش های جدید تعیین آن
P39	274	Evaluation and Identification of Carbapenem Resistant Genes in Klebsiella pneumonia Isolated from Hospitalized Patients in Ilam City	Maryam MohammadyariBalaki	مقاومت داروئی و روش های جدید تعیین آن
P40	278	Drug Susceptibility Profiling and Genetic Determinants of Drug Resistance in Mycobacterium simiae isolates obtained from Regional Tuberculosis Reference Laboratories of Iran	Sara Daneshfar	مقاومت داروئی و روش های جدید تعیین آن
P41	290	Antimicrobial activity of Cichorium intybus L. on the pathogenic genes expression of Pseudomonas aeruginosa	Atefeh Zolfaghari	مقاومت داروئی و روش های جدید تعیین آن

P42	311	Molecular study of csu C,D,E operon responsible for the biofilm formation in Acinetobacter baumannii isolates in Qom	Raziye MohamadZade	مقاومت داروئی و روش های جدید تعیین آن
P43	313	Prevalence of Methicillin-resistant Staphylococcus aureus (MRSA) and determination of antibiotic resistance-encoding genes amongst the human clinical infections collected from Isfahan, Iran	Atiyeh Ziyaechamgordani	مقاومت داروئی و روش های جدید تعیین آن
P44	317	Whether Insertion Sequence (IS) elements are involved in the emergence of carbapenems-resistant Pseudomonas aeruginosa clinical strains in Ardabil	Maryam Nazari	مقاومت داروئی و روش های جدید تعیین آن
P45	321	Evaluation of the frequency and quinolone resistance of Campylobacter spp. in raw milk samples in Alborz province by MAMA PCR method.	Mohamad Hadadi	مقاومت داروئی و روش های جدید تعیین آن
P46	326	Molecular identification of amino acid alterations in the OprD porin in clinical isolates of carbapenem-resistant Pseudomonas aeruginosa	Farzad Khademi	مقاومت داروئی و روش های جدید تعیین آن
P47	333	High-level aminoglycoside resistance and distribution of genes encoding aminoglycoside-modifying enzymes in methicillin-resistant Staphylococcus aureus (MRSA) isolated from northeastern Iran	Sajjad Yazdansetad	مقاومت داروئی و روش های جدید تعیین آن
P48	352	Antibiotic Resistance of Probiotic Strains of Lactic Acid Bacteria Isolated from Traditional Cheeses in Iran	Somaye Makzum	مقاومت داروئی و روش های جدید تعیین آن
P49	358	Investigating of resistance to aminoglycosides among Escherichia coli strains Isolated with class I integrons from surface drinking water supply sources of Ardabil province, Iran	Ali Panjalizadeh	مقاومت داروئی و روش های جدید تعیین آن
P50	362	Prescription pattern of broad-spectrum antibiotics in Ganjavian Hospital, Dezful, Southwest of Iran	Fatemeh RiyahiZaniani	مقاومت داروئی و روش های جدید تعیین آن
P51	369	Genotyping and drug susceptibility testing of Mycobacterium tuberculosis in Iran: a multi-centre study	SeyyedMohammadJavad Mousavi	مقاومت داروئی و روش های جدید تعیین آن
P52	372	Identification of oxacillinase and metallobetalactamase genes in Acinetobacter baumannii strains isolated from several hospitals in Isfahan	Kowsar Salmaninasrabadi	مقاومت داروئی و روش های جدید تعیین آن
P53	373	Identification of yeasts causing urogenital and bloodstream infections and determination of their drug susceptibility	Melika Talaeipour	مقاومت داروئی و روش های جدید تعیین آن
P54	375	Evaluation of carbapenem inactivation method for accurate detection of pseudomonas aeroginosa isolates producing carbapenemase enzymes	Masoumeh Beig	مقاومت داروئی و روش های جدید تعیین آن
P55	377	Global prevalence and distribution of	Nooshin Nazarinejad	مقاومت داروئی و روش های

		antibiotic resistance of Stenotrophomonas maltophilia clinical isolates: a systematic review and meta-analysis		جدید تعیین آن
P56	382	Molecular characteristics of antibiotic-resistant Escherichia coli and Klebsiella pneumoniae strains isolated from hospitalized patients in Tehran, Iran	Javad Sharahi	مقاومت داروئی و روش های جدید تعیین آن
P57	388	Prevalence of fluoroquinolones Resistance and OqxAB efflux pump genes in clinical isolates of Klebsiella pneumoniae	Leili Shokoohizadeh	مقاومت داروئی و روش های جدید تعیین آن
P58	392	Global prevalence and molecular epidemiology of mcr-mediated colistin resistance in Escherichia coli clinical isolates: a systematic review	Masoud Dadashi	مقاومت داروئی و روش های جدید تعیین آن
P59	406	Prevalence and pattern of antibiotic resistance of bacterial agents isolated from culture in patients with urinary tract infections referred to Khorramabad teaching hospitals in 2021	Faranak Rezaei	مقاومت داروئی و روش های جدید تعیین آن
P60	411	Inhibitory effect of Key Lime (Citrus Aurantiifolia) and Salvia (Salvia Officinalis) essential oils on Escherichia coli	Mobina Mahavar	مقاومت داروئی و روش های جدید تعیین آن
P61	414	Molecular characterization of Panton-valentine Leukocidin (PVL)-positive Staphylococcus aureus in Tehran, Iran	Zahra Najafiolya	مقاومت داروئی و روش های جدید تعیین آن
P62	419	Evaluation of antibiotic resistance pattern of Klebsiella pneumoniae isolates, collected from Miandoab hospitals	Nader Moghadam	مقاومت داروئی و روش های جدید تعیین آن
P63	422	Investigation of the frequency of resistance to Fluoroquinolones and the presence of qnrb gene in Klebsiella pneumoniae isolated from urinary tract infections in Tabriz.	Rahim Peyghami	مقاومت داروئی و روش های جدید تعیین آن
P64	428	Biofilm forming ability and agr- specific group of methicillin-resistant Staphylococcus aureus in Northern Iran	Mahsa Aghaei	مقاومت داروئی و روش های جدید تعیین آن
P65	431	Prevalence and resistance of Streptococcus pneumoniae, Staphylococcus hominis, Staphylococcus saprophyticus bacteria from acute dacryocystitis in children in Isfahan, Iran 2022	Helma Ebneali	مقاومت داروئی و روش های جدید تعیین آن
P66	435	Antifungal susceptibility and evaluation of CDR1 gene expression in fluconazole-resistant Candida albicans isolated from vulvovaginitis	Aida Esfahani	مقاومت داروئی و روش های جدید تعیین آن
P67	443	Molecular mechanism analysis of multidrug resistance (MDR) in Escherichia coli isolates	Mahsa Menshari	مقاومت داروئی و روش های جدید تعیین آن
P68	447	Determination of Colistin-Resistance Pseudomonas aeruginosa Isolates from Bovine Mastitis in Mashhad, Iran	Fatemeh Aflakian	مقاومت داروئی و روش های جدید تعیین آن
P69	448	Genotypic and Phenotypic Characterization of	Sana Falahi	مقاومت داروئی و روش های

		Antibiotic Resistance in Methicillin-Resistant Staphylococcus Aureus Isolated from Tabriz Hospitals in 2021		جدید تعیین آن
P70	449	The High Prevalence of Stx1 Gene Among Escherichia Coli Isolates from Bovine Mastitis in Mashhad, Iran	Fatemeh Aflakian	مقاومت داروئی و روش های جدید تعیین آن
P71	456	Investigating the antibiotic resistance pattern of Escherichia coli isolates from patients with urinary tract infection referred to Imam Khomeini Hospital in Shirvan city in 2021	Moein Hamidihesari	مقاومت داروئی و روش های جدید تعیین آن
P72	457	Determination of resistance to antibiotics in Corynebacterium minotissimum isolates from Tabriz, Iran	Seyedeh zahra Salemi	مقاومت داروئی و روش های جدید تعیین آن
P73	468	CRISPR-Like sequences among Helicobacter pylori isolates and their association with antibiotic resistance	Leila Yousefi	مقاومت داروئی و روش های جدید تعیین آن
P74	469	Bacterial superinfection in cutaneous Leishmaniasis	Behnaz Deihim	مقاومت داروئی و روش های جدید تعیین آن
P75	471	Panton- Valentin Leukocidin, in Methicillin-Resistant Staphylococcus aureus (MRSA) Isolates from hospitalized Patients in Rasht, Iran	Houra Pourghafar	مقاومت داروئی و روش های جدید تعیین آن
P76	482	Detection of NDM-1 producing Klebsiella pneumoniae ST15 and ST147 in Iran during 2019-2020	Zohreh RiahiRad	مقاومت داروئی و روش های جدید تعیین آن
P77	483	The prevalence of vanA gene in Methicillin-resistant Staphylococcus Aureus (MRSA) isolated from patients with bedsores	Zeinab Rezaei	مقاومت داروئی و روش های جدید تعیین آن
P78	484	Detection of New Delhi Metallo-β-lactamase-1 among Pseudomonas aeruginosa isolated from adult and Pediatric patients in Iranian hospitals	Zahra RiahiRad	مقاومت داروئی و روش های جدید تعیین آن
P79	488	Antifungal activity of green synthesized curcumin-coated silver nanoparticles alone and in combination with antifungal drugs	Shahram Mahmoudi	مقاومت داروئی و روش های جدید تعیین آن
P80	491	Comparison of the expression of Enterococcus faecium antibiotic resistance-related genes in biofilm and planktonic conditions	Mansour Goudarzi	مقاومت داروئی و روش های جدید تعیین آن
P81	492	Prevalence of carbapenemase and blaKPC gene in Klebsiella pnumoniae strains isolated from Tabriz hospitals in Iran.	Sepideh Asadi	مقاومت داروئی و روش های جدید تعیین آن
P82	499	Putative novel B-cell vaccine candidates identified by reverse vaccinology and genomics approaches to control Acinetobacter baumannii serotypes	Sheida Beiranvand	مقاومت داروئی و روش های جدید تعیین آن
P83	514	Prevalence of Methicillin Resistance Staphylococcus aureus (MRSA) isolated from Imam khomeini hospital, Tehran	Ahmad Nasser	مقاومت داروئی و روش های جدید تعیین آن
P84	520	Molecular Characterization of Antibiotic	Tayabe Avazzadeh	مقاومت داروئی و روش های

		Resistance Genes in Staphylococcus Isolated from Cell Phone Users' and Non- Users' Ears		جدید تعیین آن
P85	529	Bacteriological etiology and antibiotic resistance patterns of bloodstream infections in a tertiary care hospital in the southwest of Iran	Maniya Arshadi	مقاومت داروئی و روش های جدید تعیین آن
P86	531	Relationship between antibiotic resistance and invasion of Shigella sonnei strains	Mohammadmahdi Karimi-Yazdi	مقاومت داروئی و روش های جدید تعیین آن
P87	542	Bacterial etiology and antibiotic resistance pattern of septic arthritis in 216 patients admitted to Imam Reza Hospital, Mashhad: a 6-year retrospective study	Mahnaz Arian	مقاومت داروئی و روش های جدید تعیین آن
P88	543	effect of lactin-nisin-positive Lactococcus probiotic supernatant on Shigella flexneri biofilm.	Mohadesseh Dehghan	مقاومت داروئی و روش های جدید تعیین آن
P89	545	Bacterial community of chronic rhinosinusitis patients and therapeutic ultrasound efficacy: clinical trial study	Narjes Feizabadi	مقاومت داروئی و روش های جدید تعیین آن
P90	552	Antimicrobial susceptibility patterns and molecular characterization of plasmid-mediated quinolone resistance determinants among Salmonella and Shigella spp. isolated from pediatric patients	Marjan Rashidan	مقاومت داروئی و روش های جدید تعیین آن
P91	555	Antibiotic resistance assessment and multi-drug efflux pumps of Enterococcus faecium isolated from clinical specimens	Marjan Rashidan	مقاومت داروئی و روش های جدید تعیین آن
P92	557	In vitro formulation of Solenanthus circinnatus leaves methanolic extract and its antibacterial and antifungal inhibitory activities.	Zahra Hemati	مقاومت داروئی و روش های جدید تعیین آن
P93	571	Molecular detection of some vancomycin resistance genes of Staphylococcus aureus strains isolated from clinical samples in Thi-Qar province / South of Iraq	Seyedeh Elham Rezatofighi	مقاومت داروئی و روش های جدید تعیین آن
P94	578	Prevalence of pelA , pslA, QacE and QacEΔ1 genes and their correlation with antimicrobial resistance in Pseudomonas aeruginosa in Shiraz	Farshad Kakian	مقاومت داروئی و روش های جدید تعیین آن
P95	589	Gastrointestinal infections in hospitalized patients before and during the covid-19 pandemic (2019-2022)	Behnaz Deihim	مقاومت داروئی و روش های جدید تعیین آن
P96	593	Antibacterial effects of drug delivery system of mesoporous silica nanoparticles loaded with rifampin drug on Streptococcus pneumoniae and Pseudomonas aeruginosa	Ahmad Fatahi-Vanani	مقاومت داروئی و روش های جدید تعیین آن
P97	594	The application of the loop-mediated isothermal amplification method for rapid detection of methicillin-resistant Staphylococcus aureus	Shahi Fatemeh	مقاومت داروئی و روش های جدید تعیین آن

P98	603	Investigation of frequency and pattern of antibiotic resistance of Klebsiella oxytoca producing metallobetalactamas	Fatemeh Bahramichegeni	مقاومت داروئی و روش های جدید تعیین آن
P99	607	Molecular detection of class I integron and its gene cassette to antibiotics in Klebsiella pneumoniae strains.	Fatemeh Bahramichegeni	مقاومت داروئی و روش های جدید تعیین آن
P100	610	Inhibitory effect of pyocyanin pigment of Pseudomonas aeruginosa on Candida albicans in vitro	Fatemeh Nazarihaghighipashaki	مقاومت داروئی و روش های جدید تعیین آن
P101	615	Activity of Copper and Silver oxide NPs in forming a inhibition zone in Streptococcus salivarius and Lactobacillus rhamnosus	Soroush Moosazadeh hamzekandi	مقاومت داروئی و روش های جدید تعیین آن
P102	616	Study of growth inhibition of Streptococcus salivarius and Lactobacillus rhamnosus by Copper and Silver oxide Nanoparticles	Parisa Hosseini	مقاومت داروئی و روش های جدید تعیین آن
P103	617	Determination of Minimum Inhibitory Concentration (MIC) and Minimum bactericidal Concentration (MBC) of Copper (Cu) and Silver oxide (AgO) Nanoparticles against Streptococcus salivarius	Mehran Amir Javid	مقاومت داروئی و روش های جدید تعیین آن
P104	633	HIV-1 glycoprotein 41 molecular docking analysis and transmitted drug resistance mutations among antiretroviral therapy-naïve individuals in Iranian patients	Nastaran Khoadadad	مقاومت داروئی و روش های جدید تعیین آن
P105	634	Computational Protein–Ligand Docking to Evaluate Susceptibility to HIV Gag Inhibitors in HIV-Infected Iranian Patients	Nastaran Khoadadad	مقاومت داروئی و روش های جدید تعیین آن
P106	656	Highly Synergistic Effects of Melittin with Vancomycin against Vancomycin Resistant Staphylococcus aureus	Mohammad Hossein Ghaffari Agdam	مقاومت داروئی و روش های جدید تعیین آن
P107	657	In silico design and in vitro evaluation of anti-microbial activity of Melittin analogs	Mohammad Hossein Ghaffari Agdam	مقاومت داروئی و روش های جدید تعیین آن
P108	669	Investigation of frequency and determination of drug sensitivity of Gram-positive bacteria causing septicemia in In hospitalized patients of HAJAR Hospital, Shahrekord , Chaharmahal and Bakhtiari Province , 1400 .	Atefeh Heidari	مقاومت داروئی و روش های جدید تعیین آن
P109	671	Investigation of the prevalence of macrolide resistance of Mycoplasma pneumoniae in children: a review article	Iman Pouladi	مقاومت داروئی و روش های جدید تعیین آن
P110	675	In-vitro effect of carbapenem in combination to other antibiotics against Carbapenem-resistant Klebsiella pneumoniae	Mina Yekani	مقاومت داروئی و روش های جدید تعیین آن
P111	676	Carbapenems resistant Enterobacteriaceae isolated from surgical site infections (SSIs) from Tabriz, Iran	Mina Yekani	مقاومت داروئی و روش های جدید تعیین آن
P112	684	Nanoencapsulation of Phytosterols extracted from Pistacia terebinthus and evaluation of their antibiotic and release abilities	Maryam Meskini	مقاومت داروئی و روش های جدید تعیین آن

P113	691	Distribution assessment of Extended-spectrum beta-lactamases (ESBL) producing clinical isolates of shigella	Soheil RahmaniFard	مقاومت داروئی و روش های جدید تعیین آن
P114	693	A detection kit based on the inhibition of microbial growth for evaluating antibiotic residues in animal products	Hamid Reza Rasouli Jazi	مقاومت داروئی و روش های جدید تعیین آن
P115	700	Antibacterial Effects of Thymus Vulgaris extracts against Resistant motile Salmonella Sp. in Pheasants	Abdolreza Nabinejad	مقاومت داروئی و روش های جدید تعیین آن
P116	704	Metal-based Nanoparticles; Promising Strategy to Inhibit Quorum Sensing	Amin Haratian	مقاومت داروئی و روش های جدید تعیین آن
P117	715	Investigation of frequency and determination of drug sensitivity of Enterobacter species causing septicemia in patients hospitalized in Hajar Shahrekord Hospital, Chaharmahal and Bakhtiari Province in 1400	Atefeh Heidari	مقاومت داروئی و روش های جدید تعیین آن
P118	725	Isolation of bacteriophage against Shigella sonnei in Hospital and Municipal Wastewaters	Serveh Molaie	مقاومت داروئی و روش های جدید تعیین آن
P119	739	Frequency of Enterobacteriaceae in blood cultures and antibiotic resistance pattern in pre-COVID and during COVID period	Vahid Sharifzadeh peyvasti	مقاومت داروئی و روش های جدید تعیین آن
P120	744	Presence and antibiotic resistance of Pseudomonas aeruginosa and Acinetobacter baumannii from Intensive Care Units: An appraisal from a University teaching center, Sina Hospital, Tabriz	Somayeh Ahmadi	مقاومت داروئی و روش های جدید تعیین آن
P121	7	Studying antimicrobial effect of aqueous Sumac extract for bacteria that cause nosocomial infections by In Vitro & In Vivo method	Nafiseh Farazandehnia	کنترل عفونت های بیمارستانی
P122	8	Investigation of therapeutic applications of Cucumis metuliferus extract	Mahdi AsghariOzma	کنترل عفونت های بیمارستانی
P123	18	Isolation and identification of Burkholder cepacia from respiratory secretions of cystic fibrosis patients in East Azerbaijan, Iran	Hassan Tizfahm	کنترل عفونت های بیمارستانی
P124	30	Evaluation of the inhibitory effect of Ganoderma lucidum extract and TiO2 nanoparticle against biofilm-producing bacteria isolated from clinical samples	Ali NazariAlam	کنترل عفونت های بیمارستانی
P125	47	Bio-control of Acinetobacter baumannii by Bdellovibrio as a predatory bacteria	Neda Jafarian	کنترل عفونت های بیمارستانی
P126	73	The immunogenic role of combination of outer membrane proteins Omp34 and BauA against Acinetobacter baumannii infection in murine mode	Mohammadhasan Mirali	کنترل عفونت های بیمارستانی
P127	99	The study of prevalence of antibodies against Chlamydia pneumoniae in patients suffered	Mahdiyeh Ebrahimzadeh	کنترل عفونت های بیمارستانی

		from chronic obstructive pulmonary visiting Tabriz Emam reza and Alinasab Hospital		
P128	100	Prevalence and antibiotic susceptibility pattern of Enterobacter isolates in burn patients: A cross-sectional study in North of Iran	Mohammadreza Mobayen	کنترل عفونت های بیمارستانی
P129	101	Prevalence and profile of antibiotic susceptibility of various bacteria isolated from burn patients with ventilator-associated pneumonia (VAP): A cross-sectional study in North of Iran	Mohammadreza Mobayen	کنترل عفونت های بیمارستانی
P130	102	Prevalence and antibiotic resistance pattern of Klebsiella pneumoniae isolated from burn patients in the North of Iran	Mahsa Sadeghi	کنترل عفونت های بیمارستانی
P131	103	Risk factors related to mortality of burn patients infected with non-fermentative gram-negative bacteria in Velayat Hospital in Rasht, Iran	Mahsa Sadeghi	کنترل عفونت های بیمارستانی
P132	106	Genotyping of extended spectrum beta-lactamases (ESBLs) producing Pseudomonas aeruginosa Isolates from Nosocomial infections	Rashid Ramazanzadeh	کنترل عفونت های بیمارستانی
P133	107	Hospital-acquired infections and Antibiotic Resistant challenge in Western Asia	Arash SoltaniBorchaloee	کنترل عفونت های بیمارستانی
P134	135	Evaluation of the Effect of the Cetrimid-C, Benzalkonium Chloride and Micro-10 Disinfectants on Escherichia coli Isolated from Patients	Seyyedeh masumeh Mirnurollahi	کنترل عفونت های بیمارستانی
P135	155	The challenge of treatment multi-drug resistant strains of Acinetobacter baumannii in burn patients in Iran	Zahra Mottaghiyan	کنترل عفونت های بیمارستانی
P136	168	The Effectiveness of the Anteroom (Vestibule) Area on Hospital Infection Control and Health Staff Safety: A Systematic Review	Zahra Rafat	کنترل عفونت های بیمارستانی
P137	178	Evaluation of the effect of Savlon (Cetrimide-C), Surfosept and Sodium hypochlorite disinfectants on Klebsiella pneumoniae isolated from patients	Seyedeh Sara Seyedtaghizadeh	کنترل عفونت های بیمارستانی
P138	189	Antibiofilm activity of Cinnamomum zeylanicum essential oil against clinical strains of Acinetobacter baumannii	Malihe Bajmalourostami	کنترل عفونت های بیمارستانی
P139	190	Synergistic effect of zinc oxide nanoparticles and Bunium persicum essential oil against clinical strains of Pseudomonas aeruginosa	Malihe Bajmalourostami	کنترل عفونت های بیمارستانی
P140	240	Comparison of antibacterial activity of hypericin activated by light with hypericin not exposed to light	Mahnaz Hadizadeh	کنترل عفونت های بیمارستانی
P141	247	A combination of biofilm-associated protein (Bap) and Outer membrane protein A (OmpA)	AmirJavad Vafaei	کنترل عفونت های بیمارستانی

		protects mice against Acinetobacter baumannii infection		
P142	250	Immunization with a combination of Bap and Oma87 protects mice against Acinetobacter baumannii infection in a murine model	Marziyeh Abdollahi	کنترل عفونت های بیمارستانی
P143	261	Antimicrobial and Healing Effect of Nettle, Purslane and Hedge Nettle Extracts on Burn Infections of Staphylococcus aureus in Mice	Mahdi Arfaei	کنترل عفونت های بیمارستانی
P144	265	Antimicrobial and Healing Effects of Purslane, Green Tea and Mountain Tea Extracts on Burn Infection Caused by Staphylococcus aureus in Mice	MONA GHASEMI	کنترل عفونت های بیمارستانی
P145	270	An immunoinformatics approach to design a multi-epitope vaccine against Neisseria gonorrhoeae	Parisa Farhdikia	کنترل عفونت های بیمارستانی
P146	299	Determination of antibiotic resistance and virulence determinants of different methicillin resistant and –sensitive S. aureus (MRSA & MSSA) types isolated from Shahid Mustafa Khomaini Hospital of Ilam city by PCR, SCCmec and PFGE typing	Mehdi Abbasi	کنترل عفونت های بیمارستانی
P147	314	Evaluation the antifungal efficacy of five Iranian essential oils against fluconazole resistant Candida species isolated from patients with urinary tract candidiasis	Mehrdad Seifi	کنترل عفونت های بیمارستانی
P148	318	Antimicrobial Effect of Ajowan and Lemonbalm Extracts on Staphylococcus aureus: In vitro and Animal Model	Mahdi Arfaei	کنترل عفونت های بیمارستانی
P149	322	Antibacterial Effects of Essential Oils of Ajowan and Lemonbalm on Staphylococcus aureus: In vitro and Animal Model	MONA GHASEMI	کنترل عفونت های بیمارستانی
P150	324	Green synthesis of Cadmium Sulfide Quantum dots from Nerium Oleander leaves extract and detection of its antibacterial effects against some gram negative and gram positive bacteria	Pegah Pourbabaei	کنترل عفونت های بیمارستانی
P151	328	Investigation of antibacterial effect of a recombinant phage endolysin on Acinetobacter baumannii	Homa Noura	کنترل عفونت های بیمارستانی
P152	350	In silico study of the immunogenicity of a construct containing the extracellular loops of Acinetobacter baumannii outermembrane proteins exposed on the LCL platform	Reyhaneh Banisaeed	کنترل عفونت های بیمارستانی
P153	354	Isolation of Clostridium perfringens type D from antibiotic-associated diarrhoeal patients in Kerman hospitals of Iran	Mojtaba Alimolaei	کنترل عفونت های بیمارستانی
P154	383	A New Insight into Nosocomial Infections: a Worldwide Crisis	Elham Sheykhsaran	کنترل عفونت های بیمارستانی
P155	398	An outer membrane protein-derived peptide as	Mosayeb Rostamian	کنترل عفونت های

		Klebsiella pneumoniae vaccine candidate		بیمارستانی
P156	400	Klebsiella pneumoniae vaccines: A systematic review	Mosayeb Rostamian	کنترل عفونت های بیمارستانی
P157	503	Investigation of antimicrobial effects of lipid extracted from Streptomyces alboflavus	Marjan Seratnahaei	کنترل عفونت های بیمارستانی
P158	507	the effect of personnel's knowledge in controlling the infection	Zahra Karaminezhad	کنترل عفونت های بیمارستانی
P159	525	Essential Oils Composition and Antibacterial Activity and Antioxidant Activity of Stachys lavandulifolia Vahl from Alborz - Iran	Mona NajafiMoghadam	کنترل عفونت های بیمارستانی
P160	530	Characterization of biofilm formation and virulence factors of Staphylococcus aureus isolates from paediatric patients in Tehran, Iran	Hiva Kadkhoda	کنترل عفونت های بیمارستانی
P161	533	Surveying on biofilm-related virulence factors in Acinetobacter baumannii: A cross-sectional study, and molecular typing of isolates using the REP-PCR method	Nafiseh HosseinzadehShakib	کنترل عفونت های بیمارستانی
P162	537	Characterization of Antibacterial and Antioxidant Properties of Flowers of Ziziphora clinopodioides	Seyededalat Pishkar	کنترل عفونت های بیمارستانی
P163	540	Phytochemical, Antibacterial Activity Screening of Methanolic Psidium guajava L. Leaves Extract	Seyededalat Pishkar	کنترل عفونت های بیمارستانی
P164	547	Evaluation of Surgical Antibiotic Prophylaxis and Microbial Spectrum in Patients with Surgical Site Infection	Mahnaz Arian	کنترل عفونت های بیمارستانی
P165	556	an experimental study on the feasibility of ozonation and ultraviolet radiation for decontamination of infectious waste	Alireza Mohtasebi	کنترل عفونت های بیمارستانی
P166	569	The antibacterial activity of bacteriocin-like inhibitory substances (BLISs) extracted from clinical Pseudomonas aeruginosa strains	Hamed Charkhian	کنترل عفونت های بیمارستانی
P167	574	The prevalence of coinfections and antibiotic-resistant strains among hospitalized Covid-19 patients in Mashhad, Iran	Arastoo Vojdani	کنترل عفونت های بیمارستانی
P168	588	Emergence of OXA-10 and OXA-48 like carbapenemases among Enterobacter isolates from inpatients in southern Iran	Melika Moradi	کنترل عفونت های بیمارستانی
P169	604	Spectroscopic Determination of Total Phenol, Flavonoid Contents and Antibacterial Activity of Polylophium involucratum (Pall.) Boiss.	Shahab Ojani	کنترل عفونت های بیمارستانی
P170	605	The evaluation of the antibacterial and antibiofilm activity of phycocyanin pigment & clindamycin antibiotic in liposomes against Staphylococcus aureus isolates	SeyedMahmoud Barzi	کنترل عفونت های بیمارستانی
P171	613	Evaluation of Antibacterial Activity of Essential Oils of Aerial of Heracleum	Sedigheh Mehdinajad	کنترل عفونت های

		persicum L. from Ramsar - Iran		بیمارستانی
P172	614	Bioactive Compound, Radical Scavenging and Antibacterial Activity of Aqueous Extract of Flowers of Echium amoenum Fisch. & C.A.Mey. from Guilan – Iran	Sedigheh Mehdinajad	کنترل عفونت های بیمارستانی
P173	623	Immunogenicity of the combination of two outer membrane proteins, Oma 87 and BauA against Acinetobacter baumannii infection in a murine model	Masoumeh Sadeghpoor	کنترل عفونت های بیمارستانی
P174	629	Antibacterial effects of silver nanoparticls nursing gowns on geram- positive bacterial	Masoumeh Molabagheri	کنترل عفونت های بیمارستانی
P175	643	Determination of Minimum Inhibitory Concentration (MIC) and Minimum bactericidal Concentration (MBC) of Copper (Cu) and Silver oxide (AgO) Nanoparticles against Actinomyces viscomus	Majid Rezaei	کنترل عفونت های بیمارستانی
P176	647	Frequency distribution of secondary bacterial infections (aerobic and anaerobic) in patients admitted to the dermatology ward of Alzahra Hospital, Isfahan University of Medical Sciences	Hanieh Sharifian	کنترل عفونت های بیمارستانی
P177	658	The comparison of the antibacterial and antibiofilm activities of Zingerone and Niosome containing Zingerone against Methicillin- Resistant Staphylococcus aureus (MRSA) isolates, isolated from diabetic ulcers	Laleh Larijanian	کنترل عفونت های بیمارستانی
P178	665	Synthesis and investigation of antibacterial properties of nanosheet carbon nitride	Rojin Anbarteh	کنترل عفونت های بیمارستانی
P179	685	Synthesis and investigation of antibacterial carbon nitride	Tania Ghanidel	کنترل عفونت های بیمارستانی
P180	703	In-vitro activity of antibiotics combination against carbapenem resistant Acinetobacter baumannii	MohammadYousef Memar	کنترل عفونت های بیمارستانی
P181	748	Multidrug - resistant pathogens in burn wound and using nanoparticles as advanced therapeutic strategies	Jaber Hemmati	کنترل عفونت های بیمارستانی
P182	11	Molecular Identification of Mycoplasma¬ Hominis in Vaginal Sample of Women Referred to the Infertility Center of Fatemieh Hospital in Hamadan	Hadi Hosainpour	روش های جدید تشخیص میکروبها
P183	15	An electrochemical DNA biosensor based on a gold nanostructure for the detection of Enterococcus faecalis gene sequence	Razieh Nazari	روش های جدید تشخیص میکروبها
P184	16	DNA electrochemical biosensor for the detection of 16s rRNA gene sequence related to the Enterococcus faecalis	Razieh Nazari	روش های جدید تشخیص میکروبها
P185	61	Oral Microbiota Dysbiosis as a Prognostic Biomarker for Colorectal Cancer	Ali Zarei	روش های جدید تشخیص

				میکروبها
P186	75	Diagnosis and treatment of Merkel cell polyomavirus	Piruz Shadbash	روش های جدید تشخیص میکروبها
P187	115	Comparison of Penicillinase and β–lactamase enzymes in validation of sterility test in some of injectable β–lactam antibiotics	Fatemeh Behoftadeh	روش های جدید تشخیص میکروبها
P188	139	Designing a non-enzymatic system at constant room temperature as a signal amplification technique for the detection of Klebsiella pneumoniae	Erfan Shahbazi	روش های جدید تشخیص میکروبها
P189	242	Detection of Chlamydia abortus sheep abortion specimens by Nested PCR	SeyyedSajjad MousaviYengejeh	روش های جدید تشخیص میکروبها
P190	346	In silico analysis and experimental study on Bst DNA polymerase 1 Large fragment (Bst pol 1 L.F) in E.coli	Fatemeh Zamani	روش های جدید تشخیص میکروبها
P191	380	The effect of Bacillus subtilis natto on the gene expression level of E-cadherin in colonic carcinoma cell line Caco2	Parisa Abedi Elkhichi	روش های جدید تشخیص میکروبها
P192	390	A novel electrochemical biosensor for detection of Streptococcus penumoniae	Azam Yaghoobi	روش های جدید تشخیص میکروبها
P193	397	Biotransducer-conjugated nobel metal nanomaterials as nanobiosensors for pathogenic organisms	Atiyeh Nomani	روش های جدید تشخیص میکروبها
P194	462	Aptamer-based nanobiosensors for the detection of E.coli	Fatemeh Jalali	روش های جدید تشخیص میکروبها
P195	512	Introduction of a novel tellurite-containing selective medium for the rapid phenotypic identification method of hypervirulent Klebsiella pneumoniae isolates	Rahimeh Sanikhani	روش های جدید تشخیص میکروبها
P196	527	A comparison between a colorimetric and a fluorescent dye in a SARS-CoV-2 reverse transcriptase-loop-mediated isothermal amplification (RT-LAMP) assay	Mohsen Vaez	روش های جدید تشخیص میکروبها
P197	534	Title of the article: Investigation of new methods for detecting microbes (Batakid comparing two methods, PCR and LAMP)	Elaheh Moghoumi	روش های جدید تشخیص میکروبها
P198	601	Limit of detection evaluation of a synthetic SARS-CoV-2 RNA by RT-LAMP and Real-time PCR	Mohsen Vaez	روش های جدید تشخیص میکروبها
P199	1	Zoliflodacin: A Hope to Treat Antibiotic-Resistant Neisseria gonorrhoeae	MohammadReza Mohammadi	عفونت های ادراری و روش های نوین درمانی
P200	38	Simultaneous Molecular identification Mycoplasma and Ureaplasma in women with vaginosis	Mahla Abedini	عفونت های ادراری و روش های نوین درمانی
P201	52	Phylogroup classification and investigation the relationships between phylogroups and antibiotic resistance patterns of uropathogenic	Narjes Morovatimoez	عفونت های ادراری و روش های نوین درمانی

		E. coli isolated from pediatric urinary tract infection		
P202	80	Antimicrobial Resistance Pattern and multi drug resistance frequency in Escherichia coli Strains Isolated from Patients Referred to Teaching Hospitals in Mazandaran Province, Iran	Fatemeh Roozbahani	عفونت های ادراری و روش های نوین درمانی
P203	113	Necessity of Laboratory Screening for Bacteriuria in Elderly Population	Narges Nooritalab	عفونت های ادراری و روش های نوین درمانی
P204	120	Antimicrobial Efficacy and Prevalence of Microcins among Escherichia coli isolates	Farzaneh MohammadzadehRostami	عفونت های ادراری و روش های نوین درمانی
P205	125	Evaluation Antibacterial behavior of Silver nanoparticles on general escherchia uropathogenic	Lida Eftekharivash	عفونت های ادراری و روش های نوین درمانی
P206	166	The association between microbial and viral infectious agents with ulcerative colitis	Tohid Javaheri	عفونت های ادراری و روش های نوین درمانی
P207	315	Non-antibiotic methods in the treatment of urinary tract infection	Mahdiyeh Nabavinia	عفونت های ادراری و روش های نوین درمانی
P208	451	Prevalence of blaTEM gene among Escherichia coli strains isolated from Tabriz hospitals	Sana Falahi	عفونت های ادراری و روش های نوین درمانی
P209	532	Distribution of virulence genes among Staphylococcus saprophyticus isolated from patients with UTI	Maryam Rafiee	عفونت های ادراری و روش های نوین درمانی
P210	548	Comparative study of antifungal effect of different active herbal compounds	Mehdi Shakibaie	عفونت های ادراری و روش های نوین درمانی
P211	550	Blue light irradiation inhibits bacterial growth	Mehdi Shakibaie	عفونت های ادراری و روش های نوین درمانی
P212	591	Investigation of virulence factors and their association with antimicrobial resistance among uropathogenic Escherichia coli strains isolated from patients in Basra city; Iraq	Seyedeh Elham Rezatofighi	عفونت های ادراری و روش های نوین درمانی
P213	637	New findings from diagnostic methods of urinary infections in children	Zahra Mottaghiyan	عفونت های ادراری و روش های نوین درمانی
P214	662	Study of biofilm formation among S.saprophyticus isolated from patients with UTI	Maryam Rafiee	عفونت های ادراری و روش های نوین درمانی
P215	702	Investigation of the antibacterial effect of IDR-1018 peptide and chitosan nanoparticles on resistant Pseudomonas aeruginosa isolated from patients with urinary tract infections	Mohammadreza AsadiKaram	عفونت های ادراری و روش های نوین درمانی
P216	705	Expression of a hybrid protein composed of several antigens from uropathogenic Escherichia coli in Lactococcus lactis and confirmation of its expression on the surface of the bacteria	Mohammadreza AsadiKaram	عفونت های ادراری و روش های نوین درمانی

P217	36	Evaluation Human Papillomavirus infection and Correlation with H.Pylori infection in Adenocarcinoma gastric cancer	Mohammadreza Pourmohammad	سرطان، پیوند و بیماری های عفونی
P218	37	Evaluation of severity persistent asthma with Hemophilus influenza Type A infection in sputum of patients based on Real time PCR	Mohammadreza Pourmohammad	سرطان، پیوند و بیماری های عفونی
P219	77	Therapeutic Potential of Gut Microbiota in Colorectal Cancer	Morteza HassandokhtMashhadi	سرطان، پیوند و بیماری های عفونی
P220	82	Anticancer Effects of Caffeic Acid on A549 Non-small Cell Lung Cancer Cells	Raham Mojibi	سرطان، پیوند و بیماری های عفونی
P221	85	Epidemiology of Merkel cell carcinoma	Piruz Shadbash	سرطان، پیوند و بیماری های عفونی
P222	88	The evaluation of bacterial infection in patients with acute Lymphoblastic leukemia in induction phase of treatment with Hyper CVAD regimen	Mohammadali Mashhadi	سرطان، پیوند و بیماری های عفونی
P223	93	Invasive Aspergillosis in post-liver transplant patients	Rozita Khodashahi	سرطان، پیوند و بیماری های عفونی
P224	94	Critical COVID 19 in Solid Organ Transplatation	Rozita Khodashahi	سرطان، پیوند و بیماری های عفونی
P225	213	Cancer and Coronavirus Disease (COVID - 19) : Comorbidity , Mechanical Ventilation , and Death Risk	Faraneh Hatefi	سرطان، پیوند و بیماری های عفونی
P226	255	Investigation of the frequency of Helicobacter pylori infection in tissue samples of gastric cancer in Tabriz hospitals	Saeedesadat Ghorashizadeh	سرطان، پیوند و بیماری های عفونی
P227	284	Genotyping Helicobacter pylori and fgf7 Gene Expression in Gastric cancer	Manouchehr AhmadiHedayati	سرطان، پیوند و بیماری های عفونی
P228	342	Bacteria-cancer interactions: bacteria-based cancer therapy	Negin NajmiNoghondar	سرطان، پیوند و بیماری های عفونی
P229	455	Cytotoxic activity of exosomes carrying gold nanoparticles produced by Micrococcus yunnanensis strain J2	Mandana Jafari	سرطان، پیوند و بیماری های عفونی
P230	461	Review of Handrab and Handwash by scrub method In the first surgery And the second operation Doctors and Oncology operating room working personnel in Mashhad-spring1401	Zohreh Rokni	سرطان، پیوند و بیماری های عفونی
P231	472	Examination of handrub and hand wash scrub on first and second operation in doctors and oncology operating room personnel in the private hospital of Mashhad in the spring of 1401	Zohreh Rokni	سرطان، پیوند و بیماری های عفونی
P232	477	HTLV-1–Cell Interactions in the Development of Adult T-Cell Leukemia	Malihe Naderi	سرطان، پیوند و بیماری های عفونی

P233	515	Mutations in HBV- S gene and overlapping RT region in association to hepatocellular carcinoma	Davod Javanmard	سرطان، پیوند و بیماری های عفونی
P234	582	Bacterial etiology and antibiotic resistance pattern of bacteremia in patients with hematologic malignancies admitted to Imam Reza Hospital, Mashhad: an 8-year retrospective study	Mahnaz Arian	سرطان، پیوند و بیماری های عفونی
P235	620	Evaluation of antibacterial resistance pattern of Helicobacter pylori isolated of Patient with suspected gastric cancer	Arash Adamnejad Ghafour	سرطان، پیوند و بیماری های عفونی
P236	622	CAR-T Cells & Oncolytic Viruses against Solid Tumors	Piruz Shadbash	سرطان، پیوند و بیماری های عفونی
P237	625	Molecular characterization of virus-positive and virus-negative in Merkel cell carcinoma	Piruz Shadbash	سرطان، پیوند و بیماری های عفونی
P238	635	Study of probiotic effect of Bifidobacterium bifidum on CacoII cancer cell line	Hosein Alipour	سرطان، پیوند و بیماری های عفونی
P239	686	Prevalence of hepatitis B Virus Infection Among HIV positive patients in Zabol city(iran)	Khadije Rezaie Keikhaie	سرطان، پیوند و بیماری های عفونی
P240	687	Prevalence of Extended-Spectrum Beta-Lactamase Producing Escherichia coli Causing Bloodstream Infections in patients with leukemia undergoing levofloxacin prophylaxis	Mahdane Roshani	سرطان، پیوند و بیماری های عفونی
P241	694	intertumoral microbiome and their effect on tumors	Tahmineh Rahimi	سرطان، پیوند و بیماری های عفونی
P242	232	Survey on Prevalence of Antibiotic Resistance in Anaerobic Bacteria Isolated from Oral Infections	Maryam Sheykhzadegan	باکتریهای سخت رشد وبیهوازی ها
P243	283	Frequency of virulent Legionella pneumophila in hospital water supply systems in the west of Iran	Manouchehr AhmadiHedayati	باکتریهای سخت رشد وبیهوازی ها
P244	334	Molecular detection of Brucella spp. in the population of vaccinated and non-vaccinated sheep against brucellosis in Yazd Province of Iran.	Fatemeh Sataeimokhtari	باکتریهای سخت رشد وبیهوازی ها
P245	356	Cloning and sequencing of the etx gene from Clostridium perfringens type D strains isolated from patients with antibiotic-associated diarrhoea (AAD)	Mojtaba Alimolaei	باکتریهای سخت رشد وبیهوازی ها
P246	370	Impact of Pepsin on Transcriptional Alteration of Helicobacter pylori Virulence Genes	Amir Ebrahimi	باکتریهای سخت رشد وبیهوازی ها
P247	371	A study of the prevalence of Neisseria gonorrhoeae and its molecular characterization in Tehran, Iran	Pouria Zolfaghari	باکتریهای سخت رشد وبیهوازی ها
P248	404	Comparison Specificity of Invasive and	Faranak Rezaei	باکتریهای سخت رشد

		Serologic Methods in the Diagnosis of Helicobacter pylori in Khorrmabad City, Iran		وبیهوازی ها
P249	408	spoT gene is involved in biofilm formation and antibiotic resistance of Helicobacter pylori isolates	Leila Yousefi	باکتریهای سخت رشد وبیهوازی ها
P250	418	Decolorization of textile wastewater using thermophilic bacteria isolated from the wastewater and returned to the production line	Milad Sabertahan	باکتریهای سخت رشد وبیهوازی ها
P251	464	New toxinotyping of clostridium perfringens isolates based on molecular characterization of netB and cpe genes	Maryam Amini	باکتریهای سخت رشد وبیهوازی ها
P252	466	Evaluation of toxin production power in different types of clostridium perfringens isolates	Maryam Amini	باکتریهای سخت رشد وبیهوازی ها
P253	519	A study of prevalence of vacA d genotypes of Helicobacter pylori isolated from patients with gastrointestinal problems in Mashhad	Hana Hamid	باکتریهای سخت رشد وبیهوازی ها
P254	701	Carbapenems resistance among Bacteroides fragilis isolated from skin and soft tissue infections	MohammadYousef Memar	باکتریهای سخت رشد وبیهوازی ها
P255	29	The novel therapeutic strategy for obesity through the gut-brain axis	ROMINA KARDAN	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P256	79	The Impact of the Gut Microbiome on Toxigenic Bacteria	Rohollah Zarei koosha	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P257	84	Replacing Meal worm in aquatic diet to increase probiotic bacteria and reduce disease	Laleh Yazdanpanah Goharrizi	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P258	108	Evaluation of Lactobacillus brevis supernatant on Pseudomonas aeruginosa biofilm formation	Ava Behrouzi	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P259	130	Postbiotics and Paraprobiotics: The New Scopes in Innovative Microbial Functional Foods and Neutraceuticals	Bita Rahmani	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P260	149	Therapeutic potential of fecal microbiota transplantation in systemic lupus erythematosus	Farshid Fathabadi	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P261	169	Evaluation of species distribution and virulence factors of oral mycobiome in hospitalized patients with COVID-19: A case–control study	Zahra Rafat	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P262	170	Study of skin and nail Candida species as a normal flora based on age groups in healthy persons in Tehran-Iran	Zahra Rafat	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P263	171	Epidemiology, laboratory diagnosis and clinical aspects of fungal pulmonary infections in 384 patients hospitalized in pulmonary units in Guilan province, Iran	Zahra Rafat	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P264	172	Study of skin and nail Trichosporon species as a normal flora based on age groups in healthy	Zahra Rafat	میکروبیوتا و اهمیت آن در

		persons		بیماریها ی عفونی
P265	184	The role of probiotics in inducing apoptosis in oral cancer	Vahideh Faghanizadeh	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P266	193	Interplay of microbiome and host genetics promote inflammatory bowel disease	Mehrnaz Moattari	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P267	195	Investigation of the relationship between the gut microbiota and inflammatory bowel disease in a mouse model	Afsaneh Salimi	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P268	217	Amplification of Choosing Isolation-Sources with an Approach to Ameliorate Screening for Diverse Yeasts with Probiotic Potential: a Comparative Study	Bita Rahmani	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P269	241	Effects of Escherichia coli strain Nissle 1917 on goldfish (Carassius auratus) tissues histomorphology challenged with arsenic	SeyyedSajjad MousaviYengejeh	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P270	266	New method for Membrane Vesicle (MV) extraction from Gram-positive Bacteria, a nanoparticle useful in biomedicine and nanotechnology	Fateme RafieiAtani	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P271	267	Enterococcus parabiotic regulate inflammatory response induced by Poly (I:C) in the lungs of mice	Zahraa AlHijjaj	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P272	343	The effect of psychobiotics on consumer health	Reza Abazari	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P273	357	The effect of Bacteroides thetaiotaomicron extracellular vesicles and it’s supernatant on gene expression involved in Epithelial – Mesenchymal Transition in HCT-116 Cell line	SeyedAbdolmajid Khosravani	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P274	364	Investigating the Presence of tolC Efflux pump Gene in Urinary Isolates of Klebsiella Pneumoniae in Clinical Samples in the city of Zahedan	Mohaddeseh Daemi	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P275	368	Investigating the Presence of AcrAB Efflux pump Gene in Urinary Isolates of Klebsiella Pneumoniae in Clinical Samples in the city of Zahedan	Mohaddeseh Daemi	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P276	423	Co-aggregation of Lactobacillus reuteri isolated from yogurt against pathogenic Helicobacter pylori for reduction load of H. pylori in human	Fatemeh Bakhshi	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P277	438	Human gut and SARS-CoV-2	Javad Allahverdy	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P278	450	In vitro and in vivo effects of Pseudomonas plecoglossicida strain IAUK2313 on growth of Helianthus annuus	Fatemeh Saadatnasri	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P279	453	Growth performance, mucosal immunity and	Ali Shaker	میکروبیوتا و اهمیت آن در

		disease resistance in goldfish (Carassius auratus) orally administered Escherichia coli strain Nissle 1917		بیماریها ی عفونی
P280	486	How Dysbiosis (Microbiota interruption) leads to colorectal Cancer	Fatemeh Naeemi	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P281	736	Association of altered gut microbiota composition with chronic urticaria	Edris Nabizadeh	میکروبیوتا و اهمیت آن در بیماریها ی عفونی
P282	17	Glanders Re-emerging in Few Horses in East Azerbaijan, Iran	Hassan Tizfahm	بیماریهای زئونوز
P283	49	Antifungal activity of eugenol-loaded polyacrylonitrile nanofibers against dermatophytes	Masoomeh Shams-Ghahfarokhi	بیماریهای زئونوز
P284	86	Seroprevalence Study of Brucellosis and Toxoplasmosis Infections Among Women in Ardabil, Iran	MohammadTaghi Ahady	بیماریهای زئونوز
P285	87	The Most Effective Medicinal Plants for the Treatment of Toxoplasmosis Infection	MohammadTaghi Ahady	بیماریهای زئونوز
P286	105	Identification and prevalence of Helicobacter pylori virulence genes; babA and cagA in Wolinella spp. of the oral cavity of dogs	Zahra Jahanshiri	بیماریهای زئونوز
P287	198	Sequence analysis of the flaB2 gene among Leptospira interrogans serovars from Iran	Sepideh Haghnazari	بیماریهای زئونوز
P288	216	Measuring the effect of Ribavirin on Crimean-Congo Hemorrhagic Fever Virus(CCHFV)	Mahsa Rahnein	بیماریهای زئونوز
P289	218	The Prevalence Rate of Candida albicans in Proventricular of Poultry in Babol City	Fatemeh Salehi	بیماریهای زئونوز
P290	220	Molecular identification of virulence gene hlyE in different serovars of Salmonella isolated from human and livestock in Iran	Negar NorouziMotlaghTehrani	بیماریهای زئونوز
P291	228	Molecular detection of lsa21 gene encoding an adhesion protein of pathogenic leptospiral serovars	Zahra Rahmani	بیماریهای زئونوز
P292	237	Survey of plasma alterations of hepcidine, cholinesterase and total sialic acid in sheep with naturally infected Sarcocystosis	Amin Amirzadeh	بیماریهای زئونوز
P293	239	Evaluation of Animal Bite & Rabies Epidemiological in Kermanshah Province During 2011-2019	Mehrdad Pooyanmehr	بیماریهای زئونوز
P294	253	Study of mycobacterium, a zoonosis threat to ornamental fish; review article	Sina SalajeghehTazerji	بیماریهای زئونوز
P295	269	The effects of aqueous and alcoholic extracts of Nymphaea alba on Candida albicans and determine effective products and comparing the results to clotrimazole	Ebrahim Karimian	بیماریهای زئونوز
P296	287	Antimicrobial effect of Alternaria metabolite isolated from tomato on Staphylococcus aureus	Ebrahim Karimian	بیماریهای زئونوز
P297	307	Molecular detection of Rickettsia and	Omid Azizi	بیماریهای زئونوز

		Ehrlichia isolates in ticks collected from domestic livestock of Torbat Heydariyeh-Iran-2020-21		
P298	331	Serological diagnosis of Brucella spp. in the camel population of southern Kerman province of Iran	Arman Raisi	بیماریهای زئونوز
P299	341	Anisakis Allergy	Mehrdad Asgharnia	بیماریهای زئونوز
P300	351	A decision regarding the role of ticks as the proven and suspected vectors of CCHFV (Crimean-Congo hemorrhagic fever virus): A meta-analysis review	Hassan Nasirian	بیماریهای زئونوز
P301	401	The use of Gecko cell line in the cultivation and preparation of live attenuated Toxoplasma gondii strain	Roghayeh Ramezanpoorronizi	بیماریهای زئونوز
P302	403	Evaluation the immunogenicity of Toxoplasma gondii experimental vaccine in pregnant sheep	Seyedehzahra Bootorabi	بیماریهای زئونوز
P303	416	Report of a case of dog infection with Hepatozoon canis (Apicomplexa: Adeleorina) parasite in north of Iran	Rasta Malek	بیماریهای زئونوز
P304	427	Comparing Diagnostic Accuracy of the fliD Gene and the glmM Gene in Helicobacter Pylori	Alireza Sharifi	بیماریهای زئونوز
P305	460	Updated population genetic understanding of Mycobacterium bovis in the Iranian cattle, a search for major clonal complexes frequently observed in the world	Zahra Esmaeilpour	بیماریهای زئونوز
P306	496	Molecular identification of Echinococcus granulosus sensu lato in stray and domestic dogs in Shahrekord, Central Iran	MohammadAli Mohaghegh	بیماریهای زئونوز
P307	528	Bioactive agent for prevention & control of Mycobacterium avium subspecies paratuberculosis	Mera Sharif	بیماریهای زئونوز
P308	592	Serological survey of Toxoplasma gondii infection in dogs with breeding disorders	Darya Foolady	بیماریهای زئونوز
P309	599	Serological survey of H9N2 influenza viruse in Domestic Pigeons of Ardabil, Iran	Aidin Azizpour	بیماریهای زئونوز
P310	626	Isolation and Antimicrobial Resistance Profiles of Salmonella enteritidis From an Alexandrine Parakeet (Psittacula eupatria): a Potential Zoonotic Source	Moein Khodayari	بیماریهای زئونوز
P311	638	Evaluation of the killing effect of chitosan and chitosan- amphotericin B in vitro and in vivo	Parisa Mousavi	بیماریهای زئونوز
P312	649	Serological survey of Leptospira infection in abortions of small ruminants	Abbas Zarei	بیماریهای زئونوز
P313	666	Seroprevalence of Brucella Antibody Titer (Wright's Test) in Suspected Cases in Kashan, Iran	Sareh Bagheri	بیماریهای زئونوز
P314	673	EXPRESSION AND PURIFICATION OF	Mehdi Gharakhani	بیماریهای زئونوز

		rLOA22 OF LEPTOSPIRA INTERROGANS IN PROKARYOTIC SYSTEM		
P315	689	Analysis of MicroRNA-146a gene polymorphism in patients with brucellosis: A Case-Control Study	Sima Kazemi	بیماریهای زئونوز
P316	690	Investigating the prevalence of Listeria monocytogenes and the pathogenic genes inlA, inlB, prfA, and hlyA in abortion	Rahil KiyanpourBerjoee	بیماریهای زئونوز
P317	709	Isolation of Campylobacter from aborted cases in sheep in Qazvin province	Mohammad Rafiee Barzoki	بیماریهای زئونوز
P318	720	Isolation and molecular identification of Brucella species from human and livestock in Hamadan province by PCR method	Behnam Rafiee	بیماریهای زئونوز
P319	723	Anti-leishmaniasis activity of Rhamnus cathatica on amastigote stages of Leishmania major standard strain invitro	Bahman Rahimi Esboei	بیماریهای زئونوز
P320	724	Determining the effect of the hydroalcoholic extract of Terminalia chebula on the tachyzoite of the Toxoplasma parasite in laboratory conditions (in vitro)	Bahman Rahimi Esboei	بیماریهای زئونوز
P321	727	Prevalence and molecular characterization of Shiga toxin-producing Escherichia coli in Sheep farms of Sanandaj-Iran	Pouya Ghaderi	بیماریهای زئونوز
P322	91	Identity Confirmation of IRIBA vaccine by multiplex PCR Assay and phage typing	Maryam Dadar	تازه های بروسلوز
P323	162	Comparison of efficacy between three clinical samples (blood, urine, semen) for molecular detection of Brucella Spp infection in male dogs	Amin Ganjavi	تازه های بروسلوز
P324	264	New protein and bacteriophage immunoassay techniques for detection Brucella	Fateme RafieiAtani	تازه های بروسلوز
P325	325	Molecular Detection of Brucella spp. in camel population in southern Kerman Province of Iran	Nafiseh Malekzadeh	تازه های بروسلوز
P326	479	Epidemiology of clinical and paraclinical findings and treatment of patients with brucellosis admitted to Beheshti Hospital in Kashan during 2011 to 2021	Hadis Fathizadeh	تازه های بروسلوز
P327	510	New therapeutic and diagnostic methods in cases of Malt fever: New Insight	Bita Zandi	تازه های بروسلوز
P328	596	Clinical manifestations and paraclinical findings of brucellosis patients admitted to Imam Reza Hospital, Mashhad – a 10-year retrospective study	Mahnaz Arian	تازه های بروسلوز
P329	116	Investigation and monitoring of microbial pollution (bacteria and Giardia protozoan) in urban water and production water of household water treatment plant in Ardabil, Iran	Arezoo Abdoli	اهمیت باکتریهای در الودگی مواد غذائی

P330	179	Investigation of microbial contamination of Mahabad Dam reservoir in different seasons	Mohamadhosein Sadeghizali	اهمیت باکتریهای در الودگی مواد غذائی
P331	181	Identification of bacterial agents causing sugarcane peduncle soft rot in Khuzestan Provine, Iran	Amal Fazliarab	اهمیت باکتریهای در الودگی مواد غذائی
P332	185	Inhibition of histamine accumulation by novel histamine-degrading species of Staphylococcus sp. isolated from goats and sheep milk	Safoora Pashangeh	اهمیت باکتریهای در الودگی مواد غذائی
P333	194	Effect of Hydroalcoholic and Aqueous Extracts of Carum Copticum on Escherichia Coli Strains in comparison with Gentamicin	SeyyedAli Mozaffarpur	اهمیت باکتریهای در الودگی مواد غذائی
P334	236	The General Information About food health and Safety, A Case Study	Mehrdad Pooyanmehr	اهمیت باکتریهای در الودگی مواد غذائی
P335	282	Identification of Salmonella spp from food outbreak in Tehran during 1400-1401	Sara Shakerihosseinabad	اهمیت باکتریهای در الودگی مواد غذائی
P336	289	Prophage typing of methicillin-resistant Staphylococcus aureus in the traditional dairy products of Ilam	Mostafa Nemati	اهمیت باکتریهای در الودگی مواد غذائی
P337	329	Native Probiotic LAB Strains Inhibit the Growth of Listeria monocytogenes and S.aureus in Lactic Cheese Samples	Fahimeh Assari	اهمیت باکتریهای در الودگی مواد غذائی
P338	338	The application of different types of packaging in controlling the microbial spoilage of food	Amin Khalili	اهمیت باکتریهای در الودگی مواد غذائی
P339	396	Investigation of contamination of Fecal Escherichia coli in vegetables collected from Sistan	Haniyeh Karimimarezi	اهمیت باکتریهای در الودگی مواد غذائی
P340	417	Evaluating the Effectiveness of Natural Detergent and Disinfectant on Gram-Positive and Gram-Negative Bacteria	Zahra PourahmadGhalehJoughi	اهمیت باکتریهای در الودگی مواد غذائی
P341	553	Investigating on the biological interaction of maize seedling soft rot bacteria	Maedeh Heidari	اهمیت باکتریهای در الودگی مواد غذائی
P342	559	The safety and quality properties of raw beef meat in slaughter plants of Kermanshah province using HACCP	Yasser Shahbazi	اهمیت باکتریهای در الودگی مواد غذائی
P343	563	Determining microbial contamination of poultry plants in Kermanshah province	Nassim Shavisi	اهمیت باکتریهای در الودگی مواد غذائی
P344	587	Occurrence, Virulence Characteristics, and Serogroups of Shiga Toxin-Producing Escherichia coli Isolated from Sheep and Goats in Razavi Khorasan Province, Iran	Ali Nemati	اهمیت باکتریهای در الودگی مواد غذائی
P345	670	Antibacterial activity of disinfectant column with UV lamp on some bacteria polluting surface water	Yaser Yousefpoor	اهمیت باکتریهای در الودگی مواد غذائی
P346	719	Investigation of the most important bacteria contaminating traditional Iranian dairy	Ahmad Nasrollahzadeh	اهمیت باکتریهای در الودگی

		products		مواد غذائی
P347	154	Emergence of amoebic dysentery mimicking Covid-19: A human case report from Iran	Sina Mohtasebi	بیماریهای نوظهور و نوپدید
P348	161	Detection of SARS-CoV-2 in household dogs and cats living with COVID-19 infected owners by Real-time PCR during Delta and Omicron variant waves in Iran	Maziar Khalilizadehmahani	بیماریهای نوظهور و نوپدید
P349	186	A review of the ZIKV virus and possible preparedness for the resulting epidemic	Ali Ahmadabadi asl alamdari	بیماریهای نوظهور و نوپدید
P350	244	Design a multi-epitope vaccine against influenza A virus with a bioinformatics approach	Mina Mirzaee	بیماریهای نوظهور و نوپدید
P351	538	Epidemiological use of nested PCR targeting the QpRS plasmid associated with the chronic form of Q fever in horses of West Azarbaijan province	Manijeh Tehrani	بیماریهای نوظهور و نوپدید
P352	672	Investigating the process of infection caused by intestinal parasites in Iranian HIV positive patients: a review article	Iman Pouladi	بیماریهای نوظهور و نوپدید
P353	696	Designing of a multi-epitope protein composed of essential virulence factors of SARS-Cov-2 virus and evaluation of its immunogenicity in animal model	Mohammadreza AsadiKaram	بیماریهای نوظهور و نوپدید
P354	743	Emerging of infections caused by multi-drug resistant (MDR) and Extensively-drug resistant (XDR) Acinetobacter baumannii in hospitalized patients in Iran; A systematic review.	Mahdieh Delfi	بیماریهای نوظهور و نوپدید
P355	6	evaluating the effect of methanolic extract of Quercus persica on Pseudomonas aeroginosa in combination with specific lytic phage	Behnam Hajizadeh Sisakht	فاژ تراپی
P356	22	Bacteriophage-derived endolysins as a novel candidate for treatment of P. aeruginosa infection	Erfaneh Jafari	فاژ تراپی
P357	31	Bacteriophage isolation against MDR Enterococus strains	Zahra EzadiLaybidi	فاژ تراپی
P358	60	Evaluation the treatment of diarrhea by phage cocktail product	Golnar Rahimzadeh	فاژ تراپی
P359	128	The control of Multi-Drug Resistant Klebsiella pneumoniae wound infection by Bacteriophage in a Rat Model	Mehrdad Mohammadi	فاژ تراپی
P360	148	Isolation, characterization, and genome investigation of vB_SenS_TUMS_E4, a polyvalent bacteriophage against Salmonella enteritidis	Narges Torkashvand	فاژ تراپی
P361	316	Isolation, Characterization and Genomic Analysis of vB_PaeS_TUMS_P81, A Lytic Bacteriophage against Pseudomonas aeruginosa	Haniyeh Kamyab	فاژ تراپی

P362	402	ENZYBIOTICS ARE A GOOD ALTERNATIVE TO ANTIBIOTICS	Mahoora Rahimi	فاژ تراپی
P363	410	Isolation and Characterization of Lytic Bacteriophages of E. coli from Anzali Lagoon	Farzin BabaAli	فاژ تراپی
P364	95	Effectiveness of inactivated COVID-19 vaccines among Stem Cell Transplant Recipient	Rozita Khodashahi	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P365	134	REVERSE TRANSCRIPTION LOOP-MEDIATED ISOTHERMAL AMPLIFICATION (RT-LAMP) FOR THE RAPID DIAGNOSIS OF CORONAVIRUS SARS-COV-2	Aysar AlJebur	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P366	141	Scorpion venom: dangerous or potency for COVID-19 treatment	Narges Pashmforoosh	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P367	163	Development of a potent recombinant antibody against the SARS-CoV-2 by in-depth immunoinformatics study	Fatemeh Yaghoobizadeh	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P368	164	The successful expression of a potent recombinant scFv antibody against the SARS-CoV-2	Fatemeh Yaghoobizadeh	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P369	222	Molecular mechanisms of galidesivir as a potential antiviral treatment for COVID-19	Hesamoddin Hosseinjani	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P370	223	Novel immunological aspects of sirolimus as a new targeted therapy for COVID-19	Hesamoddin Hosseinjani	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P371	229	Spore probiotic modulates lung inflammation triggered by the viral pathogen-associated molecular pattern poly (I:C) in BALB/c mice.	Fatemeh Baghoveh	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P372	309	The effect of opium contained in the herbal medicine Alerguard (Stopcivir syrup) on reducing the respiratory symptoms of patients with COVID-19	Ali Kargar	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P373	348	Analysis of laboratory parameters used for diagnosis of COVID-19 in suspected patients in Iran	Amin Sepehr	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P374	407	Optical nanobiosensors used for HCoVs detection	Fatemeh Jalali	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P375	421	Evaluation of Association between TLR7 Single Nucleotide Polymorphism (rs179008	Negar Parsania	تازه های تشخیص، درمان و

		and rs179009) with Susceptibility to Acute SARS-CoV-2 Infection in confirmed patients in Tehran from April to May 2020		واکسیناسیون بیماری کووید - ۱۹
P376	426	Evaluation of the association between rs3775296 and rs3775291 single nucleotide polymorphisms of TLR3 gene with susceptibility to acute SARS-CoV-2 infection in confirmed patients in Tehran	Sina Nagozir	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P377	430	Assessment of Variations in RBD domain within spike protein of SARS-COV2 during different waves in South Khorasan, East of Iran	Davod Javanmard	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P378	437	Investigating single nucleotide polymorphism (SNP) of different SARS-CoV-2 variants and evaluating their effects	Javad Sarvmeili	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P379	459	Exopolysaccharide (Postbiotic) Therapy: Possible Treatment for Covid-19	Saeed Ahmadi Majd	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P380	473	COVID-19 and parasitic diseases: A systematic review	Sara Kooti	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P381	489	COVID-19-associated fungal infections in Iran: a systematic review	Shahram Mahmoudi	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P382	495	Evaluation of mortality risk factors in patients who died due to covid-19 at Boushehr shohadaye khalije fars Hospital, 2020-2021	Fatemeh Abbasi	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P383	509	Pediatric Multisystem Inflammatory Syndrome Temporally associated with SARS-CoV-2 symptoms in Iran and literature review	Davood Azadi	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P384	539	In silico study of natural chalcone derivatives against RNA dependent RNA polymerase (NSP12) of SARS-CoV-2 using molecular docking tools	Tooba Abdizadeh	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P385	602	Systematic Reviews of Different Types of Drug Delivery in the Treatment and Prevention of Oral and Dental and Cardiorespiratory Diseases in Patients and Animals Involved in the Disease	Fereshteh Afkar	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P386	609	Protection and Efficacy of the commonplace Vaccines against COVID-19	Roya Hajialibabaei	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P387	648	Stem cell therapy for COVID19: The impact of coronavirus infection on recipients of	Maryam Tabourak	تازه های تشخیص، درمان و

		hematopoietic stem cell transplantation		واکسیناسیون بیماری کووید - ۱۹
P388	660	Investigation of Anti-SARS-CoV-2 IgG and IgM Antibodies among the Shahid Hashminejad hospital staff with three different exposure levels with COVID-19 patient, Mashhad	MAHDIS GHAVIDEL	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P389	677	A review of Nerium oleander effects as herbal therapy: a possible candidate in the treatment of COVID-19	Reyhane Rasizade	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P390	678	A review of the Anti-inflammatory effects of Artemisia spp as a possible candidate in the treatment of patients with COVID-19	Reyhane Rasizade	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P391	679	A review of the antifungal effects of Zataria multiflora as a possible candidate in the treatment of secondary fungal infections in patients with COVID-19	Reyhane Rasizade	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P392	682	bioinformatic analysis of Nucleocapsid (N) gene in human coronaviruses Comparing with other animal Coronaviruses	Mahsa Abdoljabbari	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P393	722	Covid- 19 patients neutrophil against Staphylococcus aureus and Pseudomonas aeruginosa	Mona Ghazi	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P394	726	Evaluation of Bacterial Coinfection in COVID-19 Patients Referred to Educational hospitals of Isfahan	Saeed Javdan	تازه های تشخیص، درمان و واکسیناسیون بیماری کووید - ۱۹
P395	252	Meta-analysis of latent tuberculosis in healthcare workers in Iran: a retrospective review	Niloofar Kavoosi	وضعیت بیماری سل در ایران و جهان واهمیت سل مقاوم به درمان
P396	254	A case report of feline tuberculosis: diagnosis and its dangers to humans	SeyedMehdi Joghataei	وضعیت بیماری سل در ایران و جهان واهمیت سل مقاوم به درمان
P397	293	A systematic review study on Role of long non-coding RNAs (lncRNAs) in tuberculosis	Reza Saki	وضعیت بیماری سل در ایران و جهان واهمیت سل مقاوم به درمان
P398	310	Detection of resistance to rifampicin and isoniazid in Mycobacterium Tuberculosis isolates by High Resolution Melting (HRM) Real-Time PCR to set-up this method in Tuberculosis Reference Laboratory	Mina Yazdanmehr	وضعیت بیماری سل در ایران و جهان واهمیت سل مقاوم به درمان
P399	363	Detection of rifampicin resistance strains of Mycobacterium tuberculosis using multiplex	Zahra Hosseinali	وضعیت بیماری سل در ایران و جهان واهمیت سل مقاوم به

		allele-specific polymerase chain reaction (MAS-PCR) in Ardabil, Iran		درمان
P400	454	Isolation and identification of Mycobacterium from poultry and personnel of Bird's Garden of Alborz province	Niloofar Mobarezpour	وضعیت بیماری سل در ایران و جهان واهمیت سل مقاوم به درمان
P401	458	Molecular identification of Mycobacteria isolated from Alborz zoos	Zohre Ahmadi	وضعیت بیماری سل در ایران و جهان واهمیت سل مقاوم به درمان
P402	485	Development of drug resistant mycobacterium tuberculosis strains	Romina Ghodsvali	وضعیت بیماری سل در ایران و جهان واهمیت سل مقاوم به درمان
P403	490	Bio-incidence of Mycobacterium avium subspecies paratuberculosis infection in goat milk samples using IS900-PCR	Zahra Hemati	وضعیت بیماری سل در ایران و جهان واهمیت سل مقاوم به درمان
P404	551	A Novel Mutation in the Efflux Pump Rv1258c (Tap) Gene in Mycobacterium tuberculosis Clinical Isolates Resistant to First-Line Drugs in Iran	Shima Sadat Farzaneh	وضعیت بیماری سل در ایران و جهان واهمیت سل مقاوم به درمان
P405	568	Liposomal delivery system/adjuvant for subunit vaccine against tuberculosis	Melika Moradi	وضعیت بیماری سل در ایران و جهان واهمیت سل مقاوم به درمان
P406	580	Linezolid resistance among multidrug-resistant Mycobacterium tuberculosis clinical isolates in Iran	Shahi Fatemeh	وضعیت بیماری سل در ایران و جهان واهمیت سل مقاوم به درمان
P407	9	Isolation and Identification of grapevine endophytic bacteria in west Azerbaijan province	Elhan Vagharisouran	-Other related topics
P408	12	Exploitation of two selected immunogenic proteins, BauA and OmpA, for protection against Acinetobacter baumannii infection	Motahare Tamehri	-Other related topics
P409	19	Designing shRNA Targeting West Nile virus NS3 Gene as a Potential Gene Therapy Tool Using Computational Pattern	Shekofe Rezaei	-Other related topics
P410	20	In silico Design of shRNAs against Crimean-Congo hemorrhagic fever virus RdRPs gene	Shekofe Rezaei	-Other related topics
P411	21	Lentiviral gene vector transformation in Escherichia coli derived DH5α, JM109 and Stbl4 cells	Shekofe Rezaei	-Other related topics
P412	24	Isolation and identification of Gallant Super (Haloxyfop-R-methyl) degrading bacteria in canola fields	Hossein MirzaeiNajafgholi	-Other related topics
P413	25	Isolation and identification of Trifluralin Degrading bacteria in bean fields	Hossein MirzaeiNajafgholi	-Other related topics
P414	26	Bacterial Vaccine	Farzaneh Dianatdar	-Other related topics

P415	39	Effect of bacterial starter culture under various temperatures on Kermanshahi roghan fatty acid profiles during the long time storage	Maryam Chalabi	-Other related topics
P416	43	Immunogenicity of the Recombinant Cryptococcus neoformans HSP70, a potential Candidate for Developing an ELISA kit	Pooya Jafari	-Other related topics
P417	44	The prevalence of ESBLs and biofilm formation in Escherichia coli isolated from urinary tract infection in Isfahan, Iran	Elham Haghighifar	-Other related topics
P418	45	The therapeutic effect of the pexiganan peptide on antibiotic resistance nosocomial pathogens models	Parvin Askari	-Other related topics
P419	46	Investigated the therapeutic effect of Tilapia Piscidin 4 (TP4) peptide on antibiotic resistance nosocomial pathogens in vitro and in vivo	Parvin Askari	-Other related topics
P420	59	Ca19Zn2(PO4)14 Nanoparticles: Synthesis, characterization and its effect on the colonization of Streptococcus mutans on tooth surface	Ali Shakeri moghaddam	-Other related topics
P421	64	In vitro assessment of native probiotic bacteria isolated from Lorestan Nomads Dairies	Mohaddaseh Ramezani	-Other related topics
P422	65	Bacillus cereus with an ability of oil bioremediation in harsh environmental conditions	Reyhaneh Shekari	-Other related topics
P423	81	Prevotella As Next Generation Probiotic	Azar Rahi	-Other related topics
P424	83	The genital hygiene habits and sexual behaviors associated with urinary tract infection in pregnant women	FATEMEH NASIRIAMIRI	-Other related topics
P425	89	Investigation of IL-2 and IFN-γ to EBV peptides in stimulated whole blood among multiple sclerosis patients and healthy individuals	Nastaran Rafiee	-Other related topics
P426	96	Inhibitors of fungal growth from natural origins	Fatemehsadat Jamzpour	-Other related topics
P427	104	Anti-bacterial and Anti-Quorum Sensing Properties of Dionysia Revolute Boiss against Secondary Bacterial Infections of COVID-19 Patients; An in-vitro Study	Farhad Moradi	-Other related topics
P428	121	An Evaluation of Antibacterial Effects of Human Amniotic Fluid on Pathogenic and Probiotic Bacteria in Vitro	MohammadMoein Mesbahzadeh	-Other related topics
P429	123	Synthesis silver nanoparticles using Peucedanum officinale extract (PO@AgNPs) and investigation antibacterial and antioxidant activities	MohammadMoein Mesbahzadeh	-Other related topics
P430	127	The anti-trichomonial effects of Methanolic extract of Rhamnus cathartica and nanoamodine on Trichomonas Vaginalis	Bahman Rahimi Esboei	-Other related topics
P431	136	Survey of Metalo beta Lactamase genes, bla	Mohammad Ahanjan	-Other related topics

		IMP1, INT 1 in Acinetobacter baumanii isolated from burn patients Zare Hospital of Sari		
P432	138	The Effects of Medicinal Plant Extracts of Salvia Xanthochelia on Hepatitis C Virus Replication in Cell Culture	Lida Eftekharivash	-Other related topics
P433	144	Identification of urease positive bacteria other than Helicobacter pylori in endoscopy (stomach biopsy samples) of patients with gastritis and investigation of antibiotic resistance of isolated bacteria	Mohammad Ahanjan	-Other related topics
P434	146	Improving ethanol tolerance in a commercial yeast strain by a combination of mutation and evolutionary engineering	Fatemeh Sheikhi	-Other related topics
P435	147	Increasing ethanol resistance in Saccharomyces cerevisiae using Adaptive laboratory evolution	Mahnoush Vosough	-Other related topics
P436	150	Inverse correlation between serum of anti-pneumococcal and ferritin levels after pneumococcal vaccination in splenectomised beta thalassemia major	Abdolreza Sotoodeh Jahromi	-Other related topics
P437	151	Seroloprevalence of Hepatits G Virus (HGV) in beta-Thalassemia Patients Jahrom-Iran, 1399	Abdolreza Sotoodeh Jahromi	-Other related topics
P438	159	Molecular discrimination of cryptic Candida albicans species complex isolated from patients in southeastern Iran	Setareh AghaKuchakAfshari	-Other related topics
P439	167	Electrospinning as a novel strategy for Encapsulation of Bifidobacterium animalis subsp. Lactis BB12 in Chitosan and Inulin nanofibers	HouriSadat Mousavi	-Other related topics
P440	174	Epidemiology, risk factors, species distribution, and antifungal susceptibility of candidemia among hospitalized patients with COVID-19	Zahra Rafat	-Other related topics
P441	176	Fabrication of Nano Ester Fibrs by pure PHB from wild type Azospirillum brasilense	Soheila Abbasi	-Other related topics
P442	177	Effect of harmel aqueous extract on LPS-induced NO production in human mononuclear cells in vitro	Fatemeh Hajighasemi	-Other related topics
P443	188	Evaluation of Shigella flexneri invasion by plaque formation assay	Mohammadmahdi Karimi-Yazdi	-Other related topics
P444	196	Detection of porphyromonas gingivalis DNA in the synovial fluid of rheumatoid arthritis patients bt real-time PCR	Solmaz MirMahdavi	-Other related topics
P445	199	Spa Typing of Methicillin-Resistant Staphylococcus aureus isolated from broilers in Ilam	Fazel Pourahmad	-Other related topics
P446	200	Isolation, Identification and Bioproprospecting the Antibacterial Activity	Fazel Pourahmad	-Other related topics

		of Actinobacteria Associated with Chamomile sp.		
P447	204	Investigation of biofilm formation among clinical isolates of Klebsiella pneumoniae in Bushehr province, Iran.	Hamed Hatami	-Other related topics
P448	211	Up-Regulation of VEGF in THP1 leukemic cells by lipopolysaccharide in vitro	Fatemeh Hajighasemi	-Other related topics
P449	212	recombinant PepX peptidase from Lactobacillus fermentum hydrolyzes gliadin protein in vitro	Laya Heydari	-Other related topics
P450	219	Antibacterial activity of kefir drinks prepared under different fermentation conditions	Hadi Koohsari	-Other related topics
P451	221	Antibacterial activity of several kombucha beverages prepared with different herbal teas and under different fermentation conditions	Hadi Koohsari	-Other related topics
P452	225	Bacteria-induced antimicrobial peptides secretion in Tenebrio molitor hemolymph	MohammadTaghi Mousazadeh	-Other related topics
P453	226	Isolation and Recognition of the Hyaline and Dematiaceae Fungi from Broiler Poultry feed in Amol City, Mazandaran	Mahdi DadashiFirouzjaei	-Other related topics
P454	227	Evaluation of the frequency of different species of Aspergillus from the lungs of extinct chickens in Aviculture in Babol county	Mahdi DadashiFirouzjaei	-Other related topics
P455	233	Multipathogen Detection in Patients with Respiratory Tract Infections; Identification of Non-Respiratory Viruses Using Multiplex Real Time Polymerase Reaction (PCR)	Zahra Heydarifard	-Other related topics
P456	234	Human adenovirus 6 identification in tonsillar tissue of children with tonsillar hypertrophy	Zahra Heydarifard	-Other related topics
P457	245	Isolation and identification of probiotic bacteria from dairy sewage	Zahra Hamzehali	-Other related topics
P458	249	Antibiotic resistance in farmed carp in Guilan province	Monireh Faeed	-Other related topics
P459	251	The effects of Galega Officinalis as ingredients of functional food on the treatments of type 2 diabetes patients	Maryam TamaskaniZahedi	-Other related topics
P460	256	Optimization of Gold Nanoparticle Production by Exopolymer of Chlamydomonas Spp	Nasim Nasiri	-Other related topics
P461	257	Bioremediation of Heavy Metals by Indigenous Probiotic LAB strains in Invitro Condition	Mahdieh Mostafidi	-Other related topics
P462	258	probiotics Modulate allergic asthma	Fatemeh Hajighasemi	-Other related topics
P463	259	Vaccino-informatics study of Bordetella pertussis toxin subunit 1 (PTXa), Corynebacteriumdiphtheria toxin (Tox) and Clostridium tetani Tetanus toxin (TetX) to develop a tri-valent DTP synthetic protein as candidate vaccine	Zahra Salahi	-Other related topics
P464	262	A qualitative investigation of the antimicrobial potential of two lactic acid	Sana Yahyazadehjasour	-Other related topics

		bacteria supernatant against prevalent skin pathogenic bacteria		
P465	271	Simian Virus 40 DNA in Immunocompetent Children with Respiratory Disease	Sina SalajeghehTazerji	-Other related topics
P466	275	Design of shRNAs against Yaba monkey tumor virus by insulin metalloprotease-like protein gene	Soren Nooraei	-Other related topics
P467	276	Antifungal Resistance in Clinical Isolates of Candida albicans species complex in Southeastern Iran	Setareh AghaKuchakAfshari	-Other related topics
P468	279	Investigating the dominant microbial population and predicting anaerobic naphthalene degrading genes in the Nayband Gulf	Mahsa Harirforoush	-Other related topics
P469	280	Molecular docking simulation of Anti parasitic properties of the main active ingredient of Nigella sativa in the inhibition of N-myristoyltransferase	Zahra Dehghan khalili	-Other related topics
P470	281	Risk factors and histopathological profile for unresponsive cases with anthroponotic cutaneous leishmaniasis: A case-control study on treatment outcome	Mehdi Bamorovat	-Other related topics
P471	286	Optimization of the bio-hydrogen production by a phototrophic bacterium	Mohammadreza Karamian	-Other related topics
P472	288	Molecula detection of probiotic bacteria isolated from Mauremys caspica stool	Amin Pouresmail	-Other related topics
P473	292	Co-infection of sexually transmitted pathogens with human papilloma virus in cervical sample: A multicenter study in Iran	Mahsa Shelerangkon	-Other related topics
P474	294	Dolutegravir versus efavirenz; A comparison of the effectiveness of two antiretroviral regimens in the treatment of HIV patients	Arian Amali	-Other related topics
P475	296	Comparison the antibacterial effect of green-synthetized nano-silver with calcium hydroxide in infected canals with Enterococcus Faecali	Majid Zare-Bidaki	-Other related topics
P476	306	Investigating the effect of MSI-99 antimicrobial peptide on MexAB-OprM efflux pump of Pseudomonas aeruginosa using molecular docking	Zohreh GholizadehSihamzgi	-Other related topics
P477	344	Synthesis of metal nanoparticles using different microorganisms	Negin Abdali	-Other related topics
P478	345	The use of actinomycetes in the production of secondary metabolites, including antibiotics, in dealing with MRSA strains	Seyed Mohammad Nekoueinaeini	-Other related topics
P479	347	Investigating the antibacterial and healing effect of medicinal plant extracts along with silver sulfadiazine in the treatment of burn infection	Hamid Reza Faqih Rad	-Other related topics
P480	353	Study on correlation between Demodex mites	Shokoofeh Zadehnasir	-Other related topics

		density and blepharitis.		
P481	355	Assessing the prevalence of certain bacterial infections in infertile and pregnant women	Fatemeh Sameni	-Other related topics
P482	359	Research on the relationship between Demodex mites density and redness and inflammatory dermatoses	Shokoofeh Zadehnasir	-Other related topics
P483	360	Methicillin-resistant Staphylococcus aureus in healthy horses in Marvdasht city	Hassan Cheshmi	-Other related topics
P484	361	Study on correlation between demodex folliculorum density and itchig	Maedeh Saveh	-Other related topics
P485	366	Assessing the prevalence of certain bacterial infections in infertile and pregnant women	Fatemeh Sameni	-Other related topics
P486	376	Effects of Esculin as an antimicrobial compound on pectate lyase enzyme of Pectobacterium carotovorum by molecular dynamics simulation	Ali Khakpour	-Other related topics
P487	379	Study on the routes of Demodex mites transmission	Maryam Misaghi	-Other related topics
P488	384	Influenza A virus and related secondary bacterial infections	Elham Sheykhsaran	-Other related topics
P489	386	Infantile Botulism: One of the Multiple Etiologies of Acute Hypotonia in Infancy	Parastoo Sharifian	-Other related topics
P490	389	Mycoplasma pneumoniae infection among children: a systematic review and meta-analysis	Parastoo Sharifian	-Other related topics
P491	394	Separation of alkaliphilic indigene reducing agent bacteria from Iron mine wastewaters and using them to eliminate cyanide from solution	Niloufarsadat Taher	-Other related topics
P492	395	Bacterial synthesis of spinally multi metallic Nanoparticle by indigene Iron mine bacteria	Niloufarsadat Taher	-Other related topics
P493	399	Probiotic and its relationship with diseases	Zahra Amoozad	-Other related topics
P494	405	The Role of Viruses in Preventing Anoikis and Tumor Spread	Zahra SobhiAmjad	-Other related topics
P495	409	The use of microalgae in the production of functional foods	Sahar Asadpour	-Other related topics
P496	412	Relationship between Bacterial Genital Infections in Pregnancy Outcomes: A Systematic Review and Meta-Analysis	Amjad Ahmadi	-Other related topics
P497	420	Using the Plackett-Burman design in optimization of cultural parameters of probiotic Lacticaseibacillus casei isolated from dairy products	Morteza MohajeriAmiri	-Other related topics
P498	424	Antibacterial and antibiofilm activities of nanoemulsion containing Nigella sativa essential oil on multi-drug resistant strains of Staphylococcus aureus and Pseudomonas aeruginosa.	Milad Afrooz	-Other related topics
P499	429	Evaluation of Antibacterial Combination Activities of Honey and Alcoholic Extract of	Sajjad Jafari	-Other related topics

		Crocus sativus Plant on Staphylococcus aureus: An in vitro Study		
P500	434	Investigation of allergenicity of antimicrobial peptides Magainin and MSI-99 using in silico method	Mohaddeseh Mohsenpour	-Other related topics
P501	440	Determination of Antimicrobial Susceptibility Testing of Acinetobacter Baumannii and Escherichia coli Isolates from The Heart Blood of Aborted Fetuses in Shiraz, Iran	Abolfazl RafatiZomorodi	-Other related topics
P502	441	Prevalence of Mycobacterium avium subsp. paratuberculosis in subclinically infected dairy cattle in Mashhad by Ziehl-Neelsen staining, culture, and PCR	Tahereh GholamhosseiniMoghaddam	-Other related topics
P503	442	EPIYA Motif Genetic Characterization from Helicobacter pylori Isolates in Distinct Geographical Regions of Iran	Fatemeh Estaji	-Other related topics
P504	446	A new pathovar of Pseudomonas amygdali as causal agent of bacterial leaf spot and die-back of hazelnut	Nargues FalahiCharkhabi	-Other related topics
P505	463	A review of the antimicrobial and anti-biofilm effects of Quercetin as a possible candidate for treating infected patients with pseudomonas aeruginosa	MohammadTaghi Mousazadeh	-Other related topics
P506	465	Occurrence of Klebsiella oxytoca as causal agent of palm date offshoot rot	Alma Abedinzadeh	-Other related topics
P507	480	Isolation and identification of nanocellulose producing bacteria from vinegar	Parisa Nikkhah	-Other related topics
P508	481	Occurrence of palm rots disease caused by Citrobacter koseri, a new plant pathogen	Alma Abedinzadeh	-Other related topics
P509	487	The world of the fetal microbiome	Sadaf Irani	-Other related topics
P510	493	Isolation of probiotic bacteria of traditional milk in Qom province and investigation of their adhesion to Caco2 cell line	Muhammad Asgari	-Other related topics
P511	494	Prevalence and Expression of Genes of Type II Antitoxin Toxin Systems in Clinical Isolates of Methicillin-Resistant Staphylococcus aureu	Pezhman Karami	-Other related topics
P512	498	An update on prevalence of slow-growing mycobacteria and rapidgrowing mycobacteria retrieved from hospital water sources in Iran – a systematic review	Pezhman Karami	-Other related topics
P513	500	Prevalence of Helicobacter felis and Helicobacter heilmannii and coinfection with Helicobacter pylori in gastric biopsy specimens in endoscopic ward of Shahid Beheshti Hospital, Hamadan, Iran	Pezhman Karami	-Other related topics
P514	501	The glycerol effect on Docosahexaenoic acid production in salt-resistant bacteria	Zahra Fathi	-Other related topics
P515	511	The investigation of antibacterial effects of Lawson (Henna extract)-loaded porous silica	Mahsa Sedighi	-Other related topics

		nanoparticles		
P516	513	Isolation of enterotoxigenic Escherichia coli (ETEC) from children medical center hospital, Tehran	Ahmad Nasser	-Other related topics
P517	518	Evaluation of the effect of soil actinomycetes extracts on the growth of pathogenicity of fluconazole-resistant strains of Candida albicans	Mahtab Karami	-Other related topics
P518	522	A systematic review of the antimicrobial effects of different plant extracts (Scrophularia striata) as a possible candidates in the treatment of infectious diseases	Sajjad Jafari	-Other related topics
P519	523	Phyto-Mediated Silver Nanoparticles for Antibacterial Performances by Salicornia Extract	Mona NajafiMoghadam	-Other related topics
P520	524	Evaluation of the antimicrobial effect of molds isolated from animel feed on gram positive bacteria	Hedyeh Taghizadeh	-Other related topics
P521	535	Investigations of Portulaca oleracea Compounds with Helicobacter pylori Virulence Factors CagA and VacA Using Molecular Docking in Gastric Cancer	Nastaran Nikkhou	-Other related topics
P522	536	Evaluation of the effect of soil bacteria extracts on growth of pathogenicity of fluconazole resistant strains of Candida tropicalis.	Sepideh Zolghadr	-Other related topics
P523	541	In vitro Qualitative Phytochemical Analysis and Antibacterial Activity of Ethanolic Extract of Flowers of Rheum ribes L. from Tonekabon - Iran	Samin Amirkhani	-Other related topics
P524	544	Antibacterial Activity of Methanolic Extract of Pistacia atlantica Fruits using Disk Diffusion Method for the Treatment of Urinary Tract Infections	Samin Amirkhani	-Other related topics
P525	546	Investigation of Phytase Production by a Strain of Aspergillus niger in Submerged Fermentation of Orange peel	Atefeh Hamzeh	-Other related topics
P526	549	Bacterial etiology of fever episodes of splenectomised patients in three medical centers in the city of Mashhad in northeastern Iran	Mahnaz Arian	-Other related topics
P527	560	Anti-biofilm potency of PepR, a viral-derived peptide, against drug-resistant Pseudomonas aeruginosa	Behrouz Taheri	-Other related topics
P528	561	Microbial decolorization of acid red 18 by a novel bacterial strain	FATEMEH HEYDARI	-Other related topics
P529	562	High frequency of phenotypic resistance against ampicillin in Shiga toxin-producing Escherichia coli strains isolated from sheep carcasses in Kerman	Parvin Mohseni	-Other related topics

P530	565	Study of phenotypic antimicrobial resistance to cephalosporins in Shiga toxin-producing Escherichia coli strains isolated from sheep carcasses in Kerman	Parvin Mohseni	-Other related topics
P531	566	Prevalence of antibiotic resistance against colistin in Escherichia coli strains isolated from sheep carcasses in Kerman	Parvin Mohseni	-Other related topics
P532	567	Identification of Infectious Laryngotracheitis antibodies in broiler flocks in ce Guilan provin	SeyedehAftab Momeni	-Other related topics
P533	570	The Screening of Rubella Virus, Cytomegalovirus, Hepatitis B Virus, and Toxoplasma gondii Antibodies in Prepregnancy and Reproductive-Age Women in Tabriz, Iran	Edris Nabizadeh	-Other related topics
P534	572	The study of the antibacterial effect of peptides obtained from the microbial degradation of feather by Bacillus Tequilensis BK206	Kowsar Bidari	-Other related topics
P535	573	Isolation and molecular identification of endophytic fungi from Licorice (Glycyrrhiza glabra L.)	Melika Esfandiari	-Other related topics
P536	575	Frequency of cagE and cagM genes in Helicobacter pylori isolated from patients with digestive disorders	Zahra Ebrahimi	-Other related topics
P537	576	In vitro and In vivo evaluation of antiendotoxin activity of the pepR peptide against endotoxin mediated shock and invasive Pseudomonas aeruginosa Infection	Zahra Farshadzadeh	-Other related topics
P538	579	Study of Infection of Broiler Chickens in Guilan Province with Fowl cholera by ELISA Method	Mobina Ghafuri	-Other related topics
P539	581	Isolation and molecular identification of two rutin-producing endophytic fungi from Caper (Capparis spinosa L.)	Melika Esfandiari	-Other related topics
P540	584	Phenotypic resistance to fluoroquinolones (enrofloxacin and ciprofloxacin) in Shiga toxin-producing Escherichia coli isolates from sheep carcasses in Kerman against	Pouneh Hajipour	-Other related topics
P541	585	Investigation of antimicrobial resistance to chloramphenicol in Shiga toxin-producing Escherichia coli isolates from sheep carcasses in Kerman	Pouneh Hajipour	-Other related topics
P542	590	Antimicrobial resistance to gentamicin in Shiga toxin-producing Escherichia coli isolated from sheep carcasses in slaughterhouse of Kerman	Pouneh Hajipour	-Other related topics
P543	597	Assessment of in vitro Antibacterial Efficacy of Phytosynthesized Selenium Nanoparticles using Polylophium involucratum (Pall.) Boiss.	Shahab Ojani	-Other related topics

		Seeds Extract Against Pathogenic Bacteria		
P544	606	Antibacterial Activity of Synthesis of Silver Nanoparticles of Methanolic Extract of Leaves of Anethum graveolens L. from Tonekabon - Iran	Mehdi Mirzaeichegeni	-Other related topics
P545	611	Evaluation of gene expression changes in two-component regulatory systems of Pseudomonas aeruginosa	Siavash Aynesazi	-Other related topics
P546	612	Bacterial Profile and Antibiotic Resistance in Patients with Diabetic Foot Ulcer: a meta-analysis	Saeed Ahmadi Majd	-Other related topics
P547	636	Comparison of bactericidal properties of argon and helium cold atmospheric plasma on multidrug resistance Pseudomonas aeruginosa	Reyhaneh Shekari	-Other related topics
P548	640	Feasibility of Ethanol Production from Whey by Kluveromyces sp.	Mahdi Eiwaznezhad	-Other related topics
P549	650	Designing of a multi-epitope vaccine candidate against Campylobacter jejuni based on bioinformatics study	Zahra Firoozi	-Other related topics
P550	651	In silico study to design a multi-epitope vaccine against to challenges caused by Listeria monocytogenes	Najmeh Alinaghi	-Other related topics
P551	652	Evaluation of immunological characteristics in order to design a multi-epitope vaccine candidate against shigella dysenteri	Mahsa Behzadmand	-Other related topics
P552	653	Antimicrobial activity of Pediococcus acidilactici PTCC 1954 and Leuconostoc mesenteroides PTCC 1953 isolated from organic meat sausages	Mohammad FaeziGhasemi	-Other related topics
P553	654	Characterization of Razi Bovine Kidney (RBK) cell line as sensitive cell for BOHV-1 virus	Masoumeh Maqami	-Other related topics
P554	655	A multi-epitope vaccine candidate design against Coxiella burnetii causing Q fever	AHMADREZA HABIBI	-Other related topics
P555	680	Application of Chitosan-Silver Nanoparticle as Theranostic Agents	Fatemeh Mahmoudimeymand	-Other related topics
P556	683	Studu on Antibacterial activity of extracted phycocyanin from spirulina platensis	Ali Sheykhinejad	-Other related topics
P557	706	Effects of probiotic therapy on immune system and inflammation in patients with multiple sclerosis	Morteza Nazari	-Other related topics
P558	707	The probiotic properties and potential of vaginal lactobacilli spp. Isolated from healthy women against some vaginal pathogens	Arezoo Asadi	-Other related topics
P559	708	Isolation and identification of Lactobacillus producing Biosurfactant and investigating its antimicrobial effects on human pathogenic bacteria	Ardalan Rahimipour	-Other related topics
P560	710	Isolation, Identification, and Evaluation of The Ability to Produce Xanthan Gum from	Amirhossein Ghadiri	-Other related topics

		Lactose by Xanthomonas campestris Isolated from Plants Infected by Bacterial Canker		
P561	712	Molecular identification of bacteria isolated from vaginal infections of infertile women	Nima ShaykhBaygloo	-Other related topics
P562	713	Optimization of bio-decolorization Acid Red 14 using bacterial strain isolated from wastewater	Fatemeh Bahramichegeni	-Other related topics
P563	716	Applications of Bacillus as probiotics for human use	Ahmad Nasrollahzadeh	-Other related topics
P564	718	Optimization of Pectinase Production from Agricultural Waste Under Solid-State Fermentation by Bacillus pumilus	Amirhossein Ghadiri	-Other related topics
P565	728	Efficacy of alcoholic extract of Heracleum persicum (Golpar) on the survival of Lactobacillus plantarum and Lactobacillus kazei in probiotic dough,	Fatemeh Dadmarzi	-Other related topics
P566	735	Detection of enteroviruses in children with acute gastroenteritis in Iran	Negar Javidihelan	-Other related topics
P567	741	A Mathematical Probabilistic Modelling for the Single Molecule Kinetics Problem	Reza FallahMoghaddam	-Other related topics
P568	742	Simple One-step Synthesis of Carrageenan Coated-Silver Nanoparticles with Antibacterial Properties	Mahsa Sedighi	-Other related topics

مقالات سخنرانی اعضاء پنل

ALTERNATIVE TREATMENT OF UNCOMPLICATED URINARY TRACT INFECTION

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Background and Aim : Urinary tract infections (UTIs) are among the most prevalent infectious diseases in general practice and of these, 80% are classified as uncomplicated UTIs (uUTIs).

Methods : Although current EAU guidelines recommend the use of antibiotics (ABs) as the first choice of treatment for the acute phase of uUTIs, several prospective randomized, placebo-controlled studies have been performed already comparing antibiotic therapy with symptomatic therapy. These results were compelling enough for the updated German Clinical Guidelines to encourage the use of the non-AB symptomatic treatment in selected cases of acute lower uUTIs with mild-to-moderate symptoms and use the Acute Cystitis Symptom Score (ACSS) questionaire for the clinical diagnostics and patient-reported outcome in females with acute episodes of uUTI (cystitis).

Results : If not only antibacterial agents but also alternative substances will be tested, clinical criteria should become the most important inclusion and outcome objectives. For the diagnostics of uUTI not only the presence but also the severity (scoring) of the so-called typical symptoms are important. Although, the presence of “a minimum number of symptoms such as frequency, urgency and dysuria AND documented pyuria” as suggested by the draft EMA guideline may have a reasonable sensitivity and specificity, to diagnose AC, for the definition of “clinical cure” a scoring system is also necessary, because it cannot be expected that in all patients with favourable clinical outcome all so-called typical symptoms will have been disappeared.

Conclusion : . In female patients with acute uUTI the Acute Cystitis Symptom Score (ACSS) questionaire already validated in several languages could be a suitable tool for better defined diagnostics and patient-reported outcome to define better clinical cure and failure in well designed clinical and epidemiological studies and for self-treatment.

Keywords : uncomplicated urinary tract infection, acute cystitis, female patients, Acute Cystitis Symptom Score, ACSS, questionaire.

Case presentation of infectious and non-infectious problem in a patient with bone marrow transplantation

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Background and Aim : VOD/SOS arises from endothelial cell damage and hepatocellular injury due to the transplantation conditioning regimen. locally released cytokines induce activation of cell adhesion molecules on endothelial cells, resulting in local cell damage and detachment and activation of the coagulation pathway, leads to fibrosis of sinusoids, followed by perivascular hepatocyte necrosis and the venular blockage characteristic of VOD/SOS. We decide to present a case of VOD after infectious problems of bone marrow transplantation.

Methods : A 29 y/o woman, known case of MDS/AML who presented with Anemia and thrombocytopeni, was selected for Allo-HSCT from her sibling (related fullmatch) ,She was HBSAg Positive patient who received Tenofovir from 6m ago.She received endoxan & busulfan for conditioning regimen from central vein catheter and then stem cell was injected. Levofloxacin , Voriconazole, and Acyclovir were administrated for prophylaxis. Cylosporine and MTX were started for GVHD prophylaxis .On day 6 , the patient became feverish with no complain.Fever & neutropenia management was performed,Meropenem 1 gr TDS was started.4 days later , fever continued with stable vital signs and no focal sign and symptom.Liposomal Amphotricin 3mg/kg was started and Voriconazole was discontinued.On Day 12 ,(2 day after antifungal therapy) She became afebrile with neutrophil recovery.Blood culture results from catheter and peripheral revealed Candida.spp.Catheter was removed and echocardigraphy and Ophthalmoscopy were normal.6 days later, she bacame febrile again associated with abdominal pain.

Results : CMV PCR &HBV DNA PCR were negative. Cyclosporine level was normal. PT,INR , Serum Alb were normal . Doppler sonography showed reversal of portal vein flow; abnormal portal vein waveform compatible with VOD/SOS depend on patient history. Liver biopsy was not performed due to patient condition. Treatment of the patient may include,Defibrotide,High-dose Methylprednisolone,Tissue Plasminogen Activator,transjugular intrahepatic porto-systemic shunt.

Conclusion : Recommendations for the Prevention of VOD/SOS in Hematopoietic Stem Cell Transplantation Recipients are: Avoid the use of hepatotoxins during conditioning (eg, azoles, acetaminophen). Identify drug-drug interactions in preparative regimens and modify as appropriate. Risk-adjust preparative regimen intensity according to hematopoietic cell

transplantation-comorbidity index. Pharmacologic monitoring of busulfan. Avoid the use of progesterone and estrogen if possible

Keywords : BMT- HSCT-Candida-VOD

Presentation of a case with SBP infection before liver transplantation

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Background and Aim : Recurrence of SBP has been reported to be 69% in 1 year. Norfloxacin 400 mg per day orally has been reported to successfully prevent SBP in (1) patients with low-protein ascites and (2) patients with prior SBP. Intermittent dosing of antibiotics to prevent bacterial infections may be inferior to daily dosing due to the development of bacterial resistance) and thus daily dosing should preferentially be used.

Methods : A 57 Y/O woman Background: Cirrhosis due to PBC Complications: GI bleeding, Encephalopathy, SBP. Drug history was: Ursobil Aldactone, Lactulose and Ciprofloxacin. She was presented in our MDT meeting and has been listed for LT (with the first priority). The patient admitted in Imamkhomeinin hospital two weeks later with Fever, abdominal pain and drowsiness. Her laboratory findings were compatible with SBP and she treated with piperacillin tazobactam and was discharged with ciprofloxacin after 5 days.

Results : Development of SBP in post-LT patients is associated with a poor prognosis In a study done by Leong et al, 18 patients (85.7%) who developed SBP ultimately died. The median time from the onset of ascites to death was 214 days (range: 10 – 1085 days). Following the first episode of SBP, the median time to death was 50.5 days (range: 4 – 549 days). Patients with Ascitic fluid PMN > 250 cells/mm3 should receive empiric antibiotic therapy e.g. Cefotaxime 2 g/ 8 h. Oral Ofloxacin (400 mg BD) can be considered in patients without: Shock, grade 2 hepatic encephalopathy, Cr> 3 mg/dl.

Conclusion : Development of SBP in post-LT patients may be associated with a poor prognosis. Early diagnosis and prompt management are two strategies to reduce mortality and morbidity of patients who received organ transplant while they have SBP.

Keywords : Liver Transplant, Solid Organ Transplant, Infectious Diseases, Spontaneous bacterial peritonitis

Infection Control of Multi-drug Resistant Gram-negative Bacteria (MDR-GNB)

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Background and Aim : According to the World Health Organization, Infection prevention and control (IPC) is a scientific approach and practical solution designed to prevent patients and health workers from being harmed by avoidable infection and as a result of antimicrobial resistance. Infections caused by MDR Gram-negative bacteria are difficult to treat, and can cause additional pain to patients and can prolong the length of stay in hospital and even lead to death.

Methods : IPC Assessment Framework, published by WHO, states the core components of infection prevention and control include: IPC program, guidelines, training, surveillance, multi-modal strategies, monitoring of practices, feedback, staffing, environmental health, and equipment for IPC at the facility level.

Results : Definitions: MDR (multidrug-resistant): non-susceptibility to at least one agent in three or more antibiotic categories; XDR (Extensive drug-resistant): susceptible to only one or two antibiotic categories; PDR (Pan drug-resistant): non-susceptibility to all agents in all antibiotic categories. Epidemiology: healthcare-associated infection (HAIs) pooled prevalence in high-income countries is 7.6% vs. low- and middle-income countries 10.1% to 15.5%. In Iran, the most common organisms according to the national report are gram-negative bacteria such as Klebsiella, Acinetobacter, E.coli, etc. More than half of the organisms are MDR. Infection control principles are general or specific; general ones like hand hygiene, proper ward's physical structure, optimizing patient nutritional status, glycemic control, system-based practices, adequate staff, education, environmental health, patient screening and decolonization, isolation measures, antibiotic stewardship and etc. And specific IPC measures like device-associated infection (DAIs) preventive bundles for ventilator-associated pneumonia, central line bloodstream infection, and catheter-associated urinary tract infection.

Conclusion : A successful infection control of MDR-GNB within a hospital needs teamwork and a multi-disciplinary approach. It's of utmost importance knowing the related definitions, epidemiology, history, and general/specific IPC principles.

Keywords : Infection Control, Multi-Drug Resistance, Gram-Negative Bacteria

TRENDS IN THE EPIDEMIOLOGY OF BRUCELLOSIS CASES IN IRAN DURING THE LAST DECADE

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Background and Aim : Brucellosis is one of the most important zoonotic diseases that impose a serious public health burden on some countries in the world. Annually, the World Health Organization reports more than 500000 new cases of human brucellosis. The disease is endemic in most parts of Iran; especially, in areas where people live in close contact with infected animals. According to data from the Ministry of Health, the average incidence of brucellosis in Iran was 22 cases per 1000000 population, with a decreasing trend of surveillance.

Methods : This study is a cross-sectional survey that was carried out from 2011-2020 in all provinces of Iran and among patients with clinical symptoms.

Results : During the last decade, a total of 173526 cases were reported from different provinces of Iran, with a higher frequency of occurrence in males (58.2%) living in rural areas (77%), as compared to those in urban areas (23%). Also, brucellosis was more common in the summer season (June) and most of the cases were via contact with infected livestock (91%) and consumption of unpasteurized dairy products (78% in rural areas and 76% in the urban areas).

Conclusion : The failure to effectively control brucellosis may be attributed to lack of knowledge about the disease, consumption of unpasteurized dairy and raw meat, lack of proper and safe vaccines for prevention and eradication programs, lack of rapid detection systems, and ineffective methods of isolating infected animals. Therefore, education and advancement of people's knowledge are key to the prevention and control of the disease.

Keywords : Brucellosis, epidemiology, Iran

ASSESSING THE TREND OF BOVINE TUBERCULOSIS IN IRAN, CHALLENGES AND APPROACHES

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Background and Aim : Bovine tuberculosis (bTB) is a bacterial disease associated with infections of Mycobacterium bovis (M. bovis), a species in the M. tuberculosis complex. The disease mostly affects cattle but can become established in other species. The purpose of this retrospective study was to study the trend of bovine tuberculosis in susceptible livestock populations of industrial herds and its trend in routine slaughter animals in slaughterhouses to identify non-tuberculin reactor animals.

Methods : Evaluation of the trend of bovine tuberculosis in susceptible livestock populations has been done over a period of 12 years. This retrospective study is based on the information and data of the GIS raw data obtained from the system. Slaughterhouse data were also statistically evaluating for non-tuberculin tuberculosis and suspected slaughter animals.

Results : Evaluation of disease trends and operations in recent years has shown that every year about 1.300 million tuberculosis test implemented in the level of eligible livestock in the country and the program of tuberculin test in 2021 relatively increased (10%) with compared to 2020. Test and slaughter of reactor animals program, monitoring of routine slaughtered animals in the slaughterhouses and accurate follow-up of non-tuberculin tuberculosis reactor animals isolated in slaughterhouse are the most important control program in the country. There has been a significant decrease of tuberculosis reactors in 2021 compared to 2020 which decreased by 20% and also the identification of non-tuberculin tuberculosis cases increased. The initial descriptive study of the BT in 2021 indicates that the Tuberculin skin test were carried out in 65% of industrial dairy farms in the country, which consist of 57% of the isolated reactors in the evaluation process in epidemiological units.

Conclusion : With the implementation of the compulsory livestock insurance program in the second half of 2019, it was promised that the level of coverage of tuberculin test in the country will be relatively increased, but what happened in the end was the resistance of some livestock epidemiological units farmers (even Dairy industrial units) in performing insurance and finally resistance in performing BT test in livestock units, which has led to a decrease in operations in 2019 (5% decrease compared to the previous year).

Keywords : Bovine tuberculosis, Iran

ZOONOTIC ASPECTS OF BURKHOLDERIA MALLEI INFECTION (GLANDERS)

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Background and Aim : Burkholderia mallei is a Gram-negative, non-motile, non-sporulating, intracellular bacterium which causes subcutaneous infection called as farcy or disseminated infection known as glanders in horses, mules and donkeys. Clinically the disease is acute, often fatal in donkeys and mules or chronic in horses. Equine glanders is a contagious and transmissible to closely exposed human. It is considered as occupational hazards to horse caretakers, equine handlers, veterinarians and laboratory workers. In India, re-emergence of equine glanders has been reported in 2006 and increasing trend of glanders was observed from 2015 onward.

Methods : The present study describes the report of targeted surveillance conducted in glanders in-contact equine handlers and veterinarians.

Results : A total of 735 serum samples from glanders in-contact humans were collected between 2016 and 2021 from different states in India. Samples were tested serologically by complement fixation test (CFT) and Hcp1 indirect ELISA. Only one sample was found to be positive for B. mallei specific antibodies and rest of the sera were found to be negative for glanders. Clinical and laboratory investigation confirm that the equine handler had contracted B. mallei infection from glanders affected equines in his premises. In India, the last reported case of naturally occurring human glanders in a British veterinarian was documented in 1911.

Conclusion : This study reports the first case of human glanders after 109 years in India. Lack of awareness among equine keepers about glanders disease and improper bio-security measures while handling of infected equines may favours the transmission of B. mallei to humans.

Keywords : Glanders, ELISA, CFT, Equines, Humans

SIGNIFICANCE OF BACTERIAL DORMANCY IN FOODBORNE PATHOGENS

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Background and Aim : In the majority of studies performed within the laboratory it is common practice to cultivate foodborne pathogens within a culture then study behavior or efficacy of decontamination methods etc. In reality, the laboratory environment is far removed from the real world in which bacteria mostly exist in a non-growing state and more than likely, under constant stress. Dormancy (hibernation) is a strategy that bacteria, including human pathogens, undergo to enhance resistance and persistence to stress. There two main forms of dormancy encountered are the persister state and Viable But Not Culturable (VBNC). The common features of both types of dormancy is enhanced resistance to stress (for example, sanitizers, heat) and inability to be cultured using standard techniques. Consequently, dormant bacteria can resist stress that would otherwise be inactivated and also cannot be detected by culturing. In addition, dormant pathogens can result in latent infections but cause illness upon revival. In the following presentation the different forms of dormancy encountered in foodborne pathogens will be described along with experimental approaches. Potential mechanism how dormancy is induced and selected for will be described. The search for agents that revive dormant bacteria will be discussed along with knowledge gaps, especially in relation to risk assessment in relation to food safety.

Methods : -

Results : -

Conclusion : -

Keywords : Dormancy, Foodborne, Pathogens

ARE RECURRENT UTI ASSOCIATED WITH MORE VIRULENT *E. COLI*?

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Background and Aim : More than 40% of women who experience acute cystitis develop recurrence which can be either relapse or reinfection based on the strains responsible for causation of new episode of cystitis. Present study was planned in order better insight of the host behavioural and bacterial characteristics that are associated with recurrent UTI in women.

Methods : A cohort of 241 women with culture proven acute cystitis were followed up for recurrence and their index episode *E. coli* was matched with recurrent strain(s) using Enterobacterial RepetitiveIntergenic Consensus (ERIC) profiles. *E. coli* were further analyzed for phylogroups, virulence genotype, virulence score (VF score) and biofilm formation capability. Questionnaire-based data was collected from participants through interview for behavioural practices and psychosocial aspects associated with recurrent UTI.

Results : 46 women had culture confirmed recurrence by *E. coli* during follow-up of one year. Acute *E. coli* from 22 women were classified as RI (recurrent infection) isolates as the index and first recurrence were caused by same strain of E. coli while remaining 24 women were assigned to SI(single infection) group. Pathogenicity island gene malX (p=0.02), toxin gene cytotoxic necrotizing factor cnf1 (p=0.00) and VF score ((1.95 vs. 1.58, p =0.04).) were significantly associated with RI isolates. Phylogroup B2 formed majority in RI isolates, whereas SI had significant number of isolates belonging to phylogroup A. RI isolates were significantly better biofilm producers then SI isolates (p = 0.01). Family history of UTI in a first degree female relative and constipation were the strongest independent risk factors for recurrent cystitis (OR=2.61, 95%CI=1.17-5.81; OR=2.61, 95%CI=1.16-5.84), other included stress incontinence (OR=2.16, 95%CI=1.07-4.33).

Conclusion : *E. coli* associated with recurrence had higher mean VF scores and stronger biofilm formation capability thus appear to be more virulent and malX seems to have a role in causing recurrence. Many behavioural risk factors reflect cultural and ethnic lifestyle and most of the risk factors for initial infection are potentially modifiable but sufficient to also pose risk for recurrence.

Keywords : UTI, *E. coli*

Investigation of microbiological characteristics of canned tomato paste product in IRAN

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Background and Aim : Tomato paste is one of the processed tomato products that has a long shelf life and is used as an important food ingredient all over the world. According to global statistics, Iran is among the top ten producers of tomato paste in the world, Iran ranks sixth to seventh among producers in the world, and is among the ten producers that play a role in international trade.

Methods : In order to investigate the possible contamination of canned tomato paste in the country, 46 samples of canned tomato paste in the amount of 184 cans of 800 grams were purchased from the market. The samples incubate at of 30C◦ ± 1C◦ for 14 days and 55 C◦ ± 1C◦ for 7 days.

Results : The contents of both test containers were tested separately for mesophilic bacteria, thermophilic bacteria, mold and yeast. Out of 46 samples of canned tomato paste, 29 samples (63%) showed contamination with thermophilic bacteria.

Conclusion : phenotypic and genotypic tests were performed to determine the type of thermophilic bacteria on the obtained colonies and the type of the desired species was examined in pathogenicity.

Keywords : canned tomato paste, thermophilic bacteria, mesophilic bacteria

Neglected Microbial Infections at a Glance: (Strategies and Tactics)

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Background and Aim : Neglected tropical diseases (NTDs) are a variety of severe diseases that are mainly prevalent in tropical regions. The sources of these diseases are multi-factorial and without eradicating their causative factors, all creatures will be affected by the consequences of them. Identification of the epidemiological situation, reservoirs and carrier's resources and the basis of their continuity or outbreaks events should be considered.

Methods : WHO Member States are grouped into six regions and each region has a regional office. Using the data collected by the health sectors and centers for disease control could be reliable sources for choosing the best path.

Results : The occurrence of Neglected Microbial Infections is complex and often associated to regional and economic conditions and nature of causative agents. The frequency of the events make their public-health control challenging.

Conclusion : In spite of the mobilization of the involved countries' capacity, there were limitations to eradicate the corona pandemic. Thus to rely on a ten-year short-term road map to prevent, control, eliminate or eradicate of Neglected Microbial Infections may not be feasible.

Keywords : Infection, Disease Eradication, World Health Organization

Most common microbial foodborne diseases analysis

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Background and Aim : In this session, we will talk about the most common microbial associated with foodborne diseases including:Gastritis: Helicobacter pylori, _ Salmonella species, Shigella species, Campylobacter jejuni and coli, Escherichia coli (STEC, EIEC, ETEC, EPEC, EAEC), Vibrio cholerae, V. parahaemolyticus, Bacillus cereus, Yersinia enterocolitica, Edwardsiella tarda, Pseudomonas aeruginosa, Aeromonas species, Plesiomonas shigelloides, Bacteroides fragilis, Clostridium botulinum, C. perfringens, Food intoxication: Staphylococcus aureus, Bacillus cereus, Clostridium botulinum, C. perfringens, Antibiotic-associated diarrhea: Clostridium diffcile, Staphylococcus aureus

Methods : Selected Bacteria Associated with Foodborne Diseases:Aeromonas species(Meats, produce, dairy products), Bacillus cereus (Fried rice, meats, vegetables), Brucella species(Unpasteurized dairy products, meat), Campylobacter species(Poultry, unpasteurized dairy products), Clostridium botulinum(Vegetables, fruits, fish, honey), C. perfringens(Beef, poultry, pork, gravy), Escherichia coli(Beef, unpasteurized milk, fruits and juices, vegetables, lettuce), Francisella tularensis(Rabbit meat), Listeria monocytogenes(Unpasteurized dairy products, coleslaw, poultry, cold-cut meats), Plesiomonas shigelloides(Seafood), Salmonella species(Poultry, unpasteurized dairy products), Shigella species(Eggs, lettuce), Staphylococcus aureus(Ham, poultry, egg dishes, pastries), Streptococcus group A(Egg dishes), Vibrio species(Shellfsh), Yersinia enterocolitica(Unpasteurized dairy products, pork)

Results : Selected Bacteria Associated with Waterborne Diseases:Aeromonas species (Gastroenteritis, wound infections, septicemia), Campylobacter species, Escherichia, coli, Plesiomonas shigelloides, Salmonella species, Shigella species, Yersinia enterocolitica(Gastroenteritis) Francisella tularensis (Tularemia), Legionella species (Respiratory disease), Leptospira species(Systemic disease), Mycobacterium marinum(Cutaneous infection), Pseudomonas species(Dermatitis), Vibrio species(Gastroenteritis, wound infection, septicemia)

Conclusion : Intestinal protozoa: Amebae (Entamoeba histolytica, E.polecki), Ciliates (Giardia duodenalis, Dientamoeba fragilis, Neobalantidium coli , Coccidia (Cystoisospora belli, Sarcocystis Sp., Cryptosporidium Spp., Cycclospora cayetanensis. PHYLUM: MICROSPORA(MICROSPORIDIA) Encephalitozoon, Enterocytozoon, Nosema, Trachipleistophora. Entomophthoromycosis: Entomophthorales Basidiobolus, Conidiobolus

Keywords : Microbial foodborne diseases, Microbial waterborne diseases, Bacterial, viral, protozoan

MICROBIOME ANALYTICS IN THE 21ST CENTURY: PERSPECTIVES AND CAVEATS

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Background and Aim : Humans exist as meta-organisms comprised of both the macroscopic host and its symbiotic commensal microbiota. With approximately 100 trillion cells, bacteria outnumber host cells by at least a factor of 10 and express at least 100-fold more unique genes than their host's genome. The tremendous enzymatic capability of the microbiome results in a plethora of metabolites found in humans which play a fundamental role in nearly all aspects of host physiology and disease development including metabolic, cardiovascular and even neuro-psychatric illnesses. Since 2000, large-scale 16S rRNA or metagenomic studies have dramatically expanded the knowledge about diversity of the human gut microbiome. Approximately 80% of the bacteria found by molecular tools are uncultured so far, and hence can be characterized only by high throughput sequencing and adequate bioinformatics analysis. Applying our patented NGS-quality control tools we completed four European external quality assessments (EQAS) comparing results from different next generation sequencing (NGS) centers with special emphasis on critical preanalytic steps, nucleic acid preparation and bioinformatic data processing. Furthermore, our goal is to achieve a functional understanding of bidirectional microbe-host interactions in health and diseases (e.g. Graft versus host disease and depression), beyond largely descriptive compositional and metagenomic analyses.

Methods : not applicable

Results : not applicable

Conclusion : comprehensive survey

Keywords : Microbiome

MICROBIOTA COMPOSITION, HOST GENE-EXPRESSION AND INFLAMMATORY BOWEL DISEASES

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Background and Aim : Dysbiosis emerges as a key factor in IBD pathogenesis. The aim of the present study is to profile changes in the gut microbiome and transcriptome in patients with inflammatory bowel disease and to correlate the potential changes with the administration of anti-TNF agent Infliximab in order to investigate their potential to predict patient response to anti-TNF therapy

Methods : Mucosal biopsy samples from IBD patients and nine healthy controls (HC) were examined for differences in microbiota composition (16S rRNA gene sequencing) and mucosal gene expression (RT-qPCR) at baseline and upon completion of IFX treatment, accordingly, via an in silico pipeline.

Results : Significant differences in microbiota composition were found between the IBD and HC groups. Several bacterial genera, which were found only in IBD patients and not HC, had their populations dramatically reduced after anti-TNF treatment regardless of response. Alpha and beta diversity metrics showed significant differences between our study groups. Correlation analysis revealed six microbial genera associated with differential expression of inflammation-associated genes in IFX treatment responders at baseline. This study shows that IFX treatment has a notable impact on both the gut microbial composition and the inflamed tissue transcriptome in IBD patients.

Conclusion : Our study reveal enterotypes that correlate with transcriptome changes and help differentiate IFX responders versus non-responders at baseline, suggesting that, in combination, these signatures can be an effective tool to predict anti-TNF response.

Keywords : microbiota, IBD, genetics

Laboratory diagnosis challenges of COVID-19

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Background and Aim : COVID-19 is a respiratory infectious disease caused by SARS-CoV-2, was first identified in Chinese patients. Early detection of positive cases such as COVID-19 patients and asymptomatic carriers is one of the main factors of prevention and further spread of infection in the population and pandemic control. During the COVID-19 pandemic, researchers have developed various diagnostic tests for detection of the SARS-CoV-2 based on various methods.

Methods : The diagnosis methods for detection of SARS-CoV-2 contain molecular test for viral genes detection and the immunological methods including human specific antibodies detection and viral antigens detection and point-of-care (POC) tests. There are challenges in diagnosis for each method, and each of them has advantages and disadvantages in diagnosis of COVID-19.

Results : Currently, real-time reverse transcriptase polymerase chain reaction (RT-PCR) is the most used diagnostic assay and gold standard method in many countries for diagnosis of COVID-19 as recommended by world Health Organization (WHO). The numerous RT-PCR protocols were developed with different sensitivity and specificity based on diagnosis of different genes of SARS-CoV-2 such as envelope (E) gene, RNA dependent RNA polymerase (RdRp) gene, spike (S) gene, nucleocapsid (N) gene and ORF1b region of virus genome.

Conclusion : The RT-PCR based on use of one or two gene targets and antigen detection tests such as some POC tests are used for diagnostic purpose, while serologic test for detection of specific antibodies against SARS-CoV-2 proteins used for assessment of seroconversion after vaccination or exposure to the virus.

Keywords : COVID-19, SARS-CoV-2, Diagnosis

ANTIBACTERIAL RESISTANCE IN PEDIATRIC BURN PATIENTS

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Background and Aim : Burn injuries are a global public health problem and still remain the leading cause of disability and unintentional death.

Methods : The risk of infections is relatively high due to the immunosuppressing effect of burns, invasive therapeutical procedures, and length of hospitalization. In pediatric burn patients, mortality rates due to sepsis still remain high. Infected burn wound serves as an important source for most of the cases of sepsis.

Results : The development of antibiotic resistance causes a big challenge in the treatment of bacterial infections in both adult and pediatric patients. Furthermore, resistance to multiple antibiotic classes reduces the probability of adequate empirical coverage, with possible unfavorable outcomes. Vulnerability to infections and increasing antibiotic resistance among organisms put burn patients at high risk of infection by multidrug-resistant (MDR) organisms. Hospital cleaning practices, antibiotic therapy without knowledge of circulating bacterial strains, and excessive and prolonged use of antibiotics have led to the development and selection of multidrug-resistant bacteria. The MDR/XDR/PDR gram negative bacteria, MRSA/VRSA/VRE have become increasingly common in hospital settings, necessitating the understanding of institutional specific circulating strains.

Conclusion : Moreover, healthcare professionals managing burn patients require in-depth knowledge of bacteria causing infection and their antimicrobial resistance patterns to direct empirical therapy.

Keywords : Antibacterial resistance, pediatric,burns

Situation of Glanders and isolation and identification of Burkhulderia mallei from suspect horses in Iran in last year

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Background and Aim : Glanders, is a highly contagious and fatal re-emerging zoonotic disease that is caused by the host-adapted equine pathogen Burkholderia mallei. The long-lasting assumption on geographical restriction of Glanders has been cracked due to globalization. Besides, in the industrialized world the poor experience and lowered awareness of involved professionals against the longley-eradicated glanders have resulted in re-introduction of the disease. Iran, in the heart of the Middle-East, remains a stronghold for glanders which is enzootic in the country similar to its flanking neighbours. A rising trend in the disease outbreak has been noted in recent years that might be a reflection of increasing potential hotspots. The molecular genotyping works conducted on limited B. mallei isolates collected in the last 10 years in Iran are surprisingly not in support of a homogenic population of the pathogen. Whether this observation indicates a heterogenic indigenous population of M. bovis accommodating clones and sub-clones being active in the region from the past or we are watching exotic strain coming to settle, we will not know unless more comprehensive molecular epidemiology researches have been completed. This work was mainly conducted to collect more B.mallei isolates.

Methods : Field and laboratory follow ups were conducted on equids that proved positive in the routine IVO-operated CF tests. If possible lower eyelid malleination was also tested. In animals destined to euthanize, postmortem specimens from suspected internal organs and wounds, and in CF negative animals and swabs were taken for bacterial culture and investigations. At laboratory specific bacterial culture media both liquid and solid were employed to improve pathogen recovery rate from the specimens.

Results : These efforts lead to a successful isolation of the pathogen as four isolates were recovered from glanders-suspected horses in Alborz, Kermanshah, Tehran and Kordestan provinces. Biochemical and molecular assays confirmed identity of the isolates as B. mallei. Further genotyping work is still ongoing to characterize the strains.

Conclusion : While CF test delivers conclusive results, it is an expertise and resource-demanding test that might not be available in all laboratory settings. Given this fact, application of complementary tests including malleination and bacterial culture will help with accuracy of disease diagnosis.

Keywords : Glanders, Burkholderia mallei, Iran, CF, bacterial culture

Reviewing the potential role of probiotic yoghurt in weight management and glycemic control in type2 diabetes

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Background and Aim : In the last decades, obesity have become the main challenges of people in developing countries, as it causes many diseases including type 2 diabetes, hypertension, etc. Accordingly, researchers have studied the effects of probiotic yoghurt on the body weight management and prevention of type2 diabetes. Yogurt is a popular fermented product in the humans' diet with specific nutrients such as calcium and protein which may have especial effects on appetite control and glycemia. Lactobacillus bulgaricus and Streptococcus thermophiles are two main bacteria, which may positively alter gut microbiota. Probiotic yogurt contains active, live cultures during the storage time and consumption. Additionally, probiotic yogurt usually contains more beneficial bacteria in comparison with conventional yogurt

Methods : this study reviewed the specific properties of probiotic yogurt as a unique product among the other probiotic foods and its action in weight loss, energy balance and type 2 diabetes control

Results : According to the results of several epidemiological and clinical studies, probiotic yogurt consumption might increase the loss of body fat and decrease the food intake which leads to body weight loss. In addition, probiotic yogurt might decrease the glycemic and insulin response while it can alter hormone response of gut as well as its microbiota.

Conclusion : Hence, daily intake of standard portion of probiotic yogurt provides a contribution to energy metabolism regulation and body health, strongly.

Keywords : yogurt ,probiotic, weight management,type2 diabetes

COMBINATORIAL EFFECTS OF ANTIBIOTICS AND ENZYMES AGAINST BACTERIAL BIOFILMS

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Background and Aim : Antimicrobial Resistance (AMR) and the formation of biofilms are the main challenges of today's medicine because it has become a global problem that affects the treatment of multiple infections and impacts public health. Infections caused by these multi-resistant or biofilm forming bacteria potentially reduce the possibility of effective therapy; this situation increases morbidity and mortality and treatment costs, and new and innovative strategies need to be devised. Biofilm-dispersing enzymes degrade the extracellular polymeric matrix surrounding bacterial biofilms, and increase their susceptibility to antibiotics and immune cells. Co-treatment using antibiofilm agents with antibiotics appears to hold great promise as one such strategy. In this study the effects of anti-biofilm activity of some enzymes alone and in combination with antibiotics from various classes on the degradation of dual-species biofilms of Pseudomonas aeruginosa and Staphylococcus aureus were evaluated.

Methods : The efficacy of trypsin, β-glucosidase, and DNase I enzymes on the degradation of dual-species biofilms of Pseudomonas aeruginosa and Staphylococcus aureus in a wound-like medium are investigated. Moreover, the reduction of minimum biofilm eradication concentration (MBEC) of meropenem and amikacin was evaluated when combined with enzymes.

Results : The minimum effective concentrations of trypsin, β-glucosidase, and DNase I enzymes to degrade biofilms were 1 µg/ml, 8 U/ml, and 150 U/ml, respectively. Combination of 0.15 µg/ml trypsin and 50 U/ml DNase I had a significant effect on S. aureus-P. aeruginosa biofilms which resulted in the dispersal and dissolution of all biofilms. In the presence of the enzymatic mixture, MBECs of antibiotics showed a significant decrease ($p < 0.05$), at least 2.5-fold.

Conclusion : In conclusion, it was illustrated that the combination of trypsin/DNase I enzymes targeting different components of biofilm matrix, can be considered as an anti-biofilm agent and an appropriate candidate to degrade S. aureus-P. aeruginosa biofilms.

Keywords : Trypsin, β-glucosidase, DNase I, biofilm, Pseudomonas aeruginosa, Staphylococcus aureus

THE CURRENT STATUS OF ANTIBIOTIC RESISTANCE IN STAPHYLOCOCCUS AUREUS

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Background and Aim : Staphylococcus aureus remain to be an important nosocomial pathogen in the word. The growing numbers of antimicrobial-resistant S. aureus place a significant burden on healthcare systems and have important global economic costs. The present study investigated the current status of antibiotic resistance in S. aureus.

Methods : A searched via PubMed, Google Scholar, Web of Science and Scopus was performed for relevant articles that reporting the status of antibiotic resistance in S. aureus around the word. The search terms were Staphylococcus aureus, antimicrobial resistance and resistance gene.

Results : Many different mechanisms including i-horizontal gene transfer which encoded by mobile genetic elements such as plasmids and transposons ii- the staphylococcal cassette chromosome and iii- mutations in chromosomal genes have an important role in S. aureus antibiotics resistance. In the literature the most important mechanisms of drug resistance are including drug modification/alteration, modification of drug binding sites/targets, changes in cell permeability resulting in reduced intracellular drug accumulation in S. aureus. The resistance rate to most antibiotics increasing during the current decade in S. aureus in most of the countries.

Conclusion : Regarding to the high resistance rate to antibiotics and diversity of antimicrobial resistance genes in S. aureus isolates, it needs to be more monitored by public health surveillance in different countries. Continuous monitoring and characterization of S. aureus resistance genes and mechanisms could be helpful in controlling the rising rate of antibiotic resistance. It is particularly important to avoid empirical use of antibiotics and trying for discover novel antibiotics because of emergence of multidrug resistance S. aureus.

Keywords : Staphylococcus aureus, antimicrobial resistance, resistance gene

Urinary Tract Infection: Different Therapeutic Strategies

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Background and Aim : Urinary tract infections (UTIs) are among the most common microbial infections in humans and represent a substantial burden on the health care system. Uropathogenic Escherichia coli (UPEC) strains are the most prevalent causative agent of UTIs. Other bacteria like proteus mirabilis, klebsiella pneumonia are among causative agent. The routine therapy of UTIs is based on the use of antibiotics such as β-lactams, trimethoprim, nitrofurantoin and quinolones in many countries. Increasing antibiotic resistance and their side effects on human body show the need to develop alternative strategies such as vaccine against UTIs. Different vaccines based on the whole cells (killed or live-attenuated vaccines) and antigens (subunits, toxins and conjugated vaccines) have been evaluated against UTIs pathogens. Furthermore, other therapeutic strategies such as the use of probiotics and antimicrobial peptides are considered against UTIs.

Methods : We in our group for more than a decade focused our research on different strategies for UTI treatment. Multi-epitope vaccines using insilico studies, based on epitope mapping of different virulence factors, using various adjuvants, other strategies, using Lactobacillus bacteria (LAB) as probiotic expressing virulence factors, were used. Anti-Sense Oligonucelotides (ASO) to inhibit target genes were also examined.

Results : Although all these attempts resulted in desirable humoral and cellular immune responses or inhibited target genes respectively; however, due to lack of suitable animal model are still in experimental phase. Among latest attempts we focused on use of Anti-microbial peptides (AMPs) that inhibit the biofilm formation in combination with antibiotics, which seems have promising prospective as alternative therapeutic strategy.

Conclusion : In conclusion based on our findings it seems that if vaccines should be developed for the treatment it should be made based on prevalent serotypes circulating in the country. Moreover, search for more AMPs with antibiofilm ability in combination with antibiotics to be used for treatment is other way to tackle the disease.

Keywords : UTI, virulence factors, vaccines, AMPs

Advances in diagnosis approaches of invasive fungal infections in haematological malignancy patients

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Background and Aim : Invasive fungal infections (IFI) remain important causes of morbidity and mortality in hematologic malignancy patient's population. It is clear that new approaches to the management of IFIs are required. Recent advances in diagnosis now allow the use of very sensitive imaging techniques with an extremely low negative predictive value. New diagnostic methods facilitate an early diagnosis of invasive fungal disease and allow for utilization of a pre-emptive treatment approach, which may ultimately lead to improved treatment outcomes and reduced toxicity.

Methods : The aim of this article is to review classical and new diagnostic tools for IFIs in hematologic malignancy patient's and to summarize current limitations of these methods.

Results : Since conventional diagnostic tools such as culture lack sensitivity and specificity, alternative diagnostic assays have been developed. In recent years, progress has been made in the development and evaluation of sensitive sero-diagnostic assays, including detection of genomic DNA sequences and fungal antigens, which aid in a rapid, early diagnosis of IFI. Both serology and PCR can be used to monitor the response to antifungal therapy. The optimal use of non-culture-based methods is in prospective screening of patients at high risk.

Conclusion : The early diagnosis of IFIs still remains a problem as existing tools lack sensitivity or specificity. Therefore, the combination of microscopy, culture-based methods, and serological and molecular techniques is necessary to allow early detection of IFIs.

Keywords : Invasive fungal infections; new approaches; haematological malignancy

New methods in the diagnosis of viral infections

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Background and Aim : Viral infections are the most important infectious agents in human diseases. Accurate and quick diagnosis of viral infections is very important in controlling these infections.

Methods : In this study, three new methods of NGS, PCR and hybridization are examined for the diagnosis of covid-19, enteroviruses and EBV.

Results : New diagnostic methods should be used to identify emerging infectious agents, but these methods still have weaknesses.

Conclusion : The results of this study show that new technology is very important in the quick and accurate diagnosis of viral infections. In addition, traditional methods such as cell culture cannot be ignored.

Keywords : Viral infection- New Detection- NGS

THE POSSIBLE ROLE OF MAP AND HERVS IN THE TYPE 1 DIABETES ONSET.

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Background and Aim : Type 1 diabetes (T1D) is an autoimmune disorder, characterized by the production of autoantibodies to the pancreatic beta-cells. In previous studies, we indicated that Mycobacterium avium subspecies paratuberculosis (MAP) could be a potential risk factor for T1D, suggesting that MAP infection could induce immune imbalance. Emerging evidence has also indicated that Human endogenous retrovirus (HERVs) may play a role in etiopathogenesis of TD1. Indeed, the envelope proteins of HERV-W and HERV-K families have been detected in serum and pancreas of patients with T1D, for these reasons we investigated the role of MAP and HERVs in a Sardinian pediatric population with T1D by analyzing the humoral response and variation over time toward peptides derived from both, the external pathogen and the endogenous retrovirus in T1D patients (from the onset up to 12 years from the diagnosis) and healthy controls.

Methods : Statistical significative different response was observed in antibody titre against all MAP and HERVs peptides between patients at T1D Onset vs. HCs ($p<0,0001$). A statistically significative and progressive decline was observed in antibody level as early as the first year of the disease. On the other hand, this pattern occurred with all peptides but not for HERV-K which remains constant from the onset until the age of six years.

Results : Our results support the hypothesis that both pathogens are linked to T1D etiology, and also that HERVs activation can be induced by certain infectious agent such as MAP. The results are in line with this hypothesis, given the high reactivity expressed in patients T1D onset for all peptide fragments evaluated. The progressive decrease in antibody titer over the years could reflects the development of an active autoimmune process at the onset. A contribution of MAP in this process could result from molecular mimicry with homologous epitopes such as Zinc transporter 8 (ZnT8) and Proinsulin (PI), leading to autoimmune responses.

Conclusion : Taken together, these findings support the hypothesis that MAP and HERV could act as risk factors for T1D, suggesting that they may serve as potential biomarkers.

Keywords : Mycobacterium avium subspecies paratuberculosis, Human Endogenous Retroviruses W and K, Type 1 Diabetes

NOVEL ANTIMICROBIAL WITH ACTIVITY AGAINST MDR GRAM NEGATIVE BACTERIA

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Background and Aim : In recent years several novel antimicrobials with activity against multidrug-resistant Gram-negative bacilli have become available. Among the novel antimicrobials are ceftazidime-avibactam, meropenem-varborbactam, imipenem-relebactam and cefiderocol. The novel antimicrobials rarely cover all bacterial resistance mechanisms and it is of utmost importance to use them rationally. This presentation reviews the activity of the novel antimicrobial as well as the potential for resistance development. Methods for reliable antimicrobial susceptibility testing are also presented, and it is emphasized that susceptibility cannot be assumed, but needs to be confirmed by testing. The presentations also briefly discusses some antimicrobials that are still in the development pipeline.

Methods : -

Results : -

Conclusion : -

Keywords : multidrug-resistant

Medical laboratory Roles and Challenges in detection and reporting antimicrobial resistance

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Background and Aim : Rising trend in bacterial resistance to antibiotics is recognized as a major global threat to public health. It is estimated that antimicrobial resistance would account for 10 million deaths per year worldwide by 2050. In between Emergence of multidrug resistant bacteria that may require new technologies for detection and reporting needs specific attention. This lecture is aimed to briefly explain the main roles of laboratory to strengthen antibiotic stewardship activities while mentioning some of the current challenges in detection of antimicrobial resistance.

Methods : Understanding different processes related to patient management in a health care facility and reviewing the impact of integration and involvement of laboratories in infection prevention and control activities reveals important role of laboratory in achieving antibiotic stewardship objectives.

Results : Guidance and information provided by laboratories to determine local microbial susceptibility pattern can help to generate appropriate surveillance data. On the other hand by using new rapid diagnostics, laboratories can decrease test turnaround time that not only shortens time needed for selecting most appropriate treatment but also help to avoid misuse or overuse of antibiotics. Cascade or selective testing and reporting according to available formulary is another way that helps to provide appropriate guidance for updating empirical therapeutic algorithms. Main challenges that our facilities encounter include availability of quality diagnostic material to detect emerging resistant strains, access to updated standards and guidelines to generate comprehensive institutional antibiogram profile and optimize empiric antimicrobial therapy and issues related to specimen collection and handling procedures.

Conclusion : All these benefits could be achievable if laboratories are integrated in an organized multidisciplinary system with strong communication between clinicians, laboratory staff, and pharmacists that facilitate correct specimen collection, proper flow of necessary data and information as well as appropriate and standardized testing.

Keywords : Antimicrobial resistance- Antibiotic stewardship- Antibiogram-Emerging resistance

The effects of Microbiota in immune system

Ghamartaj Khanbabaee [1] *

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2. *Matin Pourghasem Department of Pulmonology, Mofid Pediatrics Hospital, Shahid Beheshti University of Medical Sciences, Tehran, Iran.*

Background and Aim : Background : In recent years, there have been many investigations on the microbiota and its effects on the human immune system and the mechanisms of immune modulation and disease prevention or migitation.

Methods : Method : The importance of microbiomes has been studied more as a defensive factor in the human body system.By colonization resistance,they fight against pathogens,increase the immune system potency and the resistance level of epithelial barrier. They also play a role in the absorption of micronutrients .The interaction between human microbiota and the host's immune system plays an important role in the process of infectious, pulmonary, gastrointestinal , metabolic and autoimmune diseases, so understanding this relationship can lead to developing novel diagnostic and therapeutic methods.There are reports of manipulation of intestinal microbiota in the treatment of GI diseases.use of probiotics, that are particular strains of microbiota, has favorable effects on host immunity and against pathogens, in addition to being useful in the treatment of intestinal disorders, it has also been promising in the treatment of lung diseases.One should consider the role of genetics, diet and environmental factors such as antibiotics in the composition of intestinal microbiota,moreover the dynamics of the GI system during infancy, which is easily influenced by extrinsic factors that leads to the conversion of microbiota composition. The relation between microbiota and infectious diseases has a two-way pattern, as the microbiome fights against pathogens, its composition may also be affected after a severe infectious disease such as sepsis and can lead to intensification of the disease and even organ failure. By increasing the growth of indigenous agents, the microbiota counteracts the colonization of pathogens, which is possible through competitive metabolic interactions, direct killing of the pathogen, localization in intestinal niches, and induction of the host's immune response. Following the structural disturbance of the microbiota, the risk of infectious and inflammatory diseases increases.

Results : Results : Microbiota has an important impact on health and illness, and various serious diseases are directly or indirectly affected by it ; and if considered in therapeutic modalities will have many benefits for the patients.

Conclusion : Conclusion : By understanding the interaction between the microbiome, the body's immune system, and pathogenic agents, we can reach to a clinical perspective in diagnosing the diseases, and developing preventive and therapeutic solutions.

Keywords : Micobiologist, immune system, serious disease

MOLECULAR INSIGHTS INTO UNCOMPLICATED UTI FROM COMMUNITY SETTINGS

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Background and Aim : Urinary tract infection (UTI) is one of the most common bacterial infections in clinical practice worldwide in both community and healthcare settings, that cause significant morbidity and mortality. Approximately 150 million people are diagnosed with UTI every year, costing in excess of 6 billion dollars, worldwide. Escherichia coli and Klebsiella spp. are the two clinically relevant organisms accounting for 75%-90% of uncomplicated and complicated UTI. The distribution and susceptibility pattern of uropathogens may vary according to time, place and underlying condition. Routine urine culture testing is recommended prior to initiation of treatment. Today, Antimicrobial Resistance (AMR) is a major threat to human health and belongs to the priorities of World Health Organization. Widespread use of antibiotics without antibiotic susceptibility testing is a major reason for this. Uncomplicated UTI is one of the common conditions at the community level treated empirically and regarded as a potential cause for the emergence of AMR. The increasing dissemination of Extended Spectrum β- Lactamases (ESBLs) producing uropathogens in the community renders clinical treatment difficult. Limited information is available regarding community-acquired UTI from rural areas.

Methods : We conducted a prospective multicentric-cross-sectional study at the community level targeting patients attending the Out Patients Department (OPD) of the rural health centers from four geographical regions (North, South, West and East) of India to determine the epidemiology, antibiogram profile, and identification of ESBL producers.

Results : Total of 397 out of 5297 (7.5%) urine samples from clinically suspected UTI patients were found positive causing significant bacteriuria (Adults:Paediatrics 7.9:1, Male:Female 1:1.8). Diabetes melitus was observed as the commonest risk factor followed by renal stone. Approximately 79.1% of total cases were caused by E.coli (64%) and K. pneumoniae (15.1%) and uniformly predominated in all the geographical regions.

Conclusion : This is alarming data from a large-scale nationwide community study indicating the increasing prevalence of ESBL-producing and carbapenem-resistant E.coli isolates in the community. This study outlines the UPEC isolates harbouring multidrug-resistant genes along with the high-risk clones. There is a high prevalence of virulence markers and resistance genes among these isolates from both symptomatic and asymptomatic bacteriuria patients. Hence, regular AMR surveillance with judicious usage of antibiotics, and policy restriction is highly essential to formulate the guidelines, especially in developing

countries. Strict infection control measures and regular surveillance is required to limit its spread in the community; thereby preventing the imminent threat of an epidemic of antimicrobial resistance in future.

Keywords : Urinary tract infection, Escherichia coli, Antimicrobial resistance

Brucellosis Diagnostic Approaches

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Background and Aim : Brucellosis is a neglected tropical zoonotic disease that threatens the food production and public health sectors. It is of considerable animal welfare and economic importance and is underreported in most parts of the world, especially in developing countries. Brucellosis has been reported in domestic animals and humans in Iran. The burden of the disease is unclear, and the awareness remains questionable. It became necessary for this review to be carried out to highlight the diagnostic approaches used to confirm brucellosis in animals and humans.

Methods : So far, reports of brucellosis in previous studies have been based on serology only. Seroprevalence data of Brucella antibodies in animals indicate the risk of human brucellosis. There is no reports to identify Brucella species circulating in Iran.

Results : It could largely be attributed to a lack of standard laboratories for testing and the lack of consumables. The way forward will require a surveillance system for brucellosis in the country, educating all sectors affected and drafting a diagnostic protocol for high-risk individuals.

Conclusion : They do not portray a comprehensive human brucellosis situation where the disease is endemic. Accurate microbiological, molecular and epidemiological evidence of brucellosis within the country is lacking. Hence, the need for a nationwide survey using the standardized methodology to understand.

Keywords : Brucella, Brucellosis, Diagnosis, Iran

Phage therapy: a new therapeutic solution for infected wounds

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Background and Aim : Wound infections have been explained as severe conditions especially in hospitals. In addition to extensive tissue damage and nonhealing wounds, septicemia can increase the mortality rate of wound infections. The most important causative agents of wound infections are included: Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, and Pseudomonas aeruginosa. Because of high prevalence of antibiotic resistant bacteria and limitations to discovery of new effective antibiotics, finding new approaches to combat bacterial infections has been inevitable recently.

Methods : In this study, we reviewed the results of using bacteriophages against wounds MDR (Multi-drug resistant) bacterial infections focusing on experimental assays, animal models and clinical trials. Phages effectiveness in wound healings was surveyed based on previous reports.

Results : According to the results, phages have high potential to prevent wound infections by MDR bacteria, faster healing of the infections and removing bacterial biofilms with lower toxicity than antibiotics. Animal models were used to determine the phages activity against the infections. Using combinational therapy (phage-antibiotic) and phage cocktails were reported as more efficient methods to control the infections and also reducing the antibiotic resistances. In addition, using new delivery systems could be very helpful in wounds phage therapy.

Conclusion : In spite of successful experiments of phage therapy indicating high potential of bacteriophages to prevent and remove wound infections, more studies are needed to extensive therapeutic uses of bacteriophages and manufacturing the regularly therapeutic phage-based products.

Keywords : bacteriophages, multidrug-resistant bacteria, wound infection

UTI AND URINARY CATHETERS

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Background and Aim : The most frequent hospital associated infection (HAI) is urinary tract infection (UTI). Hospital associated UTI is linked with a urinary catheter in 70-80% of the cases. Therefore, strategies to reduce catheter associated UTI (CAUTI) are of most importance.

Methods : The following questions should be answered on every patient with urinary catheter: the real need for catheter insertion, duration, appropriate type and size of catheter. The following considerations should also be followed: a proper technique of insertion, and proper maintenance.

Results : The most important determining factor for the development of CAUTI is the duration of catheter maintenance. The risk of CAUTI is 3-7% daily and around 100% after 30 days. Internal catheters should not be used to control incontinence in the elderly. Intermittent catheterization is a better alternative for patients with bladder emptying problems. Using a sterile technique of insertion is an important key, however, the need for antiseptic cleaning of the meatus is not established. Using catheters and reservoirs with a closed system helps in reducing CAUTI and any break in the closed system necessitates the change of catheter with its reservoir. The benefit of bag irrigation and using antiseptics for the disinfection of reservoirs is not established. Using short time intervals for change of catheters is not recommended and is associated with increased infection rates in some studies. Indications for change of catheters include: obstruction, infection, and disrupted closed system. Antibiotics are not recommended routinely when inserting or changing catheters. The use of complex drainage systems with antibiotics/valves is not recommended and does not reduce symptomatic UTI. The use of silicone catheters is not associated with less UTI but is associated with less encrustation and is used in cases of frequent obstruction.

Conclusion : Key elements for the prevention of CAUTI are establishing a real need for catheterization in candidates and using alternatives to internal catheters in selective patients, minimal duration of catheterization in case needed, using sterile technique of insertion and maintainance of closed system. The use of expensive coated catheters or reservoir systems have not been associated with reduced CAUTI in most studies.

Keywords : Urinary tract infection

ANTIMICROBIAL PRESCRIBING ETIQUETTES IN SIMPLE AND COMPLICATED UTI

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Background and Aim : Urinary tract infections (UTIs) are among the most frequent infections in clinical practice requiring a considerable number of antibiotic prescriptions.

Methods : The prescribing pattern in a healthcare facility can be understood by carrying out point prevalence surveys or detailed audits. Questionnaires and surveys can also be utilized. It is important to appreciate that antimicrobial policies based on local antibiograms and education play an important role in nudging the clinician to prescribe antibiotics judiciously. Targeted antibiograms should be built for facilitating evidence based antimicrobial prescriptions.

Results : It is important to bear in mind that management of cystitis and pyelonephritis, as well as simple and complicated UTI is markedly different. Nitrofurantoin, trimethoprim–sulfamethoxazole, fosfomycin, and pivmecillinam are useful first-line agents for cystitis. They are effective against ESBL producers and thus are extremely useful empirical agents. Empirical use of fluoroquinolones, third generation cephalosporins, aminoglycosides, carbapenems should be reserved for pyelonephritis and other complications. In this age of mounting AMR it is useful to know non-pharmacological prevention strategies for recurrent UTI with patients as it is becoming clear that community involvement is equally important in the combat against AMR. Adhesion blockers such as D-mannose, replacement topical estrogen therapy in postmenopausal women, probiotics, oral immunostimulants are being promoted for use in women to prevent cystitis.

Conclusion : While it is important to refer and adhere to national guidelines, it is even better to develop local antibiograms and guidelines in order to dispense optimum treatment and to halt the onward march of AMR.

Keywords : Urinary tract infection, Antibiograms

Brucellosis treatments

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Background and Aim : Brucellosis is the most common zoonotic infection and is an important public health problem in Iran.The purpose of brucellosis treatment is to control the disease and prevent its complications and relapses. Currently, in uncomplicated brucellosis there are two recommended antibiotic combinations Treatment for 6 -8 weeks.The first regimen is doxycycline 100 mg /BD plus intramuscular streptomycin 1 g once daily or gentamicin 5 mg/kg/ day . The second regimen is doxycycline plus rifampin 600 to 900 mg/ once daily. However, in terms of recurrence and failure, the first regimen is superior to the second ,there are clinicians who favor the use of the second combination because it is rather cheap, easy to use, and available . Combination regimen based on quinolones is also the second line of treatment. In children and pregnant women (12-36Months), trimethoprim/sulfamethoxazole and rifampin for have been recommended. In complicated or treat diffilt cases a three-drug regimen is recommended for 3 to 5 months. Finally, the possibility of relapse or treatment in all the above regimens should be considered in the patient and The patients should be followed clinically.

Methods : -

Results : -

Conclusion : -

Keywords : -

Disseminated invasive aspergillosis after liver transplantation despite good graft function

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Background and Aim : Invasive aspergillosis (IA) is one of the most serious causes of death after liver transplantation (LT). IA is the second most common fungal infection, and its mortality rate exceeds 80%.

Methods : A 30-year-old man presented to our hospital because of fulminant hepatitis . who underwent liver transplantation from a deceased donor. Pretransplant screenings for donor and recipient such as HIV, HBV, HCV, HDV, CMV, EBV, and syphilis for donor and HIV, HAV, HBV, HCV, HDV, CMV, EBV, VZV, PPD, IGRA, and syphilis for the recipient were negative.

Results : Although he appeared to have good graft function, After 5days post transplantation vital signs revealed a temperature of 101.2°F, pulse 98 beats per minute, respirations 30 breaths per minute, blood pressure 137/99 mm mercury, and a room air oxygen saturation of 87%. Chest CT scan revealed pleural effusion and nodular lesion.Bronchoscopy &BAL revealed positivity for Aspergillus PCR, and GM. Simultaneously he had skin ulcer on abdomen.Therapy was soon modified to Voriconazole combined with caspofungin.

Conclusion : The present report describes the case of very early onset of IA after LT.

Keywords : Invasive aspergillosis, Liver transplantation, Antifungal treatment

Prevention and control of human rabies in Iran

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Background and Aim : Prevention of human rabies in Iran

Methods : Implementation of bite and rabies prevention programs in humans based on the current health system, community culture, and people at risk especially children and other people at risk is very important. These activities conducting by using the latest national guideline, that prepared base on reference books and the World Health Organization, and papers and other recommendations of international organizations.

Results : 100% of human rabies cases are fatal, it is necessary to pay special attention to educating the community in order to prevent animal bites and also to refer to rabies prevention center after bites. The national guideline for prevention and control of human rabies has been prepared by the National Committee. Principles of fallowing animal bit are: 1- Treatment of the wound 2- Complete debridement of crushed and necrotic parts 3- Disinfection of the wound with betadine solution or 40 to 70% ethyl alcohol 4- No suturing of the wound site 5- if indication injection of rabies immunoglobulin and vaccine and completion of vaccination period 6- Injection of anti-tetanus immunoglobulin and vaccine 7- Antibiotic treatment 8- Care of the invading animal 9- Sampling of the suspected invasive animals Even after severe injury, post-exposure prevention for rabies is 100% effective. For each wound immediately wash with soap and high-pressure water for at least 15 to 20 minutes and Use disinfectants such as povidone-iodine or other compounds that can kill the virus.

Conclusion : According to the implementation of the national guidelines for human rabies prevention, register more than 260,000 human bitted cases in 2021. Due to the lack of animal bitted to refer to rabies prevention center 16 human cases of rabies were registered in 2021. It is hoped that by raising community awareness and improving coordination between the veterinary organization and ministry of health, and the Department of Environmental, we will see the rabies elimination in humans.

Keywords : Human rabies

Brucellosis in livestock: Seroepidemiology, risk factors and preventive strategies to manage the disease in Famenin, Iran

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Background and Aim : Brucellosis is an infectious disease in humans and livestock. The disease is endemic in many regions of Iran, e.g. Hamedan province. Knowledge of infection rates and associated risk factors is essential to control and prevent the disease. The main purpose of the present work was to determine the prevalence of brucellosis and associated risk factors in cattle, sheep, and goats in Famenin, Hamedan province, West of Iran.

Methods : Blood samples of 1758 animals (sheep, goats, and cattle) were obtained in different rural regions of Famenin. The samples were evaluated to detect Brucella-antibodies using Rose Bengal Plate Test (RBPT), Wright Standard Tube Agglutination Test (SAT), and 2-Mercapto-Ethanol (2-ME) techniques. The risk factors associated with the disease such as age, gender, history of vaccination, and abortion in animals were evaluated.

Results : The prevalence of brucellosis was detected at 1.3% among individual animals and 11% among herds. This rate was 1.43% for sheep and 1.05% for goats. No seropositive case was detected in cattle samples using RBT, STAT, and 2-ME. There was no significant difference between positive samples in sheep and goats. The antibodies to the Brucella infection were 2.73% with RBPT and 1.30% with SAT and 2-ME. There were no significant correlations between brucellosis rate and the presented variables except gender in sheep. Brucellosis in rams was 5.7 times higher than in ewes ($P<0.0001$).

Conclusion : This is a comprehensive evaluation of animal brucellosis parallel to humans cohort study in the Famenin region for the first time. Although the rate of brucellosis in animals is low in the region, explaining the risk factors to farmers, mass vaccination, regular screening of animals, and culling the positive animals are very important for controlling and reducing the disease in the region.

Keywords : Animal, Brucellosis, Endemic, Risk factors, Prevention.

Clostridioides difficile specific bacteriophages and the outlook for phage therapy in intestinal infections

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Background and Aim : Clostridioides difficile (C. difficile) has driven consideration as an emerging pathogen responsible for the global spread of outbreak strains, its dynamic epidemiology, and the increasing frequency, acuteness, and health care charges correlated with C. difficile infections (CDI). The increasing emergence of antibiotic-resistant C. difficile has prompted an exploration of alternative therapeutic options. A promising approach for controlling bacterial disease is the employment of bacteriophages.

Methods : C. difficile was isolated from stool samples of hospitalized CDI suspected patients in Tehran, Iran. PCR confirmed and determined bacterial toxin profiles. Double-layer agar and spot method were employed for isolating C. difficile bacteriophage from hospital sewage which were subsequently imaged by transmission electron microscopy. The phage's one-step growth curve, efficiency, and host range were investigated in-vitro.

Results : Twenty-one of the 28 isolated C. difficile from 185 stool samples were toxigenic (11.3%). Six toxin profile was determined. The highest prevalence belonged to (tcdA+, tcdB+, cdtA-/cdtB-) isolates. Bacteriophage isolation from hospital sewage by NaCl was better than with CaCl2 salt; however, isolation with MgSo4 salt was unsuccessful. According to the TEM image, a phage belonging to the Siphoviridae family was isolated. The phage was stable at 25 to 45℃ and between 3 to 11 pH. The phage was effective in decreasing C. difficile count in-vitro. A one-step growth chart with nonlinear regression analysis showed high correspondence with the logistic growth pattern, with an estimated latent phage period of around 30 minutes. Among the 28 toxigenic C. difficile isolates with six toxin profiles, the phage has shown a lytic effect against 70% of those strains.

Conclusion : It appears that lytic phages have the potential of becoming an alternative therapeutic option for mitigation of CDI since it has advantageous functions in eliminating C. difficile and has no effect on other bacteria in the gut microbiome.

Keywords : Clostridioides difficile , CDI, Bacteriophage

Delamanid-containing regimens and multidrug-resistant tuberculosis

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Background and Aim : Multidrug-resistant tuberculosis (MDR-TB) is a life-threatening condition needing long poly-chemotherapy regimens. As no systematic reviews/meta-analysis is available to comprehensively evaluate the role of delamanid (DLM), we evaluated its effectiveness and safety.

Methods : We reviewed the relevant scientific literature published up to January 20, 2022. The pooled success treatment rate with 95% confidence intervals (CI) was assessed using a random-effect model. We assessed studies for quality and bias, and considered P<0.05 to be statistically significant.

Results : After reviewing 626 records, we identified 25 studies that met the inclusion criteria, 22 observational and 3 experimental, with 1276 and 411 patients, respectively. In observational studies the overall pooled treatment success rate of DLM-containing regimens was 80.9% (95% CI 72.6-87.2) with no evidence of publication bias (Begg's test; P >0.05). The overall pooled treatment success rate in DLM and bedaquiline-containing regimens was 75.2% (95% CI 68.1-81.1) with no evidence of publication bias (Begg's test; P >0.05). In experimental studies the pooled treatment success rate of DLM-containing regimens was 72.5 (95% CI 44.2-89.8, P <0.001, I2: 95.1%) with no evidence of publication bias (Begg's test; P >0.05).

Conclusion : In MDR-TB patients receiving DLM, culture conversion and treatment success rates were high despite extensive resistance with limited adverse events.

Keywords : TB MDR-TB delamanid bedaquiline effectiveness safety

MYCOBACTERIA-BRONCHIAL EPITHELIAL CELLS CROSSTALK THROUGH TYPE I INTERFERON SIGNALING

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Background and Aim : The first interaction of mycobacteria with the host occurs in bronchial epithelial cells. Although underlying mechanisms remain unclear, the crosstalk between mycobacteria and host cell plays a crucial role in the initiation and subsequent direction of adaptive immune responses.

Methods : We developed ex vivo and in vivo models using microparticles generated from Mycobacterium abscessus (MAB) to study this crosstalk. For ex vivo model, Normal Human Bronchial Epithelial (NHBE) cells were applied to develop a lung on chip technology. For In vivo model, we used 6-week-old age C57Bl/6 male mice. They were challenged intratracheally with MAB microparticles for 4 doses with 3-day intervals.

Results : RNAseq analysis identified 1759 differentially expressed genes comparing NHBE cells with and without MAB microparticles challenge. 410 genes had a 2.5-fold change (FC) or greater. NHBE cells significantly enriched the IFN I signaling pathway after exposure to MAB microparticles. Protein overexpression of IFN I family (2′-5′-Oligoadenylate Synthetase 1, Interferon-induced GTP-binding protein Mx1, Interferon-stimulated gene 15) was found in bronchial epithelial cells following exposure to MAB cell wall microparticles. Significant overexpression of IFN I family proteins and genes were found in mice lung after intratracheal inoculation of microparticles.

Conclusion : Type I IFN initiates a significant local immune response after exposure of bronchial epithelial cells to cell wall of mycobacteria. Our study proposes that “limited bronchial infection” is a more appropriate biologic definition instead of “mycobacteria colonization” when environmental mycobacteria are isolated in sputum without the presence of other diagnostic criteria of mycobacterial disease.

Keywords : Mycobacteria, Local immune response, Normal human bronchial epithelial

NOVEL METAL(LOID)-BASED AND PLANT-BASED ANTIBACTERIAL COMPOSITIONS AND USES THEREOF AGAINST BACTERIAL BIOFILMS

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Background and Aim : Antibiotic resistance, biofilm, and persistent infection is a challenge in the healthcare system. Our research group focuses on exploring the efficacy of Metal(loid)-based antimicrobials (MBAs) towards novel infection control solutions. In this study, we explored MBAs and Plant-Based Antibacterial Compositions (PBCs) to discover novel antibacterial components.

Methods : Synergistic antibacterial potentials of MBAs screened systematically in a total of, 5760 combinatorial MBAs concentrations, in lab media and infection related simulated wound fluid against six WHO concerned bacteria. The silver nitrate (Ag)-potassium tellurite (Te) combination was identified as the most effective MBAs. A quite same experiment carried out to identify the most effective PBCs. In a binary screening method, the selected PBCs and PBCs we screened for the best combination formula. To understand the molecular mechanisms of MBAs and PBCs, especially their synergism state, in a comparative study, we defined the differentially expressed gene profile under MBAs and PBCs alone and in their optimal synergistic combination using the RNA-seq approach. The study was complemented with metabolomics and direct biochemistry assays. We also evaluate the stress effect and toxicity on the animal model system of Caenorhabditis elegans.

Results : The Te and Ag had significantly better biofilm inhibition and biofilm eradication efficacy as well as the most effective anti-biofilm synergism potency against indicator strains and clinical isolates. The PBCs-PBCs mix not only was more effective than common antibiotics, but also prevented bacterial recovery, decreased the risk of future resistance chance, and it was effective at lower concentrations. Our OMICS study showed, all of our selected PBCs utilized the same pathway for their antibacterial effects. They are mostly targeting bacterial cell membrane in the initial step rather than other mechanisms, which could be part of the explanation as to why they are not toxic to the eukaryotic cells. MBAs mainly affected four cellular processes including sulfur homeostasis (mainly), reactive oxygen species (ROS) response by targeting [Fe-S] centres, energy pathways, and the bacterial cell membrane. The C. elegans animal model showed co-application of MBAs-PBCs has reduced toxicity over the individuals and provides increased their antioxidant properties to the host.

Conclusion : This study is leading towards a novel antimicrobial formulation that is effective in also preventing and eradication of persistent infection and biofilms.

Keywords : Biofilm, Metalloid, Silver nitrate, Potassium tellurite, synergism.

Gut-Liver Axis

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Background and Aim : There is a complicated relationship between the liver and intestines. In this regard, genetic, environmental factors and diet play a role. What is important in the intestine is the presence of gut microbes, it is said that they are numerous and even ten times as the number of human body cells.

Methods : Anatomical connection, including the bile duct system, liver and portal veins, and general blood flow, further strengthens this connection and crosstalk, and creates a balance between the immune system and tolerance against pathogens and antigens. Any type of dysfunction of gut microbes and even the liver leads to a change in the intestinal population in the form of Dysbiosis, and become the important topic of research in the development of inflammatory bowel disease, diabetes, obesity, metabolic syndrome, fatty liver and cardiovascular diseases in recent years

Results : A clear example of this Dysbiosis is fatty liver and steatohepatitis and cirrhosis caused by it, which factors such as diabetes, obesity, metabolic syndrome provide the basis for the development of inflammation and liver damage. Microbial products in the form of DAMPs, PAMPs stimulate the immune cells of the liver and finally lead to activate the Stellate Cell (HSC), which results in the secretion of collagen and causes liver fibrosis and cirrhosis.

Conclusion : Gut microbial agents by affecting the intestinal lymphocytes lead to the production of antibodies that target hepatocytes or cholangiocytes and lead to the exacerbation of diseases such as PBC, ALH and PSC

Keywords : Gut-Liver Axis, Dysbiosis, tolerance, microbes

مقالات سخنرانی

بیست و سومین کنگره بین المللی میکروب شناسی ایران

O1-137: Emergence of colistin resistant K.pnenomonia isolates in Payvand clinical and specialty laboratory ; a 6 month survey

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Background and Aim : Emergence of multi drug resistant bacteria (MDR, resistant to 3 classes of antibiotics) and more serious extensively drug-resistant bacteria (XDR, almost resistant to all or all approved antimicrobial agents) are global challenges. Colistin, is the last available antibiotic for treatment of carbapenem resistant enterobacteriacea. So, in this study emergence of colistin resistant K. pnenomonia isolates in Payvand clinical and specialty laboratory was evaluated in a 6 month study.

Methods : From Sep 2021 to March 2022, 5736 different clinical samples from 5865 patients who referred to Payvand clinical and specialty laboratory were included in this study. Further colony isolation was done based on standard protocol using bacterial media, streak culture and routine incubation at 37ºC. Bacterial identification and antimicrobial test (AST) was done by using automated Vitec2 system (Biomerieux, France) and using GN 2 and GN76 cards respectively based on the CLSI protocol. The AST were reported as minimum inhibitory concentration (MIC). Colistin resistant was done on selected XDR K. pnenumonia isolates using N240 card. Further statistical analysis was done.

Results : 863 of 5736 (15.04%) of clinical samples (including: broncoalveolar lavage (Bal), sputum, wound, blood and urine) were culture positive. Of them 130 isolates were identified as K. pneumonia and 16.92% (22/130) of them were resistant to all tested antibiotics (including: Amp, TZP, CFZ, Fox, Caz, CRO, FEP, ERTA, IMP, An, GM, CP, Levo, FM and SXT) and identified as extended drug resistant (XDR). These 22 XDR K. pneumonia strains were isolated from 12 female and 8 male patients. 12/22 K, pneumonia isolates showed intermediate resistant (I) and 10 were colistin resistant(R).

Conclusion : Although, sample collection of only a clinical laboratory in Tehran is a limitation of this study but high rate of XDR K. pneumonia with no susceptibility to colistin seems alarming and needs especial notification on antibiotic stewardship, infection control and antibiotic prescription.

Keywords : klebsiella pneumonia, Colistin, resistant

O2-152: Enhanced anti-biofilm activity of the minocycline-and-gallium-nitrate-containing niosomes against Acinetobacter baumannii in the mouse pneumonia model

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Background and Aim : Acinetobacter baumannii is a worldwide health issue due to its high antibiotic resistance and ability to construct biofilms. Nanoparticles (NPs) with high biocompatibility, high penetrating power and low medication dose can successfully treat antibiotic-resistant infections. This study will use a mouse pneumonia model to evaluate the anti-biofilm effectiveness of niosomes containing minocycline and gallium nitrate (GaN).

Methods : This study's clinical sample was isolated among diverse bacterial biofilms developed on the lungs of patients hospitalized in Logman hospital, Tehran, Iran. The biofilm of A. baumannii was considered the most lethal strain to be evaluated. To increase their anti-biofilm characteristics, Minocycline and GaN were encapsulated in niosomes as biocompatible drug carriers. The niosomes' size, zeta potential, shape, stability, drug entrapment efficacy, drug release pattern, MIC, and MBC were studied. It was generated by giving A. baumannii suspension intranasally to anesthetized mice whose immune systems had already been compromised twice by cyclophosphamide. The infection was proven before the mice were treated using PCR. After treatment, the lungs were excised sterile and stained with (Hematoxylin and eosin) H&E to determine histologic symptoms, inflammation, and intercellular secretions. The drugs' cytotoxic effects were assessed in the liver and spleen

Results : The niosomes investigated contained minocycline, and GaN had an average size and zeta potential of 230 nm and -40 mV. Niosomal formulations feature a high rate of drug entrapment and a delayed drug release rate. Niosomes containing minocycline and GaN eradicated biofilms after 1, 3, and 5 days. The mice given the combination of the two compounds required less time to be treated than the animals given the single medication (minocycline).

Conclusion : The therapy group survived longer than the control group. The minocycline and GaN-loaded niosomes could be considered promising candidates for treating the infections caused by A. baumannii and biofilm formation.

Keywords : Niosome; Minocycline; Gallium Nitrate; Pneumonia Model; Acinetobacter baumannii;

O3-273: Evaluation of the effect of probiotics pichia kudriavzevii on NBT test of IL-17 secretion in mice with Candida systemic infection

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Background and Aim : Candidiasis is one of the most common opportunistic fungal infections in humans and animals. The disease is caused by a yeast fungus called Candida albicans. Candida albicans is a natural flora in humans and animals, and their growth and reproduction are usually limited by the immune system and other microorganisms.

Methods : In this study, 28 female Wistar rats (6-8 weeks) with a weight range (180-200) g were divided into 4 groups: group A: healthy rats as control, group B: rats infected with Candida Albicans with ID (ATCC 10231) and concentration (2 × 106 cfu/ml), group C: rats treated with Pikia yeast with concentration (107 cfu/ml), group D: Candida-infected and yeast-treated rats At the end of the 15-day period, the animals were facilitated to measure blood factors: including interleukin-17 and to evaluate the function of phagocytes in terms of respiratory explosion (NBT test). Colonization of Candida albicans colonies in liver tissue and all tissues were isolated and homogenized and cultured in SDA medium.

Results : Evaluation of serum protein: Interleukin 17 between experimental groups and comparison with each other showed no significant change ($P < 0.05$). but the function of oxidative respiratory burst of neutrophils (NBT test) had a significant increase in the infected group treated with probiotics compared to the infected group ($P < 0.05$). In the study of Candida albicans colonies in the infected group and the infected group treated with probiotics, the lack of colony growth was compared with the infected group.

Conclusion : The results of the research indicate that Pikia kudriozoui probably inhibits Candida albicans by increasing the respiratory burst function of neutrophils, so the results of liver and kidney tissue culture in terms of evaluating Candida albicans confirm this possibility. Therefore, it is suggested to use probiotics as a therapeutic supplement and possibly strengthen the body's immune system during candidal infections in order to prevent the disease process and control it.

Keywords : Candidiasis, Probiotics, Picia chondrocytes, Interleukin 17, NBT test.

O4-319: First report of poxtA, cfr, and optrA genes related to linezolid resistance from human clinical Enterococcus spp. isolates in Iran

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Background and Aim : Enterococci can acquire linezolid resistance through chromosomal mutation or the uptake of mobile genetic elements containing particular linezolid resistance genes including cfr, optrA, and poxtA. The study aims were to analyze the antibiotic susceptibility patterns of Enterococcus isolates, including phenotypic resistance identification, followed by detection of cfr, optrA, and poxtA genes in MDR isolates.

Methods : In this descriptive study (cross-sectional), 175 non-duplicate enterococcal isolates were obtained from different clinical specimens at the Al-Zahra, Amin, and Khorshid hospitals in Isfahan. After the biochemical confirmation of the strains, the PCR amplification of genes (ddl) was performed to determine the enterococci species. The antibiotic resistance profile of Enterococcus isolates was investigated based on CLSI 2022's instructions and analyzed using Whonet 2021 software. then used a multiplex-PCR method to detect optrA, cfr, and poxtA from whole genomic bacterial DNA. The confirmation of the gene detection process was done by genome sequencing. Statistical analyses were performed using SPSS version 26 software. A significance level of $P < 0.05$ was used to define significant results.

Results : Among our isolates, E. faecalis predominated 73.7%. As well, vancomycin and linezolid-resistant enterococci constitute 29.7% and 4.0%, respectively. Nevertheless, MDR prevalence among E. faecium was 91.1%, 68.9% among E. faecalis, and 66.6% among other species of Enterococcus. Our results showed that the prevalence of optrA was 71.4% and that of poxtA and cfr was 42.8% among linezolid-resistant enterococci and there is a significant relationship ($P < 0.05$) between resistance to linezolid and the presence of each of these three genes.

Conclusion : This is the first study to describe the linezolid resistance genes cfr, optrA, and poxtA in Iran, and to investigate their prevalence in clinical Enterococcus spp. isolates at Isfahan University of Medical Sciences hospitals. It should be considered alarming if even one specimen is found expressing optrA, poxtA, or cfr, where genes for resistance can spread between clinical settings and non-clinical settings, as well as between different species.

Keywords : Enterococcus spp., linezolid-resistance, poxtA, cfr, optrA

O5-323: The synergic effect of Levilactobacillus brevis IBRC-M10790 and vitamin D on Helicobacter pylori-induced inflammation

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Background and Aim : Owing to the emergence and spread of multidrug resistance mechanisms in Helicobacter pylori, achieving successful H. pylori eradication has become exceedingly difficult. Thus, this study for the first time determines the effect of a novel combination of vitamin D and probiotic on the pathogenesis of H. pylori.

Methods : We established an in vitro experimental system using AGS human gastric carcinoma cells and explored the synergistic effect of Levilactobacillus brevis and vitamin D on H. pylori. L. brevis live bacteria, pasteurized, cell free supernatant (CFS), and extracellular vesicles (EVs), as well as their combination with vitamin D were used during this study. We assessed the anti-inflammatory and anti-oxidative effects of these combinations using RT-PCR and ELISA, respectively. We further performed adhesion assay to evaluate the influence of L. brevis and vitamin D on the adherence of H. pylori to gastric epithelial cells.

Results : Our results demonstrated that L. brevis and vitamin D possess anti-inflammatory and anti-oxidative effects against H. pylori infection in AGS cells. However, the combination of vitamin D with the probiotic strain (particularly L. brevis live bacteria and CFS) can more efficiently reduce the production of pro-inflammatory cytokines IL-6, IL-8, IFN-γ, and TNF-α from the gastric epithelium. Moreover, vitamin D and L. brevis exhibited an additive impact preserving the integrity of the epithelial barrier through increasing the production of tight junction protein ZO-1. Furthermore, this combination can potentially reduce H. pylori adherence to gastric epithelial cell.

Conclusion : These results indicate the additive advantage of vitamin D and probiotic co-treatment to attenuate H. pylori-induced inflammation and oxidative stress. Consequently,

probiotic and vitamin D co-supplementation can be considered as a novel therapeutic approach to manage H. pylori infection.

Keywords : Helicobacter pylori, Levilactobacillus brevis IBRC-M10790, vitamin D, extracellular vesicle, AGS cells

O6-374: Phenotypic and genotypic characterization of carbapenem-resistant Pseudomonas aeruginosa isolates from Hamadan, Iran

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Background and Aim : In recent years, the prevalence of carbapenem-resistant Pseudomonas aeruginosa isolates has become a worldwide concern. Rapid and accurate detection of carbapenemase-producing P. aeruginosa isolates is so important. The aim of this study was to evaluate the performance of the phenotypic methods such as Modified Hodge test (MHT), CarbaNP (CNPt), combined double-disk synergy test (CDDT), and carbapenem inactivation method (CIM) for rapid and accurate detection of clinical carbapenemase production of P. aeruginosa isolates.

Methods : This study was performed on 97 P. aeruginosa strains, which were isolated from clinical samples in Hamadan hospitals, western Iran in 2017-2018. Antibiotic susceptibility testing was performed using disk diffusion and minimum inhibitory concentration (MIC) by E-test method. We evaluated the performance of MHT, CarbaNP, CDDT, and CIM tests in comparison to polymerase chain reaction (PCR) for the detection of carbapenemase-producing isolates. Additionally, the presence of carbapenem-resistant genes was investigated using the PCR method.

Results : Our findings showed that the highest resistance was to cefoxitin (94.8%). Moreover, among the carbapenem antibiotics, the highest resistance was to imipenem (49.4%). Among the 49 carbapenem-resistant isolates, 42 (85.7%) isolates were MIC positive. The results of phenotypic tests showed that CarbaNP, CIM, CDDT, and MHT tests were positive in (48/49, 97.95%), (46/49, 93.87%), (27/49, 57.44%), and (25/49, 53.19%) of isolates, respectively.

Conclusion : CarbaNP and CIM tests showed high sensitivity, specificity, positive predictive values (PPV), and negative predictive values (NPV) compared to PCR in P. aeruginosa isolates. CarbaNP and CIM tests are highly sensitive and specific tests for identifying carbapenemase-producing P. aeruginosa isolates.

Keywords : Carbapenemase, Metallo-β-Lactamases, Pseudomonas aeruginosa

O7-564: The effect of ampicillin/sulbactam-colistin-eluting noisome nanoparticles against the expression of biofilm-associated genes (pgaA, pglL) of Acinetobacter baumannii isolates

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Background and Aim : Acinetobacter baumannii is an emerging cause of nosocomial infections. The isolation of strains resistant to multiple antibiotics is increasing at alarming rates. The demonstrated ability of nosocomial strains to grow as the biofilm is believed to play a significant role in their persistence and antibiotic resistance. This study aimed to evaluate the effect of ampicillin /sulbactam-colistin eluting noisome nanoparticles against the expression of biofilm-associated genes of Acinetobacter baumannii isolates.

Methods : In this study, among40 clinical samples, 10 high biofilm-forming isolates were detected. Niosomes were prepared using the thin-film hydration method and were characterized by zeta potential measurement and Field Emission Electron Microscope (FE-SEM). The ampicillin /sulbactam-colistin entrapment efficiency was determined. The expression levels of biofilm-associated genes(pgaA, pglL) were quantified by the Quantitative Real-Time PCR method. Statistical analysis was performed using one-way ANOVA test.

Results : The round-shaped ampicillin /sulbactam-colistin eluting noisomes were 230 nm and had -25mV zeta potential. The encapsulation of ampicillin /sulbactam and colistin in the niosomes was 78% and 89%, respectively. Noisomes containing ampicillin /sulbactam-colistin could significantly reduce the expression of pgaA and pglL ($p<0.05$).

Conclusion : The results indicated that ampicillin/sulbactam-colistin- loaded niosomes reduced the expression of genes related to biofilm formation and the antibioflim activity of ampicillin/sulbactam-colistin- eluting niosomes was confirmed.

Keywords : Acinetobacter baumannii; biofilm-associated genes; niosome nanoparticle

O8-632: Fabrication and optimization of amoxicillin-loaded niosomes: An appropriate strategy to increase antimicrobial and anti-biofilm effects against multidrug-resistant strains of Staphylococcus aureus

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Background and Aim : In this study, different formulations of amoxicillin-loaded niosomes were fabricated using the thin-film hydration method and their physicochemical properties were determined using scanning electron microscopy (SEM), dynamic light scattering (DLS), and Fourier-transform infrared spectroscopy (FTIR). The optimum prepared niosomes had a spherical morphology with an average size of 170.6±6.8 nm and encapsulation efficiency of 65.78±1.45%

Methods : he drug release study showed that the release rate of amoxicillin from niosome containing amoxicillin was slow and 47±1% of the drug was released within 8 hours, while 97±0.5% of the free drug was released. In addition, amoxicillin-loaded niosome increased the antimicrobial activity by 2-4 folds against multidrug-resistant (MDR) Staphylococcus aureus strains using broth microdilution assay. Moreover, at ½ minimum inhibitory concentrations, amoxicillin-loaded niosome significantly enhanced the anti-biofilm activity compared to free amoxicillin. Amoxicillin-loaded niosome had negligible cytotoxicity against HEK-293 normal cell line compared to free amoxicillin. The free niosomes exhibited no toxicity against HEK-293 cells and presented a biocompatible nanoscale delivery system. Based on the results, it can be concluded that amoxicillin-loaded niosome can be used as a promising candidate for enhancing antimicrobial and anti-biofilm effects against MDR strains of S. aureus.

Results : All the noisome formations were prepared based on the Design of Experiments described in Table 1. Influence of various variables such as surfactant: Span 60: Tween 60 and cholesterol on the entrapped efficiency percentage and the size of noisome are shown in . The niosome size ranging 170.6±6.8– 248.5±1.7 nm and entrapment efficiency (EE %) ranging 45.36±1.1– 65.78±1.45% were achieved. The 1:1 and 50:50 molar ratio of cholesterol and Span 60: Tween 60 resulted in smaller niosomes with high EE%. The optimum niosome formulation was successfully fabricated and their physicochemical was determined for the desired criteria based on the experimental design. The optimized formulation particle size is 170.6±6.8 nm, and the EE% 65.78±1.45 %

Conclusion : In this study, various niosome formulations containing amoxicillin were fabricated and their antimicrobial and anti-biofilm effects were investigated. Our findings demonstrated that amoxicillin-containing niosome reduce antimicrobial effects by 2 to 4 times and had biofilm inhibitory effects against multidrug-resistant Staphylococcus aureus strains compared to free amoxicillin. The results of cytotoxicity also demonstrated that amoxicillin-loaded niosomes reduced the cytotoxicity of amoxicillin. According to the results of this study, it can be concluded that niosome is a suitable drug delivery system for antimicrobial purposes

Keywords : Amoxicillin, Niosome, Staphylococcus aureus, Antimicrobial, Anti-biofilm

O9-737: Molecular characterization of virulence and antibiotic drug resistance pattern of Acinetobacter baumannii and distribution of intrasplasmid replicase genes and sequence types

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Background and Aim : Despite the progress in the antibiotic resistance mechanisms in Acinetobacter baumannii, a more informative knowledge on the genetic characterization is required to drive their recent evolution. The present study emphasized on molecular epidemiology of carbapenem resistance, efflux pumps, porins, biofilm capacity and quorum sensing, and sequence analysis of plasmid replicons.

Methods : The study was performed on 112 A. baumannii isolates. Antibiotic susceptibility testing was done by disk diffusion and agar dilution. Presence of oxacillinase and metallo β-lactamase genes was detected by PCR. The level of expression of efflux pumps and porins was investigated by Real-time PCR. Biofilm capacity was analyzed using microtiter plate method followed by quorum sensing and virulence related genes. Sequence typing and PCR-based replicon typing were performed by PCR.

Results : All A.baumannii isolates revealed the presence of gyrB and rpoB genes. Resistance to cephalosporins, carbapenems, fluoroquinolone, trimethoprim-sulfamethoxazole, and piperacillin/tazobactam was observed in all isolates (considered MDR and carbapenem resistant A.baumannii (CRAB) strains). Resistance to all classes of an¬tibiotics except colistin and ampicillin/sulbactam was observed in 30 A.baumannii isolates (designated XDR strains). Presence of blaOXA-51-like was a distinct feature. blaOXA-23-like and blaOXA-24/40-like genes were observed in most of the strains. Presence of blaNDM and blaIMP were detected in CRAB strains while, no CRAB strain was positive for blaVIM, blaSIM, blaGIM and blaSPM. The ISAba1 element was present in the majority of CRAB strains. The real-time PCR showed higher expression of adeB and adeJ genes while decreased expression level was observed for carO, omp33-36 and oprD porin genes. Biofilm activity was observed at various levels and all isolates were positive for bfmSR, csuE, pgaA, abaI and pgaD while, bap and

bla-PER1 were not detected by all the isolates. All isolates were also positive for the Type I fimbriae, PilT motility related genes and ompA virulence gene. Sequence-based typing revealed all isolates belonged to European (EU) clone II. Replicase typing showed rep6 and rep2 genes had highest frequency.

Conclusion : Presence of virulence feature in majority of clinical isolates confirms the endemicity of A.baumannii and appraise the nosocomial nature of the bacteria. Predominance of multiple CRAB strains is an alarming concern.

Keywords : Acinetobacter baumannii; Carbapenem resistance genes; molecular epidemiology; Biofim; Virulence; Typing

O10-738: Genetic characterization of Klebsiella pneumoniae: Five year experience in ICU admitted patients

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Background and Aim : Klebsiella pneumoniae being widely recognized as a nosocomial, multidrug-resistant and a heterogeneous pathogen which requires critical genetic characterization to be discovered to provide more comprehensions about the characterization of this pathogen in various infections. We aimed at to characterize 124 ESBL producing, carbapenem and quinolone resistant clinical K. pneumoniae isolates collected over a five year period, through serotyping, determination of virulence factors, antibiotic resistance testing, and enterobacterial repetitive intergenic consensus-polymerase chain reaction (ERIC-PCR).

Methods : All typical colonies of K.pneumoniae isolated were initially confirmed by PCR and tested for being hyper virulent phenotypically followed by antimicrobial susceptibility test. MICs of ciprofloxacin was determined by E-test. Multiplex PCR based screening was done for plasmid mediated quinolone resistance (PQMR), integrase genes and efflux pump genes. The Mast® D68C test detected the presence of ESBLs and AmpCs phenotypically, and later presence of ESBL and AmpC genes was observed by PCR. Presence of carbapenemase genes were evaluated by PCR. Capsular serotyping and capsule-associated virulence genes were studied using the molecular method. All strains were fingerprinted by ERIC-PCR.

Results : All K.pneumoniae isolates had a positivity for the internal transcribed spacer region (K. pneumoniae 16S–23S) confirming as K. pneumoniae. Of all isolates, 59% were typeable. Majority of isolates (88.9%) were resistant to cephalosprins while, ciprofloxacin and carbapenem resistance was evident in 41.3% and 24% strains respectively. ESBL production was observed in 73% isolates. Frequency of qnrA, qnrB and qnrS was 3.7%, 10.5% and 9.7% respectively while 47.6% and 4.8% isolates were positive for aac(6')-Ib and 4.8% qepA respectively. Integron 1 and 2 and both 1 and 2 were noticed in 38.1%, 17.5 and 6.3% respectively. We identified 17 different ERIC patterns. Frequency of blaOXA-48, blaKPC, blaNDM, blaVIM and blaIMP genes was found as 78.8%, 14.75%, 19.67%, 11.47% and 4.91 respectively. Our study evidenced virulence-associated genes including, capsules, encoding

lipopolysaccharides, regulators of hypermucoviscosity, adhesins, iron acquisition systems, enterobactin, allantoin metabolism and those which help to overcome innate host immunity.

Conclusion : Our findings highlights the importance of surveillance of K. pneumoniae in clinical infections. The genetic surveillance is important in understanding the pathogenic characteristics of K. pneumoniae isolates.

Keywords : Klebsiella pneumoniae; Serotyping; Virulence factors; Antibiotic resistance; ERIC-PCR

O11-90: Detection Of virulence factor genes in isolated Legionella pneumophila isolates from hospital water sources

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Background and Aim : Owing to the fact that Legionella presence in water sources does not necessarily lead to onset of disease, several factors such as inhaled bacteria dose, virulence factors and diversity of serogroups can be considered as contributing factors. The main aims of this study was to Using culture for Legionella monitoring in hospital water samples, risk assessment by an invasion of the HeLa cell and investigate the presence of major virulence factor genes as well as the ability to form biofilms in the Legionella isolates.

Methods : In this study 100 water samples collected from hospitals of Iran university medical sciences, from water sources and were examined. 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. Using Favor gene kit, DNA of the samples was extracted, and then the PCR reaction for 16srRNA genes was done using proprietary primers. Virulence genes (mip, rtx, lvh, dot, hsp60) and biofilm formation were subsequently analyzed among the isolated Legionella pneumophila

Results : Out of water samples, 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%) were with 104GU/L and 2 cases (4/76%) were with <104 GU/L. PCR assay for the virulence genes showed that all 12 (100%) isolates were positive for mip genes, 9 (75%) were positive for dot gene, 8 (66.66%) were positive for hsp, 6 (50%) were positive for lvh, and 4(33.33%) for rtx. Two of the isolates displayed higher ability to form biofilm in reference to the standard strain.

Conclusion : This study reveal that water sources in hospital colonized by virulent legionella and should be continuously monitored to avoid elevated concentration of legionella and visible biofilm formation.

Keywords : Legionella pneumophila, rtx, dot, hsp60, mip, lvh, 16srRNA, biofilm formation, virulence genes, PCR, Realtime PCR, invasion

O12-142: Bdellovibrio bacteriovorus as living antibiotic against some Enterobacteriaceae members and extensively drug-resistant (XDR) clinical pathogens

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Background and Aim : Bdellovibrio-and-like organisms (BALOs) are a group of predatory microorganisms that attack and kill other Gram-negative bacteria for growth and reproduction, acting as potential living antibiotics and biocontrol agents. This study describes the isolation, identification, biological properties, and bacteriolytic activity of the first Bdellovibrio sp. with a broad prey range from Iran.

Methods : One BALO strain with high predatory potency was isolated from the rhizosphere soil using Escherichia coli as prey. It was identified and designated as Bdellovibrio bacteriovorus strain SOIR-1 through plaque assays, biological properties, transmission electron microscopy (TEM), Bdellovibrio-specific PCRs, and 16S rRNA gene sequence analysis. The antibiotic resistance pattern of some clinically isolated Gram-negative pathogens was determined through the standard Kirby-Bauer disc diffusion method. Finally, the predatory potency and bacteriolytic activity of SOIR-1 toward some Enterobacteriaceae members and antibiotic-resistant clinical pathogens was also evaluated through the plaque formation assays and lysis analysis in the broth co-cultures, followed by monitoring the OD600, CFU/ml, and PFU/ml parameters.

Results : TEM, Bdellovibrio-specific PCRs, and analysis of 16S rRNA gene sequence revealed the close relationship of SOIR-1 with strains of Bdellovibrio bacteriovorus. The strain SOIR-1 grew within the temperature range of 25-37 °C and the pH range of 6.0-8.0, with the optimal predatory activity at 30 °C and pH 7.4. It had the highest and lowest predatory activity toward Shigella dysenteriae and Pseudomonas aeruginosa with a killing rate of 89.66% and 74.83%, respectively. All clinical isolates showed the properties of extensively drug-resistant (XDR). Regarding the XDR clinical isolates, SOIR-1 showed the highest and lowest bacteriolytic efficiency against Acinetobacter baumannii (84.33%) and Pseudomonas aeruginosa-369 (55.16%), respectively.

Conclusion : Considering the hypothesis of Bdellovibrios heterogeneity, identification of new isolates contributes to a deeper understanding of their diversity, their ecological roles in different ecosystems, and their promising potential as living antibiotics or biocontrol agents. Bdellovibrios with broad bacteriolytic nature has not previously been reported in sufficient detail from Iran. The results of this study showed the great potential of native B. bacteriovorus SOIR-1 as a living antibiotic in the control and treatment of diseases caused by Enterobacteriaceae as well as Gram-negative XDR pathogens, regardless of their antimicrobial resistance state.

Keywords : Predatory bacteria; Bdellovibrio bacteriovorus; Isolation; Iran; Bacteriolytic activity; Antimicrobial resistance

O13-209: Promising antibacterial effect of impregnated nanofiber mats with a green nanogel against clinical and standard strains of Pseudomonas aeruginosa and Staphylococcus aureus

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Background and Aim : Pseudomonas aeruginosa and Staphylococcus aureus are two important pathogens that cause many maladies such as skin diseases in humans. Resistance to common antibiotics is a major challenge for health care systems worldwide; new green antibacterial agents have become crucial. In this study, ingredients of Mentha longifolia essential oil were first investigated; pulegone (46.97%), eucalyptol (12.22%), piperitenone (6.13%), carvone (4.16%), and limonene (3.42%) were identified as five major ingredients. Electrospun nanofibers of polycaprolactone-alginate nanofibers with 188 (±36) nm diameter were then prepared.

Methods : The nanofibers were characterized using ATR-FTIR analysis, SEM analysis, and water contact angle meter. They did not show cytotoxic effects on HFFF2 cells, a human skin normal cell line. After that, a nanoemulsion-based nanogel of M. longifolia EO was prepared and physically impregnated on the surface of the nanofibers mats. Antibacterial effects of the prepared prototype at three concentrations (2.5, 5, and 10 mg/mL) with exposure times of 1, 3, and 24 h were investigated against clinical and standard strains of P. aeruginosa and S. aureus.

Results : At a 5 mg/mL concentration with 1 h exposure, the growth of a standard strain of P. aeruginosa ~80% was decreased. After increasing exposure time to 24 h, growth of both standard and clinical strains ~90% reduced. Furthermore, at a 10 mg/mL concentration with exposure times of 3 and 24 h, ~100% reduction in the growth of all exanimated bacteria strains was observed.

Conclusion : The chemical composition of M. longifolia EO was first investigated using GC-MS analysis. Electrospun nanofibers of polycaprolactone-alginate nanofibers were then prepared; they did not show cytotoxicity on a normal human skin cell line (HFFF2). After that, nanoemulsion-based nanogel of M. longifolia EO was prepared and physically impregnated on the surface of the nanofibers mats. Finally, the antibacterial effects of the prepared prototype against clinical and standard strains of P. aeruginosa and S. aureus were investigated; their growth was reduced to ~ 0%. As the green ingredients of the prepared prototype and its promising efficacy, it could thus be used as a potent antibacterial agent in wound dressing or cleaning pads.

Keywords : Mentha longifoliaEssential oilElectrospinningPolycaprolactone-alginate nanofibers

O14-327: New endolysin against Acinetobacter baumannii: antibacterial effect

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Background and Aim : Nowadays, antibiotic-resistant bacterial infections are the second leading cause of death in the world. Endolysins are the phage enzymes can destroy bacterial cell wall, therefore, they can be used for development of new antibacterial drugs. One of the most important bacteria causing more than 80% of nosocomial infections is Acinetobacter baumannii. In this study the antibacterial effect of new recombinant engineered endolysin was investigated against A. baumannii.

Methods : For this purpose, designed recombinant endolysin was expressed in E. coli BL21(DE3) using pET expression system and purified by nickel chromatography column. The column output checked by SDS-PAGE to confirm its purity. Then, the protein concentration calculated with Bradford method. To investigate the antibacterial effect of the fusion protein, plate lysis assay performed, on Acinetobacter baumannii PTCC 1855 according to CLSI 2018 protocol. As well, Mueller-Hinton Agar (MHA) medium and Trypticase Soy Agar (TSA) medium were used for antibacterial effect evaluation. Consequently, 0.5 McFarland (OD~0.13) sample was prepared from bacterial liquid culture (24h). The bacterial suspension was cultured as dense lawn by sterile swab on TSA and MHA medium. The initial concentration of the recombinant enzyme was 600µg /ml, which was diluted 1:2 with a suitable buffer containing 0.5 mM EDTA as a membrane permeabilizer. 20µl of each sample dropped on the plates and incubated overnight at 37oC.

Results : The results showed that recombinant endolysin had a significant inhibitory effect on A. baumannii on TSA plate. In addition, MHA medium, had an inhibitory effect on the enzyme and prevented the formation of zone of inhibition.

Conclusion : According to the obtained results, the engineered fusion protein has a good inhibitory effect on this bacterium and by further studies for improving its activity it can be considered as a possible new alternative for antibiotics available in market

Keywords : Acinetobacter baumannii, Anti-Bacterial Agents, Recombinant Fusion Protein, Peptidoglycan Hydrolase.

O15-349: FliC Protein from Enterobacteriaceae Family revealed a Promising Epitope-Delivery Platform

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Background and Aim : Flagella are filamentous organelles with essential roles in bacterial physiology, such as motility and chemotaxis. Studies have shown that more than 50 genes are complicated in the assembly and function of flagella. Flagellin (FliC) is an essential subunit of flagella in motile bacteria. The flagellin subunit, encoded by the fliC gene, has a tubular structure at the distal end of flagella. The atomic model of flagellin as a component of the 11 proto-filaments was constructed from electron micrographs. The 3D structure of the FliC protein showed that this protein typically has four main domains, consisting of D0, D1, D2 and D3. The D0 and D1 domains are required to mediate flagellar polymerization. Analysis of the sequence diversity of the FliC protein in the Enterobacteriaceae family may provide insight into the pathogenic strategy of these bacteria in the context of interaction with pathogen -associated molecular patterns. In addition, the efficacy of FliC as an adjuvant or a component of the multi-epitope vaccine has been demonstrated.

Methods : We analyzed 392 full-length FliC proteins from the Enterobacteriaceae family. In the first step, isoelectric pH, molecular weight, and amino acid composition of FliC protein sequences were calculated using the ProtParam program. Next, the tertiary structure of the FliC proteins and its interaction with zebrafish TLR -5 was performed. Sequence alignments were performed using ClustalW software and the curricular phylogenetic tree was depicted using MEGA -7 software and iTOL web server. Finally, we evaluated the interaction of FliC proteins of Enterobacteriaceae family with TLR-5 to find the strongest docking.

Results : Physicochemical properties and multiple sequence alignments revealed that FliC has a unique characterization in each genus. However, D1 as the binding domain site associated with TLR-5 exhibited high sequence conservation and the FliC protein of S. enterica subsp. enterica had the strongest interaction with TLR-5.

Conclusion : FliC protein of S. enterica subsp. enterica can be considered as a promising epitope -delivery platform. In addition, phylogenetic analysis revealed that FliC may be acceptable marker for distinguishing genera in the Enterobacteriaceae family.

Keywords : Enterobacteriaceae Family, FliC, Epitope-Delivery Platform

O16-478: Mycoplasma pneumonia and Chlamydia pneumonia infection in patients admitted to Beheshti hospital in Kashan with community-acquired pneumonia

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Background and Aim : Mycoplasma pneumonia and Chlamydophila pneumoniae has been associated as a cause of community-acquired pneumonia (CAP) worldwide. The aim of this study was to determine the prevalence of C. pneumoniae and M. pneumoniae infections in patients admitted to Beheshti hospital in Kashan with CAP.

Methods : This descriptive cross-sectional study was performed on 160 patients with CAP admitted to Beheshti Hospital in Kashan. Serological tests for Mycoplasma and Chlamydia pneumonia were used to evaluate IgG and IgM by the ELISA method. A questionnaire including demographic data, hospitalization time, clinical and paraclinical findings were completed. Data analyzed by SPSS software (20 version).

Results : M. Pneumonia antibody IgM and IgG detected in 19 (11.9%) and 132(82.5%) cases respectively. C. Pnemoniae antibody IgM and IgG in 16(10%), and 151(94.4%) cases found positive. There was no significant relationship between M. neumoniae and Chlamydia pneumonia infections with sex, underlying illness, the severity of pneumonia, ICU admission, hospital death, hospitalization time, CRP, hematocrit and platelet count. While there was a significant relationship between M. Pneumonia with chief complaint ($p<0.001$) and age ($p = 0.122$). Also, a significant relationship was seen between C. pneumonia with white blood cell count ($p = 0.001$) and changes in chest radiography ($p = 0.001$).

Conclusion : The results of this study indicate a high prevalence of M. Pneumoniae and C. Pneumoniae in CAP patients. Therefore, in the empirical treatment of pneumonia patients, appropriate antibiotics against these two atypical organism seems necessary.

Keywords : Community-acquired pneumonia, Chlamydia Pneumoniae, Mycoplasma Pneumoniae

O17-502: A survey on ESBL, MBL Enzymes, and AcrAB-TolC Efflux Pump Frequency Correlation with MDR in Clinical Enterobacter spp.

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Background and Aim : Enterobacter cloaca and Enterobacter aerogenes are opportunistic pathogens that cause nosocomial infections. Multidrug resistance, in particular, the presence of Extended-spectrum beta-lactamase enzymes, Metallo-beta-lactamases, and efflux pumps have posed major problems in treatment. The aim of this study was to evaluation of ESBL, MBL enzymes, and AcrAB-TolC efflux pump in Enterobacter isolated from hospitals of Hamadan and Tehran.

Methods : A total of 42 isolates were identified as Enterobacter species and were evaluated for antibiotic susceptibility using the disk agar diffusion method, the MIC of cefotaxime was using the E-test strip. PCR method was used to identify ESBL, MBL beta-lactamase, and AcrAB-TolC efflux pump genes, using the Double-Disk Synergy Test and Imipenem-EDTA combined disc. Statistical analysis was performed using SPSS software (Version 24).

Results : Ceftazidime had the highest percentage of antibiotic resistance (71.5%), while TGC had the lowest resistance to antibiotics (4.6%). 76% of the isolates were resistant to cefotaxime (MIC test) and 74.6% of the isolates were MDR. In phenotypic analyses, 88.5% of isolates were ESBL positive and 6% were MBL positive. Furthermore, PCR test results for ESBL genes revealed that the largest presence of genes was connected to TEM (96%), SHV (66%), and CTX-M (68%), which were among six separate gene groups. CTX-M genes CTX-M1 (72%) and CTX-M15 (68%) were discovered in the isolates. Furthermore, the frequency of AcrAB-TolC efflux pump genes was Acr-A, Tol-C, and Acr-B, 28%, 18% and 12%, respectively.

Conclusion : The high incidence of Enterobacter strains to produce ESBLs with the TEM, SHV, and CTX-M genes found in this study has been identified as a severe concern in hospitals, posing serious issues for infection management and antibiotic therapy. On the other hand, there was a correlation between the existence of the IMP Metallo-beta-lactamase genes and the development of antibiotic resistance, also the presence of the AcrAB-TolC efflux pump genes. Colistin, amikacin, tigecycline, and imipenem have a low resistance to isolates and can be used to treat infections.

Keywords : Enterobacter cloacae, Enterobacter aerogenes, ESBL, MBL, AcrAB-TolC, Efflux pumps, Biofilm

O18-508: New treatment of bacterial infections caused by Escherichia coli based on exosomes secreted from stem cells

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Background and Aim : Exosomes derived from MSCs are used to detect and treat bacterial and viral infections. Exosomes help in the healing process by delivering miRNA and mRNA, peptides, proteins, cytokines, and lipids, as well as communicating with other organs in the body. The advantages of these Extracellular vesicles (EVs) cells are their small size, high stability, low function, repair of tissue damage caused by infection, and reduced inflammatory factors. The current study's purpose was to determine the use of Exosomes for treatment. E. coli belongs to the Enterobacteriaceae family, which is known to cause various infectious diseases. We will cover the two treatments for disorders induced by exosomes. E. coli is implicated in the formation of liver abscesses, which may lead to mortality in cases with comparable infections and inflammatory solid reactions. AIEC is another strain of E. coli that causes common Crohn's disease. To survive in intestinal epithelial cells, these bacteria enter macrophages and generate inflammation and cytokines. As the initial line of bacterial therapy, we utilized antibiotics.

Methods : In both studies, qRT-PCR methods were used to evaluate the number of exosomes and assess the inflammatory response in the infected cells. Then, we purified and secreted Exosomes released by T84 cells (Exo-uninfected) and infected human intestinal epithelial and revealed addition of them.

Results : According to the analysis of the combination of imipenem and exosomes derived from stem cells, there is a significant synergistic effect and a decrease in the secretion of inflammatory cytokines, nitric oxide, and the amount of apoptosis in infected cells. Analyzes indicate that transmission of these miRNAs was significantly increased from exosomes to recipient cells to inhibiting autophagy-mediated clearance of intracellular AIEC

Conclusion : Due to increased drug resistance, Escherichia coli, which leads to a wide range of diseases, the use of exosomes as an effective non-antibiotic treatment method has been applied in these studies against infections caused by this bacteria there are some limitations to this study that need to be acknowledged and considered in future.

Keywords : Escherichia coli, Exosome, bacterial infections

O19-661: Investigation of the relationship between the presence of genes involved in type II toxin-antitoxin systems in Acinetobacter baumannii and resistance to specific antibiotics

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Background and Aim : The purpose of this study was to investigate the relationship between the presence of genes involved in type II toxin-antitoxin systems in Acinetobacter baumannii and resistance to specific antibiotics.

Methods : Seventy clinical isolates of A. baumannii were collected from variuos clinical samples. Antimicrobial Susceptibility test was determined by disk diffusion. Type II TA system-related genes including GNAT, XRE -like, hipA, hipB, hicA, hicB were screened using PCR. The relationship between the presence of toxin and antitoxin related genes and resistance to specific antibiotics was investigated.

Results : The highest rate of resistance and sensitivity was observed against Cefepime (77.14%), and Ampicillin/sulbactam (42.85%) respectivley. All A. baumannii isolates were considered as MDR. In this study, three TA loci were identified for A. baumannii including GNAT/ XRE-like, HicA/HicB, and HipA/HipB and their prevalence was 100%, 42%, and 27.1%, respectively. There was no significant relationship between the prevalence of these systems and the origine of A.baumannii . Our data showed significant correlations between the presence of HicA/HicB system and resistance to ceftazidime, meropenem, imipenem, and cefepime (P-value <0.05), and the presence of HipA/HipB system and resistance to ceftazidime, meropenem, imipenem, and cefepime (P-value <0.05).

Conclusion : The existence and expression of genes involved in the toxin-antitoxin system may play a role in the resistance to specific antibiotics and increase the spread and maintenance of multidrug resistance in bacteria.

Keywords : Acinetobacter baumannii, Toxin-antitoxin (TA) systems, Antibiotic Resistance

O20-114: Comparison of reduced graphene oxide and Multi-Walled Carbon Nanotubes modifications on glassy carbon electrode for Escherichia coli detection

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Background and Aim : Escherichia coli is an indicator in the quality control of pharmaceutical and other samples. This study was aimed to compare the classical methods and biosensors for E. coli detection.

Methods : A reference electrode (Azar Ag/AgCl electrode), a counter electrode (platinum wire), and a glassy carbon electrode as working electrode were used for E. coli detection. Reduced graphene oxide (rGO) which synthesized with modified Hammer method and also Multi-Walled Carbon Nanotubes (MWCNTs) were immobilized on glassy carbon electrode (GCE) separately. Then, AuNPs decorated on them with chronoamperometric and reduction method and activated with the mixture of 5 mM N-hydroxysuccinimide (NHS) and 2 mM 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride (EDC) at 33°C for 2 h. Then, they were exposed to polyclonal E. coli antibody for 1 hour at 33°C. After washing with PBS)pH 7.4(and drying, 5 µl of 0.5 W/V% Bovine Serum Albumin solution was immediately immobilized on the modified electrode. Morphology and structure of rGO and MWCNTs and AuNPs were verified by SEM as well as the surface of bare glassy carbon electrode before and after modification. Square-Wave Voltammetric and Cyclic Voltammetric techniques were used for detection of E. coli in different samples. On the other hand, for classic method, serial dilutions of E. coli ATCC 8739 were prepared and cultured on Tryptic Soy Agar and incubated at 37oC for 72 hours. Results were compared with biosensor detections. Salmonella enterica ATCC 14028, Pseudomonas aeroginosa ATCC 9027, Bacillus subtilis ATCC6633 and Staphylococcus aureus ATCC 6538 reference strains were used for examining the specificity of the optimized electrode.

Results : GC/rGO/AuNPs/BSA modification had not significant change in currents in compare with GC/MWCNTs/AuNPs/BSA. There was similar sensitivity of detection in polluted samples in compare with plate method. LOD of biosensor with GC/MWCNTs/AuNPs/BSA was about 3.02 CFU/ml without interference with other bacteria.

Conclusion : In spite of two methods of AuNPs immobilization, SEM pictures established that current deviation with Au was not applicable in GC/rGO/AuNPs/BSA modification.

Presence of MWCNTs with AuNPs could effect on spread of electrode area and conductivity. There was no significant deviation between classical and biosensor analysis.

Keywords : Reduced graphene oxide, Biosensor, E. coli, Multi-Walled Carbon Nanotubes, AuNPs

O21-111: Urinary tract infection in diabetes: Uropathogens, related factors, and antimicrobial sensitivity at Sari, Iran

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Background and Aim : : Based on the high frequency of UTI in diabetic patients and consequently using more antibiotics, this study aimed to determine the common uropathogens in diabetic patients, etiological factors, antibiotic resistance patterns, and MIC to improve insight in this infection, treat better, prevent inappropriate antibiotic use, and reduce community resistance.

Methods : In this cross-sectional study, having common UTI symptoms and possible risk factors were collected via the questionnaire from 302 patients with diabetes for analyzing. The taken urine samples were cultured for diagnosing UTI. For every positive sample, disk diffusion tests were done. Those antibiotics with the highest rate of resistance and intermediate resistance were selected. The E-test was then used for further examination and MIC determination.

Results : Of the total 302 samples, 22.5% were detected as UTI positive. Isolated bacteria were 59.4% and 40.59% of the various gram-positive and negatives species, respectively. The most predominant bacteria were S. agalactiae (25%). There is clear correlation between UTI and having fever (p-value= 0.034), urgency (p-value=0.04) as symptoms and renal failure (p-value= 0.006), recent hospitalization (p-value= 0.018), and diabetes duration (p-value=0.028) as risk factors. Antibiogram showed that the most sensitivity to piperacillin-tazobactam (96%) in gram- positives and gentamicin (100%) in gram-positive and negatives. Besides, the results of the E-test compared with disk diffusion.

Conclusion : The study showed that first-line drugs commonly used in UTI are not appropriate for diabetic patients. It seems using other antibiotics according to isolated bacteria and antibiogram tests considering for better UTI treatment among diabetic patients.

Keywords : Urinary tract infection (UTI), Diabetes Mellitus (D.M.), Antibiotic resistance, Uropathogens, Bacteriuria

O22-526: Evaluation of immunogenic efficacy of Hma.FdeC.UpaB.CTB recombinant protein in associated with chitosan against Uropathogenic Escherichia coli

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Background and Aim : Urinary tract infections (UTIs)are the most common bacterial infections and usually caused by Uropathogenic Escherichia coli (UPEC). Serious challenges such as chronic recurrent UTIs, the need for long-term prophylactic antibiotic therapy in the antibiotic resistance era highlights the necessities for effective preventive methods, such as vaccination against UTIs.

Methods : FdeC, Hma, UpaB and also Ctb (as build-in adjuvant) were chosen to design a multi-epitope subunit vaccine containing Bcell linear epitopes using different bioinformatic methods. Recombinant protein expression was performed using the BL21(DE3)/pET28 expression system and purified through a Ni-NTA column. The designed proteins were encapsulated in chitosan nanoparticles. Female 6–8 weeks old BALB/c mice were immunized intranasally with vaccine protein or chitosan-encapsulated vaccine protein. Total IgG, IgG isotypes (IgG1, IgG2a) and IgM responses of immunized mice were measured by ELISA to determine antibody responses.

Results : Expression of the vaccine protein was confirmed by SDS- PAGE and western blot. The analysis of antibody assay shows that vaccine protein in associated with chitosan significantly stimulates humoral immunity.

Conclusion : Our results showed that intranasal administration of the designed vaccine formulated with chitosan has the potential to stimulate the protective humoral immune response against UPEC.

Keywords : Urinary tract infections, multi-epitope subunit vaccine, chitosan

O23-393: Prevalence , Molecular identification and Antifungal susceptibility pattern of Candida species from the Oral cavity of hospitalized patients with kidney transplantation in Iran

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Background and Aim : Oral candidiasis considered as a major complication of mucus membrane infection of immuno-compromised patients, such as, those undergoing kidney transplantation. The aim of this study was to identify Candida species and evaluate drug susceptibility testing of isolates in oral cavity of hospitalized patients with kidney transplantation.

Methods : Two separate swabs were taken from oral cavity of 40 patients before and after transplantation (step1 and step 2 respectively) , transferred to sterile falcon tubes and cultured on Sabouraud' Dextrose Agar medium (SDA) and 21- plex PCR was used for identification of Yeasts . Anti fungal drug susceptibility testing(AFST) was performed against fluconazole and itraconazole according to CLSI micro dilution standard method (M27, A3/ S4).

Results : C. glabrata was the most prevalent species in step 1 with (65%) and step 2 (60%). C. albicans in step 1 (33%) and step 2 (38%) accounted to the second level ,and Rhodotorula was ranked last frequency (2%). C. glabrata (n=4) isolates from step 1 were resistant to fluconazole, in step 2, C. glabrata (n = 20) were itraconazole sensitive ,whereas, C. albicans isolates were fluconazole resistant in both step 1 and step 2 (n=7 and n = 6 respectively) ,on the other hand one isolate was itraconazole resistant in the priviously mentioned step.

Conclusion : Based on obtained findings, in kidney transplant patients C,glabrata represented as the main causative agents of oral candidasis ,focusing on the importance of non-albicans Candida in oral cavity of patients . According to AFST results ,an increased number of resistant isolates shed light on performing antifungal tests for achieving the best outcome of patients in order to prevent therapeutic failure.

Keywords : Candida species, Molecular identification ,Antifungal drug susceptibility testing,Kidney transplant patients

O24-304: DNA-aptamer-nanographene oxide as a targeted bio-theragnostic system in antimicrobial photodynamic therapy against *Porphyromonas gingivalis*

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Background and Aim : The aim of this study was to design and evaluate the specificity of a targeted bio-theragnostic system based on DNA-aptamer-nanographene oxide (NGO) against Porphyromonas gingivalis during antimicrobial photodynamic therapy (aPDT).

Methods : Following synthesis and confirmation of NGO, the binding of selected labeled DNA-aptamer to NGO was performed and its hemolytic activity, cytotoxic effect, and release times were evaluated. The specificity of DNA-aptamer-NGO to *P. gingivalis* was determined. The antimicrobial effect, anti-biofilm potency, and anti-metabolic activity of aPDT were then assessed after the determination of the bacteriostatic and bactericidal concentrations of DNA-aptamer-NGO against *P. gingivalis*. Eventually, the apoptotic effect and anti-virulence capacity of aPDT based on DNA-aptamer-NGO were investigated.

Results : The results showed that NGO with a laky, scale-like, and layered structure in non-cytotoxic DNA-aptamer-NGO has a continuous release in the weak-acid environment within a period of 240 h. The binding specificity of DNA-aptamer-NGO to *P. gingivalis* was confirmed by flow cytometry. When irradiated, non-hemolytic DNA-aptamer-NGO were photoactivated, generated ROS, and led to a significant decrease in the cell viability of *P. gingivalis* ($P < 0.05$). Also, the data indicated that DNA-aptamer-NGO-mediated aPDT led to a remarkable reduction of biofilms and metabolic activity of *P. gingivalis* compared to the control group ($P < 0.05$). In addition, the number of apoptotic cells increased slightly ($P > 0.05$), and the expression level of genes involved in bacterial biofilm formation and response to oxidative stress changed significantly after exposure to aPDT.

Conclusion : It is concluded that aPDT using DNA-aptamer-NGO as a targeted bio-theragnostic system is a promising approach to detect and eliminate *P. gingivalis* as one of the main bacteria involved in periodontitis in periopathogenic complex in real-time and in situ.

Keywords : Aptamer, *Porphyromonas gingivalis*, Antimicrobial photodynamic therapy, Nanographene oxide

O25-55: Diversity of the gastric microbiota in the Helicobacter pylori infected and non-infected patients and its link to transcriptional changes of gene mediators in the NF-κB inflammatory pathway among patients with chronic gastritis

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Background and Aim : The role of gastritis, as a serious disease, in the formation of gastric cancer and its interplay with microbial infections remains largely unknown. We aimed to investigate diversity of bacterial communities and their links with alteration in transcriptional levels of genes associated with the NF-κB inflammatory pathway in the gastric tissue.

Methods : Gastric biopsy samples of 168 patients with gastric disorders were provided. Histological examination of the biopsies and their culture on specific and general culture media were done to show histological changes and isolation of Helicobacter and non-Helicobacter bacteria, respectively. Among the patients with moderate chronic gastritis, 16S rRNA gene sequencing were done on a healthy individual, 8 H. pylori infected and 5 H. pylori non-infected patients. Discriminative indicator bacteria, alpha and beta diversity of the characterized bacterial taxa in each group of the patients and their correlations with relative expression values of NF-κB pathway were evaluated.

Results : These results showed significant microbiome diversity between the patients with H. pylori infection compared with non-infected patients. The enrichment of members of the oral microbiota in H. pylori-negative patients was seen in the studied cases. Epsilonbacteraeota in H. pylori-infected and Firmicutes in the non-infected patients were the most prevalent phyla. LEfSe analysis proposed members of Helicobacteraceae and Streptococcaceae as main indicator organisms in the H. pylori-positive and H. pylori-negative patients, respectively. It seems that the interaction between the characterized gastric microbes and the expression levels of inflammatory and carcinogenic genes is complex.

Conclusion : Our results showed colonization of the stomach by a variety of bacterial taxa in patients with moderate chronic gastritis. Although members of the microbiota from the oral cavity and upper respiratory tract were detected as common bacteria associated with gastritis

in the H. pylori-negative patients, establishment of their role as true pathogens or a bystander and their links with induction of inflammatory response need further studies.

Keywords : Helicobacter pylori; Microbiota; Gastritis; NF-κB pathway; 16S rDNA

O26-695: Changes in the microbial genomic pattern of the blood of patients with Crohn's disease in the flare and remission phases

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Background and Aim : Crohn's disease (CD) has a chronic course, which environmental, genetic and bacterial flora are the main factors causing this condition. There is a lack of data about the role of bacteria in Crohn’s disease incidence and its relation with gradual changes of bacterial biomarkers in blood of CD patients.

Methods : Nineteen CD patients were enrolled in this study. CD activity scores, biological, clinical and demographic data of the patients were recorded during 3-months follow up. Aerobic and anaerobic bacteriological culture was done on blood samples and 16SrRNA sequencing were done on extracted DNA from PBMCs.

Results : Bacteriological culture showed bacteriemia with Streptococcus spp. and Clostridium spp. in two active CD patients. Bacterial population in flare phase of active patients were significantly higher than their remission phase. This difference was mostly associated with the decrease in the population of gram-negative bacteria such as salmonella, sphingomonas, bradyrhizobium and gram-positive bacteria such as streptococcus, enterococcus and lactobacillus in remission phase.

Conclusion : Bacterial diversity was decreased in remission phase of CD patients. The quantity and diversity of bacterial genera were involved in severity of CD patients.

Keywords : Crohn’s disease; Gene expression; 16SrRNA sequencing; Bacteremia

O27-117: Isolation and Molecular Identification of Mycobacterium from Milk Samples of Tehran Province's dairy Farms

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Background and Aim : A study was performed in the Persian capital province of Tehran to assess frequency of Para tuberculosis in its operating cattle farms.

Methods : As many as 8,000 cows were screened by a home-made ELISA system. Milk specimens were collected from detected reactor to perform confirmatory PCR-16srRNA, PCR-IS900 and PCR IS1311 experiments plus bacterial culture on specific media in search for Mycobacterium avium subsp Para tuberculosis (MAP).

Results : While among the 25 ELISA positive animals, eight cases produced positive results in PCRs only three appeared positive in MAP isolation. In deduction, we assume when it comes to selection of control measures against Ptb

Conclusion : In an environment with presumably high prevalence of Ptb like Tehran, ELISA is a much more sensible detection system compared to the zero false-positive method of bacterial culture.

Keywords : Isolation, Farms in Tehran Province, Mycobacterium avium subsp. Para tuberculosis, Johne's disease

O28-639: Evaluation of transgenic Leishmania major expressing mLLO-BAX- EndoG -SMAC in the apoptosis of itself parasite and the infected macrophages in vitro and in vivo.

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Background and Aim : Cutaneous leishmaniasis is a parasitic infection against which no confirmed vaccine has been reported so far. Because of escaping the parasite from the host immune system or preventing macrophage apoptosis, it seems the expression of pro-apoptotic proteins of macrophage (BAX- SMAC) and parasite (EndoG) by transgenic Leishmania major can limit differentiation and proliferation of parasites and the ability to cause infection by accelerating the apoptosis process of macrophage and L.major. So, this research investigated the impact of transgenic L. major including mLLO-BAX- EndoG -SMAC in macrophage and L.major apoptosis acceleration

Methods : The coding sequence mLLO-BAX- EndoG -SMAC was designed and integrated into the pLexyNeo2 plasmid. The designed sequence was inserted under the 18srRNA locus into the L. major genome using homologous recombination. Then, mLLO-BAX- EndoG -SMAC expression was studied using the Western blot, and the transgenic parasite pathogenesis was investigated compared to wild-type L. major in vitro and in vivo. Also, the collected macrophage -free supernatants at 12, 24 and 48 h post- stimulation and infected mice sera obtained at 3, 4 and 5 week post-infection were subjected to ELISA analysis for TNF-α, IL-10, IL-12 cytokines and BAX, EndoG and Bcl-2 proteins and compared with ulcer size and parasitic bar of spleen. The groups were compared using ANOVA test at the significant level of $p < 0.05$.

Results : PCR and Western blot results approved the proper integration and expression of the mLLO-BAX- EndoG -SMAC under the 18srRNA locus of L. major, respectively. The flow cytometry results revealed faster apoptosis of transgenic Leishmania-infected macrophages compared to wild-type parasite-infected macrophages. Also, in vitro, at 12h, apoptosis promotion of macrophage and transgenic L.major was correlated with increased production of IL-12, TNF-?, BAX, Endo G and reduced production of IL-10 and Bcl-2. In vivo, increased and decreased levels of the mentioned cytokines were associated to the reduction of the lesion size and the parasitic burden of spleen in transgenic L.major- infected mice compared to wild type- infected mice.

Conclusion : This study recommended transgenic L. major including mLLO-BAX- EndoG - SMAC construct as a pilot model for providing a protective vaccine against leishmaniasis.

Keywords : Leishmania major, transgenic, apoptosis, macrophage

O29-97: Safety and immunogenicity of live attenuated IRIBA vaccine in a mouse model

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Background and Aim : Brucellosis is one of the most important zoonotic diseases in livestock and humans, which is associated with abortion in animals and fever in humans, It has a high prevalence in Iran. IRIBA vaccine strain is a mutation of Brucella abortus strain 2308 that lacks the lipopolysaccharide o chain. Cows vaccinated with IRIBA are protected against abortion. The aim of this study was to evaluate the safety and immunogenicity of IRIBA vaccine, produced by Razi vaccine and serum research institute.

Methods : For this purpose, according to the OIE sampling instructions, the required number of samples were randomly selected from three batches of IRIBA vaccine produced for reduced and full dose of IRIBA vaccine. Evaluation of vaccine safety and immunogenicity of IRIBA was performed according the OIE protocol.

Results : Mice vaccinated with this vaccine showed no growth of IRIBA in cultured spleens of vaccinated mice. The condition of the spleen was also normal. Vaccine immunogenicity evaluation in vaccinated mice also showed that the vaccine tested had satisfactory results. The immune response of unvaccinated mice showed that the value of Brucella in their spleen was at least 4.5 units and in mice vaccinated with reference vaccine (RB51) and RAZI vaccine (IRIBA) was less than 2.5 units. There was also no significant difference in the immunogenicity of mice vaccinated with the reference vaccine.

Conclusion : The results of this study showed that the use of IRIBA vaccines is safe and induce sufficient immunity for protective against B. abortus.

Keywords : Brucellosis, Safety ,immunogenicity , IRIBA,vaccines

O30-187: Effect of eliminating hdcA gene of Staphylococcus epidermidis TYH1 on Histamine production

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Background and Aim : The possible adverse effect of histamine on human health has made it a detrimental aspect to the quality and safety of many fermented food products especially fish sauce.

Methods : In present study, hdcA gene in Staphylococcus epidermidis TYH1 was knocked out and its effect on histamine production was evaluated. HdcA encodes histidine decarboxylase, an enzyme that produces histamine from histidine. Both strains of TYH1, the wild type (WT) and mutant (ΔhdcA) were then incubated in tryptic soy broth (TSB) supplemented with histidine (0.5 mM). The histamine content determined by capillary zone electrophoretic (CZE) analysis. Safety assessment of this mutant of food origin was conferred by virulence genes.

Results : It was found that S. epidermidis TYH1 exhibited production of histamine (50.09?0.06 ?g/mL), while ?hdcA strain of TYH1 exhibited no histamine forming activity. Safety assessment of ?hdcA revealed the presence of nuc gene, while superantigenic toxins and coa genes were not observed. Therefore, it has the ability to be used as a starter culture to decrease the histamine content in any fermented food products.

Conclusion : Our study findings may contribute to provide a novel approach of promoting the food safety of fish sauce and other fermented food products regarding the regulation of histamine content.

Keywords : Staphylococcus epidermidis; histamine; histidine decarboxylase; capillary electrophoresis; enterotoxin

O31-558: Applications of Cold Plasma and UV Radiation Technologies in Disinfection and Increasing the Shelf-Life of Food and Agricultural Products

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Background and Aim : While a vast array of foods and agricultural commodities along with their associated pathogens are daily produced, there is no a such single universal technology to meet all the requirements. Hence, providing the technological industries with the variable options to meet its specific needs is, however, necessary. The food safety management reflects in the establishment of effective strategies to decrease the risks for the microbiological safety in the production of agricultural and food materials. Hence, the cold plasma and UV radiation technologies are strongly compatible with the most of existing packaging and quality improvement procedures

Methods : Both the cold plasma and UV radiation technologies offer the high microbial inactivation efficiency at the low temperatures, i. e., below 50°C. Hence, while the shelf-life extension is allowed, the supply chain efficiency is significantly improved. The UV and plasma applications are free of water or solvent. Hence, they are introduced as the environmentally friendly technologies.

Results : The UV photons and the active chemical species emitting from the plasma discharge sources act rapidly on the entire of foods surface in the most cases. The cold plasma and UV radiation are seemingly benign to many food products.

Conclusion : These technologies are able to reduce the preservative uses. These technologies leave no residues and, given sufficient time is provided for the recombination reactions to proceed. Besides, these sources need only a low energy input. Importantly, both the plasma and UV technologies are applicable for both the solid and liquid food products.

Keywords : Food Safety, Cold Plasma and UV-C Radiation Technologies, Shelf-Life Extension

O32-681: Are molecular methods a suitable alternative to gold standard methods in Salmonella detection?

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Background and Aim : Salmonella is one of the most common causes of foodborne outbreaks worldwide. The cultured-based method is considered a gold standard for the detection of Salmonella. Due to being cost-effective and time-consuming, there is an urgent need to investigate a rapid and cheap method. This study aimed to evaluate different methods to detect the Salmonella genus, serogroups, and serovars.

Methods : Poultry farm feces samples from 21 cities in Iran were collected from January 2016 to December 2019. The samples whose microbiological cultures were positive were subjected to serological assay and multiplex polymerase chain reaction (m-PCR) to detect serogroup A, B, C1, C2, D1, E, and H and also FliC. Besides, m-PCR was used to characterize different Salmonella serovars. The chi-square test was used to compare the discriminatory power of the different methods.

Results : Out of 2300 Poultry feces samples, 173 (7.5%) and 166 (7.2%) samples were detected as Salmonella by cultivation and m-PCR. Hence, the molecular method's sensitivity compared to cultivation was equal to 0.96 (CI=95%). The same results were obtained with m-PCR and serological in evaluating H antigenic subgroups. Therefore, the two methods' matching rate in detecting all H antigenic subgroups was 100%. Thus, the relationship between the results obtained from both methods was quite significant in the Contingency table statistical test ($P < 0.01$).

Conclusion : The results were confirmed effortlessly within a short period (24-36 hours) compared to 3-8 days for the conventional microbiological methods. Even though our results are preliminary, the m-PCR assay would offer a valuable alternative to microbiological culture.

Keywords : Salmonella; Poultry; feces, Multiplex PCR, microbiological Culture

O33-439: Isolation of lytic bacteriophage ECP-ST against Antibiotic Resistant Escherichia coli strains isolated from urinary tract infection

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Background and Aim : Uropathogenic E. coli (UPEC) is a Gram-negative bacterium and the cause of a wide range of (UTI) urinary tract infections. This bacterium is resistant to many antimicrobial agents and has become a major problem for societies. Therefore, new methods of controlling infections resistant to antibiotics are much needed. Meanwhile, bacteriophages can be used as a suitable alternative treatment, which are less resistant to them and also have few side effects. In this regard, the aim of the present study is to isolate lytic bacteriophage against several resistant strains of E. coli isolated from urinary tract infections.

Methods : In this research, in order to collect resistant E. coli bacteria strains, which are the cause of urinary tract infection, different samples of E. coli isolated in Isfahan medical diagnosis laboratories were collected. Then biochemical diagnostic tests as well as disk diffusion antibiogram test were performed for them to check antibiotic resistance. Also, sewage and river water samples were used for the isolation of specific bacteriophages and were examined by two-layer agar method and spot tests and overlay tests.

Results : In this research, we used bacteria that were resistant to cefepime, ceftazidime, imipenem, and ciprofloxacin, and finally we obtained bacteriophage ECP-ST. This bacteriophage had lytic properties against eight bacterial strains out of twenty five strains collected. And it has transparent plaques with a diameter of 2 to 3 mm, and their image was observed under the electron microscope, which shows that the ECP-ST phage has a symmetrical series and a retractable tail.

Conclusion : According to the results of this research, ECP-ST phage can be a suitable option for the preparation of phage mixture against UPEC strains for the treatment of urinary tract infections.

Keywords : Bacteriophage ; uropathogenic E. coli ; Urinary Tract Infection ; Multi Drug Resistance

O34-521: Phage cocktail as wonderful bio-nanoparticles for the prophylaxis and treatment of burn wound infection caused by multidrug-resistant bacteria in a mouse model.

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Background and Aim : Multi-drug resistance has become a major problem for the treatment of pathogenic bacterial infections. The use of bacteriophages is an attractive approach to overcome the problem of drug resistance in pathogens that cause fatal infections. Our study aimed to collect methicillin resistance Staphylococcus aureus and multi drug resistant Pseudomonas aeruginosa and Acinetobacter baumannii from patients with burn wounds and then isolate specific lytic bacteriophages against these pathogens. Then apply their cocktail as alternative therapeutic agents in a mouse model of mixed infection.

Methods : MDR-bacterial strains were collected from the microbiology laboratory of Motahari hospital. Bacteriophages were isolated from hospital sewage by double-layer agar method and tested in vitro for lytic activity against resistant isolates as well as some biological features. Morphological characteristics were identified by transmission electron microscopy (TEM). The isolated phages were named ΦS1, ΦPsd1sw, and ΦA1sw for lytic phage of methicillin-resistant Staphylococcus aureus and multi-drug resistant Pseudomonas aeruginosa and Acinetobacter baumannii respectively. We also examined the therapeutic potential of ΦS1, ΦPsd1sw, and ΦA1sw Bacteriophages cocktail for prophylaxis and treatment of mixed bacterial infection in 5groups of Six-week-old male Swiss mice (weight ~25-30 g per mouse) during 14 days by colony counting method.

Results : Morphological identification of ΦS1, ΦPsd1sw, and ΦA1sw Phages by transmission electron microscopy showed that these virion particles belonged to Myoviridae (ΦS1) and siphoviridae (ΦPsd1sw and ΦA1sw) family, with clear plaques without halo that demonstrate the lytic activity of isolated phages. In this study, the administration of a phage cocktail within one dose could prevent (group I: before bacterial infection) and treat (group II: after bacterial infection) mixed bacterial infection in comparison with control groups (almost ten-fold decrease in colony count number). Our data also demonstrated that administration of two-dose (one dose day1 and one dose on day 8 after infection) phage cocktails may be more effective prophylaxis and treatment for mixed infection than one dose cocktail (5 fold decrease).

Conclusion : In vitro and in vivo analysis of the phage cocktail demonstrated perfect lysis against the corresponding MDR-bacteria, and this cocktail may be promising as the first choice for prophylaxis against wound infection. Hence, our results suggest that this bacteriophage cocktail could be a potential therapeutic option for treating septic wounds caused by S. aureus, P. aeruginosa, and A.baumannii.

Keywords : MDR, bacteriophage, phage cocktail, S. aureus, P. aeruginosa, A.baumannii.

O35-668: Use of specific Lytic nano-phage (combination of bacteriophage and nanotechnology) in the treatment of drug-resistant tuberculosis in vitro

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Background and Aim : The emergence of multidrug-resistant tuberculosis (MDR), which means tuberculosis is caused by an isolate of Mycobacterium tuberculosis that is at least resistant to isoniazid and rifampin, is of global importance. Unlike antibiotics, bacteriophages act specifically and do not disturb the natural balance of microflora. Therefore, they are present at the place of infection where their existence is more necessary and they destroy their host, the bacterium that causes the infection, in a precise way. The purpose of this research is to investigate the efficiency of isolated specific bacteriophage against drug-resistant Mycobacterium tuberculosis bacteria and its combination with SLN solid lipid nanoparticles as nanocarriers in laboratory conditions.

Methods : In order, isolation of Mycobacterium tuberculosis from clinical samples, primary isolation of bacteriophage, purification of bacteriophage, determination of bacteriophage morphology, determination of host and specificity of bacteriophage, test to determine the sensitivity of isolated bacteriophage to temperature and pH, preparation of respiratory spray (MDIS) containing specific lytic bacteriophage Using solid lipid nanoparticles (SLN), Mycobacterium tuberculosis bacterium was investigated in terms of invasiveness and the effect of its specific bacteriophage on the specific cell line.

Results : Bacteriophage isolated with different concentrations has shown a good ability to reduce the number and eliminate Mycobacterium tuberculosis bacteria. The specific bacteriophage plaques isolated against the studied bacteria were specific and against other pathogenic bacteria, they have no lytic function.

Conclusion : This study has shown that bacteriophage or a combination of phage can reduce or completely eliminate Mycobacterium tuberculosis bacteria in laboratory conditions. These results showed that the treatment by bacteriophages has the potential to be used as an alternative proposed method to prevent the use of antibiotics in order to reduce or eliminate Mycobacterium tuberculosis infection. Therefore, they can be used as biologically capable tools against bacteria in practical conditions.

Keywords : Bacteriophage, M. tuberculosis, Drug resistance, Nanotechnology

O36-140: The assessment of antibiotic resistance changes in the Covid-19 pandemic during 2020-2022: An epidemiological study

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Background and Aim : The coronavirus disease 2019 seems to change antibiotic resistance pattern. Certain conditions in the Covid-19 era may be contributing to the rise of AMR. Due to the limitation of information on the impact of Covid-19 on antimicrobial resistance (AMR), the purpose of this research aimed to investigate the antimicrobial resistance of E. coli, P. aeruginosa, K. pneumoniae, and A. baumannii in Hasheminezhad hospital in 2 years of Covid-19 pandemic and compare the antibiotic resistance pattern in 9 seasons of the outbreak.

Methods : 1672 clinical samples were collected from January 2020 (21 Jan) and January 2022 (30 Jan) in Mashhad, Hasheminezhad Hospital. Conventional microbiological procedures for identifying gram-negative bacteria and antibiotic susceptibility testing are considered regarding the clinical and laboratory standards institute (CLSI) 2021. Also, two years of pandemic between January 2020 and January 2022 were divided into 9 periods according to the seasons.

Results : The most resistance in E. coli, K. pneumoniae, P. aeruginosa, and A. baumannii were to Ampicillin (89.6%), Ampicillin (98%), Nalidixic acid (100%), and Cefazolin (97.7%) respectively. There was no significant difference in Ceftriaxone, Levofloxacin, and Nitrofurantoin for K. pneumoniae and Ciprofloxacin for A. baumannii. For E. coli, the most change in antibiotic resistance in Cefazolin was between Fall 2020 (58.6%) and Summer 2021 (85.9%). For K. pneumoniae, the most change in antibiotic resistance in Imipenem was between Spring 2020 (20%) and Summer 2021 (83.7%). For P. aeruginosa, the most change

in antibiotic resistance in Meropenem was between Summer 2020 (82.8%) and Spring 2021 (100%). For A. baumannii, the most change in antibiotic resistance in Cefepime was between Winter 2020 (80%) and Summer 2021 (100%).

Conclusion : This study for the first time revealed that E. coli, P. aeruginosa, K. pneumoniae, and A. baumannii strains have a higher level of antibiotic resistance pattern than what was seen in similar studies conducted before the pandemic which will further restrict treatment choices and jeopardize global public health.

Keywords : Antibiotic Resistance, COVID-19 Pandemic, Escherichia coli, Pseudomonas aeruginosa, Klebsiella pneumoniae, Acinetobacter baumannii

O37-285: CORROBORATE A NEW SURROGATE VIRUS NEUTRALIZATION TEST FOR THE DIAGNOSTIC PURPOSES OF HUMORAL IMMUNITY AGAINST SARS-COV-2

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Background and Aim : The humoral response has a crucial role in immunity against SARS-CoV-2, which is elevated by infection and vaccination. Currently, several technics have been established to evaluate the neutralizing antibodies (NAbs) levels in the blood serum. In this manner, antibodies against Spike glycoprotein of SARS-CoV-2 are the most important targets. The aims of this study were humoral immunity assessment in individuals with different backgrounds and validation of a new surrogate virus neutralization test against SARS-COV-2.

Methods : We compared the conventional virus neutralization test (cVNT) as a gold standard and anti-S Electrochemiluminescence immunoassay (eCLIA) (Roche Diagnostics, Switzerland) with a surrogate virus neutralization test (sVNT) (iFlash-2019-nCoV Nab assay, YHLO, China) in vaccinated, recovered and hybrid immunized population.

Results : Our finding demonstrates that a reduction in humoral immunity against SARS-CoV-2 may occur over time. By The cVNT titers ? 1:16, 74.5 U/ml and 49.4 IU/ml for anti-S eCLIA and sVNT represent the semi-equal thresholds respectively.

Conclusion : According to our observations, increasing the herd immunity against SARS-CoV-2 by vaccination is critical to be taken into account. Furthermore, we suggest that sVNT could be a reliable routine serologic assay that performs high specificity, without cross reactivity.

Keywords : SARS-CoV-2, neutralizing antibodies, sVNT, eCLIA, cVNT

O38-330: Evaluation of lncRNA EGOT and ISG15 expression in SARS-CoV-2 infection

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Background and Aim : The recent coronavirus disease 2019 (COVID-19) pandemic, caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), activates antiviral immune responses and uncontrolled inflammatory reactions. Recent studies have demonstrated that long noncoding RNAs (lncRNAs) which are a class of non-coding RNAs with more than 200 nucleotides in length, have various biological functions and participate in the regulation of immunity signaling pathways in viral infections. Several investigations have indicated the lncRNA Eosinophil Granule Ontogeny Transcript (EGOT) levels can be up-regulated in SARS-CoV-2 infection. The NF-κB pathway is EGOT inducer and therefore, EGOT takes part as a negative regulator in the type I interferon response. On the other hand, the interferon I immunity response and ISG15 expression level can be increased by EGOT depletion. The same pattern is also observed in other viral infections, such as HCV chronic infection. This present survey aimed to assess the blood levels of EGOT and ISG15 lncRNAs in COVID-19 patients in comparison with healthy controls.

Methods : In this case-control study, blood samples were collected from 14 COVID-19 patients in comparison with 14 healthy controls who were enrolled at Taleghani Hospital, Shahid Beheshti University of Medical Science. Total RNA was isolated by RiboEX™ total RNA extraction solution (GeneAll, Seoul, South Korea). After cDNA synthesis, quantitative

real-time PCR was used to detect levels of EGOT and ISG15. Expression levels were assessed using the GraphPad Prism software through the 2-ΔΔCt method.

Results : The result indicates that the gene expression level of EGOT in SARS-CoV-2 infected patients is up-regulated compared to the control group (Fold change=11.073), but the opposite result has been observed for ISG15 expression level and it was down-regulated (Fold change=0.2217). A significant difference was found in blood levels of EGOT and ISG15 between patients and control group (P values 0.0383 and 0.0053, respectively).

Conclusion : According to these results, there is a correlation between EGOT and ISG15 expression levels and SARS-CoV-2 infection. Also, increased level of EGOT acts as a negative regulator of interferon I immunity response by blocking the expression of ISG15 and other ISGs which can lead to promoting viral replication. It seems EGOT lncRNA can be a useful key therapeutic target for the treatment of COVID-19 patients.

Keywords : COVID-19, SARS-CoV-2, lncRNA, interferon I

O39-504: The autophagy-related Beclin-1 expression as a potential diagnostic biomarker for COVID-19.

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Background and Aim : SARS-CoV-2 is a novel beta-coronavirus that causes the current COVID-19 pandemic. Previous studies have shown that coronaviruses use various cellular mechanisms such as autophagy to increase their replication. Autophagy is responsible for the selective removal of dysfunctional organelles, intracellular pathogens, and misplaced proteins, as well as the regulation of the immune response. Then autophagy is closely related to the host inflammatory response. Autophagy has a protective role in reducing the excessive release of cytokines in ARDS[1-3]. Analysis of transcriptome data in the lung cell line infected with SARS-CoV-2 has shown a change in the autophagy response[4]. SARS-CoV ORF-9b protein could induce autophagy and activate NF-κB[5]. Induction of autophagy also seems to be one of the primary functions of cGAS-STING. The cGAS-STING pathway induces autophagy directly via Beclin-1 or LC3-dependent pathways[1]. Inhibition of autophagy in the first stage of COVID-19 may lead to the regulation of the interferon antiviral response and inhibition of viral replication. Activation of autophagy in the late stage of the disease could lead to reduce inflammation and balance the immune response. For these reasons, autophagy-related therapeutic maybe useful for COVID-19[6]. The aim of this study is to evaluate the expression level of autophagy-related Beclin-1 in COVID-19 patients compared to healthy controls.

Methods : In this case-control study, blood samples were taken from 15 patients with COVID-19 and also 15 healthy controls. After total RNA extraction and cDNA synthesis, we used Real-time PCR to evaluate the expression level of Beclin-1. The data were analyzed by $2^{-\Delta\Delta Ct}$ method. ROC curve analysis was also performed to evaluate diagnostic accuracy.

Results : The result shows that expression level of Beclin-1 in COVID-19 patients was up-regulated compared to the healthy controls (Fold change=1, p value=0.03). The area under the curve (AUC) of Beclin-1 for diagnosing COVID-19 compared to controls was 0.88 (95%

CI= 0.75 to 1, p value=0.00) and the optimal cut-off value was calculated to be >0.0009 (Sensitivity 100%; Specificity 73.33%).

Conclusion : According to our results, blood Beclin-1 expression levels may serve as a potential biomarker for COVID-19 diagnosis.

Keywords : COVID-19, SARS-CoV-2, Autophagy, Biomarker

O40-153: Targeted Gene inactivation in Salmonella typhi by CRISPR/Cas9

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Background and Aim : Targeted gene inactivation (TGI) is a widely used technique for the study of genes' functions. There are many different methods for TGI, however, most of them are so complicated and time-consuming. New promising genetic engineering tools are developing for this purpose. In the present study, for the first time we inactivated a virulence gene from Salmonella Typhi (S. Typhi), located in the bacterial chromosome using CRISPR/Cas9 system.

Methods : For this aim, pCas9plasmid containing Cas9 enzyme and required proteins for HDR recombination was prepared and transferred to S. Typhi by electroporation. On the other hand, a specific guide RNA (gRNA) was designed using CRISPOR online tool. Synthetic gRNA was cloned into pTargetF plasmid. Also, a DNA fragment (HDR) was designed to incorporate into the bacterial chromosome following the cleavage of the bacterial genome by Cas9 enzyme. pTargetF containing gRNA and HDR were co-transferred to S. Typhi containing pcas9 plasmid. The transformed bacteria were screened for recombination using PCR, restriction digestion and sequencing.

Results : The results of PCR, restriction digestion and sequencing showed the successful recombination of S. Typhi, in which the gidA gene is disrupted. At last, foreign plasmids were cured by adding IPTG and growing in 37 ˚C.

Conclusion : In the present study we developed a rapid and specific method for targeted gene inactivation in a bacterial species, S. Typhi. This procedure can be exploited for disruption of other Salmonella's genes as well as other bacteria.

Keywords : Targeted gene inactivation (TGI); CRISPR/Cas system; Salmonella Typhi, gidA gene; Live attenuated vaccines.

O41-205: Screening of antioxidant activity of cyanobacteria species isolated from Khoor-e-Khooran mangrove forest, Persian Gulf, Iran

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Background and Aim : Cyanobacteria are photoautotrophic oxygenic bacteria that have acquired special attention due to their nutraceuticals and medical importance. Microbial antioxidants are noncarcinogenic, non toxic and biodegradable compounds compared to synthetic antioxidants. The aim of this study was to evaluate the antioxidant activity of isolated cyanobacteria from the Khoor-e-Khooran mangrove forests.

Methods : Water samples were collected from 12 selected stations from 25 cm below the surface in a 500 mL dark glass bottle. 100 µL of each sample was inoculated on the BG 11 medium and incubated at 28˚C under 12 hours light and 12 hours darkness for 2 weeks. The purified isolates were identified according to morphological characteristics. DPPH radical scavenging activity of the isolated bacteria were determined based on the microdilution method.

Results : We isolated 51 cyanobacterial isolates from collected water samples. Phormidium and Oscillatoria were dominant genera with frequency percentages of 45% and 35% respectively. The antioxidant determination of extracted metabolites from the isolated cyanobacteria showed that 24% of the isolates scavenged DPPH radicals with IC50 values ranged from 46.1 to 676.4 µg/ml.

Conclusion : These results revealed cyanobacterial diversity of the exploration area in the Khoor-e-Khooran mangrove wetland. The potent strains could be considered as potential sources of microbial antioxidants in future studies.

Keywords : Marine cyanobacteria, Microbial antioxidants, Mangrove forests, Persian Gulf

O42-248: Effects of dietary Enterococcus faecium supplement on the gut microbiota and growth performance in Sander lucioperca

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Background and Aim : E. faecium was isolated from the intestinal tract of Sander lucioperca collected from fish farms in Guilan,northern part of Iran.

Methods : Antagonistic activity of different doses of the probiotic was studied against A. hydrophila and the most effective dosage was selected for in vivo experiments. Fish were fed with probiotic; E. faecium dosage including 108, 1010cfu/g and without probiotic (control sets) for 8 weeks,

Results : The results showed the weight gain (WG) and Specific growth rate (SGR) were significantly increased by dietary administration of E. faecium (108, 1010cfu/g) supplemented after 8 weeks. The Feed conversion ratio (FCR) in E. faecium administered fish was significantly lower than the control. Rate of total bacteria and probiotics in intestinal tract, after 60 days of feeding with probiotic in groups fed E.faecium a dosage of 108, 1010cfu/g increased compared to control as well as its survival rate after administration of 1010cfu/g E. faecium in which was significantly higher ($P<0.05$) than other groups (86.6%).

Conclusion : Optimal dosage and dietary administration of 10 10 cfu/g for E.faecium in showed significant effect on growth performance, immunity parameters and survival in Sander lucioperca.

Keywords : Enterococcus faecium ,Sander lucioperca,growth rate,gut microbiota

O43-425: Antibacterial Effects of Bacteriocin secreted by Lactobacillus reuteri against pathogenic Helicobacter pylori

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Background and Aim : Helicobacter pylori causes gastritis, ulcers and gastric cancer. H. pylori has infected more than 50% of the population worldwide. Due to the side effects of antibiotics and strains resistance, the disadvantages of this type of treatment will be greater than its benefits. Reducing H. pylori in the stomach by selective interaction of bacterial cells as an effective method to compete with stomach pathogens is optimal and it may be effective as a blockage in the treatment of H. pylori

Methods : In this study, various samples of dairy products in different parts of the country were used to isolate the L. reuteri strain. Microscopic observation, biochemical and molecular tests and sequencing were performed to confirm the strain. Molecular and biochemical tests were performed to H. pylori identification. Anti-Helicobacter pylori activity of Lactobacillus strains by three cell-free supernatant (CFS) types was detected. Activity of non-neutralized and non-heat-treated (CFSs1), non-neutralized and heat-treated (CFSs2), pH neutralized and non-heat-treated (CFSs3) against H. pylori strains was evaluated. Inhibition zone test for H. pylori was performed using L. reuteri strains. lactic acid produced by L. reuteri was neutralized.

Results : An agar-well diffusion method was used to assess CFS effect on H. pylori growth. The inhibition zones of high concentrations of CFSs were more obvious, indicating that CFS had the potential ability to inhibit H. pylori growth. According to results, the agar-well diffusion test showed significant inhibitory effects of L. reuteri against H. Pylori. Formation of inhibition zone was significantly due to presence of antimicrobial metabolites (e.g. bacteriocin) not secretive acid lactic.

Conclusion : In summary, based on these results it can be found that the L. reuteri which is a probiotic can be applied in therapeutic application for treatment of disease related to H. pylori in gastrointestinal tract. Bacteriocin-like inhibitory substance activity can be an advantage for the probiotic choice for H. pylori infection control. If bacteriocin produced by L. reuteri has antimicrobial properties against Helicobacter pylori, it can be considered as a new generation of probiotics, postbiotics.

Keywords : L. reuteri, H. pylori, bacteriocin, agar-well diffusion, postbiotic

O44-433: Molecular epidemiology and genetic background of PVL-positive S. aureus clinical strains isolated from Iranian patients using a combination of multilocus sequence typing (MLST) analysis

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Background and Aim : Staphylococcus aureus (S. aureus)-associated disorders vary from skin infections to life-threatening invasive diseases, such as bacteremia, sepsis, and endocarditis, mediated by a variety of virulence factor. Panton-Valentine Leukocidin (PVL) is a two-component toxin produced by some S. aureus strains in varying amounts. The population structure and clones of PVL-positive S. aureus strains are changing in different healthcare facilities in different countries. The present study aimed to obtain a more complete description about the molecular epidemiology and genetic background of PVL-positive S. aureus clinical strains isolated from Iranian patients using a combination of multilocus sequence typing (MLST) analysis

Methods : A total of 28 PVL-positive S. aureus strains were detected from 600 S. aureus isolates between February 2016 and March 2019 from different hospitals in Tehran, Iran. MLST was performed for all S. aureus strains using previously reported primers specific for seven housekeeping genes, including arcC, aroE, glpF, gmk, pta, tpi, and yqiL, according to the previously described protocol. The sequences of the PCR products were compared to those of the existing alleles available on the MLST website (https://pubmlst.org/saureus/) and analyzed online to assign allelic profile (sequence type, ST) and the associated clonal complex (CC).

Results : The isolates encompassed 21 different sequence types (STs), of which 16 STs did not have matching profiles in the MLST database and were subsequently designated to ST5147-ST5162 after submitting the data to the website (https://pubmlst.org/saureus/).Other STs identified was, ST30 (6/28, 21.4%), ST1996 and ST1136, (2/28, 7.1%), ST121 and ST22(1/28, 3.57%).Based on eBURST analysis, the isolates were clustered into five CCs, including CC30, CC22, CC1, CC8, and CC5 and nine singleton.

Conclusion : Although different clones were identified in this study, CC30 (31.6%) and CC22 (21%) were identified as the dominant clones among PVL-encoding S. aureus strains. Also, both CC22 and CC30 clones have been reported to be predominant in Asian countries.

The predominance of CC22 and CC30 clones among PVL-positive strains in Iran is of great concern, as these clones appear to be highly transmissible with a propensity to spread worldwide. This study promotes a better understanding of the molecular epidemiology and evolution of PVL-positive S. aureus strains in Iran.

Keywords : Staphylococcus aureus, PVL, MLST,

O45-663: Detection of Panton-valentine Leukocidin (PVL) Gene Isoforms of Staphylococcus aureus Isolates from different hospitals in Tehran, Iran

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Background and Aim : PVL is a two-component toxin produced by some S. aureus strains in varying amounts. To date, at least 22 single-nucleotide polymorphisms (SNPs) have been identified in the lukSF-PV genes based on phylogenetic analysis. PVL-positive S. aureus strains could be classified into four major haplotype groups (R, H1, H2, H3) based on non-synonymous variations in the PVL sequence at nucleotide positions 527,663, and 1396. This study attempts to determine isoforms PVL-positive isolates in clinical samples and the molecular characterization of PVL-positive isolates.

Methods : In this study, 600 isolates of S. aureus were collected between February 2016and March 2019 from different hospitals in Tehran, Iran.A total of 28 PVL-positive S. aureus strains were detected. A PCR-based sequencing method was applied to determine SNPs in the lukSF-PV genes of all S. aureus strains. PCR amplifications were performed using a primer pair (lukS-F GTGGTCCATCAACAGGAGGT and lukF-R TGGTCCCCAACCATTATTCA) specifically designed to generate a 1107 bp fragment (nucleotides 440 to 1546) of the lukSF-PV genes.

Results : As expected, the sequences were highly conserved, but nucleotide variations were observed at seven sites (positions 470, 527, and 663 located in the lukS locus and positions 1304, 1318, 1393, and 1396 located in the lukF locus) using the lukSF-PV genes of MRSA strain USA300 as a reference. Among the isolates, 19 (67.9%) isolates were of H variant and the remaining nine (32.1%) isolates were identified as R variant, Also, H variants were further classified into H1 (4/28, 14.3%) and H2 (15/28, 53.6%) groups. Furthermore, H1 variants were further divided into H1a (n = 3) and H1b (n = 1) groups. Additionally, H2 variants were grouped into H2a (n = 14) and H2b (n = 1) groups.

Conclusion : Since the infections caused by PVL-positive S. aureus strains have high virulence and regional differences in the prevalence of PVL gene and its isoforms may affect the clinical spectrum of staphylococcal infections, so knowledge about the prevalence of strains containing PVL gene and isoform distribution can be helpful in estimating their

pathogenicity and implementing better treatment policies. Both R and H variants were detected among S. aureus strains in Iran

Keywords : Staphylococcus aureus, Panton-valentine leukocidin, PVL haplotyping, Iran

O46-667: Fabrication of a label-free electrochemical biosensor based on reduced graphene oxide-sodium diethyldithiocarbamate-polypyrrole nanocomposite for herpes simplex type 1 detection

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Background and Aim : Herpes Simplex Type 1 (HSV-1) is a human virus with a high prevalence rate on a global scale, affecting around 3.7 billion people under 50 years of age. This virus is able to cause a great variety of latent, acute, and chronic conditions such as oral, genital, and neonatal herpes. In order to control its spread, regular screening and development of novel detection methods that have high sensitivity and specificity, yet are affordable, seems to be of utmost necessity. The aim of this study was to construct and evaluate electrochemical-based biosensors to identify the gpB gene of HSV-1 virus.

Methods : First, in order to increase the sensitivity, graphene oxide nanocomposite, polypyrrole, and sodium diethyl dithiocarbamate were used on the surface of glass carbon electrode. The HSV-1 virus single-stranded DNA probe was then fixed on the surface of the modified electrode. Subsequently, hybridization between probe DNA and target DNA was reduced by the interaction of hydrophobic π-π bonds between graphene oxide bonds, and single-stranded DNA sequences were studied by differential pulse voltammetry. The microscopic properties of the glass electrode modified by Fourier scanning electron microscopy (FESEM), AFM and X-ray Analysis (EDXA) were reviewed to confirm the performance of the electrode on the DNA of the probe and after hybridization with the target DNA. Also, the specificity of the proposed biosensor was determined by a positive cell culture sample of HSV-1, a positive sample of HTLV-1 (non-complementary sample), a mixed sample (HSV-1 + and HSV-1 -), and a negative sample that were compared with PCR results

Results : Diagnostic range of the biosensor was between 500 × 10-15 to 150 × 10-12 Mol/L with a minimum detection limit of 350 fM. The performance of this biosensor was evaluated by studying cell culture samples and PCR results. We found that the results obtained from cell culture samples were in accordance with laboratory results.

Conclusion : The results showed that the designed biosensor had an acceptable performance, and its detection sensitivity and selectivity for HSV-1 virus were satisfactory. The results show the possibility of developing a new portable system for the detection of herpes simplex virus type 1.

Keywords : Nanocomposite, Glass carbon electrode, DNA electrochemical biosensor, Herpes simplex virus type 1, HSV-1

O47-688: Mathematical Modeling of Prediction of Antibacterial Properties of the Combination Honey with Alcoholic Extracts of Black Cardamom, and Zataria multiflora

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Background and Aim : Mathematical modeling is widely used by scientists in biological fields. Using modeling can help to choose the best method of predicting and controlling a biological mechanism. Mathematical models can estimate quantities that cannot be directly accessed. On the other hand, during the last forty years, many efforts have been made to find new antibiotics that are clinically useful. It is felt to use natural substances and plant extracts to control and treat infections. Since honey and Zataria multiflora and Black Cardamom plants contain effective antimicrobial substances such as thymol, carvacrol, parsimol, resorcinol and hydrogen peroxide, They have the ability to kill or inhibit the growth of some pathogenic microorganisms, Therefore aim of this study is to predict the mathematical model of antimicrobial effects of honey, Zataria multiflora and black cardamom on Escherichia coli bacteria.

Methods : The model was created for this combination, and then this model was implemented in MATLAB software to obtain the most optimal parameters. Then, the antibacterial properties of the above compounds were extracted and evaluated in the laboratory environment with the obtained parameters.

Results : Our mathematical model measured the cultivation time on the desired solutions showed that the concentration of the solution is related to the suppression of bacterial growth., The combination of honey 30%, Zataria multiflora 35%, and Black Cardamom 35% had an inhibitory and lethal effect on Escherichia coli ATCC25922 bacterium, MIC/MBC=1000 µg/ml.

Conclusion : The obtained results were in coincide with the evaluation of the model, which finally showed the antimicrobial properties of the above compounds correctly. These compounds have inhibitory effects on Escherichia coli, Therefore, the use of mathematical

models to predict the effects of organisms and optimal controls on laboratory methods seems to be a useful tool.

Keywords : Mathematical prediction, Modeling, Antibacterial, Honey, Black cardamom, Zataria multiflora.

O48-746: Recombinant CD137-Fc, applications for modulation inflammation induced by some bacteria and viruses, such as novel coronavirus.

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Background and Aim : CD137 (ILA/4- 1BB), a member of tumor necrosis factor receptor superfamily, is one of the most important T cell costimulatory molecules. Interaction of this molecule with its ligand transmits a two- way signal that activates both T lymphocyte and antigen presenting cells. The soluble form of CD137 (sCD137) reduces the activity of its membrane isoform and is associated with T lymphocyte activation induced cell death. Recombinant CD137- Fc may be used to treat Infections caused by some microbes including Listeria monocytogenes and novel coronavirus.

Methods : The 1276 bp DNA sequence encoded CD137- Fc recombinant protein was prepared and subcloned into lentiviral vector and expressed in transduced CHO- K1 eukaryotic cells. Western blot analysis, and enzyme- linked immuno sorbent assay tests were performed. The IL-6 and IL-8 levels as inflammatory cytokines were measured using the ELISA kits

Results : Different assays results demonstrated that the expression of the 70- kDa CD137- Fc molecule was detectable without any degradation. IL-6 and IL-8 were significantly decreased in the sample exposed to soluble CD137-Fc protein. While in the samples that were exposed to the membrane CD137, there was a significant increase in IL-8.

Conclusion : This study helps to confirm previous research suggesting the use of this recombinant protein as a promising solution for the treatment of some infections. This product is widely used in novel medical treatments, including cell- based immunotherapy such as dendritic cells, CAR T, and CAR NK therapy. This product can be effective in the treatment of Listeria monocytogenes infections Because of its effect on increasing the activity of neutrophils in the region, also is useful in the treatment of the 2019 coronavirus disease pandemic Because of its effect on reducing cytokine-induced inflammation.

Keywords : Recombinant protein CD137- Fc, Listeria monocytogenes infections, coronavirus inflammation, autoimmune disorders, cancer immunotherapy, sCD137. Thanks to Iran National Science Foundation for their fina

مقالات پوستر

بیست و سومین کنگره بین المللی میکروب شناسی ایران

P1-23: Antibacterial effect of Zingiber officcinalis extract on salmonella isolated from patients referred to health centers in East Azerbaijan province in 1400

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Background and Aim : Increasing the antibiotic resistance of bacteria against antibiotics has increased the use of herbs with low side effects alongside conventional drugs. The aim of this study was to investigate the antibacterial effect of ginger extract on Salmonella isolated from health care providers

Methods : In this study, 50 human Salmonella isolates were isolated from the health centers of East Azerbaijan province. First, using enriching, selective, differential, biochemical media based on specific bacteriological tables and also using commercial antisera. Regarding Salmonella O and H antigens, we determined that our bacterium belonged to the genus Salmonella. Salmonella was evaluated for ginger extract as well as for common antibiotics used in medical laboratories.

Results : The results of the study showed that out of 70 suspected Salmonella samples, 50 were Salmonella isolates, of which 35 (70%) were sensitive to ginger extract, 10 (20%) were intermediate and 5 (10%) are resistant. While the results of antibiogram to common medical antibiotics are the most sensitive to sperfloxacin 32 cases (64%) stiffness zoxime 31 cases (62%), naldexic acid and ampicillin with 30 cases (60%), Ceftriaxone is 15 cases (30%), cephalexin is 10 cases (20%) and cefazolin is 5 cases (10%).

Conclusion : Due to the increasing resistance of bacteria to antibacterial drugs, in the present study it was shown that ginger extract has more antibacterial properties compared to antibiotics used in medicine, than salmonella isolaties and from this extract can be used along with other antibiotics in medical centers.

Keywords : Salmonella,Antibiotic,Ginger,Antibacterial effect, East Azerbaijan province

P2-32: The prevalence of flouroqinolon resistance and presence of qnrA and qnrS gens in Escherichia coli isolated from Tabriz, Sina and Alzahra hospitals»

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1. *hale babaeipour*

Background and Aim : Abstract Aims and introduction: Escherichia coli is the most important member of normal intestinal flora in humans and animals. E. coli is one of the most important bacterial agent can causing opportunistic infections. Quinolones are synthetic and commonly used antibiotics for treatment of multiple clinical infections in the world. Quinolones are clinically important antibiotics, as an ideal component, because of high potency, broad-spectrum activity, good bioavailability and a potentially low incidence of side-effects. Antibiotic resistance to quinolones is increasing in the world. Thus, this study was designed to evaluate the resistance to fluoroquinolone antibiotics and investigate the frequency of plasmid-mediated qnrA, qnrB, and qnrS genes among Escherichia coli isolated of hospitalized patients in Tabriz Alzahra and Sina hospitals, Iran 2019.

Methods : Material and method: In the present study, 100 E. coli isolates were collected. Antibiotic susceptibility test was carried out by using disc diffusion method. Amplification and detection of qnrA, qnrB, and qnrS genes were carried out by polymerase chain reaction (PCR) with specific primer.

Results : Results: The most effective antibiotic against E. coli isolates was Gentamaycin (78%) but 98% of isolates were resistance to Ampicillin. 62% and 24% of Escherichia coli isolates were Nalidixic acid and Ciprofloxacin-resistant, respectively. qnr genes demonstrated in 5 isolates. qnrS were observed in 4 isolates, and qnrB were identified in one isolates. No qnrA gene was identified in this study.

Conclusion : Conclusion: According to the results, Because of different antibiotic resistance patterns in various geographical regions, antimicrobial treatment should be based on local experience. Therefore, prescribing correct antibiotics can prevent the extension of antibiotic resistance through qnr borne bacteria in the future.

Keywords : E. coli, Fluoroquinolones resistance, qnrA, qnrB,qnrS

P3-35: Molecular evaluation of vancomycin-resistant genes in Enterococcus faecalis isolated from clinical specimens

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Background and Aim : Enterococci can cause a variety of nosocomial infections from bacteremia and bloodstream infections to meningitis, urinary tract infections, and various organs. Nosocomial infections and antibiotic resistance have increased the importance of enterococci. This study was performed to evaluate the molecularity of vancomycin Enterococcus faecalis genes isolated from clinical specimens using the PCR technique.

Methods : In this study, 100 urine samples from patients with suspected enterococcal infections were collected from different hospitals in Markazi province. Enterococcus species were identified by standard methods and antibiotic susceptibility testing was performed according to the standard CLSI disk diffusion method. Then the frequency of vanA and vanB genes was examined by PCR.

Results : Out of 100 isolated samples, 36 samples of Enterococcus faecalis were identified, and using the multiplex PCR method to evaluate the presence and frequency of vanA and B genes, in 4 isolates of the vanA gene and 5 isolates of the vanB gene were observed. The highest frequency was related to the vanB gene.

Conclusion : In general, the results of this study showed that Enterococcus faecalis strains are genetically diverse, indicating the polyclonal prevalence of strains in clinical specimens. Due to the abundance of antibiotic-resistant strains especially vancomycin among enterococci, control and preventive measures are necessary.

Keywords : Enterococcus faecalis, vanB , Vancomycin, Real-Time PCR

P4-40: In vitro activities of cellulase and ceftazidime, alone and in combination against Pseudomonas aeruginosa biofilms

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Background and Aim : Biofilms are a main pathogenicity feature of Pseudomonas aeruginosa and has a significant role in antibiotic resistance and persistent infections in humans. We investigated the in vitro activities of antibiotic ceftazidime and enzyme cellulase, either alone or in combination against biofilms of P. aeruginosa.

Methods : P. aeruginosa PAO1 and two clinical isolates of P. aeruginosa recovered from the patients with burn wound were used in this study. The MIC (minimum inhibitory concentration) and MBC (minimum bactericidal concentration) of ceftazidime was determined. The bactericidal activity of cellulase on planktonic cells of P. aeruginosa was evaluated. Biofilm formation was assessed by the colorimetric microtiter plate assay. Moreover, the activities of cellulase and ceftazidime, alone and in combination, on biofilm attachment, biofilm formation, and minimum biofilm elimination concentration (MBEC) were evaluated.

Results : Both ceftazidime and cellulase significantly decreased biofilm formation in all strains in a dose-dependent manner. Combination of enzyme at concentrations of 1.25, 2.5, 5, and 10 U/mL tested with 1/16× MIC of antibiotic led to a significant reduction in biofilm biomass. Cellulase showed a significant detachment effect on biofilms at three concentrations of 10 U/mL, 5 U/mL, and 2.5 U/mL. The MIC, MBC, and MBEC values of ceftazidime were 2 to 4 µg/mL, 4 to 8 µg/mL, and 2048 to 8192 µg/mL. When combined with cellulase, the MBECs of antibiotic showed a significant decrease from 32- to 128-fold.

Conclusion : Combination of the ceftazidime and the cellulase had significant anti-biofilm effects, including inhibition of biofilm formation and biofilm eradication in P. aeruginosa. These data suggest that glycoside hydrolase therapy as a novel strategy has the potential to enhance the efficacy of antibiotics and helps to resolve biofilm-associated wound infections caused by this pathogen.

Keywords : Biofilm inhibition, Ceftazidime, Cellulase, MBEC, Pseudomonas aeruginosa

P5-41: Prevalence of Staphylococcus aureus nasal carriage and methicillin- resistant S. aureus among medical students of Shahid Sadoughi University of Medical Sciences in Yazd, Iran (2020-2021)

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Background and Aim : Staphylococcus. aureus is the second agent of nosocomial infection. About 30% of health care staff in hospitals is nasal carrier of this species. Improper use of antibiotics has led the bacterium to resist against methicillin named MRSA. The aim of this study was to represent the prevalence of nasal S. aureus and MRSA among medical students and consequently, determination the susceptibility of the isolates against different antibiotics.

Methods : In this cross – sectional study, a total of 300 nasal swabs were collected from intern and stager medical students in Shahid Sadoughi hospital of Yazd. Samples were then subjected to related tests for diagnosis of S. aureus species. Following methicillin resistance determination all were further antibiogramed using 10 selected antibiotics disks by disk diffusion method. The data were analyzed using SPSS 16 ver.

Results : Results showed that 62(21%) of samples were found to be positive for S. aureus in which 18 (29%) Samples were MRSA. Among the positive cases, 33(53.2%) were female and 29 (46.8%) were male students. The MRSA carriers were significantly higher intern than in stager (p=0.045). In addition, university entrance of year 2013 were significantly more infected with MRSA in compared to those 2016 entrance year (p=0.02). Antibiotic sensitivity test revealed that all isolates were completely resistance to penicillin, but 100% sensitive to both Gentamycin and Rifampin antibiotics.

Conclusion : High prevalence of S. aureus and MRSA carriers is mainly due to both medical and Physicians' contamination. Therefore; it seems necessary not only to point out the students but treat them with effective antibiotics. In addition screening all the medical staff for detection of S .aureus together with MRSA and taken them under adequate treatment.

Keywords : Staphylococcus. aureus, MRSA, medical students, Antibiotic resistance.

P6-50: Chemical and Judgmental Examination of Niosomes or Vesicles of Non-Ionic Surfactants

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Background and Aim : ABSTRACT Niosomes or vesicles of nonionic surfactants are very small layered structures obtained from a mixture of nonalionic surfactants of alkyl or diakyl polyglycerol ether and cholesterol and then hydration in aqueous (aqueous) medium. Today, overuse of antibiotics in the treatment of human and animal diseases has caused the multidrug resistance of bacteria to antibiotics. In addition, if a new type of antibiotic is used, resistance genes will begin to appear. After a period of widespread transmission to other bacteria, the spread of resistance and the need for new antibiotics, which requires millions of dollars. Vancomycin is used to treat infections of many gram-positive and gram-negative bacteria. Consumption of this antibiotic is very high due to the bacterial resistance that has been created against it as well as the side effects that it causes in some parts of the body. Many studies have been done on antibiotics to find a solution to eliminate the toxicity caused by their long-term use.

Methods : Niosome preparation methods Niosome preparation methods include: thin film hydration, freeze-drying, reverse phase evaporation, ether injection, sonication, micro fluidization, bubble, etc., which are described below.

Results : Niosomes Benefits ➢ These vesicles are water-based carriers, which increase patient satisfaction compared to oily drug forms.

Conclusion : Conclusion The aim of the study by Abdulaziz et al. in 2014 was to optimize norfloxacin niosomes to increase antibacterial activity and reduce bacterial resistance. In this study, Pseudomonas aeruginosa, a bacterium that forms a biofilm, was used as the test organism. Different norfloxacin niosomes were examined in vitro and in vivo for antibacterial activity in comparison with aqueous drug solution, respectively. The effect of norfloxacin niosomes on biofilm formation was investigated

Keywords : Newsome,Dialkyl polyglycerol Ether,Antibiotic,Vancomycin,Bacteria

P7-51: Co-delivery of doxycycline and hydroxychloroquine to treat brucellosis: an animal study

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Background and Aim : Evaluation of various biochemical and immunological parameters in infectious diseases is one of the best indicators for diagnosis and treatment process. The main goal of this project is to determine the effect of hydroxychloroquine and doxycycline loading into solid-lipid-nanoparticles (DOX-HCQ-SLN) on both acute and chronic phases of brucellosis.

Methods : In addition, evaluate some biochemical factors, trace elements and inflammatory elements. Blood serum levels of Zn, Fe, Na, K, hepatic biochemical parameters (AST, ALT, ALP, TBil) were remarkably different between infected and healthy rats.

Results : Vitamin D was decreased and CRP was increased in chronic and acute brucellosis. Quantitative evaluation of these mentioned parameters can be useful to diagnose brucellosis in advance.

Conclusion : Due to the good effect of the synchronized use of hydroxychloroquine and doxycycline in the form of nanoparticles, the manipulation of these nanoparticles can help for better treatment and also reduction in brucellosis re-infection.

Keywords : Brucellosis, trace elements, biochemical parameters, nanoparticles

P8-54: The effect of vancomycin-loaded niosomes on MRSA strains of Staphylococcus aureus and expression of mecA, hla, and hlb genes

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Background and Aim : Abstract Introduction and Objective: Niosomes have received a lot of attention today due to their better penetration and controlled release. This study aimed to evaluate the antimicrobial effect of vancomycin-loaded niosomes on the microbial species of staphylococcus aureus.

Methods : Materials and methods: In this study, 250 clinical samples of different patients' specimens including blood, wounds, skin, and urine were collected from different medical centers (Imam Hossein, Atieh, and Sarem) in 2020. To synthesize nanodrugs, vancomycin was encapsulated in nosocomial nanocarriers by thin-film hydration, and optimization was performed based on the three main characteristics of nanocarriers. The process of drug release from nanocarriers and stability were investigated. Then, the antimicrobial properties against microbial species of staphylococcus aureus were investigated, and finally, the expression of mecA, hla, and hlb genes was determined using the real-time PCR technique.

Results : Results: According to the designed tests, a Span60 to Tween60 ratio of 50:50 and lipid content of 300 ?mol were selected as the optimal form. The optimal nanoliposomes showed a size of 190.7 nm, a particle dispersion index (PDI) of 0.177, and retention efficiency of 71.22%. The process of drug release from the nanocarrier showed about 50% drug release from the niosome during 24 hours and about 60% after 72 hours. Stability studies over 3 months at two temperatures of 25 °C and 4 °C on the optimal sample showed that the samples stored in the refrigerator were more stable. The antimicrobial properties of the vancomycin-loaded niosomes against the mentioned microbial species showed better results compared to the free form of the drug. The nanoparticle was also able to further reduce the expression of virulence genes including mecA, hla, and hlb compared to the free form of the drug.

Conclusion : Conclusion: The favorable physical properties, efficient antimicrobial effects, and low toxicity make vancomycin-loaded niosome nanocarriers a suitable candidate for the treatment of some common bacterial wound infections. Keywords: niosome, vancomycin, bacterial infection, thin-film hydration, virulence gene.

Keywords : Keywords: niosome, vancomycin, bacterial infection, thin-film hydration, virulence gene.

P9-57: Multidrug-resistant Pseudomonas aeruginosa from sputum of patients

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Background and Aim : Antimicrobial resistance (AMR or AR) is the ability of a microbe to resist the effects of medication that once could successfully treat the microbe. Pseudomonas aeruginosa is a common encapsulated, Gram-negative, rod-shaped bacterium that can cause disease. Pseudomonas aeruginosa (P. aeroginosa) is one of the opportunistic pathogens, which is the main cause of prevalent hospital infections worldwide

Methods : this study aims to isolate and determine antimicrobial resistances patterns of Pseudomonas aeruginosa from Patients admitted to educational hospitals at the Urmia University of Medical Sciences, Iran. Clinical samples from hospitalized patientsn were collected. Then, Samples were processed and identified by standard protocol. The Pseudomonas aeruginosa positive cases was tested for antibiotic resistance kl by Kirby-Bauer disc diffusion method (according to Clinical and Laboratory Standards Institute guidelines

Results : results Among culture positive patients, 100 bacterial isolates were recovered, as Pseudomonas aeruginosa. Of the Pseudomonas aeruginosa isolates, 10% were from sputum, and remained cases from other body aspirates. The highest number of the resistance was the one againist SXT with 100% resistance. MERO , CTR and ZOX that used just for 1/3 of samples had 100% resistance,too. We had more than 60% resistance to all tasted antibiotics except CO . resistace to CO was very rare (25%)

Conclusion : P. aeruginosa is not extremely virulent in comparison with other major pathogenic bacterial species – for exampleStaphylococcus aureus and Streptococcus pyogenes – though P. aeruginosa is capable of extensive colonization, and can aggregate into enduring biofilms.[However, if a person is in a hospital or has a weakened immune system, the threat becomes very severe. In these situations, a Pseudomonasinfection can be life-threatening.The good news is that these infections are treatable, especially with an early diagnosis.

Keywords : Multidrug-resistant Pseudomonas aeruginos sputum of patients

P10-68: Screening and Assessment of Two Potential Bacterial Samples for Antimicrobial Activity

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Background and Aim : Antibiotic is a substance produced by microorganisms that inhibits or fully destroys other microorganisms. Since its discovery, diseases caused by bacterial infections have significantly reduced and the health of millions of humans around the world has improved. However, emergence of antibiotic-resistance strains is becoming a major concern because soon the current antimicrobial drugs will lose its effectiveness. There is a need for new antibiotic discovery as the rate of antibiotic-resistant strains is rising. In this study, tests were carried out to assess the antimicrobial activity of microorganism 3d-2 isolated from originally from Broga Hill, Malaysia and sample BCC2 which was found by accident from a contaminated B. cereus plate.

Methods : Initially, cross-streak test method was done to estimate probable antimicrobial activity from the mentioned bacterial samples. Kirby-Bauer test was performed using solvent extracts derived from liquid-liquid extraction and antibiotic Rifampicin (50mg/ml) stock, tested against ATCC-approved; Bacillus cereus (ATCC 11778), Staphylococcus aureus (ATCC 25923), Micrococcus luteus (ATCC 10240), E. coli (ATCC 25922) and E. coli-Migula (ATCC 11303) on Mueller Hinton agar. Thin Layer Chromatography (TLC) was performed for extracts from 3d-2 and BCC2.

Results : Cross-streaking for both samples provided no clear inhibition zones. Kirby-Bauer test's inhibition zones showed that the extract using diethyl ether, from sample BCC2 had the strongest results against Staphylococcus aureus (11mm). TLC approved the largest Rf value was equal to 1.66 and derived from bacteria BCC2 (mixed with Ethyl ether extract) which basically is considered more polar than ones from 3d-2, yet extracts from both bacterial strains were certainly polar. Similarities between Rf values of samples and other common antibiotics show, it is probable that sample 3d-2 and BCC2 are producing compounds that similar to penicillin and gentamycin respectively.

Conclusion : In conclusion, the antimicrobial compound of both 3d-2 and BCC2 are predicted to be a narrow-spectrum, belonging to unknown antimicrobial drug category. Further tests and studies need to be done in future as the identifications are not for certain.

Keywords : Antimicrobial resistance, Microbial susceptibility, Disk Diffusion Antimicrobial Tests, Antibacterial agents, Thin Layer Chromatography

P11-70: Stevia rebaudiana leaf extract mediated green synthesis of cerium oxide nanoparticles for antibacterial activity and photocatalytic degradation of Tetracycline

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Background and Aim : Cerium oxide(CeO2-NPs) are multifunctional oxide metal nanoparticles that have been considered by many due to their unique properties including antimicrobial, antifungal, semiconducting, and photocatalytic activity.

Methods : The CeO2 nanoparticles were prepared using S. rebaudiana leaf extract via a simple green method. The prepared nanoparticles were further characterized by Raman spectroscopy, X-ray diffraction (XRD), Fourier transform infrared spectroscopy (FT-IR), field emission-scanning electron microscopy (FE-SEM).

Results : The FE-SEM results confirmed that the CeO2 nanoparticles were nano size (10-50 nm). The antibacterial activity of CeO2-NPs against Pseudomonas aeruginosa and Enterococcus faecalis has shown that the minimum inhibitory concentration (MIC) was 6.25 and 12.5 µg/mL and Minimum Bactericidal Concentration (MBC) were 12.5 and 25 µg/mL respectively. In the presence of CeO2 –NPs (under optimal conditions: catalyst dosage = 0.75 g/L, TC concentration = 5 mg/L, pH=10), about 80.68% of tetracycline (TC) was degraded after 45 min UV-irradiation that it's indicative of the acceptable photocatalytic property of CeO2-NPs.

Conclusion : We believe that the obtained novel photocatalyst may be widely utilized in different fields including photocatalytic decomposition of organic compounds, dye-sensitized solar cell and air purification and so on.

Keywords : Cerium oxide, Biosynthesis, Antibacterial activity, Photodegradation, Stevia rebaudiana, Tetracycline

P12-76: Evaluation of Biofilm Formation in Methicillin Resistant Staphylococcus aureus isolated from human

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Background and Aim : Antibiotic resistance and biofilm formation ability is one of the survival strategies in human pathogenic Staphylococcus aureus, which by affecting different parts of the body, causes high costs and prolongs the patient's treatment period. The aim of this study was to determine methicillin-resistant S. aureus (MRSA) in body fluids of patients referred to Tabriz hospitals by PCR method and the evaluated of biofilm formation in those isolates with the aim of determining the relationship between biofilm formation and methicillin resistance.

Methods : For this purpose, 70 swab samples of body fluids were collected from different hospitals. For initial detection of S. aureus biochemical tests were used and PCR test with amplification of nuc gene was used to confirm the diagnosis. To identify MRSA isolates, a fragment of the mecA gene was amplified. Microtiter plate method was used to evaluate the biofilm production.

Results : From the 70 samples, 45 S. aureus (64.28%) were isolated by biochemical and molecular tests. The results of mecA gene amplification showed that from 45 confirmed isolates of S. aureus, 23 isolates (51.11%) contained mecA gene. Data obtained from biofilm formation results showed that 31 isolates (68.88%) of S. aureus were able to produce biofilms with different degrees. In total, out of 31 clinical isolates, 22.22% (n = 10) of isolates were able to produce strong biofilm, 28.88% (n = 13) of isolates were moderate biofilm and 17.77% (n = 8) of isolates were poor biofilm producers. Of the 23 isolates of MRSA, all isolates (100%) were able to produce biofilms. In total, out of 10 strong biofilm-producing isolates, 9 isolates belonged to methicillin-resistant isolates, and among the moderate and weak biofilm-producing isolates, 12 and 2 isolates belonged to methicillin-resistant isolates, respectively.

Conclusion : Overall, the results of the present study show that most strains of S. aureus isolated from various cases of clinical infections in humans are resistant to the methicillin which can be related to the production of isolates biofilms. Therefore, the results of this study can help in the accurate selection of appropriate antibiotics in treatment and prevent further spread of antibiotic resistance in bacteria.

Keywords : Antibiotic resistance, Biofilm, mecA gene, Methicillin, Staphylococcus aureus

P13-110: Genetic diversity, Distribution of Carbapenem Resistance Genes and Evaluation of the biofilm production in Uropathogenic Escherichia coli isolates from patients with urinary catheter in North of Iran

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Background and Aim : Infections due to carbapenem-resistant Enterobacteriaceae (CRE) are associated in patients with urinary catheter alarming rate of emergency status. The aim of this study was to investigate the antimicrobial resistance patterns and molecular mechanisms of carbapenem resistance among UPEC. Additionally, the potential of isolates to produce biofilms, as well as their clonal and genetic diversity, were investigated.

Methods : A cross-sectional study was accomplished on a collection of 76 non-duplicate UPEC isolates obtained from CAUTIs from May 2021 to September 2021. The modified carbapenem inactivation method (mCIM) and EDTA-modified carbapenem inactivation method (eCIM) test was performed for the detection of carbapenemase and metallo-β-lactamase activity. Also, the presence of carbapenemases genes were determined using PCR assays. In 96-well microtiter plates, biofilm development was evaluated. ERIC-PCR was used to investigate the clonal and genetic variety of isolates.

Results : A total of 76 confirmed UPEC isolates were obtained from patients mentioned to teaching hospital in Babol, Iran. The results of antibiotic susceptibility testing revealed high rate of antibiotic resistance against nalidixic acide (81.6%) and trimethoprim-sulfamethoxazole (80.3%). Among UPEC isolates, 63.2% and 13.2% of UPEC isolates were positive for MBL production. The frequencies of the studied genes are in order of blaNDM (14.5%), blaoxa-23 (2.6%) and blaoxa-48 (2.6%). Forty–two isolates (55.3 %) were positive to the capability of biofilm formation. ERIC-PCR revealed that UPEC isolates could be categorized in nine clusters A-I and five isolates were categorized as singleton.

Conclusion : The high prevalence of MDR and carbapenemase producing isolates among the UPEC strain in this investigation is concerning. Moreover, the blaNDM was the most frequent cause of producing metallo-beta-lactamase and carbapenemase. Furthermore, a high incidence of biofilm producer isolates, which was found in hospitalized patients, is a severe

problem in this study. Also, analysis revealed a partial genetic similarity among the studied isolates, indicating that the same UPEC clones may have spread to other hospital units.

Keywords : Escherichia coli, UPEC, UTI, carbapenem resistance, biofilm

P14-118: Antibiotic Resistance of Staphylococcus aureus Isolated from Nasal Cavity of Patients Hospitalized in IMAM HOSSEIN Hospital, Hashtrud

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Background and Aim : Staphylococci are metabolically active can grow on many cultivated environments..They usually have cluster and irregular shape. Staphylococcus aureus is the main pathogen among the staphylococci causing infections at different organs in humans as well as animals . It is one of the most important pathogen that prioritised by the World Health Organizaion in 2016.

Methods : The aim of this study was to evaluate the antibiotic resistance of Staphylococcus aureus isolates cultured from nasopharyngeal clinical specimens in Imam Hossein Hospital of Hashtrood. Therefore ,180 specimens were collected from patients andcultured and subsequently identified by biochemical tests

Results : Based on the result of the study of crop characteristics and biochemical separation tests,25 samples of the test (13.9%) of staphylococcal aureus infection were reported,of which all 25 cases of staphylococcus aureus were coagulase positive.All isolated staphylococcus aureus was evaluated for antibiotic resistance with antibiotics ,vancomycin,erythromycin,ciprofloaxin,clindamycin,cefocytosin,oxacillin,ampicilin,chloram phenicol,amoxicillin clavulanic,penicillin,cefazolin by disc diffusion method.That In accordance with the CLSI protocol

Conclusion : The result showed that due to the high antibiotic resistance to some antibiotics such as ampicilin,penicillin,erythromycin,performing the diffusion method before the ude of antibiotics,comprehensive research in other areas of the province and the antibiotics and Supplemental experiments such az MIC are recommended.Mean while ,all positive samples were stored in microbial bank of the Infectious Disease Research Center and tropical diseaes.

Keywords : staphylococcus aureus,Antibiotics,Antibiotic resistance,Hashtrood,Disc diffusion method

P15-119: Knowledge and attitudes towards antibiotic usage: a cross-sectional survey of Zabol population in 2017

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Background and Aim : One of the causes of antibiotic resistance is inappropriate use of antibiotics. Improper use of antibiotics can be influenced by many factors such as knowledge and attitudes towards antibiotic usage. This study was intended to investigate the level of knowledge and attitude type about antibiotic use and their correlation in people of Zabol, Iran.

Methods : in 2017, as a cross-sectional study, 109 persons were included in the study by sample size calculation and random sampling method. A questionnaire included 13 and 7 questions were answered by target population to assess knowledge and attitudes, respectively, via a 5-point Likert Scale from very strong agreement to very strong disagreement. The level of knowledge (low, medium, high) and the type of attitude (positive, negative) were determined by knowledge and attitude scores. The results were analyzed by descriptive statistics and nonparametric tests such as K-Square, Spearman, Pearson, Mann-Whitney, Kruskal-Wallis using SPSS software with statistical significance at $p < 0.05$.

Results : The reliability of the questionnaire relevant to knowledge and attitude were 51% and 57.6%, respectively. The level of knowledge of the subjects was low ($p < 0.05$) and their attitude type was negative ($p < 0.05$). The correlation between knowledge level and attitude type was positive, direct and poor ($p > 0.05$).

Conclusion : The results of this study indicate the need to change public attitudes and improve the level of knowledge of the population about the use of antibiotics.

Keywords : Attitude, Knowledge, Antibiotic use, Zabol

P16-129: The prevalence of plasmid-mediated quinolone resistance genes among Escherichia coli strains isolated from urinary tract infections in southwest Iran

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Background and Aim : Background: The extensive and inappropriate use of quinolones, frequently used as an effective treatment for urinary tract infection (UTI) patients, has led to resistance to these antibiotics. This study was designed to determine the prevalence of quinolone resistance and plasmid-mediated quinolone resistance (PMQR) genes among extended-spectrum beta-lactamase (ESBL)-producing Escherichia coli isolates.

Methods : Methods: One hundred and fourteen E. coli isolates were collected from patients' urine samples. The susceptibility of iso¬lates to selected antibiotics was tested by the Kirby-Bauer disk diffusion method. ESBL-producing isolates were identified phenotypically using a combination disk test. Using specific primers, the frequency of aac (6')-Ib, qnrA, qnrB, qnrC, qnrD, qnrS, and qepA genes was investigated by polymerase chain reaction (PCR).

Results : Results: Among 26 ESBL-producing isolates, the highest resistance rate was observed toward nalidixic acid (80.8%) and ciprofloxacin (61.5%), respectively. Ninety-seven (85%) of all isolates harbored at least one PMQR gene, the most frequent one being the aac (6')-Ib-cr variant (47.4%). The coexistence of aac (6')-Ib-cr variant and qnrB were the most broadly distributed genotype among quinolone resistance isolates. Notably, none of the isolates contained the qnrC, qnrD, and qepA genes.

Conclusion : Conclusions: Our results highlight the significant prevalence of PMQR genes in ESBL-producing E. coli isolates in this region. Also, the aac (6')-Ib-cr variant was the most frequent gene, particularly in ESBL-positive isolates. A regular periodic monitoring program is needed to control and hinder the spread of antibiotic resistance and contributed genes among UTI-causing E. coli isolates.

Keywords : Escherichia coli, Urinary tract infection, Quinolone, ESBL, qnr

P17-131: RAPD-genotyping of carbapenem-resistant Acinetobacter baumannii isolated from burn wound infections

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Background and Aim : According to studies, carbapenem-resistant Acinetobacter baumannii strains are important nosocomial pathogens, especially in burn patients, and classified as an urgent threat. The aim of current study was to investigate OXA-type carbapenemase genes, and RAPD-genotyping of carbapenem-resistant A. baumannii strains in burn patients.

Methods : In this research, 106 non-repetitive A. baumannii strains isolated from burn wound infections were evaluated for susceptibility to antimicrobial agents. Polymerase chain reaction (PCR) was used to detect OXA-type carbapenemase genes and the genetic relatedness among A. baumannii isolates was studied by random amplification of polymorphic DNA (RAPD) typing.

Results : All isolates identified as multidrug- and carbapenem- resistant A. baumannii and carried blaOXA-51-like genes. The blaOXA-23-like genes were the most predominant OXA-type carbapenemase genes (92.5%), followed by blaOXA-24/40–like (85.8%), and blaOXA-143-like and blaOXA-58-like genes were not identified among studied isolates. RAPD- PCR revealed that the tested A. baumannii strains are clustered in to 5 RAPD genotypes with ≥ 80% similarity.

Conclusion : The results of the present study indicate a high prevalence of XDR- A. baumannii strains, which is alarming. In addition, it seems that blaOXA-23-like and blaOXA-24/40–like genes play an effective role in the development of carbapenem resistance in the studied strains.

Keywords : Acinetobacter baumannii; carbapenem-resistant; RAPD-genotyping

P18-132: Antimicrobial Resistance Frequency in Carbapenemase Producing and Biofilm Forming Clinical Klebsiella pneumoniae Isolates in Northwest of Iran

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Background and Aim : Klebsiella pneumoniae is an opportunistic bacterium, which is globally recognized for its high prevalence and antimicrobial resistance. Carbapenemase production and biofilm formation are critical resistance and pathogenesis mechanisms in K. pneumoniae. This study evaluated the prevalence of three prevalent carbapenemase related genes and four frequent biofilm related genes in K. pneumoniae isolates regarding drug resistance in Zanjan, Iran.

Methods : In this cross-sectional study, 104 clinical K. pneumoniae samples were collected from educational hospitals, Zanjan, Iran. Isolate identification and confirmation were done using standard biochemical tests and PCR. Disk diffusion antibiotic susceptibility testing was performed according to NCCLS guidelines. Phenotypic confirmatory test for ESBL producing isolate recognition was performed according to CLSI guidelines. Minimal inhibitory concentrations were measured with ETEST. Biofilm formation degree was evaluated using Stepanovic's microtiter plate colorimetric method. Multiplex-PCR was performed to detect the presence of carbapenemase production genes blaVIM, blaNDM, and blaOXA-48 and biofilm related genes LuxS, Fimh1, wza, and mrkD. Statistical analysis of the results was performed using SPSS 19.

Results : The highest resistance rate was against ampicillin (100.0%) followed by cefotaxime (72.1%). Among the 104 K. pneumoniae isolates, 52 (50.0%), and 31 (29.8%) strains were determined as MDR and XDR, respectively. Moreover, 21 (40.4%) strains were determined as ESBL producing. Among a total number of 50 slime producing K. pneumoniae strains, 7 (14.0%), 15 (30.0%), and 28 (56.0%) strains exhibited high, moderate, and weak levels of biofilm formation, respectively. A number of 41 (78.8%) strains were susceptible to colistin, and 10 (19.2%) were resistant. Chi-square exact (Fisher exact for luxS) demonstrated insignificant difference between strong and moderate biofilm production related genes.

Conclusion : The study demonstrated increased rate of carbapenemase production and biofilm formation in K. pneumoniae strains in the region, highlighting the importance of properly updated antimicrobial prescription guidelines regarding epidemiological data.

Keywords : Beta-lactamases, Biofilm, Drug resistance, Klebsiella pneumoniae

P19-133: ANTIMICROBIAL RESISTANCE DURING COVID -19 PANDEMIC

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Background and Aim : COVID-19 is known as a new viral infection the virus has spread globally and resulted in a pandemic. As of March 2021, the virus has infected 125 million people and has resulted in 2.7 million deaths worldwide. Similar to COVID-19, antimicrobial resistance (AMR) represents a global public health threat that has been termed “the slow pandemic” to emphasize its more treacherous. Infections due to resistant pathogens result in ~700,000 deaths annually. This number has been evaluated to increase to 10 million deaths annually by the year 2050. Secondary bacterial infections play crucial roles in mortality and morbidity associated with COVID-19. This study aims to provide overview of findings on COVID-19 and AMR as well as to provide recommendations toward antimicrobial surveillance.

Methods : The databases used to search for the relevant articles for this review include Pub Med and Google Scholar. The following keywords were used in the search: Antimicrobial resistance, antibiotic resistant bacteria and COVID-19.

Results : This study has been reported that 72% of COVID-19 patients attending hospitals have received antimicrobial agents, despite only 8% being co-infected by bacteria or fungi. the use of antimicrobials to treat COVID-19 WAS increase ARO prevalence including extended-spectrum ?-lactamase (ESBL)- producing Klebsiella pneumoniae, carbapenem-resistant Delhi metallo-?-lactamase (NDM)-producing Enterobacterales, Acinetobacter baumannii, methicillin-resistant Staphylococcus aureus (MRSA), pan-echinocandin-resistant Candida glabrata and multi-triazole-resistant Aspergillus fumigatus.

Conclusion : There is a necessity to practices of better anti-microbial for curtailment of secondary infection rates particularly among COVID-19 patients. In addition, not needed treatment antibiotic therapy or prophylaxis to patients with mild COVID-19 or to patients with suspected or confirmed moderate COVID-19, the increased public awareness for infectious diseases and infection control issues, the strengthening of the One Health perspective as outlined by the Centers for Disease Control and Prevention. These factors may help prevent the appearance of MDROs during this pandemic. where it is reducing community import and transmission of resistant bacteria.

Keywords : Antimicrobial resistance, antibiotic resistant bacteria and COVID-19.

P20-143: Investigating in-vitro antimicrobial activity, biosynthesis, and characterization of silver nanoparticles, zinc oxide nanoparticles, and silver-zinc oxide nanocomposites using Pistacia Atlantica Resin

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Background and Aim : Background: In the present study, a fast and straightforward method was presented for the preparation of silver nanoparticles (AgNPs), zinc oxide nanoparticles (ZnNPs), and silver-zinc oxide nanocomposites (Ag-ZnNPs).

Methods : Methods: Biosynthesis was carried out using resin extraction from Pistacia Atlantica as a reductant and capping agent. In-vitro antimicrobial activities of these particles, silver nitrate (AgNO3), and zinc nitrate (Zn (NO3)2) were also evaluated in comparison with resin extracts. Synthesis of the nanoparticles and nanocomposites was characterized and confirmed by ultraviolet-visible spectroscopy (UV–vis), X-ray diffraction n (XRD), Fourier-transform infrared spectroscopy (FTIR), field emission scanning electron microscopy (FESEM) equipped with an energy dispersive spectroscopy (EDS) and transmission electron microscope (TEM). Then, antimicrobial activity was tested against Klebsiella pneumonia, Escherichia coli, Staphylococcus aureus, and Proteus mirabilis using the agar well diffusion method.

Results : Results: Maximum inhibition zones were observed for resin-AgZnNPs and resin-ZnNPs (21.1 ± 0.002 mm), demonstrating their antibacterial activity, while Zn (NO3)2 had the smallest inhibition zone (5.4 ± 0.06 mm).

Conclusion : Conclusions: These results are promising in terms of their potential ability to be used against pathogenic bacteria.

Keywords : Pistacia atlantica resin extract, Nanoparticles, Nanocomposite, Antibacterial activity

P21-145: Inhibitory effect of clove plant extract on Staphylococcus aureus bacteria in vitro and its comparison with selected antibiotics

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Background and Aim : Nowadays due to the increasing incidence of antibiotic resistance,the need to find new and safe antibacterial compounds has become one of the main priorities of medical researches. Staphylococcus aureus is a vital bacterial pathogen that is considered as one of the significant causes of nosocomial infections. Antibiotics in this bacterium and the emergence of resistant strain of vancomycin are now a major hospital challenge in the field of infection control. Today, the use of plants in the treatment of resistant infections is considered as an antibacterial source. In this study, the inhibitory effect of clove on the standard strain of Staphylococcus aureus in vitro by disk diffusion method was investigated and the results were compared with standard therapeutic antibiotics

Methods : In this study, Staphylococcus aureus was cultured on Mueller Hinton agar (MHA) and incubated for 24 hours, additionally 0.5 McFarland suspension was prepared. Afterwards, grinding the clove plant an aquatic extract was prepared from the clove powder. In order to determine the sensitivity, 3 wells were created in each culture medium and different extracts were administered separately from 10,15,25,50,75 to 100 µl, respectively. It was poured into the wells and simultaneously other selective antibiotics of Vancomycin, Chloramphenicol, Tetracycline were placed in other plates. After measuring the created growth inhibition halos, the obtained results were evaluated and the diameter of growth inhibition halos was measured carefully.

Results : The outcomes of this experiment showed that the halos created by the clove herb are surprisingly effective and in some volumes are equal to the selected antibiotics. On the other hand, the more extract's concentrations were increased, the larger inhibition halos were created. Subsequently, the results of this study showed that the largest growth inhibition halo was related to the volume of 75 and 100 ?l with diameter of 29 and 30 mm and the smallest 20 mm with a volume of 10 ?l were measured. The halo of non-growth of bacteria in the presence of vancomycin and tetracycline antibiotics was reported to be 24 and 27 mm, respectively.

Conclusion : The results indicate that the aqueous extract of clove plant is strongly effective in preventing the growth of Staphylococcus aureus and can be used as a plant alternative to selected antibiotics in the treatment of infections caused by Staphylococcus aureus

Keywords : Staphylococcus aureus, Clove, Aqueous extract

P22-156: Evaluation of antifungal effects of Zinc oxide nanoparticles (ZnO-NPs) and Amphotericin B (AMB) on different Candida spp in vitro condition

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Background and Aim : Candidiasis is a fungal infection caused by yeasts from the genus Candida. In recent decades, the use of zinc oxide (ZnO-NPs) has been used due to the large energy band gap, chemical, thermal stability, high oxidation dependence, and non-toxicity was increased. This study aimed to evaluate of antifungal effects of zinc oxide nanoparticles (ZnO-NPs) and Amphotericin B (AMB) on different Candida spp in vitro condition

Methods : In the present study, the susceptibility of different Candida species to ZnO-NPs and AmB was determined by broth microdilution (BMD).

Results : The results indicated that the ZnO-NPs showed antifungal activity against pathogenic Candida spp. The MIC (Minimum inhibitory concentration) and MFC (Minimum fungicidal concentration) of ZnO-NPs were 64 to 128 µg/ml and 256 to 512 µg/ml, respectively. In comparison, MIC and MFC of AmB were 8 to 16 µg/ml and 16 to 32 µg/ml, respectively.

Conclusion : The ZnO-NPs showed antifungal activity against pathogenic Candida spp, but these antifungal properties are less than AmB.

Keywords : Candidiasis zinc oxide nanoparticles AmB

P23-157: Evaluation of Apoptosis effect of Amphotericin B (AmB) on different Candida spp.

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Background and Aim : Candidiasis is the most common fungal infection, primarily due to the increasing numbers of immune and medically compromised patients. Apoptosis is a common method of programmed cell death, characterized by depolymerization of the cytoskeleton, cell shrinkage, chromatin condensation, nuclear fragmentation, and phosphatidylserine transport to the cell surface. The purpose of present study was to measure the apoptosis effect of Amphotericin B (AmB) on different Candida spp.

Methods : The apoptotic effects of MIC concentration of Amphotericin B for each Candida species were detected by the flow cytometric method.

Results : The flow cytometry results showed that the highest apoptotic effect of AmB was observed on C. kruzei and, the minimum apoptosis effect of AmB was seen on C. lusitaniae.

Conclusion : Our results showed that Amphotericin B (AmB) has an apoptosis effect on different Candida spp. The apoptosis effect induced by AmB varied in different Candida spp.

Keywords : Apoptosis Candidiasis AmB

P24-160: Evaloation of antimicrobial resistance of bacteria isolated from cutaneous, soft tissue and visceral abscesses

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Background and Aim : Microbial agents producing abscesses in the skin, viscera and soft tissues include various types of aerobic and non- aerobic bacteria. The most important are Staphylococcus aureus, streptococcus, Escherichia coli, Pseudomonas, Bacteroides and klebsiella. The main treatment of abscess, pushing out through drainage or split abscess. After removing the necrotic tissue and pus, The antibiotic should be used to treat the disease. The aim of this study was to determine the aerosol production of abscess in skin, viscera and soft tissue and then to evaluate their susceptibility to different antibiotics.

Methods : Specimens of bacterial isolated from skin abscesses and infections and other connective tissue components that were identified, cultured and antibiogram into the microbiological laboratory of the Tabriz children center were extracted and then clinical information was obtained from patients. The data included the age, sex, location of the infection ,its association with hospital infections (in case of suspicion of nosocomial infections) and the manner of intervention, including aspiration,surgical drainage,or of type of antibiotic therapy

Results : clinical and laboratory data of patients with skin and soft tissue admitted to Tabriz children's hospital. 100 samples of positive blood culture were selected during 5 years and used for evaluation of drug resistance pattern. In this study 52.3 % of the patients were males and 47.7% were females. Of the 100 positive culture cases ,47.7% were Staphylococcus aureus ,8% Klebsiella and 8% Esherichia coli .46.6% of cases included soft tissue abscesses,33% of visceral absesses and 20.5 % of skin abcesses, The results of the antibiogram showed that Staphylococcus aureus versus penicillin was 79.5% oxacillin34.1% ,amikacin 26.2% clindamycin ,29.3% erythromycin,35%cefalexin,12.5% ceftizoxime and ceftriaxone 22% and Vancomycine 2.4% are resistant

Conclusion : The susceptibility and resistance pattern of Staphylococcus aureus is unpredictable and multiple resistance is common .At present resistance to Vancomycin is low ,of course. This level of resistance should be confirmed by more precise methods such as MIC or E test measurements. Obviously .the use of Vancomycine should be limited to the treatment of serious infectious disease and in cases of non critical infectious disease acquired

by the community Antibiotics such as cephalexin and clindamycin can still be used .In this study ,high levels of resistance to penicillin are also evident.

Keywords : Microbial Resistance, Antibiotics, Abscess, Soft tissue

P25-182: Phenotypic Identifcation and Genotypic Characterization of Plasmid-Mediated AmpC β-Lactamase-Producing Escherichia coli and Klebsiella pneumoniae Isolates in Iran

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Background and Aim : One of the mechanisms of Klebsiella pneumoniae and Escherichia coli resistance to β-lactam antibiotics is the production of β-lactamase enzymes. Among these are the AmpC β-lactamases, which confer resistance to a class of antibiotics. However, little is known about the AmpC β-lactamases of K. pneumoniae and E. coli clinical isolates in Qazvin, Iran. This study was designed to assess the AmpC β-lactamases-producing strains and also identify the prevalence of AmpC β-lactamases genes.

Methods : Antimicrobial susceptibility tests were performed on 435 K. pneumoniae and E. coli isolates using disk difusion technique. Plasmid-mediated AmpC genes were studied using a multiplex PCR assay. The AmpC β-lactamase-producer isolates were studied by employing cefoxitin disk difusion test, AmpC induction test, AmpC cefoxitin-EDTA test, and boronic acid disk test.

Results : Our results showed that of 46 (18.4%) cefoxitin-insensitive E. coli isolates, 10 (21.7%) were positive for AmpC ?-lactamase genes, among them 4 (8.69%) isolates were positive for blaDHA genes and 6 (13%) for blaCIT genes. Of 57 (30.4%) cefoxitin-insensitive K. pneumoniae isolates, 10 (17.5%) were positive for AmpC gene with 4 (6.34%) and 6 (9.5%) isolates positive for blaDHA and blaCIT genes, respectively. However, no MOX, ACC, FOX, or EBC genes were detected in the isolates. Considering the results of diferent confrmatory phenotypic tests, the AmpC cefoxitin-EDTA test showed a higher discriminatory power for detecting AmpC ?-lactamase-producing strains. The specifcity and sensitivity of AmpC cefoxitin-EDTA were 77%, 100% for K. pneumonia and 70%, 90% for E. coli higher than the other two tests, respectively. Also, the authors demonstrated high prevalence rate for resistance to certain antibiotics, such as cefuroxime, trimethoprim-sulfamethoxazole, ampicillin, and cefotaxime.

Conclusion : In conclusion, our study provided valuable information regarding the plasmid-mediated AmpC β-lactamase gene content, antibiotic resistance, and confrmatory phenotypic tests for AmpC β-lactamases in E. coli and K.pneumoniae isolates from clinical sources.

Keywords : AmpC β-lactamases -Escherichia coli- Klebsiella pneumoniae-

P26-191: Evaluation of the role of efflux pumps in multidrug-resistant Escherichia coli ST131 isolated from blood samples in hospitalized patients in Tehran, Iran

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Background and Aim : Nowadays antibiotic resistance is one of the biggest concerns for human beings. In this regard, group ST131 E.coli isolates were repeatedly associated with fluoroquinolone resistance and the most virulent strains belonging to phylogroup B2. Among different mechanisms of antibiotic resistance, the role of genetically-encoded efflux pumps such as acrAB-TolC, Mdfa, Mdtb in MDR resistance should be considered in these bacteria.

Methods : In this cross-sectional study, 124 blood samples were collected from hospitalized patients in different wards of the two educational hospitals during 2020. To confirm that the isolated bacteria is E.coli several biochemical tests have been done. To understand the antibiotic resistance pattern, antibiogram tests were performed according to the Kirby-Bauer method according to the CLSI guideline. In the next step, E.coli ST131 was recognized phylogenetically, and the role of efflux pumps was investigated in them.

Results : The distribution of different strains in hospital wards shows that the most prevalent of both E. coli sequence type was related to the emergency department. In this study, the highest antibiotic resistance was to nalidixic acid and ampicillin (78.2%). On the other hand, the highest sensitivity was to tigecycline, ertapenem, and imipenem. According to the combined disc method, 57 isolates were identified as ESBL-producing strains. Among these, 29 isolates belonged to phylogenetic group B2. In the meantime, 20 isolates were finally identified as type 131 sequences by PCR method.

Conclusion : Improper use of over-the-counter antibiotics causes irrecoverable damages to human health. This may cause the advent of multi-drug resistant (MDR) phenotypes by several mutations. Our study mentioned the improving role of efflux pumps and the increase of quinolone resistance in E.coli ST131. New implementations of drug treatment by using alternative drugs combining with efflux pump inhibitors can be beneficial against these infections.

Keywords : Efflux pump, multidrug resistance (MDR), Fluoroquinolone, Escherichia coli ST131

P27-197: Evaluation of the emergence of Acinetobacter baumannii isolates containing VIM and SIM and drug resistant MDR genes isolated from surfaces and equipment of Tehran medical centers by PCR

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Background and Aim : Excessive and indiscriminate use of antimicrobials in the hospital and community environment are the most important coding factors that lead to the emergence, evolution and acquisition of new resistance of bacteria to antimicrobials. The aim of this study was to investigate the emergence of Acinetobacter baumannii isolates with drug-resistant VIM and SIM genes isolated from the surfaces and equipment of the NICU ward of Tehran Pediatric Medical Centers by PCR

Methods : : In this descriptive cross-sectional study, which was performed over a period of 2 months, out of a total of 120 samples that were sent to the microbiological laboratory of West Tehran. Forty species of Acinetobacter baumannii were identified and isolated using culture methods and biochemical tests. VIM and SIM genes were identified by PCR.

Results : The resistance of the isolates to the antibiotics of imipenem and meropenem and lincomycin 40 isolates (100%) and ceftozoxime and oxytocin 36 isolates (90%) and gentamicin 34 isolates (85.97%) and ciprofloxacin (98%) Ceftazidime was 39 isolates (99%) and cefotaxime and cefexime were 27 isolates (69.4%) and ampicillin and tetracycline were 28 isolates (70.2%). And 40 isolates (100%) were sensitive to cholestin and the mean minimum lethal concentration of imipenem and meropenem antibiotics among 24 isolates (60.3%) was MIC ≥ 64 ug/ml. The frequency of VIM and SIM genes in resistant isolates is 7 isolates (19.4%) and 1 isolate (3.2%), respectively

Conclusion : In this study, the importance of the emergence of drug-resistant Acinetobacter baumannii isolates was investigated. And the genotype of this species in relation to antimicrobial substances in different parts of the world, including Iran, and this requires extensive studies by researchers .

Keywords : Acinetobacter baumannii, beta-lactamase genes, drug resistance.

P28-201: Antibacterial activity of propolis nanoparticles against Enterococcus faecalis biofilm

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Background and Aim : The presence of bacterial biofilm and its products in the root canal of necrosis is main etiological factor in the development of apical periodontitis. Antibiotics are used in the treatment of biofilms but the current trend is towards the identification of natural products in disinfection. Nanoparticles are able to penetrate bacteria and bacterial biofilms, so they can be a potential agent for controlling the growth of bacterial infections. The aim of this study was to investigate the antimicrobial efficacy of propolis nanoparticle (PN) as an endodontic irrigant against E. faecalis biofilm in vitro.

Methods : In the present study, PN was prepared by the ultrasonication method. Scanning electron microscopy and dynamic light scattering were used to measure the size and morphology of the produced nanoparticles. The PN and sodium hypochlorite (5.25% NaOCl) were evaluated in vitro against E. faecalis (PTCC 1778) by disk diffusion and broth micro-dilution method. The biofilm formation was assessed through the crystal violet staining and MTT assays.

Results : The results indicated that PN was effective against E. faecalis biofilm. However, NaOCl showed strong antibacterial activity even at low concentrations. PN was able to inhibit the E. faecalis biofilm adherence at a sub-MIC concentration. Moreover, Electron micrographs indicated the inhibition of biofilms compared to control biofilms.

Conclusion : PN was able to inhibit the adhesion of E. faecalis biofilm that could be due to the reduced particle size, better nanoparticle penetration and the synergistic impact of main components in propolis. Further research is needed to investigate the synergistic effect of PN in combination with endodontic irrigants and to understand their mechanism of action.

Keywords : Antibacterial, Biofilms, E. faecalis, Nanoparticles

P29-208: Determination of the efflux pump-mediated resistance prevalence in Pseudomonas aeruginosa strains isolated from clinical samples in shiraz

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Background and Aim : Pseudomonas aeruginosa is one of the most frequent Gram-negative pathogens responsible for nosocomial infections. One of the problems in treating patients infected with this bacterium is the development of antibiotic resistance by various mechanisms. Mex efflux pumps play a key role in the development of multiple resistance to antimicrobial drugs. The aim of this study was to investigate the pattern of antibiotic resistance and determine the frequency of genes encoding Mex AB, Opr M efflux pump in isolated strains in Shiraz.

Methods : In this study, in order to determine antibiotic resistance and the frequency of genes encoding the efflux pump, 81 samples of Pseudomonas aeruginosa were collected from clinical centers in Shiraz and diagnostic tests were performed to confirm bacterial identity. To evaluate the antibiotic susceptibility, the agar disk diffusion test was used by Kirby-Bayer method according to the standard (CLSI). Identification of MexAB-OprM efflux pump genes was performed using PCR

Results : According to the results, MexD and OprJ genes have the lowest resistance with 64% and OprM gene has the highest resistance with 96%. Also, the diameter of the growth inhibition zone by antibiotics obtained from antibiotic resistance by NCCLS method showed that these bacteria are resistant to all antibiotics studied. Also, the resistance of Meropenem (100%), Ceftazidime (100%) and Ceftizoxime (100%) was higher among all antibiotics and the lowest resistance was related to Cefepime (14%), also Ciprofloxacin (8%) antibiotic is sensitive.

Conclusion : The results of this study indicate an increasing antibiotic resistance among Pseudomonas aeruginosa strains. Increased expression of MexAB-OprM efflux pump genes is one of the common mechanisms in the resistance of Pseudomonas aeruginosa isolates to antibiotics. Identifying resistance mechanisms can be useful in controlling and treating such resistant strains.

Keywords : Pseudomonas aeruginosa, Antimicrobial resistance, Efflux pump, Resistance genes, PCR

P30-210: Investigation of Antifungal susceptibility test against Aspergillus flavus species isolated from patients with pulmonary aspergillosis

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Background and Aim : Subject: Aspergillus species are responsible for the highest mortality rates among patients with fungal infections. Aspergillus flavus is the common cause of invasive aspergillosis and pulmonary aspergillosis (PA) in immunocompromised patients. Millions of people worldwide are at risk of aspergillosis each year, especially individuals with impaired immune function and those with low numbers of neutrophils, solid organ transplant recipients. The triazole antifungal drugs, itraconazole, voriconazole, caspofungin, and amphotericin B, are recommended as first-line drugs in the treatment and prophylaxis of aspergillosis. Azole-resistant Aspergillus flavus species have been increasingly identified in the last decade.

Methods : Method: This study will be designed to identify and determine the MIC of clinical isolates of A. flavus according to CLSI M38-A2 guidelines. Sixty-six Aspergillus flavus isolates were identified based on the microscopic and macroscopic criteria and molecular identification by sequencing the beta-tubulin (benA) gene.

Results : Results: MIC/MEC range for caspofungin was 0.003–2 μg/ml, compared to 0.06–4 μg/ml for itraconazole, 0.25–8 μg/ml for voriconazole, and 0.125–8 μg/ml for amphotericin B. Aspergillus flavus was the most susceptible to caspofungin (MEC50 = 0.06 μg/ml) and the most resistant to amphotericin B (MIC50 = 2 μg/ml). Resistant to voriconazole, itraconazole, caspofungin, and amphotericin B were reported for 2, 12, 6, and 5 isolates, respectively. Caspofungin exhibited the lowest MEC50/MIC50 (0.06 mg/mL), followed by itraconazole (0.25 mg/mL), voriconazole (0.5 mg/mL), and AMB (2 mg/mL).

Conclusion : Conclusion: This information is necessary to improve patient management and when an outbreak dealing with drug-resistant infections occurs.

Keywords : Aspergillus flavus , beta-tubulin, AFST

P31-224: In Vitro evaluation of susceptibility of Trichomonas vaginalis isolates to MetronidazoleI in Alborz province

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Background and Aim : Trichomonas vaginalis is a common sexually transmitted protozoan parasite. Metronidazole, a 5-nitroimidazole, is the drug of choice for treating T. vaginalis infection. Since some patients are resistant to metronidazole, thus, the present study aimed to explore the susceptibility to metronidazole of isolates of T. vaginalis in aerobic and anaerobic conditions.

Methods : Forty-five clinical T. vaginalis isolates from vaginal secretions and urine sediment were collected from women and men referred to clinics, medical diagnostic laboratories, and hospitals in Karaj. The isolates were purified by repeated cultures on TYM medium supplemented with 10 % calf serum, antibiotic (100 µg/mL ceftriaxone and 50 µg/mL ciprofloxacin), and fungicides (2.5 µg/mL amphotericin B). 105 live parasites were added to all 24-wells tissue culture plates. To evaluate the effect of metronidazole on Trichomonas vaginalis parasites, the concentrations of 2, 4, 8, 16, and 32 µg/ml were prepared and all groups were kept at 37°C for 24 and 48 h. For MIC (minimum inhibitory concentration), the viabilities of the trophozoites in the wells under various aerobic and anaerobic conditions were assessed by examining visually the motilities of the cells with an inverted microscope after 24 and 48 h of incubation. For MLC (minimum lethal concentration), the contents of each of the wells were inoculated into the bottoms of tubes containing 5 ml of fresh TYM medium, and the tubes were examined for the presence of motile after five days.

Results : The results of MIC and MLC of T. vaginalis isolates showed that all 45 isolates had MIC and MLC ≤16 µg/ml. Since resistance to metronidazole was defined as MIC ≥50 µg/ml, all isolates were sensitive to metronidazole. Although there were no metronidazole-resistant cases, the lethal effect of metronidazole on the parasites was more effective in anaerobic than aerobic conditions. In addition, the results showed that the death rate of parasites increases with the increase in incubation time.

Conclusion : Although the results of this research have shown that no isolates resistant to metronidazole were found, they should be treated in a way that prevents the production of resistant strains.

Keywords : Trichomonas vaginalis, Metronidazole, In Vitro, MIC, MLC, Alborz

P32-230: Evaluation of the simultaneous exposure to diclofenac and gentamicin on some virulence factors of Pseudomonas aeruginosa

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Background and Aim : Pseudomonas aeruginosa is a Gram-negative bacterium which is an opportunistic human pathogen capable of causing a wide array of life-threatening infections, including ventilator-associated pneumonia, urinary tract infections, burn, wound injuries, bone and joint infections. Diclofenac is a non-steroidal anti-inflammatory drug (NSAID) which has shown considerable antimicrobial activity. Also, combination therapy of antibiotics with nonsteroidal anti-inflammatory drugs (NSAIDs) has shown significant synergism. This study was conducted to evaluate the effect of simultaneous use of diclofenac and gentamicin on the virulence factors of clinical isolates of P. aeruginosa.

Methods : Bacterial identification and isolation was performed using differential biochemical assays. The antibiotic resistance pattern was determined by the disk diffusion method and the Minimum Inhibitory Concentration (MIC) of diclofenac and gentamicin against P. aeruginosa was determined by broth microdilution assay. Bacterial swarming and twitching motility of isolated strains exposed to diclofenac, gentamicin, and diclofenac + gentamicin at sub- MIC concentration were also evaluated.

Results : According to the results, the bacterial strains were Gram negative, catalase positive and non-fermentative rods able to grow in cetrimide agar. The MIC of diclofenac and gentamicin were determined 5120 and 128 µg/ml. The average inhibition zone around gentamicin disks impregnated with diclofenac were 23 and 24 mm for pathogenic and ATCC strains, respectively, which were significantly greater than the inhibition zones around the antibiotic alone. Also, bacterial swarming and twitching motility was significantly decreased in the presence of both drugs compared with either agent alone.

Conclusion : According to the study, diclofenac and gentamicin have a promising synergic activity against P. aeruginosa which could be used for therapeutic approaches. However, further studies are needed in this area.

Keywords : diclofenac, Pseudomonas, infection, gentamicin.

P33-231: Antiparasitic activity of pyocyanin pigment produced by Pseudomonas aeroginosa against Trichomonas vaginalis

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Background and Aim : Pyocyanin pigment is a blue redox compound that is metabolically active and has therapeutic effects on eukaryotic and prokaryotic cells. The opportunistic pathogen Pseudomonas aeruginosa is the only non-fermenting lactose gram-negative bacterium that produces the pigment pyocyanin. Trichomonas vaginalis is a flagellar protozoan that causes trichomoniasis, the most important non-viral sexually transmitted disease in the world. The main treatment for this infection is metronidazole, which scientists are looking for new ways to treat due to the observed side effects and drug resistance. This study aimed to investigate the effect of pyocyanin pigment extracted from Pseudomonas aeruginosa on Trichomonas vaginalis and also the effect of pyocyanin toxicity on the PC12 cell line.

Methods : For this purpose, Pseudomonas aeruginosa RTCC1474 strain was purchased from Razi Vaccine and Serum Research Institute and pyocyanin pigment was extracted from this bacterium with the help of chloroform. The relative purity of the pigment was confirmed by thin layer chromatography, spectrometry UV-Vis and FTIR and We examined its effect on different concentrations against Trichomonas vaginalis parasite and PC12 cell line.

Results : Pyocyanin pigment at concentrations of 10000µg / ml in 24 hours and concentrations of 5000 and 2500 µg / ml in 48 hours inhibited parasite growth 100%. Its IC50 level in 48 hours was 17.44 µg / ml and the CC50 of this pigment was obtained on the cell line at 930 µg / ml. All experimental steps were performed with three replications and statistical results were obtained with the help of GraphPad Prism software version 9.

Conclusion : According to the results, this pigment was effective against Trichomonas vaginalis parasite, and its selective index on cell line was 53 times (SI = 53.32), so more and more comprehensive studies to investigate the composition of pyocyanin in vitro and in vivo are suggested.

Keywords : Pyocyanin pigment, Pseudomonas aeruginosa, Trichomonas vaginalis, Cell line, IC50

P34-243: Susceptibility of clinically isolated strains of methicillin resistant Staphylococcus aureus to vancomycin in Tehran

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Background and Aim : Several drug-resistant bacteria have emerged in recent decades, which have challenged many antibiotics' effectiveness, particularly in hospital infections, and many healthcare settings have incurred a lot of costs as a result. The impressive ability of Staphylococcus aureus to acquire resistance to numerous other antibiotic classes, including methicillin-resistant S.aureus (MRSA) strains, has major ramifications for current and future treatment options against this pathogen. As long as the early 1960s, vancomycin has been considered to be the administrated drug to treat MRSA infections in hospitalized patients, although the Centers for Disease Control (CDC) reported Vancomycin intermediate-resistant (VISA) in the United States in 2002 after being identified in Japan for the first time in 1997. In terms of significance, this study was concerned to evaluate the level of MIC and MBC of vancomycin on MRSA isolated from the clinic.

Methods : S.aureus clinical samples were collected from 100 hospitalized patients at different parts of the Imam Khomeini and the Sina hospitals. Following biochemical tests for confirmation of Staphylococcus aureus, 60 strains of MRSA were identified and isolated by antibiotic susceptibility tests, and MICs and MBCs were determined by broth microdilution and agar disk diffusion. By broth microdilution method, we identified two strains of Vancomycin Intermediate S.aureus and the other sensitive strains to Vancomycin. Death kinetics of selected resistant strains were evaluated.

Results : Among selected strains, Vancomycin is more effective against the MRSA S1 strain which is considered most sensitive than against the MRSA S95 and the MRSA S152 strains. The MRSA S95 and MRSA S152 strains have almost similar death kinetics, but MRSA S1 has a relatively faster death rate due to its sensitivity to vancomycin.

Conclusion : Even though no vancomycin Resistant S.aureus strains were not found in the present study, the frequency of VISA strains poses a drastic threat, not only to Iran's future health but also to those around the world due to facing more resistant strains.

Keywords : Staphylococcus aureus, Vancomycin, MRSA, Vancomycin intermediate-resistant (VISA)

P35-246: Inhibitory effect of prodigiosin pigment produced by Serratia marsecsenes on Trichomonas vaginalis

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Background and Aim : Microbial pigments are a type of secondary metabolite that can play a good role due to its antimicrobial properties. Prodigiosin is an antimicrobial tri-pyrrole pigment that can be extracted from Serratia marcescens . Trichomonas vaginalis is a protozoan that enters the human reproductive system and causes trichomoniasis. Trichomoniasis is the most common non-viral sexually transmitted disease treated with metronidazole. Side effects and drug-resistant are the two main problems of this drug that make doctors look for new treatments. This study aimed to extract prodigiosin pigment from Serratia marcesens to evaluate the antiparasitic properties of this pigment against Trichomonas vaginalis in vitro.

Methods : For this study, Serratia marcescens strain RTCC 2281 was purchased from Razi Institute and mass cultivated. The pigment prodigiosin was extracted using Ethyl acetate and acetone tools and the relativity of the pigment was confirmed by TLC chromatography, UV-Vis spectrophotometr, and FTIR and its effect on Trichomonas vaginalis and PC12 cell line was examined in different concentration.

Results : Prodigosin pigment at 10000 µg / ml in 24 hours and 5000 µg /ml and 2500 in 48 hours caused 100%, 92.89% and 84.26% growth inhibiton of the parasite. Its IC50 in 48 hours 112.8 µg / ml and the CC50 of this pigment on the PC12 cell line reached 84.4 µg / ml. All test steps were performed with three replications and the statistical results were calculated using Graphpad Prism software version 9.

Conclusion : According to the results, this pigment was tested on Trichomonas vaginalis and its selective index on the cell line was 7.46 times (SI = 7.46), so it can be concluded that prodigiosin pigment had an antiparasitic effect and More And more comprehensive study of prodigiosin composition in vitro and in vivo is suggested.

Keywords : Prodigiosin pigment, Serratia marcescens , Trichomonas vaginalis, Cell line, IC50

P36-260: Prevalence of Streptococcus anginosus group in outpatients population

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Background and Aim : Streptococcus anginosus group including S.anginosus , S.constellatus and S.intermedius are part of intestinal, oral cavity and vaginal flora in human. Recently they recognized as significant pathogens due to its ability to cause invasive pyogenic infections. The aim of this study was to clarify the role of this bacteria in infections.

Methods : A total of 40 patients were diagnosed with urinary tract infections , abscess formation, skin lesion and throat culture caused by S. anginosus group through microbiological methods between june 2021 and june 2022.

Results : Urinary tract infection found in 20 cases(50%) , abscess was observed in 12(30%) , skin lesion and throat culture were 6(15%) and 2(5%) respectively.

Conclusion : Urinary tract infection caused by the Streptococcus anginosus group tended to be observed in male patients with comorbid disease and to more frequently in older female. Most common sites in abscess formation was parotide and bartolin glands. Although infections caused by S.anginosus group were susceptible to Penicillin, Cephalosporines and Fluoroquinolons but Tetracyclin and Erythromycin were the most antimicrobial resistant.

Keywords : Streptococcus anginosus group, outpatient, infection

P37-268: Diclofenac increases the susceptibility of Pseudomonas aeruginosa to gentamicin through the inhibition of bacterial efflux pumps

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Background and Aim : Pseudomonas aeruginosa is an opportunistic human pathogen exhibiting innate resistance to multiple antimicrobial agents. This intrinsic multidrug resistance is caused by synergy between a low-permeable outer membrane and a number of multidrug efflux systems. Non-steroid anti-inflammatory drugs have shown the antimicrobial potential to be used in combination with antibiotics against bacterial pathogens. Diclofenac is a non-steroidal anti-inflammatory drug (NSAID) which has been shown to increase the susceptibility of various bacteria to antimicrobials and demonstrated to have broad antimicrobial activity. Therefore, the current work was conducted to evaluate the synergistic effect of diclofenac with gentamicin and its effect on inhibition of efflux pumps activity in clinical P. aeruginosa strains.

Methods : Gentamicin resistance was determined using disk diffusion method and the synergism of diclofenac and gentamicin was investigated using the checkerboard titration assay. Finally, the efflux pump activity was determined by ethidium bromide (EtBr) cartwheel method.

Results : The average inhibition zone around gentamicin disks impregnated with diclofenac were 23 and 24 mm for pathogenic and ATCC strains, respectively, which were significantly greater than the inhibition zones around the antibiotic alone. The checkerboard titration assay revealed synergism of the drugs with fractional inhibitory concentration (FIC) of 0.5. At the end, the cart wheel method showed that diclofenac in combination with gentamicin was able to reduce the extrusion of ethidium bromide from bacterial cytoplasm.

Conclusion : This study showed that simultaneous treatment with diclofenac and gentamicin can target efflux pumps activity of P. aeruginosa that could be a promising approach against drug-resistant P. aeruginosa infections, after further characterization.

Keywords : Diclofenac, Efflux pump, Pseudomonas aeruginosa, Gentamicin

P38-272: Evaluating the Frequency of blaIMI Gene in of Klebsiella pneumoniae Isolated from Patients in Isfahan Hospitals and Determining their Antibiotic Resistance Pattern

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Background and Aim : Klebsiella pneumoniae is an opportunistic, gram-negative, rod-shaped bacterium that belongs to the Enterobacteriaceae family. The spread of antibiotic resistance endangers the effectiveness of treatment and increases health care costs. Also, antibiotic resistance leads to the death of hundreds of thousands of people every year. Horizontal gene transfer plays an important role in the transfer of antibiotic resistance genes from one species to another. This study was conducted with the aim of determining the pattern of antibiotic resistance and investigating the frequency of blaIMI gene in Klebsiella pneumoniae isolated from patients in Isfahan hospitals.

Methods : This descriptive cross-sectional study was conducted on Klebsiella pneumoniae clinical isolates collected from hospitalized patients from Isfahan hospitals during one year. The strains were identified by biochemical tests. Antibiotic susceptibility was evaluated by disc diffusion method according to CLSI 2021 standard protocols for antibiotics ceftriaxone, gentamicin, cefotaxime, ciprofloxacin, amikacin, imipenem, ertapenem, meropenem and doripenem. Also, the presence of blaIMI gene was investigated using PCR molecular method.

Results : From 50 clinical strains of Klebsiella pneumoniae the most and the least antibiotic resistance is related to the ceftriaxone (86%) and amikacin (38%), respectively. Based on PCR results, blaIMI gene was not observed in any of the strains.

Conclusion : The results of the present study showed that due to the increase in the resistance of the strains to ceftriaxone, the treatment of infections causing by this isolates are major problem in future. Also, other mechanisms such as efflux pumps and mutations in purines play a significant role in creating drug resistance. Therefore, it is necessary to recognize the mechanisms of resistance and prescribe appropriate antibiotics.

Keywords : Klebsiella pneumoniae, antibiotic resistance, horizontal gene transfer

P39-274: Evaluation and Identification of Carbapenem Resistant Genes in Klebsiella pneumonia Isolated from Hospitalized Patients in Ilam City

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Background and Aim : Klebsiella pneumoniae is an important multidrug-resistant (MDR) pathogen, which is the most common cause of hospital and community-acquired infections. This pathogen causes various infectious diseases, including urinary tract infections, bacteremia, pneumonia, and liver abscesses. The acquisition of antibiotic resistance genes and the possibility of transferring resistance between pathogen strains leads to antibiotic resistance among opportunistic pathogens. The aim of this study was to evaluate and identify carbapenem resistant genes in Klebsiella pneumonia isolated from hospitalized patients in Ilam city.

Methods : The study included 45 Klebsiella pneumoniae isolates that were isolated from various clinical specimens. Identification of these isolates was done using microbiological tests such as gram staining and differential media. The antibiotic resistance pattern of the strains was determined by disk diffusion method according to CLSI 2021 standard. In this study, antibiotic disks gentamicin, cefotaxime, ciprofloxacin, amikacin, imipenem, ertapenem, meropenem and doripenem were used. The frequency of blaIMI and blaGES genes in the isolates was determined using PCR method.

Results : Out of a total of 124 culture samples collected during one year from the hospital laboratory, 45 samples were identified as Klebsiella pneumoniae. The results of the antibiotic sensitivity test showed that the most resistance is related to the antibiotic cefotaxime (37.8 percent). Also, the antibiotic ertapenem (8.9%) had the lowest resistance rate. PCR results indicate that blaIMI and blaGES genes are not present in any of the strains.

Conclusion : Identifying antibiotic resistance in hospital infectious agents is a major challenge in the treatment of infections. Based on the results, carbapenems are considered suitable options for the treatment of Klebsiella pneumoniae infection. However, the occurrence of this level of resistance is also worrying and indicates the need to pay attention to the proper prescription of these antibiotics.

Keywords : Klebsiella pneumoniae, hospital infections, blaIMI, blaGES

P40-278: Drug Susceptibility Profiling and Genetic Determinants of Drug Resistance in Mycobacterium simiae isolates obtained from Regional Tuberculosis Reference Laboratories of Iran

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Background and Aim : Among Non-tuberculous mycobacteria (NTM) which generally cause opportunistic infections, especially in immunocompromised hosts, Mycobacterium simiae (M. simiae) is one of the most important NTM, associated with pulmonary disease. The main concern about M. simiae infections is the extreme resistance of this NTM to antibiotics. There are limited studies about drug susceptibility testing (DST) and the causes of drug resistance in M. simiae. Hence, the current study aimed to identify the M. simiae isolates and to assess the drug resistance of the isolates using phenotypic and molecular methods.

Methods : In this study, 50 clinical pulmonary isolates suspected of NTM were collected from regional tuberculosis reference laboratories of Iran. The isolates were identified as M. simiae by using standard biochemical tests and molecular methods. DST was performed for identified M. simiae isolates and additional 35 M. simiae isolates from the department archive, against eight drugs. The mutations in gyrA, gyrB, and rrl genes in clarithromycin and moxifloxacin resistant isolates were investigated by polymerase chain reaction (PCR) followed by sequencing.

Results : Out of 50 suspected NTM isolates, 25 isolates were detected as M. simiae species based on the biochemical tests, and 18 isolates were verified based on the rpoB gene sequence analysis to achieve a total of 53 isolates when the archive isolates were included. DST results showed that all 53 isolates were resistant to isoniazid, rifampin, and clofazimine. The rate of resistance to ethambutol and linezolid were 34 (64%), and 40 (76%) respectively. The highest susceptibility rate was demonstrated for amikacin 53 (100%) and clarithromycin 45(85%), followed by moxifloxacin 35(66%). Sequence analysis showed mutations in positions 2058 and 2059 of the rrl gene, as well non-synonymous mutation at codons 389, 444, and 571 of the gyrB gene. Sequence analysis showed no mutation in the gyrA gene. drug-resistant isolates with mutations showed higher MICs compared to non-mutant-resistant isolates.

Conclusion : This study revealed amikacin, clarithromycin, and moxifloxacin as the most effective antibiotics. However, since M. simiae exhibited a high level of antibiotic resistance in vitro, therefore, species identification and determining the antibiotic susceptibility pattern of the isolates are essential before treatment.

Keywords : Antibiotic resistance; Iran; Mycobacterium simiae

P41-290: Antimicrobial activity of Cichorium intybus L. on the pathogenic genes expression of Pseudomonas aeruginosa

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Background and Aim : With the emergence of multidrug resistance (MDR) bacteria, it is necessary to find novel antimicrobial agents for treating such bacteria. Natural products are a rich source of bioactive compounds and are used for the treatment of a wide range of human infections. Recent studies primarily focus on herbal products due to their effectiveness as sources of antimicrobial compounds. For example, flavonoids have been recognized as having a protective effect in plants against phytopathogens. For centuries, flavonoid-rich herbal extracts have been used to treat human diseases. Cichorium intybus L. (Chicory) is a popular plant in traditional European and Chinese folk medicine, and it has been reported to have many ethnopharmacological properties including antifungal, diuretic, anti-inflammatory, digestive, and liver tonic. Considering the importance of herbal products as treatments for infectious diseases, the antimicrobial activity of aqueous and ethanolic extracts of the C.intybus L. from Guilan province, Iran on MDR P.aeruginosa isolates from patients suffering from UTI were examined in the current.

Methods : Aqueous and alcoholic extracts of C.intybus L were prepared using conventional methods. Bacteria were isolated from urine samples of patients with urinary tract infections (UTIs). Antimicrobial activity was evaluated by well diffusion method, MIC determination, antibiofilm assay. After observing the antimicrobial effect of the extracts, the effect of the extracts was analyzed on pathogenesis genes expression of P.aeruginosa using Real Time PCR. All the tests were repeated three times and the data were reported as mean ± SD. The data were statistically analyzed using One-way analysis of variance (ANOVA) and differences among the means were determined at $P \leq 0.01$.

Results : It seems that alcoholic extracts to be more effective than aqueous extracts. The antimicrobial tests showed that the extracts have significant antimicrobial effects. Also, molecular analysis was confirmed that medium to high concentrations of extracts significantly reduce the expression of pathogenic genes.

Conclusion : The extracts of C.intybus L. are good candidates to use in the treatment of UTI due to MDR P.aeruginosa although they need more investigation.

Keywords : Cichorium intybus L, antimicrobial, Pseudomonas aeruginosa

P42-311: Molecular study of csu C,D,E operon responsible for the biofilm formation in Acinetobacter baumannii isolates in Qom

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Background and Aim : Acinetobacter baumannii; the low requirement of this bacterium for its nutrients and its ability to use different carbon sources have increased its presence in different parts of the hospital. Acinetobacter baumannii, as an opportunistic pathogenic bacterium, is responsible for a variety of nosocomial infections, such as bacteremia, pneumonia, urinary tract infections, etc., and is widely known to cause infections in hospitalized patients, especially in ICU, surgery and burn wards. According to the latest WHO report in September 2017, Acinetobacter baumannii is considered one of the most important public health threatening bacteria. One of the important factors related to biofilm in Acinetobacter baumannii is the expression of the csu C,D,E system, which is regulated by a two-component B fm S / B fm R system.

Methods : 108 clinical isolates were collected from the hospitalized patients in different wards of Qom hospitals by Ms. Zohreh Sariikhani from 2012 to 2013. Clinical specimens included: urine, blood, burn wounds, surgical wounds, stools, and respiratory secretions. Diagnostic tests (Gram stain, McCann, TSI, catalase, oxidase, citrate, MR / VP, oxidative - fermentative (OF) and SIM) were performed to confirm the isolates. The confirmed isolates were then screened for the presence of csu A and B genes by PCR. The primers of the target genes were designed and used for molecular diagnosis. The biofilm formation ability of the isolates was determined by microplate method and the results were evaluated by Elisa Reader. The read absorption rates were strong (0.27 <), moderate (0.27> -> 0.13) and weak (0.13> -> 0.07) and very poor (0.07), respectively.

Results : Of 108 Acinetobacter baumannii isolates, 84 (78%) had csuC gene, 24 (22%) had csuD gene and 45 (42%) had csuE gene. Also 49 isolates (45.3%) produced strong biofilm, 27 isolates (25%) produced moderate biofilm, 28 isolates (26%) produced weak biofilm and 4 isolates (3.7%) had no biofilm forming ability. The results showed that on average at least 50% of the isolates express csu C,D,E genes.

Conclusion : Expression of these genes in biofilm forming isolates indicates the relationship between these two studied variables.

Keywords : Acinetobacter baumannii, biofilm, csu pili, csu C,D,E gene

P43-313: Prevalence of Methicillin-resistant Staphylococcus aureus (MRSA) and determination of antibiotic resistance-encoding genes amongst the human clinical infections collected from Isfahan, Iran

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Background and Aim : Methicillin-resistant Staphylococcus aureus (MRSA) is an emerging bacterium responsible for severe cases of antibiotic-resistant hospital and nosocomial infections. This survey aimed to evaluate the profile of antibiotic resistance-encoding genes in the MRSA bacteria isolated from different types of human clinical samples.

Methods : In the present research, 34 MRSA isolates were collected. MRSA strains were isolated from different types of human clinical samples. Isolates were approved in the laboratory using microbial culture and biochemical tests. MRSA identification was done according to overall resistance toward oxacillin (1 µg) and cefoxitin (30 µg) antibiotic discs. Polymerase Chain Reaction techniques were applied to assess the distribution of antibiotic resistance-encoding genes amongst the DNA samples extracted from MRSA isolates.

Results : MRSA distribution amongst the blood, pus, urine, and sputum samples was and 10.52%, 31.57%, 26.31%, and 23.68%, respectively. The most commonly detected antibiotic resistance-encoding genes amongst the MRA isolates were blaZ (100%), msrA (68.42%), and tetK (57.89%). However, ermB (31.57%) and aacA-D (42.10%) antibiotic resistance-encoding genes were the less commonlky identified antibiotic resistance-encoding genes. Distribution of the ermA and msrB antibiotic resistance-encoding genes were 55.26% and 39.47%, respectively. From a statistical view, significant differences were shown between the emrA and ermB ($P < 0.05$), and msrA and msrB ($P < 0.05$)

Conclusion : Role of MRSA as infectious agent with high antibiotic resistance in an Iranian human clinical samples was determined. According to high distribution of blaZ (penecillin-encoding resistance gene), msrA (macrolides-encoding resistance gene), and tetK (tetracycline-encoding resistance gene), their prescription should be done with caution.

Keywords : Methicillin-resistant Staphylococcus aureus (MRSA), Antibiotic resistance-encoding genes, Clinical infections, Prevalence.

P44-317: Whether Insertion Sequence (IS) elements are involved in the emergence of carbapenems-resistant Pseudomonas aeruginosa clinical strains in Ardabil

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Background and Aim : Carbapenems are the main antibiotics for the treatment of infections caused by multidrug-resistant (MDR) Pseudomonas aeruginosa (P. aeruginosa). The aims of this study were to determine the prevalence of gene encoding outer membrane porin protein (OprD) in carbapenem-resistant P. aeruginosa strains as well as to assess the role of insertion sequence (IS) elements in the inactivation of OprD porin and the emergence of carbapenem resistance

Methods : In the current study, imipenem-resistant (n=58), meropenem-resistant (n=42) and doripenem-resistant (n=23) P. aeruginosa were used. The presence of the oprD gene and IS elements were investigated using polymerase chain reaction (PCR) and sequencing methods. P. aeruginosa PAO1 strain was used as the positive control strain.

Results : The prevalence of oprD gene among carbapenems-resistant P. aeruginosa strains was 96.5%. However, the prevalence of IS elements was 0%

Conclusion : our results showed that IS elements are not involved in the inactivation of outer membrane porin OprD and the emergence of carbapenems-resistant Pseudomonas aeruginosa clinical strains in Ardabil

Keywords : Pseudomonas aeruginosa; OprD; Insertion Sequence

P45-321: Evaluation of the frequency and quinolone resistance of Campylobacter spp. in raw milk samples in Alborz province by MAMA PCR method.

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Background and Aim : Campylobacteriosis, as an important zoonotic disease, contributes a lot to causing human infectious gastroenteritis, and in addition to causing watery and bloody diarrhea, it also causes secondary diseases such as Guillain-Barre syndrome. Raw milk contaminated with Campylobacter is one of the most common causes of intestinal diseases The effect of consuming contaminated food. The goals of this study were to identify and separate jejuni and coli species in raw milk samples and to investigate molecular resistance to fluoroquinolones in campylobacters isolated from Alborz province.

Methods : 80 samples of cow, sheep and goat raw milk were collected between May and August. The PCR method was optimized to amplify the 400 bp fragment of the cadF gene and was performed on the sample and 10 samples were declared positive.Then, the MAMA PCR method was investigated to identify the resistance of Campylobacter to quinolones

Results : 8 samples infected with Campylobacter coli species were detected with the formation of 505 bp fragments, and none of the samples were infected with Campylobacter jejuni species and did not form 368 bp fragments, and the remaining 2 samples were detected as species other than coli and jejuni. Number of 1 sample Of the 8 positive samples of Campylobacter coli species, there was a Thr-86 Ile mutation that leads to resistance to fluoroquinolone antibiotics.

Conclusion : The results of this study showed the predominance of C. coli species in cases of Campylobacter contamination of milk samples. The low percentage of resistance to fluoroquinolone drugs in the investigated samples, shows that the use of antibiotics in the investigated animal husbandry units was not so widespread as to cause the predominance of drug-resistant bacteria

Keywords : Campylobacter-Quinolone resistance-MAMA PCR-Raw milk

P46-326: Molecular identification of amino acid alterations in the OprD porin in clinical isolates of carbapenem-resistant Pseudomonas aeruginosa

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Background and Aim : Among several antibiotic resistance mechanisms, mutations in the oprD gene may play an important role in the emergence of carbapenem-resistant Pseudomonas aeruginosa (P. aeruginosa) strains. Therefore, the current study aimed to identification of amino acid alterations in the OprD porin in clinical isolates of carbapenem-resistant P. aeruginosa collected from patients referred to Ardabil hospitals.

Methods : The presence of the oprD gene was detected using polymerase chain reaction (PCR) technique in carbapenem-resistant P. aeruginosa strains and then five strains positive for oprD gene were selected randomly and sent for DNA sequencing. The results were compared with the reference strain PAO1.

Results : As shown in Figure 1, the most frequent amino acid alterations in the OprD porin were 210 A→I, 202 Q→E, 190 A→K, 186 A→P, 170 L→F, 115 T→K and 103 S→T.

Conclusion : Our results revealed that mutations in the oprD gene play are involved in the emergence of carbapenem-resistant P. aeruginosa strains in Ardabil city hospitals.

Keywords : Pseudomonas aeruginosa; OprD; Mutation.

P47-333: High-level aminoglycoside resistance and distribution of genes encoding aminoglycoside-modifying enzymes in methicillin-resistant Staphylococcus aureus (MRSA) isolated from northeastern Iran

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Background and Aim : The resistance genes encoding aminoglycoside modification enzymes (AMEs) are now widely prevalent in different populations of Staphylococcus aureus. The study aimed to determine the frequency of AMEs-encoding genes and their expression profile analysis in clinical isolates of MRSA.

Methods : A total of 105 S. aureus isolates were obtained from the different clinical samples; then were identified by current biochemical tests. The MRSA strains were identified by standard phenotypic and genotyping methods. The antibiotic resistance patterns of the isolates were characterized by agar disk diffusion and MIC methods. The distribution of the AMEs, mecA, femA, and femB genes was determined by multiplex PCR. The expression profile of AMEs-encoding genes was evaluated by quantitative real-time PCR.

Results : The aminoglycoside resistance rates of kanamycin, tobramycin, gentamicin, amikacin, and netilmicin were 47.6%, 46.6%, 45.7%, 45.7%, and 26.6%, respectively. 16.1% and 1.9% of isolates were MDR and XDR phenotypes, respectively. The aac(6')/aph(2'') was the most prevalent (47.8%) AME-encoding gene, followed by ant(4')-Ia (30.4%) and aph(3')-IIIa (21.7%). The high-level expression of AMEs was also detected for aac(6')/aph(2'').

Conclusion : Our study demonstrated that the coexistence of several AMEs and the spread of the resistance determinants in MRSA clinical isolates are alarming and may contribute to the broadening of aminoglycoside resistance spectra and limit treatment options for staphylococcal infections.

Keywords : Staphylococcus aureus; Aminoglycoside; AMEs-encoding genes; mecA; Drug resistance

P48-352: Antibiotic Resistance of Probiotic Strains of Lactic Acid Bacteria Isolated from Traditional Cheeses in Iran

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Background and Aim : Antimicrobial resistance poses a threat to human health. Considering that lactic acid bacteria (LAB) could act as a reservoir of antibiotic resistance (AR) genes, LAB strains intended to be used as food or drug should be monitored for their safety. This study aimed to isolate LAB from traditional cheese, to evaluate its potential as a probiotic, and to identify the antibiotic-resistance patterns of these strains to 20 different antibiotics. The presence or absence of 15 selected antibiotic-resistance genes was also studied.

Methods : A total of 15 cheese samples were collected from 3 sampling sites from different provinces of Iran including Gilan, Kermanshah and Hamedan. These isolates were screened for their probiotic potential by selective tests, including resistance to low pH and bile salts, hemolytic activity and tolerance to digestive enzymes pepsin and trypsin tests. The 16S ribosomal ribonucleic acid (16S rRNA) genes from the selected potential probiotic LAB were amplified. Antibiotic susceptibility testing (against 20 antibiotics such as ampicillin, chloramphenicol, clindamycin, cefixime, ciprofloxacin, cefotaxime, erythromycin, cefoxitin, gentamycin, kanamycin, meropenem, nitrofurantoin, ofloxacin, oxacillin, penicillin G, rifampicin, streptomycin, tetracycline, trimethoprim/sulphamethoxazole, vancomycin was performed. The potential probiotic LAB strains was examined for the detection of 15 AR genes using PCR, including, aac(6')-Ie-aph(2")-Ia, ant(6)-Ia, aph(3')-IIIa, blaCTX-M, catA, dfrE, ermA, ermB, ermC, tetK, tetM, tetO, tetS, tetW, vanE.

Results : Three isolates (Limosilactobacillus fermentum, Lacticaseibacillus paracasei and Lactiplantibacillus pentosus) recovered from cheese samples were recognized as probiotics and passed all of the probiotic tests. The ant(6)-Ia gene was demonstrated in L. paracasei and L. fermentum. The tetM gene was found in L. paracasei. Also, the ermC gene was found in the L. paracasei. One of the isolated strains (L. pentosus) was not resistant to any of the antibiotics tested.

Conclusion : Resistance to different antibiotics is present in various species of probiotic strains in this study, which poses a substantial threat to food and drug safety. Determination of the safety of LAB for human consumption should be given more attention and monitoring.

Keywords : Lactic acid bacteria, probiotic, antibiotic-resistance

P49-358: Investigating of resistance to aminoglycosides among Escherichia coli strains Isolated with class I integrons from surface drinking water supply sources of Ardabil province, Iran

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Background and Aim : Aminoglycoside antibiotics resistance is rapidly spreading among Escherichia coli Antibiotic-resistant bacteria, such as Escherichia coli, being discharged into water sources by humans and animals, in part due to genes carried by integrons. This inquiry aimed This inquiry aimed Investigating drug resistance of aminoglycoside antibiotics in Escherichia coli strains with class I integrons in surface drinking water supply sources of Ardabil province.

Methods : Escherichia coli strains were isolated and identified applying standard biochemical and microbiological techniques from Ardabil province's water supply sources between 2021 and 2022. The class 1 integron gene was detected using the polymerase chain reaction (PCR). The disk diffusion method was used to determine antibiotic resistance and sensitivity.

Results : The Int I gene was found in 37 out of 120 isolates (30.8%). The antibiotic streptomycin had the highest resistance (100%), whereas gentamycin, tobramycinhad the lowest resistance. Gentamycin and tobramycin on the other hand, had the highest sensitivity of 100%, while streptomycin had the lowest (0%). Also, the highest level of the pollution of drinking water supply sources in the province to Escherichia coli was related to Parsabad city (40.5%) and the lowest level of pollution was related to Germi city (13.5%).

Conclusion : According to the findings of this study, the high prevalence of Escherichia coli strains resistant to the antibiotic streptomycin circulating in water sources should be considered a major concern in terms of antibiotic resistance spreading among bacteria in water.

Keywords : Antibiotic resistance, Aminoglycoside, Escherichia coli, Water sources, Ardabil province, Class I integrons.

P50-362: Prescription pattern of broad-spectrum antibiotics in Ganjavian Hospital, Dezful, Southwest of Iran

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Background and Aim : Studies based on antibiotic stewardship are essential to prevent microbial resistance (a common cause of morbidity and mortality of hospitalized patients), use antibiotics appropriately, and reduce treatment costs. This study investigated the prescription pattern of 8 broad-spectrum antibiotics in Ganjavian Hospital in Dezful.

Methods : In this cross-sectional, descriptive study, we reviewed all broad-spectrum antibiotic prescription forms including vancomycin, liposomal amphotericin B, imipenem/meropenem, teicoplanin, linezolid, caspofungin, colistin, and voriconazole during March 2018 to March 2020. All information contained in the forms, including the cause of prescription, site of infection, ward, type of microorganism, the number of prescribed doses of the drug, and the pattern of microbial resistance were recorded.

Results : We evaluated 200 patients. The most common site of infection that led to the use of broad-spectrum antibiotics were: Bloodstream infection (41%), Respiratory (24.5%), and Unknown (13%). The highest prevalence of infection was related to the general internal ward, adult ICU, and neonatal ICU (NICU). The most common bacteria reported include E. coli (19.5%), Acinetobacter baumannii (14.5%), and Pseudomonas aeruginosa (12.5%). Fifty-three percent of infections were multi-drug-resistant and 33.5% were resistant to all antibiotics tested.

Conclusion : It seems that in the near future, treating patients in hospitals will be a major challenge, and probably a percentage of in-hospital deaths will be due to resistant nosocomial infections. Therefore, emphasizing the principles of nosocomial infection control, antibiotic stewardship and continuous monitoring of the pattern of antibiotic resistance in this hospital is vital and necessary.

Keywords : Antimicrobial Stewardship, Broad-spectrum Antibiotics, Drug Resistance, Intensive Care Units (ICU).

P51-369: Genotyping and drug susceptibility testing of Mycobacterium tuberculosis in Iran: a multi-centre study

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Background and Aim : Tuberculosis (TB) is a deadly infection and caused 1.4 million deaths in 2018. Assessing the geographic distribution of major lineages of Mycobacterium tuberculosis can contribute greatly to TB control. Mycobacterial interspersed repetitive unit variable number tandem repeat (MIRU-VNTR) typing is commonly used to differentiate various lineages of M. tuberculosis.

Methods : A total of 2747 clinical specimens were collected consecutively from October 2018 through June 2019. Clinical isolates were identified as M. tuberculosis using standard biochemical tests. The standard 15-locus MIRU-VNTR typing was used for the genotyping of clinical isolates. Drug susceptibility testing was performed using the conventional proportion method.

Results : From the collected specimens, 100 were culture positive for M. tuberculosis. Using MIRU-VNTR, 99 different patterns were detected among the 100 isolates. They were distributed in one cluster comprising two strains and 98 unique patterns. Most of our isolates were similar to New-1 and Delhi/CAS strains. Of the M. tuberculosis isolates, 83 (83.0%) were pan-susceptible and 17 (17.0%) were resistant to at least one drug.

Conclusion : Our study showed that MIRU-VNTR is a useful method for studying the genetic diversity of M. tuberculosis isolates in different regional settings and will help the health authorities to construct a preventive programme for TB.

Keywords : MIRU-VNTR, Drug susceptibility testing, Tuberculosis, genotyping

P52-372: Identification of oxacillinase and metallobetalactamase genes in Acinetobacter baumannii strains isolated from several hospitals in Isfahan

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Background and Aim : Increasing of multi-drug resistant strains of Acinetobacter baumannii especially carbapenem resistance strains is a challenge for the treatment of infections. The aim of the present study was to determine susceptible pattern and frequency of carbapenem resistance genes (oxacillinase and metallobetalactamase) in Acinetobacter baumannii strains collected from different clinical samples of Isfahan hospitals.

Methods : Antibiogram profiles of the isolates were determined using disc diffusion method. Frequency of OXA_58, OXA_51, OXA_23, blaNDM, blaVIM and blaIMP genes were investigated in carbapenem resistant isolates using PCR method and positive results were sequenced.

Results : : total of 100 samples were obtained from blood, urine, wound, and tracheal cultures from Isfahan hospitals. Out of 100 bacteria identified as Acinetobacter baumannii, 60 isolates (60%) were resistant to carbapenems (meropenem and imipenem), and these bacteria were selected for antibiogram and detection of resistance genes. Result showed 100% of selected isolates were resistant to Cefotaxime, Ceftazidime, Cotrimoxazole, Gentamicin, Ampicilline-sulbactam, Ciprofloxacin and Piperacillin-Tazobactam. In addition, 8.3% and 85% of the isolates were sensitive to Amikacin and colistin respectively. Among these isolates, 100%, 100%, 4% and 24% for OXA_51, OXA_23, NDM and VIM were positive respectively. IMP and OXA_58 genes were not detected.

Conclusion : the result showed the best antibiotic against isolates was colistin. The OXA_51 and OXA_23 (oxacillinase genes) are predominant genes but IMP and OXA_58 were not local genes of carbapenem resistant in Isfahan hospitals.

Keywords : Carbapenemase, Oxaclinase, Metallobetalactamase, Acinetobacter baumannii

P53-373: Identification of yeasts causing urogenital and bloodstream infections and determination of their drug susceptibility

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Background and Aim : The incidence of opportunistic yeasts that cause life-threating bloodstream infections especially Candidiasis in humans has been increasing over recent years. These infections are difficult to treat and diagnose, in part due to the broad diversity of species that can cause the infection. In addition, resistance to one or several antifungal drugs is increasingly being reported that causes limiting therapeutic options. The aims of this study was to identify yeasts causing urogenital and bloodstream infections and determination of their drug susceptibility.

Methods : Identification of different yeasts were done by chromogenic yeast medium agar. To determine the drug susceptibility of pathogenic yeasts, minimum inhibitory concentration (MIC) method using 96-wells ELISA plates was performed. The antifungal drugs used in this study were fluconazole, voriconazole and caspofangin.

Results : Total of 30 Candida species were iolated from urine, blood and vaginal from specimens from different Isfahan hospitals were identified as 12Candida albicans, 12Candida krusei , 4Candida tropicalis, 1Candida glabrata, and 1Candida fabianii. The results showed that 50%, 90% and 93.3% of the strains were sensitive to fluconazole, voriconazole and caspofangin respectively.

Conclusion : our results showed that prodominant yeast strains were Candida albicans and Candida krusei and the caspofangin had the best antifungal effect against different Candida species.

Keywords : Drug susceptibility-Yeast agents-Urogenital infections-Bloodstream infections

P54-375: Evaluation of carbapenem inactivation method for accurate detection of pseudomonas aeroginosa isolates producing carbapenemase enzymes

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Background and Aim : Different phenotypic methods are available for identification of pseudomonas aeroginosa isolates producing carbapenemase enzymes. Carbapenem inactivation method (CIM) is a fast and inexpensive way for detection of this enzyme. The purpose of this study was to evaluate the CIM method for accurate identification of carbapenemase producing pseudomonas aeruginosa isolates.

Methods : A total of 97 clinical specimens were collected from the patients in the hospitals of Hamadan from November 2017 to May 2018, in Iran. Antibiotic susceptibility test was performed by disc diffusion method. Minimum inhibitory concentration (MIC) for imipenem was measured by E-test. Then, CIM test and polymerase chain reaction (PCR) methods were performed. Sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) of the CIM test were calculated for each of the genes. Using SPSS16 software, significance of CIM test was evaluated by chi-square test (X2).

Results : In this study, the highest and lowest levels of resistance belonged to cefoxitin 91 (93.8%) and piperacilin/tazobactam 38)39.2%). Among 97 P. aeruginosa clinical isolates, 49 (50.51%) were carbapenemase producer with positive results for CIM test in 44 (89.7%) isolates, and negative results for CIM test in 48 (49.48%) isolates. Therefore, the sensitivity and specificity of the CIM test were 90% and 100%, respectively.

Conclusion : According to the results of this study CIM method is an inexpensive test which can be easily performed and has high sensitivity and specificity for identification of carbapenemase producing P. aeruginosa isolates.

Keywords : Pseudomonas aeruginosa, PCR, CIM

P55-377: Global prevalence and distribution of antibiotic resistance of Stenotrophomonas maltophilia clinical isolates: a systematic review and meta-analysis

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Background and Aim : Stenotrophomonas maltophilia (S. maltophilia) is an opportunistic pathogen in patients taking immunosuppressive therapy, mechanical ventilation, catheters, and those hospitalized for long periods. Treatment of (S. maltophilia) is difficult because exhibits extensive resistance to a variety of antibiotics and chemotherapeutic agents. The current study aims to provide a systematic review and meta-analysis of distribution of antibiotic resistance profile among clinical isolates of S. maltophilia through case reports/case series and prevalence studies.

Methods : A systematic literature search was performed for original research articles published in Medline, Web of Science, and Embase databases from 2000 to 2021 Statistical analysis was performed using STATA 14 software to report antibiotic resistance of clinical S. maltophilia isolates worldwide.

Results : 224 studies (39 articles were case reports/case series, and 185 articles were prevalence studies) were included in current study. A meta-analysis of prevalence studies demonstrated that the most antibiotic resistance all over the world was due to levofloxacin, TMP/SMX, and Minocycline (0.144, 0.092%, and 0.014 respectively). Evaluation of the results of the case reports/case series showed that, out of 57 patients with antibiotic resistance, TMP/SMX (36.84%), Levofloxacin (19.29%), and Minocycline (1.75%) were among the most prevalent antibiotic resistance in patients. The most resistance to TMP/SMX is reported in Asia (19.29%), Europe (10.52%), and America (7.01%), respectively.

Conclusion : Considering that relatively high resistance to TMP/SMX has been recorded, more attention should be paid to the drug regimen of patients in order to prevent the emergence of multi-drug resistant S. maltophilia isolates.

Keywords : S. maltophilia, Antibiotic resistance, TMP/SMX, Minocycline, Levofloxacin

P56-382: Molecular characteristics of antibiotic-resistant Escherichia coli and Klebsiella pneumoniae strains isolated from hospitalized patients in Tehran, Iran

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Background and Aim : We evaluated the distribution of carbapenem and colistin resistance mechanisms of clinical E. coli and K. pneumoniae isolates from Iran.

Methods : 165 non-duplicate non-consecutive isolates of K. pneumoniae and E. coli were collected from hospitalized patients admitted to Iran's tertiary care hospitals from September 2016 to August 2018. The isolates were cultured from different clinical specimens, including wound, urine, blood, and tracheal aspirates. Antibiotic susceptibility testing was performed by disc diffusion and microdilution method according to the Clinical and Laboratory Standards Institute (CLSI) guideline. The presence of extended spectrum β-lactamases (ESBLs) genes, carbapenemase genes, as well as fosfomycin resistance genes, and colistin resistance genes was also examined by PCR-sequencing. The ability of biofilm formation was assessed with crystal violet staining method. The expression of colistin resistance genes were measured by quantitative reverse transcription-PCR (RT-qPCR) analysis to evaluate the association between gene upregulation and colistin resistance. Genotyping was performed using the multi-locus sequencing typing (MLST).

Results : Colistin and tigecycline were the most effective antimicrobial agents with 90.3% and 82.4% susceptibility. Notably, 16 (9.7%) isolates showed resistance to colistin. Overall, 33 (20%), 31 (18.8%), and 95 (57.6%) isolates were categorized as strong, moderate, and weak biofilm-producer, respectively. Additionally, blaTEM, blaSHV, blaCTX-M, blaNDM-1, blaOXA-48-like and blaNDM-6 resistance genes were detected in 98 (59.4%), 54 (32.7%), 77 (46.7%), 3 (1.8%), 17 (10.30%) and 3 (1.8%) isolates, respectively. Inactivation of mgrB gene due to nonsense mutations and insertion of IS elements was observed in 6 colistin resistant isolates. Colistin resistance was found to be linked to upregulation of pmrA-C, pmrK, phoP, and phoQ genes. Three of blaNDM-1 and 3 of blaNDM-6 variants were found to be carried by IncL/M and IncF plasmid, respectively. MLST revealed that blaNDM positive isolates were clonally related and belonged to three distinct clonal complexes, including ST147, ST15 and ST3299.

Conclusion : The large-scale surveillance and effective infection control measures are also urgently needed to prevent the outbreak of diverse carbapenem- and colistin-resistant isolates in the future.

Keywords : Klebsiella pneumoniae, Escherichia coli, Antibiotic resistance genes, Carbapenem, Colistin

P57-388: Prevalence of fluoroquinolones Resistance and OqxAB efflux pump genes in clinical isolates of Klebsiella pneumoniae

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Background and Aim : Considering the clinical significance of K. pneumoniae and also the factors involved in resistance to fluoroquinolones, the aim of this study was to investigate the prevalence of resistance to fluoroquinolones and also to investigate the frequency and expression level of the OqxAB efflux pump

Methods : In a cross-sectional study, one hundred isolates of K. pneumoniae were collected from clinical samples of hospitalized patients in three major hospitals. The antibiotic susceptibility of isolates was assessed by the disk diffusion agar method. The Minimum Inhibitory Concentration (MIC) of Ciprofloxacin was determined by microbroth dilution. The frequency of genes encoding oqxA and oqxB of efflux pump genes was investigated by PCR and the Real-time PCR analyzed the expression of the oqxA efflux pump gene.

Results : The frequency of K. pneumoniae isolates in ICU of hospitals was higher than in other wards (74%). High resistance to ciprofloxacin (89%) was detected. The frequency of oqxA and oqxB genes were 95% and 98%, respectively. Multidrug resistance phenotype (MDR) was observed in 65% of the strains. The oqxA expression was observed in both Ciprofloxacin-susceptible and Ciprofloxacin-resistant isolates. There was a significant relationship between oqxA expression and resistance to Ciprofloxacin.

Conclusion : According to the results of this study, the high prevalence of resistance to ciprofloxacin as well as the presence of OqxAB efflux pump genes in most K. pneumoniae strains in hospitals is a considerable and critical issue.

Keywords : Klebsiella pneumoniae, Ciprofloxacin, OqxAB, Efflux pump

P58-392: Global prevalence and molecular epidemiology of mcr-mediated colistin resistance in Escherichia coli clinical isolates: a systematic review

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Background and Aim : The continuing rise in infections caused by multidrug-resistant (MDR) bacteria is one of the most serious public-health issues in society today. Colistin is a last-resort antimicrobial drug used to treat infections caused by MDR Gram-negative bacteria, therefore resistance to this antibiotic is extremely hazardous. The current study aimed to evaluate the global prevalence and distribution of colistin resistance genes among human clinical isolates of Escherichia coli by systematic review.

Methods : PubMed, Embase and Web of Science databases were systematically searched. For further evaluation, all original English language articles that reported colistin resistance in E. coli clinical isolates published between 2000 and 2020 were examined.

Results : Of 4857 initial articles, after various stages of review and evaluation 190 related articles were selected for the systematic review. More than 79% of the publications selected in this research were published from 2014–2020. In Asia, Europe, America, Africa and Oceania, the prevalence of mobile colistin resistance (mcr)-harbouring colistin-resistant E. coli was 66.72%, 25.49%, 5.19%, 2.27% and 0.32 %, respectively.

Conclusion : The recent widespread dissemination of E. coli strains harbouring mcr genes conferring colistin resistance, especially in Asia and Europe, is concerning and requires more attention.

Keywords : Escherichia coli, mcr, Colistin, Antibiotic resistance, Systematic review

P59-406: Prevalence and pattern of antibiotic resistance of bacterial agents isolated from culture in patients with urinary tract infections referred to Khorramabad teaching hospitals in 2021

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Background and Aim : Urinary tract infection is one of the most common infectious diseases and increasing resistance of bacteria to antimicrobial agents is a major problem in the treatment of urinary tract infections worldwide. Patients diagnosed with urinary tract infection referred to Khorramabad teaching hospitals were designed and performed in 2021.

Methods : Sampling was performed using the standard mid stream method. Information about antibiotic resistance and susceptibility as well as the type of pathogen were collected and recorded by the laboratory of Khorramabad Teaching Hospitals through the report of urine culture results. After collection, the data were entered into Stata version 16 statistical software and analyzed using statistical methods.

Results : In this study, the highest frequency of reported pathogens was related toEscherichia coli(41.20% -103 patients) followed by Staphylococcus saprophyticus(20.80% -52) and Klebsiella pneumoniae(18.40% -46) , respectively. Also, the highest antibiotic resistance was reported against amoxicillin(59.2%) and then ampicillin(53.6%) and the lowest antibiotic resistance against imipenem(11.6%) and then amikacin(17.6%).In this study, between antibiotic resistance. There was a statistically significant relationship between biotics compared to amoxicillin, ampicillin and imipenem with the previous history of antibiotic use.($P < 0.05$).

Conclusion : It seems that amikacin and imipenem antibiotics are suitable drugs to start experimental treatment until the antibiogram response is ready in patients with a diagnosis of urinary tract infection.

Keywords : Urinary tract infection, antibiotic resistance, bacterial agents

P60-411: Inhibitory effect of Key Lime (Citrus Aurantiifolia) and Salvia (Salvia Officinalis) essential oils on Escherichia coli

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Background and Aim : There are many different methods to produce antibiotics for infection disease but, using of plants due to a cost effective and eco-friendly approach has been extensively noticed. These days according to the resistance of bacteria to antibiotics, scientists try to use the wide variety of plants instead of these chemical antibiotics. Key Lime, is a plant from Rutaceae which includes phenolic compounds that plays a vital role in destruction of microorganism and Salvia, is a plant from Lamiaceae which has strong antimicrobial and antioxidant properties due to the presence of active biological compounds. In this research we examine the inhibitory effect of Key Lime (Citrus Aurantiifolia) and Salvia (salvia officinalis) on Escherichia coli.

Methods : The essential oils were prepared and was used to investigate antimicrobial activity of plants on E. coli clinical isolates and reference strain (E. coli 1330). Serial dilution of essential oils (1/2, 1/4, 1/8, 1/16, 1/32, 1/64) was prepared and antibacterial effect was tested on bacteria by broth dilution method to detect MIC (minimum inhibitory concentration).

Results : The result of this research showed that Key Lime and Salvia had antibacterial effect against E. coli. MIC of Salvia and Key Lime essential oils were determined as 1/4 and 1/8, respectively. MIC of Salvia and Key Lime observed in 1/4 dilution, in which MIC was equal to MBC. The synergistic effect of Salvia and Key Lime in 1/4 dilution has antibacterial properties. The mixture of Salvia and Key Lime together in 1/4 dilution MIC had a bactericidal effect, which showed the killing effect of bacteria.

Conclusion : Therefore, these herbal compounds can be used in pharmaceutical industry to help prevent and treat infections.

Keywords : Escherichia coli, Lime, Salvia, Anti-Bacterial effect

P61-414: Molecular characterization of Panton-valentine Leukocidin (PVL)-positive Staphylococcus aureus in Tehran, Iran

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Background and Aim : Some Staphylococcus aureus strains produce Panton-Valentine leukocidin (PVL), a bicomponent poreforming toxin, which causes leukocyte lysis and tissue necrosis. Currently, there is very limited information on the molecular epidemiology of PVL-encoding S. aureus strains in Iran. This study aimed to determine genetic background of PVL-positive S. aureus clinical strains isolated from Iranian patients.

Methods : A total of 28 PVL-positive S. aureus strains were detected from 600 S. aureus isolates between February 2016 and March 2019 from different hospitals in Tehran, Iran. Antimicrobial susceptibility testing was performed according to the Clinical and Laboratory Standards Institute (CLSI) guidelines. Molecular genotyping was performed using SCCmec and accessory gene regulator (agr) typing and pulsed-field gel electrophoresis (PFGE).

Results : The highest resistance was observed against erythromycin (16/28, 57.1%). The lowest resistance was observed against linezolid (1/28, 3.6%). Moreover, 19 (67.9%) out of 28 S. aureus isolates were identified as MRSA, including CA-MRSA (14/19, 73.7%) and HA-MRSA (5/19, 26.3%). By SCCmec typing, only three types (types III, IVa, andV) were found among 19 PVL-positive MRSA isolates. The most common type of SCCmec was type IVa (10/19, 52.6%). The agr types of all 28 PVL-positive S. aureus isolates, indicated that agr type I was the predominant one (14/28, 50%). PFGE typing showed that 24 isolates were clustered into A (4 pulsotypes), B (9 pulsotypes), and C (11 pulsotypes) clusters.

Conclusion : A high prevalence of PVL-positive CA-MRSA strains was detected in Iran. Epidemiological studies have revealed that PVL gene is commonly carried by CA-MRSA having SCC mec type IV. The majority of MRSA strains in the current (50%) and previous studies in Iran carried SCCmec IV. In this study, the majority of the isolates (50%) belonged to agr type I. The agr typing results were consistent with the findings of previous studies in Iran and China. PFGE showed a high degree of genetic diversity among PVL-positive S. aureus clones. This considerable diversity in PVLpositive MRSA strains could be explained by the possibility of isolating MRSA from different sources. Application of genotyping methods such as PFGE may provide a better interpretation of MRSA transmission sources.

Keywords : Staphylococcus aureus, PVL, PFGE, Iran

P62-419: Evaluation of antibiotic resistance pattern of Klebsiella pneumoniae isolates, collected from Miandoab hospitals

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Background and Aim : Klebsiella pneumoniae is one of the important clinical pathogens and responsible for some nosocomial infections; especially pneumonia, septicemia, and urinary tract infection (UTI). Multiple drug resistance among Klebsiella pneumoniae isolates is one of the most important challenges for treating of such infections worldwide. The aim of this study was to determine the antibiotic resistance of Klebsiella pneumoniae isolates collected from Miandoab hospitals.

Methods : In this cross-sectional descriptive study, more than 250 gram-negative bacterial isolates obtained from urinary tract infections in Miandoab hospitals were studied. The selective culture media and biochemical test were used for the identification of Klebsiella pneumonia isolates. Antibacterial susceptibility of isolates was measured to Commonly used antibiotics in the treatment of UTI caused by gram-negative bacteria using disk diffusion (Kirby – Bauer) method.

Results : Out of 250 samples collected from different specimens, 96 isolates of Klebsiella pneumoniae were identified by biochemical tests. The highest antibiotic resistance of Klebsiella pneumoniae isolates to ampicillin with 100% and the lowest resistance with 13% to ciprofloxacin was observed. 36% of the isolates showed resistance to Extended-Spectrum β-Lactamase phenotypically.

Conclusion : High resistance to most of the studied antibiotics, in the studied isolates should be consider as a vital factor and must rigorously take into account in all hospital ward. Antibiogram and selection of appropriate antibiotic is recommended before starting treatment

Keywords : Antibiotic resistance pattern; Klebsiella pneumonia, UTI

P63-422: Investigation of the frequency of resistance to Fluoroquinolones and the presence of qnrb gene in Klebsiella pneumoniae isolated from urinary tract infections in Tabriz.

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1. *Rahim Peyghami*
2. *Mehdi Ghiamirad**

Background and Aim : Background and Aims Klebsiella pneumoniae is one of the important clinical pathogens and responsible for some nosocomial infections; especially pneumonia, septicemia, and urinary tract infection (UTI). Fluoroquinolones are highly effective antibiotics with many advantageous pharmacokinetic properties including high oral bioavailability, large volume of distribution, and broad-spectrum antimicrobial activity. With widespread use, antimicrobial resistance to fluoroquinolones has grown Multiple drug resistance among Klebsiella pneumoniae isolates is one of the most important challenges for treating of such infections worldwide. This study was conducted with the aim of determining the resistance of Klebsiella pneumoniae isolates collected from Tabriz hospitals against fluoroquinolone antibiotics and the presence of resistance genes in them.

Methods : Methods In this cross-sectional descriptive study, 250 gram-negative bacterial isolates obtained from urinary tract infections in Sina, Madani and Al-Zahra hospitals in Tabriz were studied. The selective culture media and biochemical test were used for the identification of Klebsiella pneumonia isolates. Antibacterial susceptibility of isolates was defined to Commonly used antibiotics in the treatment of infections caused by gram-negative bacteria using disk diffusion (Kirby – Bauer) method. The presence of resistance qnrb gene was checked by PCR using specific primers

Results : Results 96 isolates of Klebsiella pneumoniae were identified by biochemical tests. The highest antibiotic resistance of Klebsiella pneumoniae isolates to ampicillin with 100% and the lowest resistance with 30% to chloramphenicol was observed. 68% of the isolates showed resistance to Extended-Spectrum β-Lactamase phenotypically. Resistance to nalidixic acid was observed in 50 isolates and to ciprofloxacin in 4 isolates. qnrb gene was observed in 5 isolates.

Conclusion : Conclusion High resistance to most of the studied antibiotics, especially fluoroquinolones, in the studied isolates should be consider as a vital factor and must

rigorously take into account. Antibiogram and selection of appropriate antibiotic is recommended before starting treatment

Keywords : Antibiotic resistance pattern; Klebsiella pneumonia, qnrb gene,

P64-428: Biofilm forming ability and agr- specific group of methicillin-resistant Staphylococcus aureus in Northern Iran

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1. *S*

Background and Aim : Staphylococcus aureus is one of the most common causing agent of nosocomial infection, worldwide. The methicillin-resistant and biofilm-dependent infections of this bacterium has become a clinical concern in patients. This research aimed to identify biofilm forming ability and agr- specific group of clinical isolates of methicillin-resistant S. aureus (MRSA) in northern Iran.

Methods : During 2021, a total of 200 clinical isolates were identified as S. aureus by biochemical tests. The disk diffusion method was used to examine the antibiotic resistance of isolates and the microplate method was applied to investigate the biofilm production capability. In addition, the PCR method was used to determine the frequency of biofilm associated genes and agr typing of MRSA isolates. P£0.05 was considered significant.

Results : Overall, 125 (62.5%) out of 200 isolates were methicillin-resistant and 75% were multiple antibiotic-resistant. Vancomycin was the most efficient antibiotic against the isolates and highest resistant rate was against penicillin. Biofilm forming ability was detected in 99 (79.2%) methicillin-resistant isolates in which icaA and icaD were found in 85% and 78% of biofilm-producing isolates, respectively. Type 1 of the agr gene was the most common type among methicillin-resistant isolates. The frequency of biofilm associated genes showed significant association with MDR phenotype and presence of agr locus (P£0.05).

Conclusion : Present results indicate high frequency of biofilm and antibacterial resistance in methicillin-resistant S. aureus isolates in Guilan Province, northern Iran. Present data suggests reliable and rapid identification of biofilm forming MRSA strains to prevent the spread of these bacteria.

Keywords : Staphylococcus aureus, methicillin resistance, biofilm, agr typing

P65-431: Prevalence and resistance of Streptococcus pneumoniae, Staphylococcus hominis, Staphylococcus saprophyticus bacteria from acute dacryocystitis in children in Isfahan, Iran 2022

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Background and Aim : Objectives: Dacryocystitis is one of the most common eye diseases due to inflammation of the lacrimal sac. It can be of two types: acute and chronic forms. The aim of this study is identification of common bacteria causing nasolacrimal duct infection and determination of their antimicrobial susceptibility profiles in children with congenital nasolacrimal duct obstruction.

Methods : Method: This cross-sectional and analytical study was done in the ophthalmology department of Isfahan University of Medical Sciences (Iran) from January to February 2020. Identification of dacryocystitis specimens was done using phenotypic and genotypic methods. Antibiotic susceptibility tests performed by Disc diffusion method with MAST.

Results : Results: All of 10 isolates from culture of specimens belonged to gram positive cocci. Staphylococcus saprophyticus, Staphylococcus hominis and Streptococcus pneumoniae (n=1, 1.6%). Totally, highest resistance was found against erythromycin and tetracycline while vancomycin, chloramphenicol, ciprofloxacin and imipenem showed the highest susceptibility. The most sensitive antibiotics are vancomycin, chloramphenicol and, ciprofloxacin against the most common microorganisms were isolated.

Conclusion : Conclusion: The common bacteria isolated from acute dacryocystitis in our region are Staphylococcus. Ciprofloxacin, vancomycin and chloramphenicol are the most effective antibiotics against all of the isolated microorganisms. These 'regional' findings have important public health implications for the treatment and prevention of dacryocystitis in this region of Iran.

Keywords : Keywords: Dacryocystitis, antibiotic resistance, congenital nasolacrimal duct obstruction, bacteriology

P66-435: Antifungal susceptibility and evaluation of CDR1 gene expression in fluconazole-resistant Candida albicans isolated from vulvovaginitis

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Background and Aim : Vulvovaginal candidiasis (VVC) is one of the most common superficial fungal infections, and studies show that about 75% of women experience VVC at least once in their lifetime. The objective of this study was to analyse the antifungal susceptibility and the role of CDR1 gene overexpression as a mechanism of fluconazole resistance in Candida albicans isolated from vulvovaginitis patients.

Methods : The study was performed in 78 women suspected of vulvovaginitis. Isolated Candida albicans were identified using the ITS-restriction fragment length polymorphism (ITS-RFLP) technique. Antifungal susceptibility testing was performed for fluconazole, amphotericin B, ketoconazole, and itraconazole according to the CLSI M27-A3 guideline. CDR1 gene expression was conducted in fluconazole-resistant isolates using real-time PCR.

Results : Itraconazole was the most effective drug with MIC50=0.25 ?g/mL and amphotericinB was the least effective drug with MIC50=1 ?g/mL against Candida albicans among four tested antifungals with MIC range between 0.03-8 ?g/ml and 0.06-8 ?g/ml, respectively. Twelve isolates were resistant to fluconazole. The overexpression of CDR1 in fluconazole-resistant isolates was observed in 1.68–32.8-fold compared to the control strain C. albicans ATCC 10231.

Conclusion : In isolates with high MIC, CDR1 gene expression was high. It seems that resistant isolates are increasing and drug susceptibility testing is necessary to choose the appropriate drug and prevent resistance.

Keywords : Candida albicans, Vulvovaginal candidiasis, CDR1 gene expression, Antifungal susceptibility

P67-443: Molecular mechanism analysis of multidrug resistance (MDR) in Escherichia coli isolates

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Background and Aim : Excessive use of antibiotics has made Escherichia coli resistant to a large number of antibiotics. The aim of this study was to identify the molecular mechanism of multidrug resistance (MDR) in E. coli isolated from Iranian eggs.

Methods : The studied E. coli were collected from 800 egg samples of different Iranian brands in which the resistance to tetracycline, nitrofurantoin and sulfonamide antibiotics had been previously studied. From the collected samples, 12 samples of multidrug-resistant E. coli (MDR) were selected, and the presence of resistance genes in the above strains was confirmed by using specific primers and PCR.

Results : The results showed that not all strains had the resistance genes studied and the presence of Tet b gene in 50% of strains, Tet D in 25% of strains, Tet e in 35% of strains and Tet a, respectively. It was identified in 45% of strains. Sul1 gene was also observed in 25% of strains, Sul2 gene in 50% of strains and Nfsa in 30% of strains.

Conclusion : The results showed that not all identified genes were expressed under the influence of antibiotics, and only 60% of them were expressed, so only the identification of the gene in PCR and its expression in Real Time PCR indicate the sources and mechanism of resistance. Is not. The lack of expression of some genes and the lack of identification of some of the studied genes indicate the use of multidrug-resistant bacteria from other mechanisms in the development of multidrug resistance

Keywords : Escherichia coli, Multidrug resistance, Resistance genes, Real Time PCR

P68-447: Determination of Colistin-Resistance Pseudomonas aeruginosa Isolates from Bovine Mastitis in Mashhad, Iran

Abolfazl Rafati Zomorodi[1] , Gholamreza HashemitabarIn the dairy industry, bovine mastitis (BVM) is indicated as a significant concerning result of economic loss worldwide. Bacterial infections are introduced as the main reason f[2] , Fatemeh Aflakian[2] *

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Background and Aim : In the dairy industry, bovine mastitis (BVM) is indicated as a significant concerning result of economic loss worldwide. Bacterial infections are introduced as the main reason for BVM; subsequently, antibiotic therapy has been propounded as the first line of combat in mastitis cases because antibiotic residue in milk will develop diminishing antibiotic resistance to the environment. P. aeruginosa, a non-fermentative gram-negative rod-shaped bacterium, is widely associated with several infections, specially BVM. Also, P. aeruginosa is listed as a critical priority pathogen by the World Health Organization due to emerging multi-, extended- and pan-drug resistance P. aeruginosa isolates. The present study was performed to aim to assess the antimicrobial susceptibility pattern among phenotypic resistant P. aeruginosa isolates from clinical mastitis from Mashhad, northeast Iran.

Methods : The current study was conducted on a collection of P. aeruginosa isolates from clinical mastitis cases kept at the Microbiology laboratory, faculty of veterinary, Ferdowsi University of Mashhad. A total of 50 P. aeruginosa isolates from clinical mastitis cases were subjected in the current study. The Kirby-Bauer method was used to determine all isolates' antimicrobial susceptibility patterns. The colistin broth disc elution method (CBDE) was used as CLSI (2022) recommended demonstrating the colistin-resistant isolates.

Results : The antimicrobial susceptibility testing has revealed the highest resistance against meropenem 40 isolates (80%); however, aztreonam has shown a significant sensitivity (100%). Also, all isolates were sensitive to tobramycin and gentamycin. The CBDE test has determined 3 colistin-resistance isolates.

Conclusion : The emergence of colistin-resistance P. aeruginosa is a global issue that indicates antimicrobial stewardship is necessary to manage increasing antimicrobial resistance.

Keywords : Bovine mastitis, Colistin, P. aeruginosa

P69-448: Genotypic and Phenotypic Characterization of Antibiotic Resistance in Methicillin-Resistant Staphylococcus Aureus Isolated from Tabriz Hospitals in 2021

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Background and Aim : The most significant human pathogen, Staphylococcus aureus, has raised concerns due to its growing antibiotic resistance. This study's goal was to characterize the antibiotic resistance distribution among methicillin-resistant Staphylococcus aureus isolated from clinical samples of patients in Tabriz hospitals

Methods : This cross-sectional study was conducted on 242 patients hospitalized in different departments like surgery, internal medicine and infectious disease in Tabriz hospitals. The resistance pattern of isolates was determined using disc diffusion and D- test methods according to CLSI guidelines. The antibiotics used included erythromycin, linezolid, cefazolin, cefoxitin, clindamycin, and trimethoprim sulfamethoxazole. All isolates were screened for the presence of femA and mecA genes by PCR method with using special primers.

Results : All methicillin-resistant Staphylococcus aureus isolates were confirmed by PCR method using femA and mecA genes. The results showed 42, 22, 7 and 19 methicillin-resistant Staphylococcus aureus isolates were resistant for cefoxitin, cefazolin, linezolid and trimethoprim-sulfamethoxazole respectively. 15 isolates had D-shaped clear zone around proximal of erythromycin disk and 24 isolates had D-shaped zone around proximal of the erythromycin disk and small Colonies.

Conclusion : It can pose a major risk to both human health and society when methicillin-resistant Staphylococcus aureus isolates become resistant even to last-resort medicines like linezolid.

Keywords : Keywords: Staphylococcus aureus, antibiotic resistance, femA, mecA

P70-449: The High Prevalence of Stx1 Gene Among Escherichia Coli Isolates from Bovine Mastitis in Mashhad, Iran

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Background and Aim : E. coli is a gram-negative, opportunistic bacterium commonly found in the dairy cow's environment, infecting mammary glands through environmental contact. Shiga-toxin-like producing E. coli is one of the significant E. coli pathotypes that causes severe diarrhea among humans. Therefore, the distribution of E. coli isolates harboring the stx1 and stx2 genes in farm dairy is a highlighted concern for public health. The study aimed to evaluate virulence genes' prevalence, especially stx1 and stx2, among E. coli isolated from farm dairy.

Methods : The current study collected 47 E. coli isolates from clinical mastitis milk samples from a dairy farm in Mashhad. The biochemical standard tests were carried out to identify E. coli isolates. The multiplex Polymerase-chain reaction (m-PCR) assay was performed to assess the prevalence of four virulence genes, including stx1, stx2 eaeA, and hlyA genes among E. coli isolates.

Results : The most frequent genes among all isolates, as determined by m-PCR, were eaeA 42 (89.3%) and stx1 34 (72.3%). Also, the frequency of stx2, hlyA, and sta genes in E. coli isolates was found to be in 26 (55.3%), 9 (19.1%), and 4 (8.5%), respectively.

Conclusion : The high prevalence of stx1 genes among isolates from farm dairy has indicated further hygiene principle is essential in farm dairy to diminish the distribution of stx1 genes among isolates.

Keywords : Bovine mastitis, E. coli, stx1 gene

P71-456: Investigating the antibiotic resistance pattern of Escherichia coli isolates from patients with urinary tract infection referred to Imam Khomeini Hospital in Shirvan city in 2021

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Background and Aim : Escherichia coli is a ubiquitous causative agent in people with urinary tract infections, and antibiotic resistance is increasing worldwide. Therefore, early diagnosis and appropriate selection of antimicrobial drugs are necessary.

Methods : This cross-sectional study was conducted on 1550 urine samples of outpatients and inpatients who referred to Imam Khomeini Hospital in Shirvan city in 2021. The isolates were identified and identified using biochemical tests and differential culture media. The antibiotic resistance pattern of Escherichia coli bacteria was studied by disk diffusion or Kirby Baer method.

Results : In this study, out of 73 positive samples, 48 (65.7%) were Escherichia coli bacteria, the highest antibiotic resistance was related to cefazolin (64%), ampicillin sulbactam (50%), ceftriaxone (48.5%), respectively. ceftazidime (41.17%), imipenem (41.17%), ciprofloxacin (30.5%), gentamicin (7.5%) and nitrofurantoin (2.3%).

Conclusion : In general, according to the results, the most resistant antibiotics are cefazolin and ampicillin-sulbactam, which are recommended not to be prescribed due to their resistance and ineffectiveness in treatment, nitrofurantoin and gentamicin are the most sensitive antibiotics respectively.

Keywords : Urinary tract infection, Escherichia coli, antibiotic resistance

P72-457: Determination of resistance to antibiotics in Corynebacterium minotissimum isolates from Tabriz, Iran

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Background and Aim : Erythrasma is a chronic infection of the skin that appears in the body folds as flat copper spots. The causative agent of this infection is Corynebacterium minutissimum (C. minutissimum). Erythrasma can be treated with antiseptic or topical antibiotic. The aim of this study was to investigate the frequency and antibiotics susceptibility patterns of, and the presence of the erythromycin resistance gene (ermX and mefA) in C. minutissimum isolates from Tabriz, Iran.

Methods : From July 2020 to May 2022, 278 skin scrub specimens were collected from patients admitted to hospitals of Tabriz University of Medical Sciences. Specimens were incubated on the blood agar plates and isolates were identified by microbiological laboratory standards. The antibiotic susceptibility patterns were determined by the disk diffusion method and resistance genes of ermX and mefA were detected by the PCR method.

Results : Out of 278 specimens, 41 C. minutissimum isolates (14.74%) were recovered. The highest frequency of resistance was observed to penicillin (75.6%) followed by clindamycin (46.34%), erythromycin (39.2%), tetracycline (24.2%) gentamicin (19.15%), clarithromycin and neomycin (4.48%). The frequency of ermX and mefA genes were 75% and 12.5%, respectively.

Conclusion : The prevalence of erythrasma is a relatively moderate. Resistance to antimicrobial drugs was common and worrying. Resistance to erythromycin in C. minutissimum is mainly related to the ermX gene.

Keywords : Erythrasma, erythromycin, Corynebacterium minutissimum, resistance

P73-468: CRISPR-Like sequences among Helicobacter pylori isolates and their association with antibiotic resistance

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Background and Aim : Part of clustered regularly interspaced short palindromic repeats (CRISPR)-like sequences in antibiotic resistance hasn't been investigated yet. So, this research was designed to study association of CRISPR-like sequences with antibiotic resistance in H. pylori isolates.

Methods : Seventy-two isolates of H. pylori were subjected for study presence of CRISPR like sequences by PCR method and their correction with antibiotic resistance. Antibiotic resistance profile of isolates was investigated by microtiter-plate method against tetracycline, and metronidazole.

Results : The CRISPR-like region were detected in 46 (63.8%) of 72 isolates, respectively. The frequency of resistance to tetracycline, and metronidazole in CRISPR-like positive H. pylori were 36 (78%), and 36 (78%), respectively.

Conclusion : CRISPR-like sequences is involved in antibiotic resistance, so could be served as a therapeutic target and genetic markers of antibiotic resistance.

Keywords : Helicobacter pylori, antibiotic resistance, CRISPR-like

P74-469: Bacterial superinfection in cutaneous Leishmaniasis

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Background and Aim : Pathogenic bacteria are risk factor for chronic lesion of cutaneous leishmaniasis. Rapid detection of drug resistant bacteria can also contribute to the success of leishmaniasis treatment. The purpose of this study was determination of multiple drug resistance bacteria in leishmaniasis wounds.

Methods : Totally 149 wound specimens were cultured on Blood and MacConkey Agar. Identification tests such as gram staining, catalase, oxidase, triple sugar iron agar, citrate, SIM, urea agar and Methyl Red / Voges-Proskauer were used. The antimicrobial susceptibility testing to routine antibiotics by disk diffusion method and MIC(minimal inhibitory concentration), Extended spectrum beta-lactamases(ESBLs) and D-Zone test according to CLSI protocols and PCR (for mecA gene) were performed.

Results : In a cross-sectional study(Nov 2021- July 2022), 107 males and 42 females were referred to Dezful Leishmaniasis Laboratory from different urban and rural areas. All patients had ulcers for more than one month. Prevalence of bacterial secondry infection was 61.5% (S.aureus 73%, K.pneumonia 14.6%, E.cloacae 10%, and P.mirabilis 2.4%). In S.aureus isolates resistance rates to penicillin, Erythromycin, Ciprofloxacin, Clindamycin, Linezolid, Gentamicin, and Amikacin were 93.3%, 66.7%, 46.7%, 30%, 13.3%, 12.5%, 12.5%, respectively. In 4 (13.3%) S.aureus were resistance to clindamycin and positive D test. Teicoplanin MIC values were found between 0.19 -1.5 µg/ml in susceptibility ranges. Among the 30 isolates of S. aureus, mecA gene (353 bp) was amplified in 8 (27%) strains as Methicillin-resistant Staphylococcus aureus (MRSA). In gram negative bacteria, the cephalosporin or carbapenem resistance strains not detected but the ESBLs production were detected in 2 K.pneumonia strains isolated from lesions similar to cutaneous leishmaniasis.

Conclusion : Isolation of MRSA and inducible resistance to clindamycin from the samples of patients who had no history of hospitalization in the last 6 months is an alarm for the health system to use an effective treatment process to control and prevent the spread of these infections in the community.

Keywords : Antibiotic resistance, wound, leishmaniasis, MRSA, ESBL, PCR

P75-471: Panton- Valentin Leukocidin, in Methicillin-Resistant Staphylococcus aureus (MRSA) Isolates from hospitalized Patients in Rasht, Iran

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Background and Aim : Staphylococcus aureus is a Gram- positive coccus which has an appearance similar to a bunch of grapes under microscope. It produces relatively big yellow colonies on culture medium. and is often isolated from the nose, mouth and digestive tract. It is also responsible for developing the most hospitals' acquired infections and intravascular infection. Panton-Valentine Leukocidin producing strains of Staphylococcus aureus were accompanied with the infections. This study was to investigate the prevalence of pvl gene isolated from the patients hospitalized in Rasht, from the northern of Iran.

Methods : During a nine-month period, 190 clinical isolates of Staphylococcus were obtained. S. aureus strains were isolated from wounds, blood, urine, splinter, and body fluids from hospitals of Rasht, Iran. The specimens were initially inoculated in Mannitol Salt Agar and incubated at 370C for 18 - 24 hours. Colonies were examined for catalase production, coagulase, hemolysin, DNase, and Mannitol fermentation. Resistance to Methicillin was determined by either Oxacillin disk and chromosomal DNA PCR.

Results : The positive isolates were further analyzed for the presence of The pvl gene using a specific PCR primer sets and a totally of 42isolates (22.10%) were positive for pvl gene.

Conclusion : In recent years, various studies showed an increase varieties of Methicillin resistance and PVL positive Staphylococcus aureus. Therefore, considering its importance, the current study was to investigate the prevalence of pvl gene in strains isolated from hospitalized patients in Rasht, Iran.

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

P76-482: Detection of NDM-1 producing Klebsiella pneumoniae ST15 and ST147 in Iran during 2019-2020

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Background and Aim : Carbapenems are employed to treat infections caused by Gram-negative bacteria including Klebsiella pneumoniae. This research is aimed to perform phenotypic detection of β-lactamases and molecular characterization of NDM-1 positive K. pneumoniae isolates. Another objective is to investigate NDM-1 producing K. pneumoniae among children in Iran. From 2019 to 2020, altogether 60 K. pneumoniae isolates were acquired from various patients in certain Iranian hospitals.

Methods : Antimicrobial susceptibility testing was performed by disk diffusion and broth microdilution methods. In addition, mCIM and eCIM were used to confirm the production of carbapenemases and metallo-beta-lactamases (MBLs), respectively. Detection of resistance genes namely, blaNDM-1, blaIMP, blaVIM, blaKPC, blaOXA-48-like, blaCTX-M, blaSHV, blaTEM, and mcr-1 was performed by PCR and confirmed by DNA sequencing. Multilocus sequence typing (MLST) was employed to determine the molecular typing of the strains.

Results : According to the findings, the highest rate of carbapenem resistance was detected against doripenem 83.3% (50). Moreover, 31.7% (19) were resistant to colistin. Further to the above, altogether 80% (48) were carbapenemase-producing isolates and among them 46.7% (28) of the isolates were MBL and 33.3% (20) isolates were serine ?-lactamase producer. According to the PCR results, 14 isolates produced blaNDM-1. Remarkably, four blaNDM-1 positive isolates were detected in children. In addition, these isolates were clonally related as determined by MLST (ST147, ST15). Altogether ten blaNDM-1 positive isolates were ST147 and four blaNDM-1 positive isolates were ST15.

Conclusion : Based on the results, the emergence of NDM-producing K. pneumoniae among children is worrying and hence, it is necessary to develop a comprehensive program to control antibiotic resistance in the country.

Keywords : K. pneumoniae; blaNDM-1 gene; carbapenem-resistance; carbapenemase; colistin; metallo-β-lactamase genes.

P77-483: The prevalence of vanA gene in Methicillin-resistant Staphylococcus Aureus (MRSA) isolated from patients with bedsores

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Background and Aim : Introduction: Staphylococcus aureus especially Methicillin-Resistant Staphylococcus aureus (MRSA) is one of the major causes of nosocomial and community-acquired infections and nowadays it is known as a health problem in the world due to its resistance to most antibiotics. This study aimed to determine the prevalence of vanA gene in Methicillin-Resistant Staphylococcus aureus (MRSA) isolated from patients with bedsores.

Methods : Materials and Methods: In the current study, 80 clinical isolates were collected from patiens with bedsores at Loghman-e Hakim hospital, Iranmehr hospital and Tehran wound center. The samples were identified using standard laboratory tests and resistance to cefoxitin disk (30µg) and evaluating the presence of the mecA gene. The resistance of the MRSA isolates to different antibiotics was checked using the disc diffusion method. The presence vanA gene in these isolates was investigated using specific primers and polymerase chain reaction (PCR).

Results : Results: Of the studied isolates, 29 isolates were identified as methicillin-resistant. The highest antibiotic resistance level was observed against erythromycin, and clindamycin; and the lowest was determined against linezolid with 82.75%, 82.75%, and 13.8% respectively. vanA gene was detected in all of the MRSA isolates. Multidrug resistance (MDR) was observed in almost 72.41% of isolates.

Conclusion : Discussion and conclusion: The prevalence of vanA gene has increased in Staphylococcus aureus isolates resistant to methicillin and high and multiple isolates of Staphylococcus aureus resistant to common antibiotics should be considered a serious matter.

Keywords : Methicillin-resistant Staphylococcus aureus; vanA gene; nosocomial infections

P78-484: Detection of New Delhi Metallo-β-lactamase-1 among Pseudomonas aeruginosa isolated from adult and Pediatric patients in Iranian hospitals

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Background and Aim : Gram-negative bacteria cause an alarming level of resistance to carbapenems by producing carbapenemases which can become a global epidemic. According to a report about Pseudomonas aeruginosa released by the World Health Organization in 2017, carbapenem resistance is classified as highest priority. The main objectives of the present study are to evaluate the frequency of carbapenem resistance, detect Metallo-β-Lactamases and β-lactamases, identify the molecular characterization of blaNDM-1 in Pseudomonas aeruginosa isolates, and report blaNDM-1 for the first time among children in Iran. This study selected 70 clinical isolates from different cities of Iran during 2019–2020.

Methods : Disk diffusion method and Minimum Inhibitory Concentration were employed to run antimicrobial susceptibility testing. In order to detect carbapenemases and Metallo-β-Lactamases, mCIM and CDDT were used, respectively. In addition, PCR technique and DNA sequencing were utilized to identify and confirm the genes related to β-lactamases and Metallo-β lactamases (blaNDM, blaVIM, blaIMP, blaSIM, blaGIM, blaSPM, and blaKPC)

Results : The highest resistance rates were observed for Meropenem 67.1% (47) and Imipenem 65.7% (46) while the lowest resistance rate was observed for Piperacillin/Tazobactam 35.7% (25). Of all isolates, 55.7% (39) and 54.3% (38) constituted carbapenemase-producing and MBL isolates, respectively. PCR results exhibited blaNDM-1 21.4%, followed by blaIMP 7.1% and blaVIM 2.9% of genes. Moreover, 1.4% of these isolates co-produced blaNDM-1 and blaVIM genes. These isolates did not comprise blaSIM, blaSPM, blaGIM, and blaKPC genes. Three isolates of positive blaNDM-1 isolates were notably detected among children.

Conclusion : The results showed that Metallo-β-Lactamases, especially blaNDM-1, were highly prevalent among adults and children of Iran.

Keywords : Pseudomonas aeruginosa ,Carbapenem, blaNDM-1 gene, Metallo-β-Lactamase genes

P79-488: Antifungal activity of green synthesized curcumin-coated silver nanoparticles alone and in combination with antifungal drugs

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Background and Aim : Candida and Aspergillus species are the causative agents of a wide range of infections in immunocompetent and immunocompromised individuals. Drug resistance has been reported with an increasing trend during the past decades among these fungi. Accordingly, searching for alternative approaches seems necessary. Using nanomaterials alone or in combination with antifungal drugs is a promising approach. The aim of this study was to investigate the the antifungal activity of curcumin-coated silver nanoparticles alone and in combination with antifungal drugs against a set of pathogenic Candida and Aspergillus species.

Methods : A set of 30 fungal isolates including A. fumigatus (n=6), A. flavus (n=6), C. albicans (n=6), C. parapsilosis (n=6), and C. krusei (n=6) were included in this study. The susceptibility pattern of all isolates to fluconazole and itraconazole was evaluated as per CLSI method. Curcumin-coated silver nanoparticles were synthesized and their characteristics were determined. The antifungal activity of curcumin-coated silver nanoparticles was tested alone and in combination with antifungal drugs. Finally, TEM analysis was performed to determine the effect of nanoparticles on a selected strain.

Results : Based on the results of UV–Vis spectroscopy, the nanoparticles were synthesized successfully with a mean ± SD size of 29.1 ± 5.6 nm and spherical shape. Results of antifungal susceptibility testing revealed that the majority of yeasts (15/18, 83.33%) were fluconazole-resistant. Resistance to itraconazole was also noted for 4 and 7 Candida and Aspergillus strains, respectively. Curcumin-coated silver nanoparticles demonstrated promising antifungal activity, especially against Candida species with geometric mean minimum inhibitory and fungicidal concentrations much lower than fluconazole against all the studied fungi. These values were also lower than those of itraconazole in some instances, i.e. against C. albicans and A. fumigatus. In vitro combination of curcumin-coated silver nanoparticles resulted in synergistic and indifferent interactions against Candida and Aspergillus species, respectively. TEM analysis revealed that the nanoparticle result in defects in cell wall and cell membrane of Candida.

Conclusion : Curcumin-coated silver nanoparticles, either alone or in combination with antifungal drugs, have good inhibitory effects on Candida species. Accordingly, further studies for their application against other fungi and even in murine models of infection would be beneficial.

Keywords : Curcumin, silver nanoparticle, drug resistance, drug combination

P80-491: Comparison of the expression of Enterococcus faecium antibiotic resistance-related genes in biofilm and planktonic conditions

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Background and Aim : Enterococcus faecium is a persistence bacterium which its pathogenesis is drastically affected by biofilm formation. Nosocomial infections caused by E. faecium have rapidly increased, and treatment options have become more limited. This is due not only to increasing resistance to antibiotics but also to biofilm-associated infections. This study evaluated biofilm formation in clinical and environmental isolates of multi drug resistance enterococcus faecium. In biofilm positive E. faecium isolates, the expression antibiotic resistance-related genes in planktonic and biofilm conditions were compared in vitro.

Methods : In this study, 690 Enterococcus isolates were studied. 229 isolates were Enterococcus faecium. After antibiotic susceptibility testing, 113 isolates were resistant to vancomycin. Biofilm formation was investigated in resistant Enterococcus faecium isolates. Six clinical and environmental isolates were selected. To determine the enterococcal antibiotic resistance-related genes expression, we used quantitative real-time PCR to compare mRNA levels in Enterococcus faecium cultures grown in planktonic and biofilm condition to that achieved in laboratory medium.

Results : Among 690 evaluated strains of Enterococci, among the six genes associated with biofilm formation, the expression of the pbp5 gene has the highest expression; Expression increased in five isolates and unchanged in only one isolate. Next, the vanA gene increased expression in the four isolates and unchanged in tow isolates. The lowest gene expression of the vanB gene increases the expression of only one isolate and unchanged in five isolates. The increase expression of 3 selected resistance genes (vanA, vanB and pbp5) were confirmed by real-time PCR.

Conclusion : The results of the antibiotic resistance and biofilm assay, suggest that there is a persistent and biofilm-producing strains of E. faecium, which could rapidly disseminate in

patients and the environment. Therefore, applications of precautionary and management procedures are highly required.

Keywords : Enterococcus faecium, biofilm, Gene expression, real-time PCR

P81-492: Prevalence of carbapenemase and blaKPC gene in Klebsiella pnumoniae strains isolated from Tabriz hospitals in Iran.

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Background and Aim : Background and Aim: Klebsiella pneumoniae is an opportunistic pathogen that is Gram-negative. For the efficient treatment of Klebsiella pneumonia infections, carbapenems are a good option. A class of enzymes called carbapenemases is able to hydrolyze carbapenems. In order to identify the isolates of Klebsiella pneumoniae that produce carbapenemase in Tabriz, Iran, this study introduced phenotypic and genotypic approaches.

Methods : Methods: 230 Klebsiella pneumoniae isolates from several Tabriz hospitals were the subject of this study. The Modified Hodge Test (MHT) was used to detect the isolates of Klebsiella pneumoniae that produce carbapenemase by evaluating the susceptibility of isolates to antibiotics. On an agarose gel, the PCR's final products underwent electrophoresis.

Results : Results: For piperacillin and ertapenem, the rates of resistance were observed to be 84% and 50%, respectively. While we did not find MHT positive isolates in cerebral fluids or abdominal cavities, 67% of MHT positive isolates came from urine. Furthermore, the emergency units had the fewest cases (7%) and the most (72%), respectively, of MHT positive isolates in intensive care units. In none of the isolates was the blaKPC gene discovered.

Conclusion : Conclusion: In Tabriz City, Iran, Klebsiella pneumoniae isolates have a relatively low prevalence of the blaKPC gene.

Keywords : Keywords: Klebsiella pneumoniae, Carbapenemase, PCR method

P82-499: Putative novel B-cell vaccine candidates identified by reverse vaccinology and genomics approaches to control Acinetobacter baumannii serotypes

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Background and Aim : In the last decade, Multi-drug resistance (MDR)-associated infections of Acinetobacter baumannii have grown worldwide. A cost-effective preventative strategy against this bacterium is vaccination.

Methods : This study has presented five novel vaccine candidates against A. baumannii produced using the reverse vaccinology method. BLASTn was done to identify the most conserved antigens. PSORTb 3.0.2 was run to predict the subcellular localization of the proteins. The initial screening and antigenicity evaluation were performed using Vaxign. The ccSOL omics was also employed to predict protein solubility. The cross-membrane localization of the protein was predicted using PRED-TMBB. B cell epitope prediction was made for immunogenicity using the IEDB and BepiPred-2.0 database. Eventually, BLASTp was done to verify the extent of similarity to the human proteome to exclude the possibility of autoimmunity.

Results : Proteins failing to comply with the set parameters were filtered at each step. In silico, potential vaccines against 21 A. baumannii strains were identified using reverse vaccinology and subtractive genomic techniques. Based on the above criteria, out of the initial 15 A. baumannii proteins selected for screening, nine exposed/secreted/membrane proteins, i.e., Pfsr, LptE, OmpH, CarO, CsuB, CdiB, MlaA, FhuE, and were the most promising candidates. Their solubility and antigenicity were also examined and found to be more than 0.45 and 0.6, respectively.

Conclusion : Based on the results, LptE was selected with the highest average antigenic score of 1.043 as the best protein, followed by FimF and Pfsr with scores of 1.022 and 1.014, respectively. In the end, five proteins were verified as promising candidates. Overall, the targets identified herein may be utilized in future strategies to control A. baumannii worldwide.

Keywords : Putative vaccine, Acinetobacter baumannii, In silico, Genomics approaches

P83-514: Prevalence of Methicillin Resistance Staphylococcus aureus (MRSA) isolated from Imam khomeini hospital, Tehran

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Background and Aim : Staphylococcus aureus (S. aureus) almost can cause widespread disease such as endocarditis, toxic shock syndrome, osteomyelitis, and superficial skin infection. Many invasion factor include toxin, modulator of immune response, and cell wall associated proteins can help S. aureus to persist in body. S. aureus can be categorized in two type based on resistance to the Methicillin, Methicillin-sensitive Staphylococcus aureus (MSSA) and Methicillin-resistance Staphylococcus aureus (MRSA).

Methods : 80 isolated were collected during Jun 2021 to June 2022. First, isolate investigated through biochemical test include catalase and after initial confirmation as Staphylococcus aureus differentiation of MRSA and MSSA done through presence of mec gene. In the next step antibiotic sensitivity investigated through Kirby-Bauer Method on the Muller-Hinton agar.

Results : among 80 isolates, 47 isolate were identifying as MRSA by presence of mec gene, and 33 isolate as MSSA (negative for mec). The highest level of antibiotics resistance was related to the Cefoxitin. Other antibiotic that investigated in this study include Cefotaxime and Oxacillin.

Conclusion : result of this study shown that the most of isolates are MRSA. This result concludes that the antibiotic resistance is in progress. Abusing of medication of course has a major role in this enhancement.

Keywords : MRSA, antibiotic resistance, mecA protein

P84-520: Molecular Characterization of Antibiotic Resistance Genes in Staphylococcus Isolated from Cell Phone Users' and Non- Users' Ears

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Background and Aim : Introduction: Resistance to macrolide can be created by erm genes in Staphylococcus. The aim of the current study was to determine whether or not cell phone use can result in the antibiotic resistance of 16S rDNA, Coa, ermA, ermB and ermC genes in Staphylococci isolated from cell phone users' and non- users' ears.

Methods : Methods: A total of 150 isolates of Staphylococci were tested by the disk diffusion method. The isolates were examined by PCR for 16S rDNA, Coa, ermA, ermB and ermC genes.

Results : Results: According to PCR results, in two statistical societies, 65.33% cell phone users with positive Coa had only one erm, 33.33% cell phone nonusers with negative Coa had only one erm and 1.34% had a minority of genes, whereas 24% cell phone non-users with positive Coa had only one erm , 44% cell phone non-users with negative Coa had only one erm and 32% had a minority of genes. Results showed that 16S rDNA , Coa , ermA, ermB, and ermC genes in the cell phone users group were more prevalent than the other group in Staphylococci isolated from ears.

Conclusion : Conclusion: It is revealed that the presence of 16S rDNA, Coa, and erms genes had a significant relation to erythromycin and methicillin. Detection of ermA, ermB and ermC plays crucial roles in the molecular mechanisms, epidemiology of the efflux pump and methylase erythromycin ribosome. Since antibiotic resistant Staphylococci isolates may mutate and prompt constitutive resistances it is suggested that inducible resistance test should be implemented on erythromycin resistant sensitive isolates to prevent treatment failures.

Keywords : Keywords: Cell Phone, Ear, erm Genes, Staphylococci

P85-529: Bacteriological etiology and antibiotic resistance patterns of bloodstream infections in a tertiary care hospital in the southwest of Iran

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Background and Aim : Since bloodstream infections have various etiologic factors and the importance of using proper antibiotics for these infections, identifying the causative agents and antibiotic resistance patterns of isolated bacteria is critical. The present study aimed to assess the prevalence and antibiotic resistance patterns of bacteria collected from the different wards of Imam Khomeini Hospital in Ahvaz, in the southwest of Iran

Methods : This cross-sectional study was conducted in different wards of Imam Khomeini Hospital from April 2016 to March 2017 on hospitalized patients with suspected bloodstream infections. Bacteriological identification and antimicrobial susceptibility testing were performed according to standard methods.

Results : During the study period, 5023 blood samples from clinically suspected cases of BSI were obtained. Of these, 264 bacterial isolates including 87 (33%) gram-positive and 177 (67 %) gram-negative isolates were recovered. The most common gram-positive bacteria isolates were Staphylococcus aureus 33 (12.5%) followed by Enterococcus spp 20 (7.5%), Streptococcus spp with an isolation rate of 13 (4.9%), and among gram-negative bacterial isolates, the most predominant isolates were Acinetobacter baumanii 46 (17.4%) followed by E. coli 40 (15.1%), Klebsiella pneumoniae 28 (10.6%), Pseudomonas aeruginosa 27 (10.2%), and Stenotrophomonas maltophilia 27 (10.2%).About 51.5% of Staphylococcus aureus isolates were methicillin–resistant. About 50% of Enterococcus spp isolates were resistant to vancomycin. All the isolates of Staphylococcus aureus, CoNS, Micrococcus spp, and Streptococcus spp were susceptible to vancomycin. The maximum non-fermenting gram-negative bacilli (GNFB) resistant rates were observed for Cefepime, Cefazolin, and Ceftriaxone. In the case of E. coli, the highest resistance rates were 100% and 85% for Ceftazidime and Cefazolin, respectively. 100% of Klebsiella pneumoniae and Enterobacter aerogenes were resistant to Tazobactam-piperacillin and Ceftazidime.

Conclusion : Our results highlight the value of identifying the etiologic factors responsible for bloodstream infections and their antimicrobial resistant patterns that may provide necessary information for effective antimicrobial stewardship programs in hospitals.

Keywords : Bloodstream Infections; Etiology; Iran; Antibiotic Resistance

P86-531: Relationship between antibiotic resistance and invasion of Shigella sonnei strains

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Background and Aim : Shigellosis is an important infectious disease that causes the death of many people every year, especially children under 5 years old. The disease in children can occur with mild to severe symptoms. Shigellosis manifests as diarrhea, abdominal pain and fever. Usually, the most common species of Shigella in developed countries is Shigella sonnei and in developing countries Shigella flexneri. Some multi-drug resistance (MDR) Shigella strains are highly invasive, so there is a big challenge in treating patients infected with these strains. Therefore, we decided to investigate the relationship between the invasion of Shigella sonnei strains and their antibiotic resistance.

Methods : In this study, we first selected 5 strains of Shigella sonnei that were previously obtained from the diarrhea of children with shigellosis. Then we investigate their antibiotic resistance using Kirby-Bauer disk diffusion method according to the Clinical and Laboratory Standards Institute (CLSI). The antimicrobial agents were as follows: ampicillin(AMP), azithromycin(AZM), ciprofloxacin(CIP), nalidixic acid(NA), Trimethoprimsulfamethoxazole(SXT), cefixime(CFM), cefotaxime(CTX), minocycline(MN), and levofloxacin(LEV). Finally, we performed the invasiveness of the strains using the plaque formation assay test in Hela cells.

Results : All five strains were MDR and all of them were able to form plaques in HeLa cells. Strain SS2 showed the most invasiveness with the formation of 202 plaques, but this strain was resistant to only three antibiotics. Strain SS3 had the highest resistance with resistance to 7 antibiotics, but with the formation of 18 plaques, it had a low invasion power. The antibiotic resistance profile and the number of plaques are as follows: SS1: CFM, CTX, NA, AMP, SXT / 96 SS2: NA, SXT, MN / 202 SS3: CFM, CTX, NA, AMP, SXT, MN, AZM / 18 SS4: NA, SXT, MN / 15 SS5: NA, SXT, MN / 13

Conclusion : No correlation was found between the invasion rate of Shigella sonnei strains and their antibiotic resistance profile.

Keywords : shigellosis, Shigella sonnei, plaque formation assay, antibiotic resistance

P87-542: Bacterial etiology and antibiotic resistance pattern of septic arthritis in 216 patients admitted to Imam Reza Hospital, Mashhad: a 6-year retrospective study

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Background and Aim : Septic arthritis is a medical emergency potentially associated with significant complications and disability, and as such requires prompt intervention including empiric antibiotic therapy guided by regionally validated etiologic and antimicrobial susceptibility data.

Methods : In this retrospective cross-sectional study, we reviewed the medical records of all patients admitted to Imam Reza Hospital, Mashhad with a diagnosis of septic arthritis from March 2011 to March 2016. This study evaluates demographic, clinical, and paraclinical data, including culture and antibiogram results, and additionally compares these between pediatric (<15 years old) and adult (≥15 years old) age groups.

Results : A total of 216 patients were included. Of these, 158 (73.1%) were 15 years of age or older, and 58 (26.9%) were under 15 (mean age 42.22±27.53). 135 (62.5%) were male and 81 (37.5%) were female. The knee was the most commonly affected joint in both age groups, followed by the hip. The knee was more commonly involved in adults than in children, and the hip more commonly involved in children than in adults ($p<0.001$). Additionally, positive blood culture results were higher in children than in adults ($p=0.044$). The most commonly isolated organism from joint fluid in both age groups was Staphylococcus aureus, which displayed the greatest rate of susceptibility to, in order, ceftriaxone, linezolid, gentamicin, and cefoxitin (100% of S. aureus isolates), followed by vancomycin (98% of isolates), clindamycin (91% of isolates), and erythromycin (86% of isolates). The highest rates of resistance were seen with penicillin (100% of S. aureus isolates) and imipenem (50% of isolates).

Conclusion : The organism most commonly responsible for septic arthritis in both children and adults was Staphylococcus aureus, with the highest rates of susceptibility to ceftriaxone, linezolid, gentamicin, and cefoxitin, and the highest rates of resistance to penicillin and imipenem. These results should be considered in the choice of empiric antibiotic therapy for septic arthritis before access to patient-specific culture and antibiogram results.

Keywords : septic arthritis, antibiotic resistance, children, adults

P88-543: effect of lactin-nisin-positive Lactococcus probiotic supernatant on Shigella flexneri biofilm.

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Background and Aim : Shigella causes bacillary dysentery, a severe form of dysentery that is more common in developing countries. The prevalence of shigellosis is also seen in industrialized countries, especially where it is difficult to maintain proper hygiene . Histopathological analysis of colon biopsies from patients with shigellosis shows destruction of the epithelium, mucosal erosion and typical signs of inflammation. edema and infiltration of polymorphonuclear cells into the lamina propria.

Methods : in this study, samples collected from Tehran Children's Medical Center Hospital were examined and studied. To carry out this research, 110 human samples from children's diarrheal stool samples were collected from Tehran Children's Medical Center Hospital and transferred to Kerry Blair transfer medium and then cultured on different mediums including XLD and Hecton enteric agar mediums. After incubation for 24 hours at 37°C, suspected Shigella colonies were isolated and then cultured in terms of reactions on TSI medium, lysine medium, citrate, MRVP, SIM and urea. Biochemical tests (ornithine decarboxylation reaction, ONPG test, andel production, fermentation of mannitol sugars, etc.) were used to differentiate the species.

Results : According to optical density cut off value (ODc) which was 0.138, Shigella flexneri bacteria isolated from 5 patients were non-adherent. 8 patients were weakly adherent, 14 were moderately adherent, and 10 were strongly adherent. For subsequent tests, bacteria isolated from 24 patients with moderate and strong binding were used. MIC test results According to the obtained results, the lowest lethality concentration of the supernatant on Shigella bacteria isolated from patients was reported as 40 µg/ml. According to the results obtained from this test, positive nisin supernatant has increased the diameter of the halo in Gentamicin, Chloramphenicol and Cefixime antibiotics and has changed the bacteria from resistance to these antibiotics.

Conclusion : Mirenjad et al. investigated the effect of lactobacillus supernatant on multi-drug resistant isolates of Shigella Sonnei and Sh. Flexneri reviewed. The results showed that L. casei strongly inhibited the development of pathogen samples. Also, the results showed that 4 out of 18 antibiograms showed complete resistance to pathogen samples through the disc diffusion method .

Keywords : lactococous lacticShigella flexneri biofilms

P89-545: Bacterial community of chronic rhinosinusitis patients and therapeutic ultrasound efficacy: clinical trial study

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Background and Aim : Bacterial involvement in chronic rhinosinusitis (CRS) condition made it difficult to treat using available antibiotic therapy. Therapeutic ultrasound was investigated here to evaluate bacterial diversity and quantity before and after continuous/pulsed ultrasound strategy compared to control patients.

Methods : Totally, 34 CRS patients were studied in three groups, including continuous ultrasound, pulsed ultrasound and control. Bacterial culture and identification were done before and after treatment. Computed tomography scan (CT scan) and questionnaire scores were recorded two times before and after intervention.

Results : The most prevalent bacterial isolates were non-hemolytic Streptococci (34 patients), coagulase-negative Staphylococcus (33 patients), Gram-negative cocci (26 patients), Staphylococcus aureus (19 patients), Streptococcus pneumoniae (five patients) and Streptococcus pyogenes (five patients). Both continuous and pulsed ultrasound could significantly reduce the quantity of bacterial isolates after treatment. CT scan and questionnaire results support the effectiveness of therapeutic ultrasound.

Conclusion : The quantity of clinically important bacteria was significantly reduced using ultrasound treatment and recovery of patients was supported by CT scan and questionnaire scores. Alternative therapeutic ultrasound could be an effective procedure in CRS patients.

Keywords : Rhinosinusitis; Ultrasound therapy; Bacterial infection; Treatment; Computed tomography scan

P90-552: Antimicrobial susceptibility patterns and molecular characterization of plasmid-mediated quinolone resistance determinants among Salmonella and Shigella spp. isolated from pediatric patients

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Background and Aim : Diarrhea remains a serious public health problem, which could be life- threatening in children. Different pathogens can cause acute diarrhea in children, where enteric bacteria, such as Salmonella and Shigella, are among the main responsible agents. Fluoroquinolones are the most common antibiotics prescribed to treat Shigella and Salmonella infections; however, increasing rate of resistance and its spread through plasmid-mediated quinolone resistance (PMQR) genes should be considered for medication in each country. To achieve this aim, the current study was conducted to determine the frequency of quinolone resistance plasmid genes in Shigella and Salmonella isolates of pediatric patients with acute diarrhea.

Methods : In this study, Shigella and Salmonella isolates from fresh stool samples of diarrhea patients were included from May 2017 to May 2018. All the isolates were characterized by conventional phenotypic and molecular methods. The antibiotic resistance profiles and the frequency of PMQR genes were determined by standard susceptibility and molecular test methods.

Results : The highest antibiotic resistance rate among Shigella and Salmonella isolates was related to trimethoprim-sulfamethoxazole (37/40; 92.5%) and cefoxitin (5/45; 11.1%), respectively. Although qnrS, qepA, and aac(6′)-Ib-cr genes were characterized in 32.5%, 2.5%, and 2.5% of the Shigella strains, qepA (17.7%) and qnrS (4.4%) were among the common PMQR determinants in the Salmonella isolates, respectively. The reduced

susceptibility to ciprofloxacin was detected among 25% and 22.2% of PMQR-harboring strains of Shigella and Salmonella, respectively.

Conclusion : Low rates of ciprofloxacin resistance and low frequency of MDR Salmonella and Shigella isolates were characterized in this study. Most of the isolates that carried PMQR determinants presented only low-level resistance and reduced susceptibility to ciprofloxacin

Keywords : Antibiotic resistance, Salmonella, Shigella, Pediatric, Plasmid-mediated quinolone resistance (PMQR)

P91-555: Antibiotic resistance assessment and multi-drug efflux pumps of Enterococcus faecium isolated from clinical specimens

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Background and Aim : Enterococcus faecium, common commensal bacteria, is a major cause of nosocomial infections and public health concerns. Reduced sensitivity to fluoroquinolones is partly due to efflux pumps. An ongoing challenge is to search for novel inhibitors to block these efflux pumps and restore antibiotic sensitivity. In this research, we seek to investigate the interaction of ciprofloxacin and an efflux pump inhibitor (EPI), thioridazine, on the inhibition of these efflux pumps.

Methods : In this study, a total of 88 isolates of E. faecium from clinical specimens were studied from August 2017 to September 2018. All the isolates were characterized by conventional phenotypic and molecular methods. The antibiotic resistance profiles and the frequency of efflux pump genes were determined by standard susceptibility and molecular test methods. Minimum inhibitory concentrations (MICs) to ciprofloxacin (CIP) with and without thioridazine were measured by micro-broth dilution.

Results : The highest antibiotic resistance rate was related to ciprofloxacin, levofloxacin, and imipenem 96.8%, 94.3%, and 90.9% respectively. The highest frequency of efflux pump determinants, efmA was 60(68%), followed by emeA, and efrA and/or efrB genes 48(54.5%) and 45(51%) respectively. This study showed that 41(48.2%) of the isolates became less resistant to at least 2-fold or greater decrease in MIC change in the presence of an efflux pump inhibitor.

Conclusion : Our results showed that thioridazine as an efflux inhibitor can enhance the effect of CIP as an efficient antibiotic and suggested that efrAB, efmA, and emeA efflux pumps can play a role in fluoroquinolone resistance.

Keywords : Enterococcus faecium, Efflux pumps, Antibiotic resistance, Thioridazine

P92-557: In vitro formulation of Solenanthus circinnatus leaves methanolic extract and its antibacterial and antifungal inhibitory activities.

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Background and Aim : There is a global emergence of multiple drug-resistant (MDR) microorganisms because of the overuse of antibiotics. The emergence of these bacteria reduces the effectiveness of current antibiotic therapy, causing thousands of deaths. As a result, new alternative antimicrobials are urgently required to address the issue of MDR microorganisms. In this study, the antibacterial activity of methanolic extract of Solenanthus circinnatus (S. circinatus) leaves was investigated against four microorganisms, Escherichia coli (ATCC 25922), Staphylococcus aureus (ATCC 25923), Pseudomonas aeruginosa (ATCC 9027) and Candida Albicans, using the broth micro-dilution test.

Methods : The freshly collected leaves of S. circinatus were minced and exhaustively extracted (100 g) with 200 milliliters of 80% methanol for 72 hours using the percolation method. The extract was filtered and the solvent was evaporated to dryness at 50°C under reduced pressure. The dried extract was further concentrated in a speed vacuum.

Results : The result was that the extract had moderate inhibitory activity against Escherichia coli and Candida Albicans, but no inhibitory activity in other species at 50 mg/mL.

Conclusion : In conclusion, methanolic extract from S. circinatus leaves would be of interest in controlling infections with Escherichia coli and Candida Albicans.

Keywords : Antibiotics, Inhibitory Activity, Multiple Drugs Resistant, Solenanthus circinnatus

P93-571: Molecular detection of some vancomycin resistance genes of Staphylococcus aureus strains isolated from clinical samples in Thi-Qar province / South of Iraq

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Background and Aim : Glycopeptides such as vancomycin are frequently choice antibiotics for the treatment of infections caused by methicillin resistant Staphylococcus aureus (MRSA). For the last years incidence of vancomycin intermediate S. aureus (VISA) and vancomycin resistant S. aureus (VRSA) has been increasing in various parts of the world. The present study was carried out to find the presence of VISA and VRSA in Thi-Qar province-south of Iraq.

Methods : A total 315 staphylococcal isolates consisting of 130 S. aureus and 185 coagulase negative staphylococci (CoNS) were isolated from different clinical specimens from various hospitals including AL Hussein teaching hospital, AL Haboubi teaching hospital, AL Musawi hospital for children, and Burn center. All S. aureus isolates were subjected to MIC testing (against vancomycin) on Brain Heart Infusion (BHI) vancomycin screen agar test. Disc diffusion testing for Ampcillin (10 ug), Oxacillin (10 ug), Gentamicin (10 ug), Amikacin (30 ug) Vancomycin (30 ug), and cefoxitin (30 ug) was performed. The presence of mecA, vanA, vanB, vanC, vanD, and 16s rRNA genes was evaluated by PCR.

Results : Out of 130 S. aureus, 7 strains were found to be vancomycin resistant. Seven strains had growth on BHI vancomycin screen agar (vancomycin 6 ug/ml). All isolates were positive for mecA gene. vanA, vanB, and vanC were detected in 3, 2, and 2 isolates, respectively. vanD gene was not detected.

Conclusion : Conclusion: The present study for the first time reveals the emergence of VRSA from this part of south Iraq and indicates the magnitude of antibiotic resistance in and around the study area. The major cause of this may be unawareness and indiscriminate use of broad-spectrum antibiotics.

Keywords : vancomycin; vancomycin resistant Staphylococcus aureus ; vanA; vanB; vanC

P94-578: Prevalence of pelA , pslA, QacE and QacEΔ1 genes and their correlation with antimicrobial resistance in Pseudomonas aeruginosa in Shiraz

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Background and Aim : Pseudomonas aeruginosa is gram negative, motile and aerobic bacteria that pauses as a major cause of nosocomial infections and infections in immunosuppressed and burn patients worldwide. In this study, we aimed to determine the presence and prevalence of pelA , pslA , QacE and QacEΔ1 genes and the MIC for Chlorhexidine in Pseudomonas aeruginosa isolates obtained from clinical samples from Shahid Faghihi and Namazi Hospitals in Shiraz.

Methods : In this study, 120 Pseudomonas aeruginosa isolates were collected from inpatients samples (urine, blood, trachea, wound, and body fluids) from October 2020 to July 2021. After confirming the isolates, their antibiotic resistance was checked by disc diffusion method. Then the minimum inhibitory concentration (MIC) was determined for chlorhexidine. DNA was then extracted by boiling. Finally, prevalence of pelA , pslA , QacE and QacEΔ1 genes determined by PCR¬.

Results : Out of the 120 studied isolates, 66 were positive for pelA or pslA genes and 55 (54.2%) had QacE and QacEΔ1. The average MIC (n=120) for Chlorhexidine was 0.223% (2.23mg/mL) while the MIC for pelA/pslA positive isolates was 0.3466% (3.466mg/mL) and the MIC for pelA/pslA negative isolates was 0.0712% (0.712mg/mL). Cephalosporins showed the lowest overall efficacy with ceftazidime having a sensitivity of only 17.5%. Amikacin was the only tested antibiotic to show a more than 70% effectiveness, with a total sensitivity of 73.33% followed by ofloxacin with a total sensitivity of 67.5%. In addition, the sensitivity of all the tested antibiotics except for Amikacin showed a meaningful correlation with the presence of pelA/pslA genes (p-value <0.05) which further implies the role of biofilm formation in antibiotics resistance. Furthermore, 31.8% of pelA/pslA positive samples were identified as MDR in comparison to 7.41% among pelA/pslA negative ones with an average of 26.8%.

Conclusion : The nearly 5-fold increase in the MIC for chlorhexidine alongside the significantly higher prevalence of MDR strains and antibiotics resistances in pelA/pslA positive samples furthermore implies the critical role of these genes in biofilm formation and antimicrobial resistance.

Keywords : pelA gene, pslA , QacE , QacEΔ1 gene, Chlorhexidine, Pseudomonas aeruginosa

P95-589: Gastrointestinal infections in hospitalized patients before and during the covid-19 pandemic (2019-2022)

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Background and Aim : In recent years, the covid-19 pandemic as an outbreak of respiratory transmitted disease with severe acute respiratory syndrome has affected various aspects of human life. In many countries, the management of the covid infections is a priority, and many other infectious diseases may have problems in accessing the usual medical services. On the other hand, improving the health level of society during the period of Covid-19 can also be effective in reducing gastrointestinal infections. The aim of the present study is to investigate the prevalence of gastrointestinal infections and the pattern of antibiotic resistance in patients referred to Ganjavian teaching hospital during the 4-year period (2019-2022) in Dezful.

Methods : In this study, all of stool specimens were cultured on Gram negative broth, Hektoen enteric and MacConkey agar. Isolates were distinguished by biochemical tests (TSI, Citrate, SIM, Urea agar and MRVP and Phenylalanine deaminase). The bacterial diagnostic was confirmed by serological tests (Shigella, Salmonella, Enteropathogenic Escherichia coli). Then antimicrobial susceptibility were tested according to CLSI guideline for Ampicillin(10 µg), Ciprofloxacin(5 µg), Nalidixic acid(30 µg), Trimethoprim-sulfamethoxazole(1.25/23.75µg) disks.

Results : There were 151 pathogenic bacteria from 60% male and 40% female patients, 83.5% of patients were children (6 months to 12 years). The prevalence of gastrointestinal bacterial infections were 48(29.4%), 34(20.9%), 22(13.5%), and 59(36.2%), during 1397 to 1400 years, respectively. The bacteria included 133(88.1%) Shigella, 7(4.6%) Salmonella and 11(7.3%) Enteropathogenic Escherichia coli strains. The most Shigella strains were 63 S.sonnei, 61 S.flexneri, and 9 S.dysentery. The coexistence of Shigellosis and intestinal protozoans, such as Giardia lamblia, Entamoeba histolytica and Blastocystis hominis was observed in 21(13.9%) samples. The antimicrobial patterns of Shigella isolates showed that 87.4% were resistant to Trimethoprim-sulfamethoxazole, 85.7% to Ampicillin, 61% to Nalidixic acid, and 10.1% to Ciprofloxacin.

Conclusion : Our study showed that Shigella infection was the most common among the gastrointestinal infections studied during 4 years. Although in 2019, the number of patients with gastrointestinal infections in patients hospitalized in our hospital decreased, but the

frequency of antibiotic resistance during these years before and during the covid-19 pandemic did not show any significant change.

Keywords : Gastroenteritis, Antibiotic resistance, Covid 19, Shigella, EPEC, Salmonella

P96-593: Antibacterial effects of drug delivery system of mesoporous silica nanoparticles loaded with rifampin drug on Streptococcus pneumoniae and Pseudomonas aeruginosa

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Background and Aim : Bacterial resistance to many available antibiotics is a serious issue in modern medicine. Streptococcus pneumoniae is a gram-positive, alpha-hemolytic, and oxidase-negative diplococcus and is the main cause of pneumonia that causes other infections such as sinusitis, meningitis, and brain abscesses. Pseudomonas aeruginosa is a gram-negative bacillus, which is an opportunistic hospital pathogen, and due to its high resistance to common antibiotics, mortality from its infections is very common. Since the review of the literature shows that the use of nanoparticles is a way to overcome antibiotic resistance, Therefore, the aim of this study was to investigate the effects of the drug delivery system containing the antibiotic rifampin, which is a bactericidal antibiotic and is used for a variety of bacterial infections, on Streptococcus pneumoniae and Pseudomonas aeruginosa.

Methods : Mesoporous silica nanoparticles (MSN) were synthesized using CTAB and TEOS, and using APTS linker, the amine group was placed on the surface of the nanosphere, and the drug rifampin was loaded in these particles. After checking the properties of the system using DLS, BET, TEM, SEM and checking the amount of drug loading and release, the well diffusion was performed on Streptococcus pneumoniae and Pseudomonas aeruginosa bacteria strains.

Results : The results of DLS, TEM and SEM showed particles with a size of 50 nm and the BET porosity of these particles was 3.4 nm. The loading rate of nanoparticles was 12% and the release of rifampin from nanoparticles was found to be influenced by acidic pH. In the evaluation of the antibacterial test using the well diffusion method on Streptococcus pneumoniae and Pseudomonas aeruginosa respectively, free rifampin and nanoparticles loaded with rifampin were used and the results showed the diameter of the lack of growth from 9 to 13 mm and from 5 to 7 mm, respectively.

Conclusion : MSN loaded with rifampin is able to perform its release in acidic pH and is effective in the treatment of bacterial infections caused by Streptococcus pneumoniae and Pseudomonas aeruginosa.

Keywords : Mesoporous silica nanoparticles, rifampin, drug delivery system, Streptococcus pneumoniae, Pseudomonas aeruginosa

P97-594: The application of the loop-mediated isothermal amplification method for rapid detection of methicillin-resistant Staphylococcus aureus

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Background and Aim : Methicillin-resistant Staphylococcus aureus (MRSA) is an important problem associated with significant mortality and morbidity and is well known as a predominant bacterial pathogen. The aim of this study was to identify MRSA strains. In this study (June 2018 to June 2019) isolates of S. aureus were obtained from patients referred to teaching hospitals of Ahvaz, Iran.

Methods : All isolates were confirmed by conventional microbiological methods. In the following, antimicrobial susceptibility testing (AST), MRSA screening, PCR detection of MRSA, and LAMP assay were performed.

Results : Out of a total of 156 staphylococcal isolates, 126 isolates were identified as MRSA. Seventy-two (57.1%) MRSA isolates were recovered from the wound. All MRSA isolates were sensitive to vancomycin, linezolid, teicoplanin, quinupristin-dalfopristin, and tigecycline. The results of LAMP showed 100% agreement with PCR. The sensitivity and specificity of the LAMP assays for the mecA genes were 100% and 100%, respectively.

Conclusion : The LAMP assay is a rapid and simple method for the identification of MRSA. Because of its performance without the need for specific instrumentation, this method can be easily employed in medical centers for the detection of mecA.

Keywords : LAMP, mecA gene, MRSA, PCR, Rapid detection

P98-603: Investigation of frequency and pattern of antibiotic resistance of Klebsiella oxytoca producing metallobetalactamas

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Background and Aim : Klebsiella oxytoca is a gram-negative intestinal bacterium and a member of the Enterobacteriaceae family, which about one-third of people are intestinal carriers of this microbe. Beta-lactam antibiotics are used to treat Klebsiella infection. In recent years, the resistance of Klebsiella to beta-lactams has increased significantly. The aim of this research is to investigate the frequency and pattern of antibiotic resistance of Klebsiella oxytoca clinical isolates producing metallobetalactamas

Methods : In this study, the collected laboratory samples were cultured in blood agar and Mueller Hinton media, and the frequency of Klebsiella positive culture with differential and biochemical tests and the antibiotic sensitivity of the isolates with imipenem and imipenem + antibiotics. EDTA was investigated. DNA extraction was done using boiling method and genes were identified with specific primers using PCR technique.

Results : Out of a total of 100 Klebsiella pneumoniae isolates investigated, 38 isolates producing metallobetalactamases were identified. These numbers were examined for the presence of IMP and VIM genes producing metallobetalactamases. Of these, 17 isolates had the IMP gene and 12 isolates had the VIM gene

Conclusion : The prevalence of MBL gene enzyme and antibiotic resistance is high in the hospital, and it is necessary to take measures such as antibiotic susceptibility testing, rational prescription of antibiotics, and control of contributing factors.

Keywords : Klebsiella oxytoca, IMP and VIM genes, antibiotic resistance

P99-607: Molecular detection of class I integron and its gene cassette to antibiotics in Klebsiella pneumoniae strains.

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Background and Aim : Integrons are one of the mobile genetic elements that can carry resistance genes to different antibiotics. Meanwhile, the role of class I integron is important in creating and transmitting antibiotic resistance. The purpose of this study is to isolate Escherichia coli strains, molecular investigation of class I integron and gene cassettes and determine antibiotic resistance and sensitivity.

Methods : This study was conducted on 100 samples of Klebsiella pneumoniae isolated from Khorramabad hospitals. After sampling and culture on specific media and DNA extraction, the presence of class I integron gene and aadB cassette was done by PCR method. Antibiotic sensitivity and resistance test was also done by disk diffusion method

Results : After examining 100 strains, 60 samples were resistant to all antibiotics and 78 samples had multiple antibiotic resistance. The highest resistance was related to ticarcillin and cefepime antibiotics, the lowest resistance was related to gentamicin and amikacin antibiotics. Out of 100 samples of Klebsiella pneumoniae, 48 samples had int1 gene and also out of 34 positive integron samples, 23 samples had aadB cassette.

Conclusion : In this study, according to the significant statistics of the presence of class I integron and the gene cassette inserted in it in Klebsiella pneumoniae isolates and its relationship with the pattern of multiple drug resistance, it can be concluded that these elements can play an important role in the creation and transmission of antibiotic resistance. have a biotic

Keywords : Class I integron, antibiotic resistance, Klebsiella pneumoniae, gene cassette

P100-610: Inhibitory effect of pyocyanin pigment of Pseudomonas aeruginosa on Candida albicans in vitro

Fatemeh Nazarihaghighipashaki[1] *

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Background and Aim : Background and Aim: Candida albicans as an opportunistic pathogen can cause a wide range of skin and mucosal infections. Antibiotic treatments for this fungus have several side effects that cause drug resistance. In this study, the inhibitory effect of pyocyanin pigment extracted from Pseudomonas aeruginosa on the growth of Candida albicans was investigated. Methods: In this experimental study, pyocyanin peptide was extracted from Pseudomonas and its effect on Candida albicans by minimum inhibitory concentration and minimum fungicidal concentration to evaluate the antifungal effects of this substance on Candida albicans in the laboratory. it placed. Results: By studying different concentrations of pyocyanin pigment, it was shown that Candida albicans did not grow at concentrations of 5000-10000-20000-40000 and in the wells after these concentrations, growth of Candida strain was observed. Conclusion: Based on the results of this study, a certain concentration of pyocyanin can have an inhibitory effect on the growth of Candida albicans and prevent its growth; Therefore, further experiments are needed to investigate the composition of this substance and its wider use in therapeutic cases.

Methods : Methods: In this experimental study, pyocyanin peptide was extracted from Pseudomonas and its effect on Candida albicans by disk diffusion method, minimum inhibitory concentration and minimum fungicidal concentration to evaluate the antifungal effects of this substance on Candida albicans in the laboratory.

Results : Results: By studying different concentrations of pyocyanin pigment, it was shown that Candida albicans did not grow at concentrations of 5000-10000-20000-40000 and in the wells after these concentrations, growth of Candida strain was observed.

Conclusion : Conclusion: Based on the results of this study, a certain concentration of pyocyanin can have an inhibitory effect on the growth of Candida albicans and prevent its growth; Therefore, further experiments are needed to investigate the composition of this substance and its wider use in therapeutic cases.

Keywords : Keywords: Pyocyanin, Pseudomonas aeruginosa, Candida albicans

P101-615: Activity of Copper and Silver oxide NPs in forming a inhibition zone in Streptococcus salivarius and Lactobacillus rhamnosus

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Background and Aim : Human societies are still in difficulty encounter with human pathogens, despite advances in personal health and control of various diseases. One of these problems is tooth decay, which causes annoyingly high mortality and financial losses in human societies. In recent years, nanotechnology has been able to make profound developments in the research and production of various products. Therefore, in this study antibacterial effects of Copper (Cu) nanoparticles and silver oxide (AgO) are investigated through various microbial tests (discs, wells and cylinders diffusion Method) on two microorganisms of Streptococcus salivarius and Lactobacillus rhamnosus, which act as primary colonizers in the formation of dental plaque.

Methods : In the well diffusion Method, The bacterial suspension was prepared equaled 0.5 McFarland. Wells were created and 20 µl of various concentrations (500, 2500, 5000, 12500, 25000 ppm) of nanoparticles suspension were poured separately in them. In the disk diffusion method, was performed like Well diffusion, except that the disk was placed instead of creation the wells. In the cylinder diffusion method, was performed like Well diffusion, except that using sterile pins placed sterile cylinders on the plate, instead of creation the wells, and 100 µl of various concentrations (50, 250, 500, 1250, 2500 ppm) of nanoparticles suspension were poured separately on them. Sterile physiological saline was used for negative control. Incubated plates at 37 °C for 24 h. Formation or non-formation of inhibition zone studied under light and reported.

Results : Cu nanoparticles exhibited a more lethal effect than AgO nanoparticles in all three tests performed in solid media (discs, wells and cylinders). In these tests, the inhibition zone of Lactobacillus rhamnosus was larger than the Streptococcus salivarius. It was also found that by increasing the concentration of nanoparticles, their fatal rate increased significantly.

Conclusion : Based on the data obtained in this test, copper nanoparticles were detected more fatal and antibacterial than silver nanoparticles and Lactobacillus rhamnosus was more sensitive than Streptococcus salivarius. It was also found that by increasing the concentration of nanoparticles, their fatal rate increased significantly. According to other studies carried out in this area, which all prove antibacterial properties of these nanoparticles at low

concentrations, these nanoparticles can be used as antibacterial agents in combination with mouthwashes and toothpastes in the market.

Keywords : Copper, Silver oxide, Streptococcus salivarius, Lactobacillus rhamnosus, Nanoparticle

P102-616: Study of growth inhibition of Streptococcus salivarius and Lactobacillus rhamnosus by Copper and Silver oxide Nanoparticles

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Background and Aim : Human societies are still in difficulty encounter human pathogens, despite advances in personal health and control of various diseases. One of these problems is tooth decay, which causes annoyingly high mortality and financial losses in human societies. In recent years, nanotechnology has been able to make profound developments in the research and production of various products. Therefore, in this study antibacterial effects of Silver oxide (AgO) nanoparticles and Copper (Cu) are investigated through various microbial tests on two microorganisms of Streptococcus salivarius and Lactobacillus rhamnosus, which act as primary colonizers in the formation of dental plaque.

Methods : Streptococcus salivarius ATCC 10556, was purchased from the Biotechnology Cell Bank of Pasteur Institute of Iran and Actinomyces viscosus PTCC 1202 from the collection center of Iranian industrial microorganisms. Copper NPs with 40 nm and 20 nm Silver oxide NPs provided from US Research Nanomaterials. Following incubation of bacteria and different concentrations of nanoparticles including 10, 25, 50, 100 and 200 ppm, optical density of cultures were monitored for five hours every half hour. At 30, 60 and 120 minutes after incubation, colony forming unites of culture was determined.

Results : Based on the results, it is observed that Cu NPs inhibit normal growth of the bacteria in liquid culture. Inhibition power of Cu NPs was more than AgO NPs. Also, studying on CFU in liquid test indicated that samples those treated by NPs, in comparison with control culture, displayed the significant reduction in the number of bacteria.

Conclusion : Based on the data obtained in this test, Copper nanoparticles were detected more fatal and antibacterial than silver oxide nanoparticles and Lactobacillus rhamnosus was more sensitive than Streptococcus salivarius. It was also found that by increasing the concentration of nanoparticles, their fatal rate increased significantly. According to other studies carried out in this area, which all prove antibacterial properties of these nanoparticles at low concentrations, these nanoparticles can be used as antibacterial agents in combination with mouthwashes and toothpastes in the market.

Keywords : Copper, Silver oxide, Streptococcus salivarius, Lactobacillus rhamnosus, Nanoparticle.

P103-617: Determination of Minimum Inhibitory Concentration (MIC) and Minimum bactericidal Concentration (MBC) of Copper (Cu) and Silver oxide (AgO) Nanoparticles against Streptococcus salivarius

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Background and Aim : Human societies are still in difficulty encounter with human pathogens, despite advances in personal health and control of various diseases. One of these problems is tooth decay, which causes annoyingly high mortality and financial losses in human societies. In recent years, nanotechnology has been able to make profound developments in the research and production of various products. Therefore, in this study antibacterial effects of Silver oxide (AgO) and Copper (Cu) nanoparticles are investigated through various microbial tests on Streptococcus salivarius, which act as primary colonizers in the formation of dental plaque.

Methods : In each tube 1 ml bacterial suspension and 1 ml Cu and AgO nanoparticles suspension added relatively. In this case, the final volume in each well was equal to 2 ml and the final concentration of the bacterium was equal to 5 ×105. Incubated at 37 °C for 18 h. To determine the minimum bactericidal concentration (MBC), 100 µl of the tubes were taken and streaked on plates with a Muller Hinton Agar. Then they examined for bacterial growth and colony formation. For the study of Effect of nanoparticles in 24-hour culture, is done in the same way as above. Recap the tubes and incubated at 37 °C for 24 h. Result observed spectrophotometer at 600 nm wavelength.

Results : The minimum inhibitory concentration (MIC) of Copper nanoparticles for Streptococcus salivarius was 312.5 ppm, and the Minimum bactericidal concentration (MBC) was obtained 625 ppm, though for the Silver oxide nanoparticle, the MIC was 625 ppm and MBC was 1250 ppm. The growth of bacteria in the presence of nanoparticles has declined after 24-hour incubation.

Conclusion : Based on the data obtained in this test, Copper nanoparticles were detected more fatal and antibacterial than Silver oxide nanoparticles. It was also found that by increasing the concentration of nanoparticles, their fatal rate increased significantly. According to other studies carried out in this area, which all prove antibacterial properties of these nanoparticles at low concentrations, these nanoparticles can be used as antibacterial agents in combination with mouthwashes and toothpastes in the market.

Keywords : Copper, Silver oxide, Streptococcus salivarius, Nanoparticle.

P104-633: HIV-1 glycoprotein 41 molecular docking analysis and transmitted drug resistance mutations among antiretroviral therapy-naïve individuals in Iranian patients

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Background and Aim : HIV gp41 protein plays a critical role in membrane fusion, which helps HIV to infect the host cells. Three inhibitors (T20, VIR-576 and C34) were introduced recently to target this protein. However, mutations in this region might reduce their efficacy. This study, as the first report of Iran, aimed to investigate gp41 mutations amongst Iranian patients to define the possible efficiency of gp41 inhibitors in the treatment of the patient.

Methods : 30 patients' RNA sera was extracted and then amplified the gp41 region using Nested PCR. The sequences were analyzed to define mutations, physicochemical properties, post-modification positions, structural analysis, and subtyping via Bioinformatics tools and finally, the possible docking interaction of fusion inhibitors and gp41 proteins were examined.

Results : As the first report of Iran, several mutations were found in comparison with the two selected references that docking analysis showed such substitution in the interaction site of fusion inhibitors and gp41 proteins cannot reduce the fusion inhibitors efficacy. The most prevalent subtype amongst the samples was A1, and several post-modification positions including glycosylation and phosphorylation sites were identified.

Conclusion : Our findings showed that despite numerous mutations in enrolled samples, gp41 inhibitors, could still be effective in inhibiting HIV infections in Iranian patients. Additionally, the present study introduced a new gp41 region (36-44 aa) which has considerable influence in the interactions between gp41 inhibitors and gp41 protein. Moreover, subtyping results demonstrate that HIV-Pol gene is more specific region of subtyping among Iranian patients than gp41 gene.

Keywords : HIV, gp41, Drug resistance, Docking, Fusion inhibitors, Iran.

P105-634: Computational Protein–Ligand Docking to Evaluate Susceptibility to HIV Gag Inhibitors in HIV-Infected Iranian Patients

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Background and Aim : HIV Gag protein plays a critical role in virus assembly and maturation, which helps HIV to establish a productive infection. Twelve inhibitors were introduced recently to target this protein. However, mutations in this region might reduce their efficacy. This study, as the first report of Iran, aimed to investigate Gag mutations amongst Iranian patients to define the possible efficiency of Gag inhibitors in the treatment of the patient.

Methods : 40 patients' RNA sera was extracted and then amplified the Gag region using Nested PCR. The sequences were analyzed to define mutations, physicochemical properties, post-modification positions, structural analysis, and subtyping via Bioinformatics tools and finally, the possible docking interaction of Gag inhibitors and Gag proteins were examined.

Results : As the first report of Iran, several mutations were found in comparison with the two selected references that docking analysis showed such substitution in the interaction site of fusion inhibitors and Gag proteins cannot reduce the Gag inhibitors efficacy. The most prevalent subtype amongst the samples was A1-D, and several post-modification positions including glycosylation and phosphorylation sites were identified.

Conclusion : Our findings showed that despite numerous mutations in enrolled samples, Gag inhibitors, could still be effective in inhibiting HIV infections in Iranian patients. Additionally, the present study introduced new several regions which have considerable influence on the interactions between Gag inhibitors and Gag protein.

Keywords : HIV, Gag inhibitors, Drug resistance, Gag, molecular docking

P106-656: Highly Synergistic Effects of Melittin with Vancomycin against Vancomycin Resistant Staphylococcus aureus

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Background and Aim : Multidrug resistance Staphylococcus aureus(MDR) strains are increasingly emerging as serious threat for public health. Moreover, the use of vancomycin as last resort antibiotic for the treatment of MDR infections is limited because of severe toxicity in high doses The antimicrobial activity of melittin is now confirmed against a wide variety of bacteria. However, the high toxicity is one of the limiting factors for the therapeutic application of Melittin. The combinational therapy is one of strategies used to reduce toxicity of drugs because decrease of dose of drug. In this study, the antibacterial effect of melittin peptide in combination with vancomycin was evaluated to control vancomycin resistant(VRSA) clinical isolates.

Methods : In this study, melittin was purified from Iranian honey bee venom by reversed-phase HPLC. Minimum inhibitory concentration (MIC), minimum bactericidal concentration (MBC) of antimicrobial agents were determined against VRSA isolates. The cytotoxicity of melittin on HUVEK cells and human red blood cells (RBCs) was evaluated at their synergistic concentrations.

Results : MIC and MBC values for melittin were equal to 16 and 32, respectively. Results also showed that the interaction of melittin with vancomycin was highly synergistic. Induced synergism led to a decrease in melittin and vancomycin concentrations by 32 and 16-folds, respectively. So that, only 0.25 ?g/mL melittin in combination with 0.125 ?g/mL vancomycin was sufficient to inhibit VRSA isolates growth. Based on Hemolytic and MTT assay results, Melittin did not show toxic effects at 0.25?g/ml as the synergistic concentration.

Conclusion : our findings indicated that melittin showed highly synergistic effects with vancomycin with reduced toxicity. Therefore, the combination of melittin and traditional antibiotics could be a promising strategy for the treatment of VRSA infections.

Keywords : Staphylococcus aureus, vancomycin-resistant, melittin peptide, synergism,

P107-657: In silico design and in vitro evaluation of anti-microbial activity of Melittin analogs

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Background and Aim : The antimicrobial activity of melittin (MLT) is now confirmed against a wide variety of Gram-negative and Gram-positive bacteria. However, low stability and nonspecific toxicity are the main limiting factors for the clinical applications of this natural membrane-active peptide. This study aimed to design and synthesize new analogs of MLT to increase stability, reduce toxicity, and retain their antimicrobial properties against bacterial pathogens.

Methods : Initially, peptide analogs were designed computationally through single mutations in the template peptide and evaluation of their physicochemical properties. The stability of the analogs was determined by Gromacs software, and the peptides with the highest scores in antimicrobial activity and stability were selected to synthesize and further evaluations. Minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) were determined against seven standard bacterial strains. A cell viability assay was used to determine the cellular toxicity of the analogs.

Results : Two peptide analogs, M1 and M2, with higher stability and antimicrobial activity were selected based on Cell PPD data. The M1 analog was created by replacing alanine with leucine at the 15th position, and the M2 analog was designed via substituting alanine with leucine and isoleucine with arginine at the 15th, and 17th positions, respectively. According to the Gromacs results, the M1 peptide stabilized at 50 ns, and the M2 peptide maintained its alpha-helix structure in 50-200 ns, indicating more stability of the M2 analog. RMSD and RMSF results showed no undesirable fluctuations during the 200ns MD simulation. The MIC and MBC values for the M1 peptide were calculated in a range of 8-128 ?g/ml, while the M2 peptide limited the bacterial growth at 32-128 ?g/mL and killed them at 64-256 ?g/ml. Both peptides indicated less toxicity than natural MLT, based on MTT assay results. Besides, the hemolytic activity of the M1 and M2 analogs at 16 ?g/mL concentration was 41% and 14.25%, respectively, indicating a notable decrease in the hemolytic properties of the designed analogs.

Conclusion : In this study, we developed two analogs of MLT with low toxicity, low hemolytic activity, and higher stability, along with retaining antimicrobial properties against gram-negative and positive bacteria compared to natural MLT.

Keywords : Melittin, MD simulation, antibacterial activity, toxicity, peptide

P108-669: Investigation of frequency and determination of drug sensitivity of Gram-positive bacteria causing septicemia in In hospitalized patients of HAJAR Hospital, Shahrekord , Chaharmahal and Bakhtiari Province , 1400 .

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Background and Aim : Blood infections are increasingly reported in the world , since Since they are important diseases, targeted antimicrobial treatment can reduce complications in patients with septicemia. In order to have a targeted treatment, it is necessary to accurately identify the bacteria and effective antibiotics for its treatment . Gram-positive bacteria are also one of the causes of this infection, research and investigation on these bacteria and identifying the most effective antibiotics for treatment and ,as a result, reducing mortality are very important. Therefore, the purpose of this study is to investigate the frequency and determine drug sensitivity of Gram-positive bacteria causing septicemia in hospitalized patients of HAJAR Hospital, Shahrekord , Chaharmahal and Bakhtiari Province in 1400 .

Methods : In this cross-sectional-retrospective study, all blood cultures referred to Hajar hospital laboratory from April to March 1400 were examined and studied . Blood cultures were cultured in standard Blood Agar and Chocolate Agar environments and bacterial growth was checked after 24 to 48 hours . Based on the type of bacteria grown, antibiotic sensitivity was evaluated on Mueller-Hinton's culture medium in the form of disk diffusion using commercial and standard disks. Finally, the findings were analyzed using descriptive statistics.

Results : The results of this study showed that out of 6376 blood cultures, 170 samples were positive (2.66%). Among them, 67 cases (39.41%) were infected with gram-positive bacteria. The antibiogram results showed the highest sensitivity to Linezolid (97.62%), rifampin (86.11%), amikacin (73.68%) and cefoxitin (73.08%), respectively. In this study, the most drug resistances were erythromycin (84.09%), ciprofloxacin (52.63%) and cefoxitin (25%).

Conclusion : Conclusion: According to the results, most gram positive bacteria were Staphylococcus species. By analyzing antibiotics, it can be said that ciprofloxacin can still be used for septicemia caused by gram positives.

Keywords : septicemia, gram positive bacteria, blood culture, drug sensitivity

P109-671: Investigation of the prevalence of macrolide resistance of Mycoplasma pneumoniae in children: a review article

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Background and Aim : Mycoplasma pneumoniae is a common pathogen in community acquired pneumonia (CAP) in childhood. This species affects the respiratory system. Macrolide resistance in Mycoplasma pneumoniae species is increasing in the world. Therefore, the aim of this study is to review the prevalence of macrolide resistance of Mycoplasma pneumoniae in children.

Methods : We searched MEDLINE via PubMed, Scopus, Science Direct, Web of Science (ISI), Google Scholar (as English databases); Magiran, Iran Medex, Iran Doc, and SID (as Persian databases) during 1996 to September 2021using the terms: Mycoplasma pneumoniae pneumonia (MPP), community acquired pneumonia (CAP), children, Macrolide resistance.

Results : Prevalence of MPP occurs worldwide in the age range of 3 to 7 years. Recent epidemics have occurred in Korea. Although MPP is a mild and self-limiting disease, it can develop into a severe and fulminant disease. The prevalence of macrolide-resistant MPP is rapidly increasing, and has recently reached 80–90%, particularly in Asian countries. Macrolide-resistant Mycoplasma pneumoniae (MRMP) has a point mutation in the V domain of 23S rRNA, and most of the mutations are detected at positions 2063 and 2064 of the sequence.

Conclusion : Myoplasma pneumoniae strains show a good response to treatment with macrolides. Excessive use of macrolides may contribute to these mutations. MRMP can lead to clinically refractory pneumonia, shows no clinical or radiological response to macrolides, and can develop into severe and complicated pneumonia in children. Tetracyclines or quinolones can be alternatives for the treatment of MRMP.

Keywords : Mycoplasma pneumoniae, Macrolides resistance, children

P110-675: In-vitro effect of carbapenem in combination to other antibiotics against Carbapenem-resistant Klebsiella pneumoniae

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Background and Aim : The aim of the current study was to investigate in-vitro antibacterial effect of meropenem, amikacin and colistin alone and the various combinations against carbapenem-resistant Klebsiella pneumoniae

Methods : Twenty Klebsiella pneumoniae isolates were collected from clinical specimens. The resistance to meropenem were detected by the disk diffusion and determination of minimum inhibitory concentration (MIC) of meropenem by the broth micro. Inhibitory effect of antimicrobial agents on biofilm, was studied by determining the minimum biofilm inhibitory concentration (MBIC). The synergetic effect of the antibiotics combinations was studied using the checkerboard assay and the fractional inhibitory concentration (FIC)

Results : The highest synergic effect between on planktonic form was found in amikacin/meropenem (17 of 20 isolates), and the lowest synergic interaction was observed in colistin/amikacin (2 of 20 isolates). Colistin/meropenem were shown synergic effect against 11 isolates. The highest synergic inhibitory effect against biofilm was detected in meropenem/colistin (14 of 20 isolates) followed by amikacin/meropenem (6 of 20 isolates) and meropenem/colistin (2 of 20 isolates)

Conclusion : The combination of meropenem, amikacin and colistin had indicated the different effects on biofilm form and planktonic form of Klebsiella pneumoniae. Thus, a distinct testing of inhibitory effects of the antimicrobial drugs in the combination is essential for biofilm forms. Amikacin/meropenem and was more effective against planktonic and meropenem/colistin against biofilm forms of Klebsiella pneumoniae

Keywords : Meropenem resistance, Biofilm, Klebsiella pneumoniae, combination therapy

P111-676: Carbapenems resistant Enterobacteriaceae isolated from surgical site infections (SSIs) from Tabriz, Iran

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Background and Aim : The antibiotic susceptibility pattern and carbapenem resistance mechanisms of Enterobacteriaceae isolates from surgical site infections (SSIs) were investigated

Methods : Fifty-two carbapenem resistance Enterobacteriaceae isolated was isolated from SSIs. The disk diffusion and agar dilution methods were applied for determine the antibiotics susceptibility patterns. AmpC and efflux pump overexpression and carbapenemase mediated resistance were detected by phenotypic methods. The genes carbapenemase encoding genes were detected by the PCR

Results : According to the minimum inhibitory concentration (MIC) and disk diffusion, a high level of resistance were observed to most class of drugs except colistin and amikacin. No efflux pump overexpression was observed in resistance to carbapenems. Among 52 carbapenem resistant isolates, Klebsiella pneumoniae was most common (41/52; 78.84%%) followed by Escherichia coli (8/52: 15.38%), and Enterobacter spp (2/52; 3.84%). AmpC overproduction was found in Enterobacter spp. According to the phenotypic test and PCR results, the resistance to carbapenem in E. coli and K. pneumoniae was observed to be associated with carbapenems production. The most common carbapenemase gene was blaOXA-48-like (53.8%) followed by blaKPC (32.6 %) blaNDM (11. 53 %), and blaVIM (1.2%)

Conclusion : According to our results the incidence of carbapenems resistant Enterobacteriaceae is at a worrying level. The most frequent mechanism of carbapenems resistance was carbapenemase. We suggest reevaluation in the controlling program of SSIs caused Enterobacteriaceae in our health care centers

Keywords : SSIs, Carbapenem, Resistance, Enterobacteriaceae

P112-684: Nanoencapsulation of Phytosterols extracted from Pistacia terebinthus and evaluation of their antibiotic and release abilities

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Background and Aim : Plant sterols are LDL cholesterol-lowering supplements, but they have low dispersion and lack proper stability in biological conditions. One of the ways to solve this problem is to encapsulate them with other substances such as lipids.

Methods : In this study, plant phytosterols extracted from Pistacia terebinthus seed oil and squalene were nanoencapsulated by the lipids, starch, and cellulose under the coacervation technique without adding synthetic polymer surfactants in order to increase dispersion and stability. The properties of these products were identified by FTIR, UV-Vis, SEM, DLS, and GC analysis. The effective variables in this process to optimize the particle size and lipid nanoparticle loading were prioritized by Box-Benken analysis.

Results : According to the results, the particle size was 50 nm and the phytosterol loading was around 80 with high positive zeta potential. Antimicrobial activity and drug release of nanocapsules were also evaluated. Aureus, L. acidophilus, and L. casei showed inhibition in the presence of extracted nanocapsulated phytosterols compared to initial concentrations.

Conclusion : It was also found that nanoencapsulated phytosterols have stability and release control and can be used as a good nanocarrier in drug delivery.

Keywords : Phytosterols, Caffeine, Nanoencapsulation

P113-691: Distribution assessment of Extended-spectrum beta-lactamases (ESBL) producing clinical isolates of shigella

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Background and Aim : Shigella is knows as a major cause of diarrhea and around 70% of all its infections occur in children under the age of 5 years. One of the most concerning aspects of antibiotic resistance is the emergence and widespread distribution of resistance to β-lactam class drugs which is induced by the enzyme β-lactamase. Analyzing the distribution of β-lactamase is essential in optimal antibiotic administration and infection control. The current study evaluates the distribution Extended-spectrum beta-lactamases (ESBL) producing clinical isolates of shigella in a single health center in Tehran, Iran.

Methods : Fifty isolates were identified as shigella using the standard biochemical tests. The production of ESBL was assessed based on the CLSI guideline using ceftazidime and cefotaxime antibiotic discs. In this method, the inhibition zone is evaluated once for the individual antibiotics and once accompanied with clavulanic acid and a 5≤ increase in inhibition zone diameter in the presence of clavulanic acid was considered as proof of ESBL production.

Results : Based on the test results, 50 percent (25/50 isolates) were confirmed to be ESBL producing strains.

Conclusion : The emergence of ESBL enzymes in shigella strains and isolates can be considered as a global health risk for both developed and developing countries. As β-lactam class drugs are one of the most used antibiotics in Iran, information about the distribution of ESBL strains is vital in effective infection treatment and control.

Keywords : Shigella, Extended-spectrum beta-lactamases, Antibiotic resistance, beta-lactamase

P114-693: A detection kit based on the inhibition of microbial growth for evaluating antibiotic residues in animal products

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Background and Aim : Antibiotic residues in food can harm consumers by developing antibiotic resistance and the food industry by inhibiting the fermentation process. Therefore, identifying the overuse of antibiotics in meat, chicken, eggs, honey, milk, and other animal products used in the fermentation industry is a critical public health and supply chain quality control issue. Here, we have developed a kit based on microbial growth inhibition to determine animal products contaminated with excessive amounts of antibiotics above maximum residue limits (MRLs).

Methods : We used plate count agar medium containing 108 CFU/ml spores of Bacillus stearothermophilus var. calidolactis, glucose, cysteine, and bromocresol purple (BCP) as pH indicator to detect microbial growth. The pH was adjusted to 7.8±0.2. We also used some antibiotics, including trimethoprim, chloramphenicol, and streptomycin, to increase the specificity of the growth environment and sensitivity to other antibiotics. The suspension was solidified in tubes and stored at below 4 °C.

Results : Further analysis showed that this kit could detect the antibiotics penicillin G, amoxicillin, cefalexin, gentamicin, and tetracycline at the levels of MRL or below in approximately three hours. The kit has a shelf life of at least six months in the refrigerator.

Conclusion : This kit can be easily used by non-experts and does not require complicated equipment. Additionally, this can quickly, precisely, and affordably detect a wide range of antibiotics. It is applicable to a variety of different animal products, such as milk, honey, eggs, meat, and chicken.

Keywords : antibiotics residue in dairy, antibiotics detection kit, antibiotic resistance, Geobacillus stearothermophilus

P115-700: Antibacterial Effects of Thymus Vulgaris extracts against Resistant motile Salmonella Sp. in Pheasants

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Background and Aim : Thymus vulgaris is a flowering plant of the family Lamiaceae commonly known as thyme, native to Southern Europe, and has a worldwide distribution Mediterranean and neighboring countries, Northern Africa, and parts of Asia , they contain thymol and carvarol which shows anti inflammatory , antiseptic, antibiotic, and antifungal properties .Since chemical compounds showed some side effects and residues, herbal medicine will be an appropriate alternative for antibacterial needs specially for food born infections

Methods : Current report goes to a herds of Common Pheasants infected with motile salmonella sp;The birds were severely dehydrated , diarrheotic and downer. In differentiative stools culture motile salmonella Sp. were isolated, the antibiogram test for tetracyclines, neomycine, beta-lactam antibiotics, Enrofloxacin , Aminoglycosides, Cephalosoporines and Fosmycine showed 1+ to 3+ resistation

Results : Regarding to invitro and Invivo passed tests, a 1/10 (V/V) mixture of Thymus vulgaris extracts in yoghurts mixed with foods used for the birds fed 4 to 5 times a day for 5 days; At the end of herbal therapy the second stool culture showed no any motile salmonella Sp.were isolated.

Conclusion : The current WHO reports attend to resistant salmonella Sp. outbreaks in food animals which should be safe controlled for public health.

Keywords : Salmonellosis, Pheasnts, Thymus vulgaris, Resistant, treatment

P116-704: Metal-based Nanoparticles; Promising Strategy to Inhibit Quorum Sensing

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Background and Aim : Pseudomonas aeruginosa is one of the main bacteria producing biofilm. Biofilm can cause acute bacterial infection. Biofilm formation and motility in this bacterium is under the control of the quorum sensing system (QS). These bacteria can communicate with each other using messenger molecules called autoinducer molecules. Hence, disrupting QS is a promising strategy to combat bacterial infection. Several nanoparticles can be used for this purpose. There is mounting evidence that metal nanoparticles can be effectively used to block QS and inhibit the growth of bacteria, especially Pseudomonas aeruginosa.

Methods : In this study, we compared the effect of different anti-QS nanoparticles, including silver, nickel oxide, zinc oxide, gold, and selenium, on QS performed in individual studies on Pseudomonas aeruginosa - both clinical strains as well as laboratory strains. All these particles successfully inhibited biofilm production by more than 90% in laboratory strains such as PAO1 and PA14 and clinical strains extracted from cystic fibrosis patients. Another factor considered was the minimum inhibitory concentration (MIC) for each of the nanoparticles. The MIC of zinc oxide, silver, nickel oxide, selenium, and gold nanoparticles in mg/ml was 24.414, 0.078-0.156, 0.05, 0.0046-1.1844, and 0.0092-0.0369, respectively.

Results : As a result, gold nanoparticles needed the lowest concentration to stop the growth of all Pseudomonas aeruginosa strains. In the end, to determine the best option, we considered the production process and its justification as an important factor. The production of silver nanoparticles had a better economic and environmental justification. This nanoparticle can be produced by photochemical, biological and biosynthetic methods, but producing gold nanoparticles costs more.

Conclusion : Nanoparticles are very promising options for fighting antibiotic-resistant bacteria, and according to laboratory evidence, silver nanoparticles can be one of the best options for disrupting QS and fighting infectious bacteria such as Pseudomonas aeruginosa. Also, this nanoparticle can prevent the growth and production of biofilm in these bacteria.

Keywords : Pseudomonas aeruginosa, Anti-quorum sensing, Nanoparticles, Nanomedicine, Biofilm inhibition, Minimum Inhibitory Concentration

P117-715: Investigation of frequency and determination of drug sensitivity of Enterobacter species causing septicemia in patients hospitalized in Hajar Shahrekord Hospital, Chaharmahal and Bakhtiari Province in 1400

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Background and Aim : Blood infections are one of the main causes of death in the world. Gram-negative bacteria, the most abundant of which are Enterobacteriaceae, are one of the most important causes of septicemia. Finding septicemia-causing bacteria and investigating its drug resistance is a prerequisite for effective and rapid treatment and preventing the progression of infection and mortality. Therefore, the purpose of this study is to investigate the frequency and determine the drug sensitivity of Enterobacter species causing septicemia in patients admitted to Hajar Shahrekord Hospital, Chaharmahal and Bakhtiari Province in 1400.

Methods : In this cross-sectional-retrospective study, all blood cultures referred to the Hajar hospital laboratory from April to March 1400 were examined and studied. Blood cultures were cultured in the standard environments of Blood Agar, EMB, Chocolate Agar and the growth of bacteria was checked after 24 to 48 hours. Based on the type of bacteria grown, antibiotic sensitivity on Müller Hinton's culture medium as disk diffusion using commercial and standard disks has been investigated. Finally, the findings were analyzed using descriptive statistics.

Results : The results of this study showed that out of 6376 blood cultures, 170 samples were positive (2.66%). Meanwhile, the causative agent of septicemia in 42 cases (24.7%) of the samples was found to be Enterobacter species and the predominant species was Enterobacter cloacae. Have been. Antibiogram results showed the highest sensitivity to ciprofloxacin (91.9%), amikacin (84.37%), Trimethoprim / Sulfamethoxazole (81.8%) and morpheme (58.8%), respectively. In this study, 80% drug resistance to third-generation cephalosporins such as ceftriaxone and 77% to cefotaxime and 83% to cefixime were shown. Also, resistance to FEP (60), SAM (84), TIPZ (64), CAZ (64), MEN (41) percent were shown.

Conclusion : According to the antibiotic resistance of the third-generation cephalosporins, probably the genes for treatment are increasing. Arbitrary use of these antibiotics may be one of the causes of resistance.

Keywords : septicemia, Enterobacter, blood culture, drug sensitivity

P118-725: Isolation of bacteriophage against Shigella sonnei in Hospital and Municipal Wastewaters

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Background and Aim : Infections of antibiotic-resistant bacteria make their treatment difficult and sometimes impossible. Antibiotic-resistant bacterial infections cause long hospital stays, costly treatment for the patient. scientists are looking for new solutions to fight these bacteria. Phage therapy can replace antibiotic therapy, especially in multidrug-resistant bacteria. Therefore, our goal was to find bacteriophage that is effective against common gram-negative bacteria such as Shigella.

Methods : In this laboratory study, sampling of hospital wastewater and municipal wastewater was performed. The effluent samples were centrifuged at 4000 rpm for 10 minutes and the supernatant was filtered through a 0.45 µm perforated filter. Then, to strengthen the phage, 50 ml of filtered water with twice the volume of broth and bacterial nutrients was incubated for 24 hours in a shaker incubator. Two-layer agar method was used to see bacteriophage plaque. An electron microscope was used to see the isolated bacteriophage.

Results : Effective lytic bacteriophage to Shigella sonnei was found by testing on municipal wastewater. Electron microscope showed that the bacteriophage was more likely belonged to the Microviridae family. But, there were no positive test results for bacteriophage on hospital wastewater samples and other gram-negative bacteria.

Conclusion : Founded given the bacteriophage against Shigella sonnei, this important finding could be a good prospect for phage therapy of Shigella infection with antibiotic resistance.

Keywords : Bacteriophage; Antibacterial effect; Drug Resistant Bacteria; Gram Negative Bacteria, Shigella; Phage Therapy; Morphological Characteristics

P119-739: Frequency of Enterobacteriaceae in blood cultures and antibiotic resistance pattern in pre-COVID and during COVID period

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Background and Aim : Bacterial co-pathogens are commonly identified in viral respiratory infections and are important causes of morbidity and mortality especially in bacteremia or septicemia. We attempted to observe whether COVID-19 infection and antibiotics use in COVID period had an effect in bacterial frequency as well as antibiotic resistance pattern.

Methods : This retrospective study was carried out from January 2019 to July 2022. Patients and microbiological records were studied and analyzed for the presence of bacterial agents and their antibiotic susceptibility pattern.

Results : Year 2019, the period before COVID emergence, observed E.coli and Klebsiella pneumoniae as the predominant species isolated predominantly from internal ward. In terms of antibiotic resistance pattern, 27.3% E. coli isolates were sensitive to all antibiotics, 4.6% were only resistant to cefotaxime, 63.7% were simultaneously resistant to cefotaxime and ceftazidime, and 4.5% had simultaneous resistance to cefotaxime, ceftazidime and amikacin. Similarly, 26.3% K.pneumoniae isolates were sensitive to all antibiotics however, 2.6% were resistant only to ceftazidime, 50.1% were simultaneously resistant to cefotaxime and ceftazidime, 21% were simultaneously resistant to cefotaxime, ceftazidime and amikacin and 18.4% isolates were pan resistant. Year 2020, the early COVID period, observed the same bacterial isolates with similar resistance pattern. In contrast to E.coli, K. pneumoniae frequency increased in COVID patients admitted wards. Year 2021- Though the bacterial organisms were similar however, susceptibility of E.coli decreased from 27.3% to 12.5% and increased ESBL producing E.coli. Frequency of K.pneumoniae decreased to only 3 bacterial isolates. Year 2022- the lowest prevalence of COVID period, until July, only 20% E. coli isolates retained antibiotic susceptibility, 20% were resistant to cefotaxime, 10% were resistant to ceftazidime, and 50% were simultaneously resistant to cefotaxime and ceftazidime. K. pneumoniae showed increase in the antibiotic resistance with 33.3% isolates revealing simultaneous resistance to cefotaxime, ceftazidime and amikacin.

Conclusion : E.coli and K.pneumoniae were the two co-infectious agents in bacteremic or septicemia patients with COVID-19. Co-infection with other Enterobacteriaceae agent was

relatively infrequent. The investigation did not observed much difference in bacterial co-pathogens in COVID or non-COVID period. However, increase in antibiotic resistance especially ESBL production was evident in these years.

Keywords : COVID-19; Bacterial infection; E.coli; Klebsiella pneumoniae; Blood infection; Co-pathogens

P120-744: Presence and antibiotic resistance of Pseudomonas aeruginosa and Acinetobacter baumannii from Intensive Care Units: An appraisal from a University teaching center, Sina Hospital, Tabriz

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Background and Aim : Hospital-acquired infections, particularly in the intensive care units (ICUs), are becoming more frequent past several years, with Gram-negative bacterial infections presenting the highest incidence and eventually ending in long hospitalization. Among various pathogens, Pseudomonas aeruginosa and Acinetobacter baumannii are the most common bacteria in ICUs either due to their survival ability or usage of device and invasive procedures. Increasing use of antibiotics is also the likely main reason for the evolution of antibiotic-resistant P. aeruginosa and A.baumannii outbreaks in these clinical settings. We aimed at to observe the frequency of both these bacteria in various ICUs separately and assess the demographic and microbiological features associated with them in two and half years of time period to devise strategies to minimize their spread in the hospital wards.

Methods : We conducted this retrospective investigation from January 2020 to July 2022 in ICUs comprising burn, infectious, general 1 and 2, toxicology and surgery ICUs. Patients and microbiological records were studied and analyzed for the presence of P. aeruginosa and A. baumannii and their antibiotic susceptibility pattern using software WHONET programme.

Results : Year 2020 observed high frequency of A.baumannii in the general ICU 1 compared to others. On an average the frequency of A.baumannii was 61% and P. aeruginosa being 40%. Majority of A.baumannii were resistant to ciprofloxacin, ceftazidime, amikacin and meropenem, while P. aeruginosa retained high resistant to ciprofloxacin. In year 2021, the frequency of A.baumannii was more in general ICU 2 followed by surgery and infectious ICU (67% each) while, P. aeruginosa was isolated more from general ICU 1 and burns (64%). Turning of A.baumannii to carbapenem resistant was a considerable feature. Though

P. aeruginosa revealed antibiotic resistance towards all therapeutic agents however, all isolates from each ICUs showed high ciprofloxacin resistance. In year 2022, high gentamicin resistance was evident in P. aeruginosa in all the ICUs while emergence of extensive drug resistant (XDR) A. baumannii was a distinctive feature in burns ICU.

Conclusion : Increasing prevalence of P. aeruginosa and A.baumannii highlights their nosocomial nature and compel introduction of strict infection control strategies. Emergence of XDR A.baumannii in burns ICU had a clinical meaningful impact.

Keywords : Antibiotic resistance; Pseudomonas aeruginosa; Acinetobacter baumannii; Intensive care units; Extensive drug-resistant; Prevention

P121-7: Studying antimicrobial effect of aqueous Sumac extract for bacteria that cause nosocomial infections by In Vitro & In Vivo method

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Background and Aim : In this study, the antimicrobial effect of Aqueous Sumac extract, chemical compounds, antiviral effects and its antioxidant activity were investigated.

Methods : Preparation of total sumac extract, separation of extract components, measurement of antimicrobial effect of total extract and some isolated components were performed by disk diffusion method and accurate determination of MIC and MBC. In vivo study was performed using an animal model of a mouse. The cytotoxicity of the plant extract was investigated by Trypan Blue and MTT methods. The antioxidant activity of the extract was measured by free radical scavenging.

Results : The diameter of the growth aura of sumac aqueous extract in different concentrations is approximately equal to the diameter of the growth aura of the antibiotic gentamicin and acetic acid has a stronger antibacterial effect than lactic acid. Groups receiving sumac extract had a decreasing effect in terms of the number of bacteria counted in the blood with groups of mice receiving antibiotics. The level of antioxidant activity was 95.25%.

Conclusion : Sumac extract has a synergistic effect with some antibiotics and its effect is the same on resistant and sensitive strains of S. aureus and also its effect on gram-positive bacteria is more than gram-negative. The antiviral effect of the extract is probably due to the multiplication of the virus by inhibiting the expression of the above genes or disrupting the effect of proteins derived from these genes in the cell.

Keywords : Aqueous extract of sumac, Rhus coriaria.L , antimicrobial effect, antioxidant activity

P122-8: Investigation of therapeutic applications of Cucumis metuliferus extract

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Background and Aim : Cucumis metuliferus, a South African native plant, known as African horned cucumber and kiwano, is a therapeutic plant that has multiple applications in herbal medicine. The extract and essential oil of this plant have many medicinal effects including antibacterial, antifungal, antiviral, anti-tumor, anti-inflammation, etc. discussed in this study.

Methods : For this study, the keywords "Cucumis metuliferus", "African horned cucumber ", " herbal medicine ", and "plant extract" in the databases PubMed and Google Scholar between 2010 and 2022 were searched and 15 articles were chosen, studied, and analyzed.

Results : Because of the increased resistance of multiple microbes to antibiotics, the requirement for plants with antimicrobial effects is increasing. Cucumis metuliferus is one of the medicinal plants with antimicrobial properties that have efficacy in combating all microbes, especially Gram-negative bacteria, and fungi. This plant also has anti-viral, anti-tumor, anti-inflammatory, anti-oxidant, anti-aging, anti-ulcerogenic, and anti-diabetic features, which can be used as a material with various wonderful remedial usage.

Conclusion : These results suggest that the extract of Cucumis metuliferus can be used in clinical medicine as a therapeutic agent, which can be substituted for chemical drugs and antibiotics or help them in the treatment of illnesses.

Keywords : Cucumis metuliferus, African horned cucumber, kiwano, Herbal medicine, Plant extract

P123-18: Isolation and identification of Burkholder cepacia from respiratory secretions of cystic fibrosis patients in East Azerbaijan, Iran

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Background and Aim : Burkholderia cepacia complex (BCC) is among the main factors of secondary infections in cystic fibrosis (CF) patients. Infection by these organisms has been reported worldwide, being an organism with high drug resistance in hospital-acquired infections. Despite many global advances in Burkholderia infection epidemics, BBCS still causes many deaths in CF patients. This study investigates B. cepacia isolation and identification by culturing and selecting a proper molecular method and exact setting up an efficient, rapid, and specific ELISA-based method.

Methods : : Periodic 3-month tests, including culturing and biochemical tests, were conducted in East Azerbaijan Province (Iran) to detect secondary infections in CF patients from 22 September 2020 to 21 June 2021. Swab samples of secretions were simultaneously taken from CF patients' sputum for culturing and the PCR test.

Results : BBC was not isolated from 100 sputum samples in culturing and biochemical tests. Of all tested samples, five samples were diagnosed as BCC infected samples by the molecular diagnostic test.

Conclusion : Despite the widespread application of selective media and biochemical properties, BBC cannot be reliably identified even by commercial diagnostic systems. However, B. cepacia was identified with high precision in this study by selecting a proper

molecular method. It also seems that the use of the ELISA technique with native species is among the basic variables in setting up an efficient, rapid and specific method.

Keywords : Burkholderia cepacia complex, Cystic Fibrosis, PCR, ELISA

P124-30: Evaluation of the inhibitory effect of Ganoderma lucidum extract and TiO2 nanoparticle against biofilm-producing bacteria isolated from clinical samples

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Background and Aim : The emergence of antimicrobial-resistant pathogens, especially in health care units, lead to treatment failure. The formation of biofilms also is the main contributing factor to antibiotic resistance. So, the need for new antibacterial drugs is urgent. Ganoderma lucidum is a well-known mushroom that has various therapeutic properties like antimicrobial activity. TiO2 nanoparticles possess desirable inhibitory and bactericidal effects

Methods : In the present study, we evaluated the efficiency of TiO2 and Ganoderma extract against biofilms-producing Pseudomonas aeruginosa and Staphylococcus aureus. Biofilm formation was detected by the microtiter plate method. For this purpose, first, we determined the minimum inhibitory concentration (MIC) of tested compounds by the microdilution broth method. Then, MIC, sub-MIC, 2MIC, and 4 MIC concentrations effects of TiO2 and Ganoderma extract were assessed against strong biofilms-producing isolates. Synergistic interaction between TiO2 and Ganoderma extract was detected using checkerboard assay. Data were analyzed using the graph pad through ANOVA and t-test.

Results : According to our results, bacterial sensitivity to TiO2, and Ganoderma extract depended on the bacterial species. The average MICs of TiO2, Ganoderma extract, and combination of TiO2 and Ganoderma extract against P. aeruginosa and S. aureus were 389.9, 138.04, 86.8, 215.02, 78.3, and 121.09 µg/mL, respectively. The 2 MIC concentration of TiO2 and Ganoderma reduced the biofilm formation rate of S. aureus but test compounds had no significant effect on the decrease of P. aeruginosa biofilm.

Conclusion : Taken together, these findings revealed that nanoparticles and natural substances might represent the potential to be used for the development of promising antibacterial therapies, especially against gram-positive species in the coming years.

Keywords : Ganoderma lucidum extract, TiO2 nanoparticle, antibiofilm

P125-47: Bio-control of Acinetobacter baumannii by Bdellovibrio as a predatory bacteria

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Background and Aim : Management of antimicrobial-resistant Acinetobacter baumanni is a great challenge for clinical microbiologist. Whereas use the predatory bacteria is the best way to treat infection diseases caused by antibiotic-resistant bacteria, the aim of this study was to use the autochthonous Bdellovibrio potential to prey Acinetobacter baumannii as a biological control agent.

Methods : To evaluate the effect of autochthonous Bdellovibrio on Acinetobacter baumannii, as a biological control agent, plaque perdition assay, reduction in optical density (OD) and reduction in host cells viability by colony forming unit (CFU) counting in co-cultures after 0,24, 48 hours and assay of killing efficiency were carried out.

Results : Clear plaques were observed after 3-6 days of incubation. In co-cultures, the CFU enumeration of Acinetobacter baumannii was decreased after 48 hours. Also, after 48 hours, OD was decreased 0.7unit. In this research the efficiency ofBdellovibriokilling for Acinetobacter baumannii was 83%.

Conclusion : Base on the results, Bdellovibrio can prey Acinetobacter baumannii as a prey cell. Therefore utilize of Bdellovibrio spp., as biological control agent, for treatment of antimicrobial-resistant Acinetobacter baumannii infection suggested in future study

Keywords : Acinetobacter baumannii, Antimicrobial-resistance, Bdellovibrio, biological control agent.

P126-73: The immunogenic role of combination of outer membrane proteins Omp34 and BauA against Acinetobacter baumannii infection in murine mode

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Background and Aim : Acinetobacter baumannii is the most important agent of hospital-acquired infections worldwide. This bacterium has been regarded as a low-grade but an important opportunistic pathogen that causes various types of infections, including ventilator-associated pneumonia, urinary tract infection, skin and wound infections, bacteremia, and meningitis. Recombinant vaccines and specific antibodies are a new treatment strategies for such antibiotic-resistant infectious bacteria. However, a small number of bacterial surface antigens were tested that could only provide partial protection. For this reason, polyvalent (multiple) vaccines containing different antigens are needed to provide an acceptable level of protection. This study is oriented on the use of two outer membrane proteins, BauA and Omp34 as a polyvalent vaccine.

Methods : Recombinant BauA and Omp34 proteins were expressed, purified, and injected into BALB/c mice individually and in combination. Both active and passive immunizations were carried out. The mice were then challenged with a clinical isolate of A.baumannii. Then, the level of antibody in mice was measured by Indirect ELISA. The animal survival rate was also determined.

Results : Elevated antibody production was noted by ELISA in all the immunized groups. The combination of BauA and Omp34 proteins rendered good protection compared to the single administration of each protein.

Conclusion : Polyvalent vaccines that contain different antigens provide an acceptable level of protection.

Keywords : Acinetobacter baumunnii ., Recombinant protein., BauA., Omp34., Immunogenicity., Vaccine

P127-99: The study of prevalence of antibodies against Chlamydia pneumoniae in patients suffered from chronic obstructive pulmonary visiting Tabriz Emam reza and Alinasab Hospital

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Background and Aim : Chronic obstructive pulmonary disease (COPD) is the fourth leading cause of death in the world. Chlamydia pneumoniae (C. pneumoniae) is one of the most important factors in the development of this disease. The aim of this study was to evaluate the frequency of anti-Chlamydia pneumoniae antibodies in patients with COPD.

Methods : In this descriptive cross-sectional study, 195 patients with COPD participated. C. pneumoniae antibody titers were determined by ELISA and statistical analysis was performed using SPSS software and T-Test.

Results : The mean of IgG antibody was 74.62% and the mean of IgM antibody was 0.964%. There was no association between sex and antibody level, smoking, coronary artery disease and anti-Chlamydia pneumonia antibody levels.

Conclusion : The role of C. pneumoniae in exacerbation of COPD as a causative pathogen is more important than other causative agents.

Keywords : Chronic obstructive pulmonary disease, Chlamydia pneumoniae, Antibody

P128-100: Prevalence and antibiotic susceptibility pattern of Enterobacter isolates in burn patients: A cross-sectional study in North of Iran

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Background and Aim : The bacterial infections that prevail in the burnt patients continue to be a critical complication in the burnt patients and vary with time and place. Identification of bacterial pathogens with information on their antimicrobial susceptibility to burn wounds can help clinicians to select appropriate medication procedures by providing them with suitable antibiotics for empirical treatment.

Methods : In a 3-year descriptive cross-sectional study, data were collected from all patients with burn wound infection caused by Enterobacter isolates referred to the Burn Injury Hospital in northern Iran. Demographic and clinical information included age, sex, percentage of burns, ward, length of hospital stays, type of infection, outcome, and antibiotic susceptibility profile. Results were analyzed using SPSS software version 24.

Results : A total of 15 cases (2.8%) of Enterobacter isolates were recovered from 536 cases of burn wound infection. 9 cases of Enterobacter isolates (60%) were related to male patients and 6 cases (40%) were related to female patients. The mean age of patients was 43.53 19 19.5 years. Also, 9 cases of Enterobacter isolates (60%) were isolated from ICU and 6 cases (40%) were isolated from the burn surgery ward. The mean hospital stay was 14.97 ± 14 days and the mean hospital stay until the infection was 3.6 ± 3 days. Nine cases of enterobacterial isolates (60%) were reported in patients with improvement and 6 cases (40%) were reported in patients who died. The highest frequency in the type of infection is related to skin infections with a frequency of 9 (60%). The highest antibiotic resistance was related to ciprofloxacin (81.8%), followed by meropenem (80%) and gentamicin (75%). The most effective antibiotic was amikacin with 70% efficacy.

Conclusion : Enterobacter species isolation was low in the burn center we studied. However, the significant drug resistance of organisms makes them clinically important pathogens. Also, the results of a recent study on the emergence of antibiotic susceptibility to infection with Enterobacter isolates can be a serious warning to increase the cost of treatment and hospitalization, as well as reduce the quality of patients' health. Preventing it requires targeted

optimization of treatment protocols based on laboratory results or based on an antibiotic susceptibility pattern to reduce unwanted allergies.

Keywords : Burns, wound infections, antibiotic susceptibility, Enterobacter

P129-101: Prevalence and profile of antibiotic susceptibility of various bacteria isolated from burn patients with ventilator-associated pneumonia (VAP): A cross-sectional study in North of Iran

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Background and Aim : Ventilator-associated pneumonia (VAP) is one of the most important nosocomial infections, especially in intensive care unit (ICU) patients, which can increase mortality and treatment costs. Therefore, the present study identifies the etiological factors of VAP and patterns of antimicrobial resistance of these microorganisms in burn patients admitted to a burn hospital in northern Iran.

Methods : This study was performed on burn patients admitted to the hospital from March 2017 to March 2020. Patients ' files extracted information about age, sex, underlying diseases, length of hospital stay, outcome, cause of the burn, and antibiotic resistance pattern. The results were analyzed by SPSS software version 24.

Results : Out of 29 patients, 22 (75.9%) were male patients. The mean age of patients was 15.96 ± 41.21 years. Pseudomonas aeruginosa (48.3%) and Klebsiella pneumonia (17.2%) were the most common microorganisms causing pneumonia. Other microorganisms identified included Escherichia coli (10.3%), Staphylococcus coagulase-negative (6.9%), and unknown (17.2%). There was no significant relationship between the type of pneumonia-causing microorganisms with sex, age group, burn percentage, underlying diseases, burn cause, and treatment outcome ($P < 0.05$). Also, the highest resistance of the isolates was observed against the antibiotics of ofloxacin, ampicillin, tetracycline, clofazimine, vancomycin, cephalexin, cefixime, and cefoxitin. Amikacin (52.9%) and tobramycin (41.7%) were the most effective antibiotics.

Conclusion : Since the statistical relationship between patients' gender, age group of patients, percentage of burns, underlying diseases, types of burn mechanisms, and therapeutic outcome of the disease was not seen with the type of microorganisms involved, it can be concluded that the environmental flora is more than the mentioned variables are related to the type of microorganism causing pneumonia.

Keywords : pathogenic pattern, ventilator-associated pneumonia, burns

P130-102: Prevalence and antibiotic resistance pattern of Klebsiella pneumoniae isolated from burn patients in the North of Iran

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Background and Aim : Klebsiella species are among the most common bacteria isolated from burn wounds that cause severe complications in patients. In recent years, drug resistance in bacteria has increased, associated with increased mortality and treatment costs. Therefore, determining the antibiotic resistance pattern to select the appropriate treatment and planning to prevent the spread of this infection seems necessary. Thus, the present study investigates the prevalence of K. pneumonia isolates and antimicrobial resistance patterns for two years in a burn hospital in the North of Iran.

Methods : This study was performed on burn patients hospitalized from March 2018 to March 2020. Antibiotic susceptibility testing of all isolates was performed according to CLSI instructions, and the results were analyzed by SPSS software version 24.

Results : 61 cases (10.27%) of K. pneumonia isolates were isolated from 594 clinical specimens. The mean age of patients was 39.15 years. Five cases (8.2%) of these infections were related to patients with VAP. The highest antibiotic susceptibility was observed to azithromycin (68.2%), and the highest resistance to imipenem (85.7%) was observed.

Conclusion : because of the high prevalence of resistance in Klebsiella specimens, serious measures are necessary for prescribing antibiotics based on the antibiogram pattern. Infection treatment protocols based on laboratory results can prevent increased antibiotic resistance.

Keywords : Antibiotic resistance, Burn wound, Klebsiella pneumoniae, Nosocomial infection

P131-103: Risk factors related to mortality of burn patients infected with non-fermentative gram-negative bacteria in Velayat Hospital in Rasht, Iran

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Background and Aim : Burn wound infection (BWI) remains one of the most common causes of morbidity and mortality in burn patients. Gram-negative organisms have become significant agents of infections in vulnerable burn patients due to their multidrug resistance nature which possesses critical therapeutic challenges. This study describes the antibiotic resistance pattern in burn patients with non-fermentative gram-negative bacteria and investigates the factors related to mortality.

Methods : This retrospective study was performed on 152 burn patients admitted to the hospital from March 2018 to March 2021 in the North of Iran. All of these patients were infected with non-fermenting gram-negative bacteria. Demographic and clinical data including age, sex, underlying diseases, length of hospital stay, outcome, cause of burns, as well as antibiotic culture results, and antibiotic resistance pattern of isolates were collected. The results were analyzed using SPSS software version 24.

Results : Based on the results of laboratory tests, all microorganisms isolated from patients were strains of Pseudomonas aeruginosa. Among 152 patients, 121 (79.6%) were male and 31 (20.4%) were female. The mean age of patients was 39.53 years. The mean hospital stay was 11.57 days and the mean burn percentage was 42.79. 10 patients (6.6%) had intubated and 17 patients (11.2%) needed a urinary catheter. 96 patients (63.2%) recovered and 56 patients (36.8%) died. The highest antibiotic resistance of isolates was observed against gentamicin (82.9%). Resistance to ciprofloxacin, meropenem, imipenem, ceftazidime, and tobramycin was reported to be 79.6%, 79.3%, 79.2%, 73.2%, and 68%, respectively. Among the risk factors studied, the percentage of burns, intubation, and urinary catheterization were significantly associated with patient mortality. There was no significant relationship between other variables and patient mortality.

Conclusion : This study showed high levels of P. aeruginosa, a type of drug-resistant non-fermentative gram-negative bacteria in burn patients. Regular monitoring, testing, and laboratory antimicrobial monitoring are essential to guide experimental treatment in burn

patients. These methods, in turn, inhibit the emergence of multidrug-resistant organisms and reduce the morbidity and mortality of these infections. Also, since TBSA, intubation, and urinary catheter were significantly associated with mortality, it is necessary to consider more care and health measures in these patients.

Keywords : Gram-negative bacteria, Infection, Antibiotic resistance, Burn

P132-106: Genotyping of extended spectrum beta-lactamases (ESBLs) producing Pseudomonas aeruginosa Isolates from Nosocomial infections

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Background and Aim : Background: Pseudomonas aeruginosa (P. aeruginosa) nosocomial infections is one of the major problems increases mortality and mobility in patients. Objectives: The aim of this research was to determine the molecular epidemiology of ESBLs-producing P. aeruginosa genotypes isolated from nosocomial infections.

Methods : One forty-six clinical isolates of Pseudomonas spp. obtained from tertiary referral hospital. Phenotypic identification and PCR using gyrB were performed for P. aeruginosa detection. Extended spectrum beta-lactamases in samples were identified using disk approximation test and combination disk test (CDT). blaSHV and blaTEM genes were detected by PCR method. Strains were typed with pulse field gel electrophoresis (PFGE), repetitive element sequence (Rep)-PCR and Enterobacterial repetitive intergenic consensus (ERIC) –PCR methods.

Results : A total of 134 (91.78%) P. aeruginosa isolated were separated and 41.79% were related to nosocomial infection. extended spectrum beta-lactamases analyses test revealed that5.97% and 66.41% isolates harboring blaSHV and blaTEM genes, respectively. Enterobacterial repetitive intergenic consensus (ERIC) –PCR and Rep-PCR and PFGE showed 56, 55 and 55 different patterns, respectively. Pulse field gel electrophoresis indicate that pulsotypes C3 were dominant.

Conclusion : Association between, ESBLs-producing P. aeruginosa, blaSHV and blaTEM positive P. aeruginosa and ERIC, Rep-PCR and PFGE patterns ($p \geq 0.05$) were not significant. Nosocomial infection, prevalence of ESBLs among the clinical isolates of P. aeruginosa in Kurdistan was observed. Periodic review of antibiotic resistance and molecular methods to prevent the spread of infections in hospitals is required.

Keywords : Genotyping Techniques, beta-lactamase, Pseudomonas aeruginosa, Infections, Hospitals

P133-107: Hospital-acquired infections and Antibiotic Resistant challenge in Western Asia

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Background and Aim : Hospital-acquired infections or nosocomial infections (NIs) are related with different toxins or infectious agents that cause infection among patients admitted to the hospital. These infections are likely to spread through hospital boundaries during the patient's hospital Stay. This study aims to provide a detailed review of literary studies to identify the prevalence of nosocomial infections and antibiotic-resistance specifically in Western Asia countries.

Methods : The material is from scientific articles on bacteriology, microbiology, infectious diseases, drug resistance as well as searching the valid scientific databases.

Results : The findings indicated that nosocomial infections following antibiotic resistance are an emerging problem in Middle Eastern countries, leading to significant morbidity and mortality. Most frequently reported NIs in Middle East in our review are bloodstream infections (50%) and surgical site infections (50%) followed by urinary tract infections.

Conclusion : Nosocomial infections following antibiotic resistance are an emerging problem in Middle Eastern countries, leading to significant morbidity and mortality. Escherichia coli and Klebsiella species among gram-negative bacteria, Staphylococcus aureus among gram-positive bacteria and fungal pathogens such as Candida species are most reported pathogens involved in nosocomial infections, and resistance to penicillin, cephalosporin, carbapenem and fluoroquinolone antibiotics were significantly reported. However, most studies showed minimum resistance of pathogens against the drug colistin. Hence, further studies are required in Middle East to further examine and improve sensitivity of colistin in NIs.

Keywords : Antimicrobial resistance, Nosocomial infection, Western Asia

P134-135: Evaluation of the Effect of the Cetrimid-C, Benzalkonium Chloride and Micro-10 Disinfectants on Escherichia coli Isolated from Patients

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Background and Aim : Disinfectants are very important in terms of clinical applications. The use of disinfectants is recommended due to the antibiotic resistance of some hospital pathogens such as Escherichia coli. In this research, the effect of the disinfectants Cetrimid-C, Benzalkonium Chloride and Micro-10, as well as the effect of the dilution recommended by the manufacturing factories, on a number of Escherichia coli isolates was evaluated.

Methods : In this study, urine samples collected from a number of patients were examined for the presence of Escherichia coli by diagnostic and biochemical tests and the presence of bacteria was also confirmed by PCR method. Then, the effects of the recommended dilutions of the above disinfectants by the manufacturing factories were investigated on 19 Escherichia coli isolates at 5, 10 and 15 minutes after adding bacteria.

Results : Cetrimid-C, Benzalkonium Chloride and Micro-10 disinfectants inhibited the growth of all 19 strains of Escherichia coli isolated from patients in all three times of 5, 10 and 15 minutes

Conclusion : which shows the full effectiveness of the above three disinfectants in laboratories and health centers.

Keywords : Disinfectant, Cetrimid-C, Benzalkonium Chloride and Micro-10, Escherichia coli

P135-155: The challenge of treatment multi-drug resistant strains of Acinetobacter baumannii in burn patients in Iran

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Background and Aim : Acinetobacter baumannii is second cause of burn infections in Iran. The treatment of antibiotic resistant strains of Acinetobacter baumannii in burn patients has turned into a challenging puzzle. Since the skin is the first defense barrier against invasion of microbes, burn patients are prone to infect with opportunistic bacteria such as Acinetobacter baumannii due to loss of this defense barrier. It is difficult for physicians to prescribe a suitable treatment regimen for burn patients because these patients are infected with other bacteria such as Pseudomonas aeruginosa. Carbapenems were the choice for multi-drug resistant isolates (MDR) but with emergence of carbapenem resistance strains, tigecycline and colistin were chosen as alternative drugs against extensive-drug resistant isolates (XDR). The present study aimed to explore the challenge of treatment MDR strains of Acinetobacter baumannii in burn patients in Iran.

Methods : In this study various databases used to select articles in both Persian and English languages. Targeted databases were Google Scholar, PubMed, Scopus, Web of Science. The applied keywords included multi-drug resistant strains of Acinetobacter baumannii ,burn patients and Iran.

Results : In this study, all isolates were resistant to carbapenems in genotypic and phenotypic analysis, but showed sensitivity to colistin and tigecycline and this sensitivity was much about colistin.

Conclusion : Our study revealed almost all isolates from burn patients were resistant to carbapenems and the prevalence of multi-drug resistant strains of Acinetobacter baumannii is increasing.

Keywords : Acinetobacter baumannii, MDR, XDR, Carbapenem

P136-168: The Effectiveness of the Anteroom (Vestibule) Area on Hospital Infection Control and Health Staff Safety: A Systematic Review

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Background and Aim : The emergence of SARS-CoV2 in 2019 showed again that the world's healthcare system is not fully equipped and well-designed for preventing the transmission of nosocomial respiratory infections. One of the great tools for preventing the spread of infectious organisms in hospitals is the anteroom. Several articles have investigated the role of the anteroom in disease control but the lack of a comprehensive study in this field prompted us to provide more in-depth information to fill this gap. Also, this study aimed to assess the necessity to construct an anteroom area for hospital staff members at the entrance of each ward of the hospital, and specify the equipment and facilities which make the anteroom more efficient.

Methods : Articles were identified through searches of Scopus, Web of Sciences, PubMed, and Embase for studies published in English until May 2020 reporting data on the effect of the anteroom (vestibule) area in controlling hospital infections. Data from eligible articles were extracted and presented according to PRISMA's evidence-based data evaluation search strategy. Also, details around the review aims and methods were registered with the PROSPERO.

Results : From the database, 209 articles were identified, of which 25 studies met the study criteria. Most studies demonstrated that an anteroom significantly enhances practical system efficiency. The results showed that the equipment such as ventilation system, high-efficiency particulate absorption filter, hand dispensers, alcohol-based disinfection, sink, mirror, transparent panel, UVC disinfection, and zone for PPE change, and parameters like temperature, door type, pressure, and size of the anteroom are factors that are effective on the safety of the hospital environment.

Conclusion : Studies demonstrated that providing an anteroom for changing clothing and storing equipment may be useful in reducing the transmission of airborne infections in hospitals. Since the transmission route of SARS-CoV2 is common with other respiratory infectious agents, it can be concluded that a well-designed anteroom could potentially decrease the risk of SARS-CoV2 transmission during hospitalization as well.

Keywords : anteroom, vestibule, airborne infection, nosocomial infection, SARS-CoV2, hospitalization, healthcare safety

P137-178: Evaluation of the effect of Savlon (Cetrimide-C), Surfosept and Sodium hypochlorite disinfectants on Klebsiella pneumoniae isolated from patients

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Background and Aim : Klebsiella pneumoniae is an opportunistic and pathogenic pathogen that causes hospital infections. Pollution of environmental surfaces and its transmission is an effective factor in the development and spread of hospital infections, so it is necessary to eliminate bacteria from the hospital environment, especially Klebsiella pneumoniae. The use of disinfectants is effective in preventing and controlling hospital infections. In this research the effect of three disinfectants, Savlon (Cetrimide-C), Surfosept and Sodium hypochlorite with dilutions according to the manufacturer's instructions on the growth of a number of Klebsiella pneumoniae isolates from infectious urine samples has been investigated.

Methods : Urine samples from people with urinary tract infections were subjected to biochemical and PCR method confirmation tests for the presence of Klebsiella pneumoniae, and after culture, an approximate concentration of half McFarland was prepared from them. Then, the dilution effect of each disinfectant according to the instructions of the manufacturer was tested on 15 isolates by the Pour Plate Method in 5, 10, 15 minutes; The growth and non-growth of bacteria after these times were examined.

Results : Savlon (Cetrimide-C), Surfosept and Sodium hypochlorite disinfectants inhibited the growth of all 15 strains of Klebsiella pneumoniae isolated from patients in 5, 10, 15 minutes.

Conclusion : Therefore, the above three disinfectants are used in laboratories and health centers. They were completely effective and efficient.

Keywords : Disinfectant, Savlon (Cetrimide-C), Surfosept, Sodium hypochlorite, Klebsiella pneumoniae

P138-189: Antibiofilm activity of Cinnamomum zeylanicum essential oil against clinical strains of Acinetobacter baumannii

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Background and Aim : Acinetobacter baumannii is one of the most important causes of hospital infections worldwide. One of the mechanisms of antibacterial resistance of this bacterium is by biofilm formation. Considering the role of biofilms in the pathogenicity of bacteria, it seems necessary to find new treatment methods to inhibit the formation of biofilm by bacteria. One of the proposed solutions to deal with bacterial biofilm is the use of plant essential oils. The aim of this study is to investigate the antibiofilm activity of Cinnamomum zeylanicum essential oil against clinical strains of A. baumannii.

Methods : In this study, 30 clinical strains of A. baumannii were selected from the urine samples of patients referred to Milad Hospital and their ability to form biofilm based on binding to polymeric surfaces was evaluated. The minimum inhibitory concentration (MIC) of C. zeylanicum essential oil was determined by broth microdilution method against 5 strains of A. baumannii with strong biofilm, and the biofilm inhibition effect of the strains was evaluated in the presence of C. zeylanicum essential oil in concentrations of 1.2 MIC, MIC and 2 MIC by calculating CUT OFF.

Results : According to the results, out of 30 strains of A. baumannii, 24 strains (80%) formed a strong biofilm. MIC of C. zeylanicum essential oil on A. baumannii strains with strong biofilm was obtained between 0.5-1 ?l/ml. All investigated strains formed a negative biofilm after the effect of the essential oil in all its concentrations.

Conclusion : The use of medicinal plant compounds, including cinnamon essential oil, can be one of the effective strategies to deal with bacterial biofilm and reduce their resistance.

Keywords : biofilm, antibiotic resistance, essential oil, Cinnamomum zeylanicum, Acinetobacter baumannii.

P139-190: Synergistic effect of zinc oxide nanoparticles and Bunium persicum essential oil against clinical strains of Pseudomonas aeruginosa

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Background and Aim : The increasing use of antibiotics against bacterial infections has led to an increase in drug resistance and adverse side effects. Pseudomonas aeruginosa is an opportunistic pathogen that causes a wide variety of infections. The combined use of nanoparticles and herbal compounds is a new approach to increase their effectiveness against drug-resistant bacteria. This study was conducted with the aim of investigating the synergistic effects of zinc oxide nanoparticles and Bunium persicum essential oil against clinical strains of P. aeruginosa.

Methods : In this study, 30 clinical strains of Pseudomonas aeruginosa were selected from the urine samples of patients referred to Milad Hospital. the antibiotic sensitivity of strains was evaluated by the disk diffusion method. Zinc oxide nanoparticles were prepared and the composition analysis of Bunium persicum essential oil was performed. The minimum inhibitory concentration (MIC) of B. persicum essential oil and zinc oxide nanoparticles were investigated by broth microdilution method and the synergistic effect of essential oil and nanoparticles was determined by the checkerboard method.

Results : The highest antibiotic resistance of Pseudomonas aeruginosa strains was reported to the antibiotic Ticarcillin (48%) and the lowest resistance to the antibiotic ciprofloxacin (14%). The MIC of B. persicum essential oil was obtained between 0.5-4 µl/ml, and the MIC of zinc oxide nanoparticles for the studied strain was between 32-128 µg/ml. The interaction of B. persicum essential oil and zinc oxide nanoparticles showed a synergistic effect against 60% of P. aeruginosa strains.

Conclusion : The findings showed that the combined use of zinc oxide nanoparticles and Bunium persicum essential oil can be a promising option to control the emergence of multi-drug resistant bacteria.

Keywords : synergism, antibiotic resistance, Bunium persicum, essential oil, Pseudomonas aeruginosa.

P140-240: Comparison of antibacterial activity of hypericin activated by light with hypericin not exposed to light

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Background and Aim : Hypericin, a phenanthropeylene quinine pigment naturally occurring in Hypericum perforatum L., possesses a variety of therapeutic activity such as antidepressant, antiviral, antibacterial and anticancer. Hypericin is well-known as a potent natural photosensitizing agent in photodynamic therapy.The present study aimed to evaluate the antibacterial activity of Hypericin in the light and in the dark on bacteria of clinical importance.

Methods : The antibacterial activity of hypericin was tested against Staphylococcus aureus ATCC 6538 and Escherichia coli ATCC 8739 in the presence of light (590 nm, 10 J/cm2) and or in the dark using agar-well diffusion method and expressed as the average diameter of the zone of inhibition of bacterial growth around the wells.

Results : After light irradiation, the antibacterial activity for Staphylococcus aureus obtained at concentration 0. 03 mg/mL, 0.05 mg/mL and 0.1 mg/mL with inhibition diameter values 10.5, 11.5 and 14.0 mm, while in the dark, the inhibition-zone diameters were 10.0, 11.5 and 13, respectively. The antibacterial activity of Escherichia coli both in the presence of light and in the dark was slightly less than that of Staphylococcus aureus, so that the inhibition zone of mean diameters were in the range of 9-13 mm

Conclusion : The results of this study showed that there is no significant difference between light-activated or inactive hypericin in terms of antibacterial activity, and Staphylococcus aureus is more sensitive to hypericin than Escherichia coli.

Keywords : Antibacterial effect, photodynamic therapy, Hypericin, Escherichia coli, Staphylococcus aureus

P141-247: A combination of biofilm-associated protein (Bap) and Outer membrane protein A (OmpA) protects mice against Acinetobacter baumannii infection

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Background and Aim : Acinetobacter baumannii is the leading cause of nosocomial infection. A. baumannii is the etiologic agent for various illnesses including pneumonia, meningitis, and bloodstream infections. Due to multiple antibiotic resistance of the bacterium, the treatment is very difficult, and hence specific and economical test for early diagnosis and control of infection is needed. The development of such a test requires targeting specific cell surface antigens. Biofilm-associated protein (Bap), a specific cell surface protein, is directly involved in A. baumannii biofilm formation. Production of antibodies can be used for inhibition of biofilm and control of the diseases caused by A. baumannii. Outer membrane protein A (OmpA) is the most promising vaccine candidate against one of the most successful nosocomial pathogens, A. baumannii. In this study, the immunogenicity of Bap and OmpA proteins in BALB/c mice was investigated.

Methods : The conserved regions from OmpA and Bap genes determined by in-silico studies were cloned. The construct was transferred to E. coli BL21(DE3). The recombinant proteins were purified by Ni-NTA affinity chromatography. The recombinant proteins were injected into BALB/c mice. The titer of IgG was measured by the indirect ELISA method. The intraperitoneal challenge was performed with A. baumannii 19606 in immunized mice and the number of bacteria counted in the spleen, liver, and lungs of the control and test mice groups.

Results : IgG level was significantly increased in the immunized mice sera. A substantial difference was observed between bacterial counts in the organs of test and control mice after intraperitoneal challenge with A. baumannii 19606.

Conclusion : The immunization with Bap and OmpA proteins could prevent Acinetobacter baumannii infection.

Keywords : OmpA., Bap., Acinetobacter baumannii., Immunization

P142-250: Immunization with a combination of Bap and Oma87 protects mice against Acinetobacter baumannii infection in a murine model

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Background and Aim : In recent years, persistent outbreaks in hospital environments caused by multidrug-resistant strains have been making a health crisis worldwide. It is important that new approaches are developed to prevent or treat the infections caused by multi-drug-resistant strains. Immunological strategies such as active and passive immunization approaches could be considered new vital options. A surface protein commonly known as biofilm associate protein (Bap) has been identified in a bloodstream isolate of A. baumannii. Bap A. baumannii is involved in intercellular adhesion within the mature biofilm. Bap-related proteins are present on the bacterial surface and confer upon bacteria the capacity to form a biofilm, show a high molecular weight, contain a core domain of tandem repeats, and play a relevant role in bacterial infectious processes. Oma87 or BamA (β-barrel assembly machinery) has been introduced as an immunogenic outer membrane β-barrel assembly protein via reverse vaccinology by in silico analysis. The easy acquisition of resistance to antimicrobial agents in this organism leads to the failure of the therapeutic regimens. However, the protectivity of A. baumannii Oma87 is not well known. Some physicochemical properties were assessed via in silico analyses. The current research undertakes a study on the immunogenicity of recombinant Oma87 and Bap in a murine model.

Methods : The recombinant proteins were purified and then administered to mice. The titer of IgG antibodies was measured by the indirect ELISA method. We monitored the survival rate in neutropenic mice for 5 days. The intraperitoneal challenge was done with A. baumannii 19606 in immunized mice and the number of bacteria counted in the spleen, liver, and lungS of the control and test mice groups.

Results : IgG level was significantly increased at 1:128,000 dilution in immune mice sera. A high titer of a specific antibody was achieved against rOma87 even after the first injection. A substantial difference was observed between bacterial counts in the organs of test and control mice after intraperitoneal challenge with A. baumannii 19606.

Conclusion : Based on these results, Oma87 and Bap could be considered a promising vaccine candidate against A. baumannii.

Keywords : A. baumannii., Vaccine., Antibody., Infection., Oma87., Bap

P143-261: Antimicrobial and Healing Effect of Nettle, Purslane and Hedge Nettle Extracts on Burn Infections of Staphylococcus aureus in Mice

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Background and Aim : Staphylococcus aureus is one cause of hospital infections which creates a wide range of infectious illnesses. It is necessary to mention that Urtica dioica, Portulaca oleracea and Stachys schtschegleevii have more antimicrobial and healing effects. In this project, the antimicrobial and healing effects of plants extracts with silver sulfadiazine were studied on burn infections of Staphylococcus aureus in rats.

Methods : In this study, ethanolic and acetonic extracts of Urtica dioica, Portulaca oleracea and Stachys schtschegleevii were prepared in the laboratory. Then, the MIC and MBC of the extracts were determined by the dilution method in the Muller Hinton agar. In study of animal model, firstly the bacteria were inoculated with a concentration of (5×105 CFU/ml) to the wound site on rats. After 24 hours, an ointment was prepared based on MBC concentration from extracts of mentioned plants for 1g of silver sulfadiazine and was used to treat burn wounds and infections of Staphylococcus aureus.

Results : In studies conducted on rats, it was found that ethanolic and acetonic extracts of Urtica dioica, as well as the acetonic extract of Portulaca oleracea had more antimicrobial and healing effect on Staphylococcus aureus. But in the wound treated with ethanolic and acetonic extract of Stachys schtschegleevii, bleeding was seen.

Conclusion : The results of the studies showed that the ethanolic and acetonic extracts of Urtica dioica and the acetonic extract of Portulaca oleracea had more antimicrobial and restoration effects on burn wound infected with Staphylococcus aureus in rats. Ethanolic and acetonic extract of Urtica dioica had better healing effects than acetonic extract of Portulaca oleracea. As a result, extract of Urtica dioica could be used in preparation of burn ointments.

Keywords : Burn Infection, Portulaca oleracea, Stachys schtschegleevii, Staphylococcus aureus, Urtica dioica

P144-265: Antimicrobial and Healing Effects of Purslane, Green Tea and Mountain Tea Extracts on Burn Infection Caused by Staphylococcus aureus in Mice

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Background and Aim : Staphylococcus aureus is one of the principal causes of hospital infections and causes a wide range of infectious diseases. The purpose of this research is to study the healing effects of ethanolic and acetonic extracts of Portulaca oleracea, Camellia sinensis and Stachys lavandulifolia with eucerin on burn infection caused by Staphylococcus aureus in mice.

Methods : In this study, ethanolic and acetonic extracts of Portulaca oleracea, Camellia sinensis, and Stachys lavandulifolia were prepared in the laboratory. Then their MIC and MBC levels were determined by the broth dilution method. Burn wounds were created in the rats. After 24 hours, the infection with Staphylococcus aureus was inoculated to the rats at a concentration of (5×105 CFU/ml). After 24 hours, the ointment was prepared based on the MBC concentration of ethanolic and acetonic extracts of mentioned plants per 1 g of eucerin. Then it was used to treat burn wounds and infections caused by Staphylococcus aureus.

Results : In the studies conducted on mice, it was found that the acetonic extracts of Portulaca oleracea, Camellia sinensis, and Stachys lavandulifolia, as well as the ethanolic extracts of Stachys lavandulifolia and Camellia sinensis, have antimicrobial and healing effects on burn wounds caused by Staphylococcus aureus. Meanwhile, the acetonic extracts of Portulaca oleracea and Camellia sinensis and the ethanolic and acetonic extracts of Stachys lavandulifolia have better effects than the ethanolic extract of Camellia sinensis. Also, the ethanolic extract of Portulaca oleracea had the lowest level of effectiveness. Bleeding and slow recovery rates were observed in the burn site treated with the ethanolic extract of this plant.

Conclusion : The results of the studies showed that the ethanolic and acetonic extracts of Stachys lavandulifolia and Camellia sinensis, and the acetonic extract of the Portulaca oleracea, have the highest antimicrobial and healing effect on burn infection caused by Staphylococcus aureus. Therefore, these extracts can be used as an antimicrobial drug or burn ointment.

Keywords : Burn wound infection, Camellia sinensis, Portulaca oleracea, Stachys lavandulifolia, Staphylococcus aureus

P145-270: An immunoinformatics approach to design a multi-epitope vaccine against Neisseria gonorrhoeae

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Background and Aim : Neisseria gonorrhoeae is one of the most common bacterial sexually transmitted diseases (STDs) that cause inflammation of the genitourinary tract. The emergence of N. gonorrheae strains resistant to almost all classes of antibiotics available for treatment and the lack of an effective gonococcal vaccine are sufficient reasons for the necessity of urgent action for prevention and control. The aim of present study, an in silico approach was adopted to construct a multi-epitope vaccine from immunogenic proteins of N. gonorrhoeae selected to elicit a cellular immune response as well as a humoral immune response.

Methods : Five amino acid sequences of N, gonorrhoeae were retrieved from the GenBank database. Three ABCpred, BCPREDS and LBtope online servers were considered for B cells prediction and IEDB server for T cells (CD4+ and CD8+) prediction. All sequences were performed for validation, allergenicity, toxicity and physicochemical analysis using web servers.

Results : A total of 6 sequences with different lengths for linear B cell epitopes, 6 and 7 sequences were considered as epitopes of CD4+ T cells and CD8+ cells, respectively. The secondary and three-dimensional (3D) structure of the final vaccine was predicted. In addition, the complex between the final vaccine and immune receptors (TLR-4) was evaluated by molecular docking. To confirm the expression of the designed vaccine, the vaccine mRNA was amplified with the help of Java codon compatibility tool and the secondary structure was generated from Mfold. Finally, codon optimization based on Escherichia coli K12 resulted in optimal GC content and higher CAI value followed by incorporating it into the cloning vector pET28þ(a).

Conclusion : Therefore, it can be further corroborated using in vitro and in vivo assays to fulfil the global need for a more efficacious anti-Neisseria vaccine.

Keywords : Neisseria gonorrhoeae, immunoinformatic, vaccine

P146-299: Determination of antibiotic resistance and virulence determinants of different methicillin resistant and –sensitive S. aureus (MRSA & MSSA) types isolated from Shahid Mustafa Khomaini Hospital of Ilam city by PCR, SCCmec and PFGE typing

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Background and Aim : Staphylococcus aureus as a multi-capacity pathogenic bacterium which holds virulence factors of antibiotic resistance is considered as one of the threatening factor for human life. Air conditions, hospital personnel and different surfaces have important roles in transferring of this bacterium among patients and hospital wards. Due to an increasing trend of antibiotic resistance and pathogenesis ability of these strains (MRSA) globally and also in our country, a proper planning for determining of the distribution source of theses strains in the community and control of their associated infections is very necessary.

Methods : Samples were taken from air, environment, personnel and patients admitted to different wards of shahid Mstafa Khomeini Hospital in Ilam city, every four weeks for 7 months. Strains identities were determined using standard biochemical tests as well as via tracing of spa and femA genes. Identification of sensitive and residence strains to methicillin was performed using the test of sensitivity to cefoxitin via disk diffusion method and tracing of mec A gene by PCR. Antiobiogram was performed using 11 different antibiotics. The 13 virulence genes and 12 antibiotic resistance genes were studied via multi-PCR method and finally the methicillin resistance strains were typed using the SCCmec typing method. The current study aimed to determine the type of MRSA by pulsed field gel electrophoresis (PFGE).

Results : Totally 88 strains were isolated from different samples including surfaces (38.9%), personnel (26.6%), air (23%) and patients (11.9%). All strains were sensitive to linezolid, vancomycin, synercid, tigecyline, mupirocin, imipenem. Resistance to tetracycline, erythromycin, cefoxitin and gentamicin, clindamycin was 100%, 31.9%, 23.6% 13.3% and 8.9% ,8.9% respectively.Among 33 different pulsotypes, 20 pulsotypes were known as the most frequent pulsotypes and 13 pulsotypes were found as a single.

Conclusion : . Nosocomial infections by Staphylococcus aureus particularly MRSA strains are among worrisome problems in Iran. On the other hand personnel and environments of hospital wards are often responsible for distributing of staphylococcus isolates. In the current study SCCmec types detected from patients and surfaces were the same that indicated a

circulation of MRSA between patients and hospital environment. Therefore an intensive and accurate control of hospital environment for this infection is essential.

Keywords : MRSA,PFGE

P147-314: Evaluation the antifungal efficacy of five Iranian essential oils against fluconazole resistant Candida species isolated from patients with urinary tract candidiasis

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Background and Aim : Urinary tract candidiasis has been the most common nosocomial fungal infection in recent years. Candida species are considered as normal microbial flora, immune deficiency leads to dysbiosis of microbiome and the opportunistic Candida spp especially Candida albicans causes urinary tract infection. In spite of increasing antifungal resistant among fungal species the speed of commercialization of new antifungals is low. Therefore it is important to search for natural products with high antifungal efficacy and low side effects. The aim of the present study was to evaluate antifungal efficacy of five Iranian essential oils against fluconazole resistant Candida species isolated from patients with urinary tract candidiasis.

Methods : Chemical composition of Origanum majorana, Artemisia dracunculus, Cymbopogon citrate, Cinnamomum verum and Caryophyllus aromaticus essential oils was determined applying gas chromatography/mass spectroscopy (GC/MS) analysis and antioxidant activity was inspected with DDPH assay. Antifungal efficacy was done by broth micro-dilution method according to CLSI protocols.

Results : Antifungal properties of esstiential oils against fluconazole resistant Candida species showed that Cinnamomum verum, Caryophillium aromaticus, Artemisia dracunculus, Origanum vulgare and Cymbopogon citratus essential oils had MICs between 125 to 175 mg/mL (mean value: 147.7 _ 25.5 mg/mL), 700 to 1000 mg/mL (mean value: 740.9 _ 105.4 mg/mL), 1000 to 2000 mg/mL (mean value: 1454.5 _ 509.6 mg/mL), 173 to 350 mg/mL (mean value: 208 _ 55.8 mg/mL) and 125 to 175 mg/mL (mean value: 156.8 _ 24.6 mg/mL) respectively. All essential oils were identified fungicide.

Conclusion : It is concluded that essential oils are suitable to be used in resistant Candida species, nevertheless at this rate, these products could be applied as adjuvant therapy along with conventional antifungals.

Keywords : nosocomial infections, urinary tract candidiasis, essential oils, antifungal resistant, Candida spp

P148-318: Antimicrobial Effect of Ajowan and Lemonbalm Extracts on Staphylococcus aureus: In vitro and Animal Model

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Background and Aim : Infectious diseases are one of the most common diseases around the world which impose enormous financial burden on society. Staphylococcus aureus is an important causes of nosocomial infections and multidrug resistance. Although synthetic antibiotics have been able to play an important role in treatment of infectious diseases in past decades, however problems related to microbial resistance of antibiotics have caused that the medical plants to be considered as an alternative.

Methods : In this study, aqueous and ethanolic extracts were prepared from dried leaves of the Trachyspermum copticum and Melissa Officinalis, then anti-bacterial activities of the extracts for Staphylococcus aureus were experimented, first by the method of well diffusion in agar, and later the amount of the MIC and MBC of the extracts were measured by broth dilution method. In animal model study, first 5×105 CFU/ml of bacteria was intraperitoneally injected and after 24 hours, 0.5ml (as MBC concentration of each the extracts) of extracts, to female BALB/c mice was intrapertioneally injected. Then, the counting of bacterial clonies in spleen were determined with cultivation on Mueller Hinton agar after 7 days as the standard protocol.

Results : The experiment results concerning the determination of growth inhibition diameter in agar showed that the maximum of growth inhibition diameter is related to the ethanolic extract of Trachyspermum copticum (20 mm), and the minimum of growth inhibition diameter is related to ethanolic extract of Melissa Officinalis (10 mm) at the highest concentration (400 mg/ml). In conditions of in vivo, after 48 hours spleen supernatant cultivation, the average number of bacteria for ethanolic extracts of the Trachyspermum copticum and Melissa Officinalis were 1.8×103 CFU/ml and 6.6×103 CFU/ml respectively and for aqueous extract of Trachyspermum copticum was 14.6×103 CFU/ml. These results showed significantly decrease in number of bacteria in all experimental groups (p?0.5) compared to control group.

Conclusion : In general, the results of evaluations in experimental conditions and the animal model showed that ethanolic and aqueous extracts of Trachyspermum copticum and ethanolic extract of Melissa Officinalis have the effective antibacterial activity against mentioned bacteria and can be useful to treatment of nosocomial infections.

Keywords : Antimicrobial, Melissa Officinalis , Staphylococcus aureus , Trachyspermum copticum

P149-322: Antibacterial Effects of Essential Oils of Ajowan and Lemonbalm on Staphylococcus aureus: In vitro and Animal Model

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Background and Aim : Infectious diseases are one of the most common diseases around the world which impose enormous financial burden on society. Staphylococcus aureus is an important causes of nosocomial infections and multidrug resistance. Although synthetic antibiotics have been able to play an important role in treatment of infectious diseases in past decades, however problems related to microbial resistance of antibiotics have caused that the medical plants to be considered as an alternative.

Methods : In this study, essential oil was prepared from dried leaves of the Trachyspermum copticum and Melissa Officinalis, then anti-bacterial activities of the essential oil for Staphylococcus aureus was experimented, first by the method of well diffusion in agar, and later the amount of the MIC and MBC of the essential oils were measured by broth dilution method. In animal model study, first 5×105 CFU/ml of bacteria was intraperitoneally injected and after 24 hours, 0.5ml (as MBC concentration of each the essences) of essential oils, to female BALB/c mice was intrapertioneally injected. Then, the counting of bacterial clonies in spleen were determined with cultivation on Mueller Hinton agar after 7 days as the standard protocol.

Results : The experiment results concerning the determination of growth inhibition diameter in agar showed that the maximum of growth inhibition diameter is related to the essential oil of Trachyspermum copticum (30 mm), and the minimum of growth inhibition diameter is related to essential oil of Melissa Officinalis (10 mm) at the highest concentration (400 mg/ml). In conditions of in vivo, spleen supernatant cultivation, the average number of bacteria for Trachyspermum copticum and Melissa Officinalis essential oil were 2×102 CFU/ml and 6×102 CFU/ml respectively. These results showed significantly decrease in number of bacteria in all experimental groups ($p<0.5$) compared to control group.

Conclusion : In general, the results of evaluations in experimental conditions and the animal model showed that the essential oils of Trachyspermum copticum and Melissa Officinalis have the effective antibacterial activity against mentioned bacteria and can be useful to treatment of nosocomial infections.

Keywords : Antimicrobial, Essential oil, Melissa Officinalis, Staphylococcus aureus , Trachyspermum copticum

P150-324: Green synthesis of Cadmium Sulfide Quantum dots from Nerium Oleander leaves extract and detection of its antibacterial effects against some gram negative and gram positive bacteria

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Background and Aim : The spread of multiple-drug resistance in pathogenic bacteria is an increasing serious problem for medicine and the pharmaceutical industry. The aim of this study was to evaluate antibacterial effects of green synthesized Cadmium Sulfide Quantum dots (CdS QDs) against some gram negative and gram positive bacteria.

Methods : In this study was conducted during 6 mounts period from July 2021 to January 2022, the green synthesis of Cadmium Sulfide quantum dots using Nerium oleanderleaves extract using three different methods: ultrasonic (15 minutes at 37°C), microwave (15 minutes under 300W radiation), and flotation (soaking in water 3 days in Balloon packed via paraffin), was done and as Cadmium sulfide source, the dehydrated Cadmium acetate and Sulfide sodium was added, and the supernatant was filtered through filter paper. After that the antibacterial effect of these different synthetic QDs was evaluated on E.coli ATCC 25922, Salmonella enterica ATCC 14028, S.aureus ATCC 25923, and Bacillus cereus using disc diffusion method on Muller Hinton agar, and compared with ceftazidime (30µg), chloramphenicol (30µg), penicillin (10µg), and imipenem (10µg).

Results : In the evaluation of antibacterial effects of Cadmium sulfide quantum dots prepared using ultrasonic, microwave and flotation methods, it was determined that, antibacterial effects of quantum dots were stronger than ceftazidime, chloramphenicol and penicillin, while each one never doesn't have effects of imipenem.

Conclusion : Our finding showed that, aqueous and methanolic extracts of cadmium sulfide quantum dots have had antibacterial effects and the rate of inhibition growth zone in bacteria had direct relation to concentration of aqueous and methanolic extract of QDs, and gram positive bacteria were more sensitive to QDs than gram negative bacteria.

Keywords : Quantum dots, Green synthesize, antibacterial effects, Nerium oleandrum, antibiotic resistance

P151-328: Investigation of antibacterial effect of a recombinant phage endolysin on Acinetobacter baumannii

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Background and Aim : A. baumannii infection has become a critical challenge to health care systems. The most important concern about this bacterium is its increased resistance to different antibiotics. The prevalence of antibiotic resistant A. baumannii is also high in Iran. One of the methods recently used as an alternative to antibiotic treatment is to use phage endolysin enzymes to specifically eliminate bacteria. In this study, antibacterial effect of recombinant PlyF307 endolysin was examined on Acinetobacter baumannii.

Methods : After synthesis of the endolysin PlyF307 gene, the plasmid extracted and transferred to the expression vector pET28a by the enzymatic digestion. The plasmid transferred to E. coli BL21(DE3) pLysS. Then induced for expression by IPTG. Western blot method was used to confirm the expression of recombinant protein. Endolysin purified by nickel chromatography column. Then, the protein concentration calculated with Bradford method. To investigate the antibacterial effect of the enzyme, plate lysis assay performed, on Acinetobacter baumannii PTCC 1855. Tryptic Soy Agar (TSA) medium was used for antibacterial assay. In summary, 1.5×108 CFU, equivalent to McFarland Turbidity Standard No. 0.5, transferred to TSA and 20µl of each sample was dropped on the medium and then incubated at 37 °C for 18 hours. The initial concentration of the enzyme was 600µg /ml, which was diluted 1:2, 1:4, 1:8 with a suitable buffer containing 0.5 mM EDTA as a membrane permeabilizer.

Results : The results showed a 10-15 mm inhibitory zone at the inoculation site of 1:4 dilution of enzyme, which is probably due to the greater accessibility of the enzyme to the bacteria in a diluted state.

Conclusion : According to the obtained results, the PlyF307 endolysin can be candidate as antibacterial drug for Acinetobacter baumannii.

Keywords : Cross Infection, Acinetobacter baumannii, Anti-Bacterial Agents, Bacteriophages, enzyme.

P152-350: In silico study of the immunogenicity of a construct containing the extracellular loops of Acinetobacter baumannii outermembrane proteins exposed on the LCL platform

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Background and Aim : Acinetobacter baumannii has recently emerged as an important nosocomial pathogen that causes infections, especially in immunocompromised patients. In this context, introducing an effective vaccine for the prevention of infections caused by this bacterium as a cost-effective seems necessary. Therefore, this study aimed to design the best structure combined with three selected loops of OMP epitopes based on their properties to improve immune response against A. baumannii.

Methods : In this study, LCL (Loopless C-lobe) was used as a scaffold to display three surface exposed and conserved regions of OMPs epitopes including Loop3OmpA, Loop3Omp34, and Loop7BauA. In the next step, different bioinformatics tools were used to analyse this construct from different aspects such as BepiPred2 that predicts the location of linear B-cell epitopes, probability of antigenicity was predicted for selected regions using Vaxijen server (Threshold=0.4), Jpred4 used to predict three-state (a-helix, b-strand and coil) secondary structure with accuracy of >80.0%, 3D structures of the selected regions were predicted by I-TASSER server, and ToxinPred server used to identify highly toxic or non-toxic peptides.

Results : The Bepipred2 server predicted 96% linear B-cell epitopes in this construct. The regions selected by the VaxiJen server were predicted as an antigen. The results of the prediction of the secondary structure by the Jpred4 server showed that 98% of epitopes are coiled. The results of I-TASSER modeling showed that 96% of selected loops are exposed at the surface of the construct. This construct was probably not soluble as predicted by biotech software. Finally, according to the ToxinPred server results, the designed construct is predicted to be non-toxic.

Conclusion : According to obtained results, this construct can increase the function of the immunogenic epitopes and so this combination could be suggested as an appropriate vaccine candidate against A. baumannii.

Keywords : Acinetobacter baumannii , bioinformatic, OmpA, Omp34, Loop7BauA, vaccine

P153-354: Isolation of Clostridium perfringens type D from antibiotic-associated diarrhoeal patients in Kerman hospitals of Iran

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Background and Aim : Clostridium perfringens (C. perfringens) may induce severe diseases in humans such as gas gangrene, necrotic enteritis, food poisoning, antibiotic-associated diarrhea (AAD), and sporadic diarrhea (SD). C. perfringens type F causes 15% of all AAD/SD cases, and the association of the other C. perfringens types with these diseases was not reported. In this study, the incidence of C. perfringens-associated diarrhoea was investigated in hospitalized patients in the hospitals of Kerman, Iran.

Methods : A total of 151 stool specimens from AAD/SD patients were bacteriologically investigated for C. perfringens, and the isolates were analyzed for C. perfringens toxin genes (cpa, cpb, etx, iap, and cpe) by PCR.

Results : C. perfringens isolation ratio was 28.5% (43 of 151 patients) after the bacteriological and molecular examinations, which was significant among different hospitals ($p<0.01$). A total of 114 C. perfringens isolates were obtained from stool specimens. Based on the gene profiles, 35 (30.7%), 64 (56.1%), and 15 (13.2%) isolates belonged to types A, F, and D, respectively, and the other C. perfringens types were not detected.

Conclusion : C. perfringens-associated AAD is an important gastrointestinal disease in the nosocomial patient that has been frequently attributed to type F. In this study, the prevalence of AAD was determined in hospitalized patients in the Kerman province of Iran and C. perfringens type D were identified in humans for the first time while humans are not natural hosts for this type. The epidemiology of C. perfringens-associated AAD in long-term hospitalized patients were discussed.

Keywords : Clostridium perfringens; Type D; Antibiotic-associated diarrhoea; Hospital; Kerman, Iran

P154-383: A New Insight into Nosocomial Infections: a Worldwide Crisis

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Background and Aim : The term" Nosocomial" is attributed to the diseases acquired by the patient under medical care. Various microorganisms, including bacteria, viruses, and fungi, may contribute to developing nosocomial infections (NIs). Urinary tract infections (UTI), surgical-site infections (SSI), bloodstream infections (BSI), and pneumonia are the most well-known instances.

Methods : We investigated various aspects of NIs and the main causative agents of NIs, particularly bacteria, antibiotic resistance, crucial viral infections in hospitals, and a brief survey of fungal infections in various databases including Pubmed, Scopus, and Google scholar.

Results : It was concluded that specific human body tissues such as those in the lungs and urinary tract are more likely to be a target for nosocomial pathogens. The fatalities associated with these infections, particularly in the intensive care unit (ICU), are serious concerns. Transmission by health facilities has become a primary medical issue because of its spread into the community. Another medical point is antibiotic resistance which is a leading cause of prolonged periods of hospitalization and makes the treatment procedure harder and costlier.

Conclusion : Additionally, measures to prevent the spread of NIs and minimize economic loss are discussed. All physicians and medical students must be updated about different kinds of these infections, their causative agents, challenges, and how to deal with them to reduce the consequences and improve public health.

Keywords : Nosocomial infections, Bacterial and Viral agents, Infection control and prevention

P155-398: An outer membrane protein-derived peptide as Klebsiella pneumoniae vaccine candidate

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Background and Aim : There is no approved vaccine for Klebsiella pneumoniae yet. Outer membrane protein-K17 (OMPK17) is involved in K. pneumoniae pathogenesis and its immunogenicity has been shown in animal models. However, no information has been found about OMPK17 dominant immunogenic regions (epitopes) in the literature. Therefore, this study aimed to predict both T cell and B cell epitopes of K. pneumoniae OMPK17 via immunoinformatics approaches and find the best epitopic region as vaccine candidate.

Methods : Applying several prediction tools, both T cell and B cell epitopes of OMPK17 were predicted and followed by several screening steps including clustering, human similarity, immunogenicity, allergenicity, toxicity, conservancy, docking, and structural/physicochemical suitability.

Results : The results showed that there are some regions of OMPK17 that have more potential as epitopes. Comparing the best T cell and B cell epitopes led to a 25-mer peptide containing both T cell (class-I and class-II) and B cell (linear) epitopes that posses an appropriate physicochemical and structural characteristics that are required for K. pneumoniae vaccine development.

Conclusion : The in vitro/in vivo study of this peptide is recommended to clarify its actual efficiency and efficacy.

Keywords : Epitope, Immunoinformatics, Klebsiella pneumoniae, Outer membrane protein-K17, Physicochemical characteristics

P156-400: Klebsiella pneumoniae vaccines: A systematic review

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Background and Aim : The treatment of Klebsiella pneumonia, a common cause of hospital and/or community-acquired infections, is faced with significant challenges demanding the development of prevention strategies including vaccination. However, no approved and globally available vaccine exists, yet. Here, we systematically reviewed all published data on K. pneumoniae vaccines in both humans and animal models.

Methods : Without time restrictions, three electronic databases including PubMed, Scopus, and Web of Science were searched using appropriate keywords to retrieve published studies. The studies were screened and the data of those that matched our inclusion criteria were collected and analyzed.

Results : Totally, 2077 records were retrieved; of which 38 studies were included for qualitative analysis (35 studies were done on animal models and three studies were done on human samples). The most frequently used animal model was BALB/c mice. Proteins, polysaccharides, and their combinations were the most vaccine candidates used. The amount of antigen, the route used for immunization, and the challenge strategy was varying in the studies and were chosen based on several factors such as the animal model, the type of antigen, and the schedule of immunization. Almost all studies claimed that their vaccine was effective/protective, indicated by increasing survival rate, reducing organ bacterial load, and eliciting protective antibody and/or cytokine responses

Conclusion : Altogether, the information presented here will assist researchers to have a better look at the K. pneumoniae vaccine candidates and to take more effective steps in the future.

Keywords : Klebsiella pneumoniae, Systematic review, Vaccine

P157-503: Investigation of antimicrobial effects of lipid extracted from Streptomyces alboflavus

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Background and Aim : The aim of the present study was to investigate the antimicrobial activities of a Streptomyces strain that had previously been isolated from Tehran province soil samples.

Methods : Methods: A Streptomyces strain was identified from Tehran province soil samples. The strain's genus was determined using phenotypic and biochemical analyses. Using MEGA7 software, a gene tree was designed to show the relationship between isolates by the neighbor-joining method based on the nucleotide difference number model. The presence of antimicrobial metabolites was assessed in Streptomyces isolates using the Cross-Streak method. In flasks with 250 cc of BHI broth nutritional medium, the strains that exhibiting antimicrobial activities was cultivated after preliminary screening. Minimum Inhibitory Concentration (MIC) determination was performed by the microdilution method. Using concentrations established by the microdilution method, the metabolite's antibacterial activities were exanimated in fresh rabbit serum. The isolated metabolite's stability was examined at 60 °C and in the presence of proteinase K (50 mg/ml). In order to further purify the metabolite, precipitates of the metabolite were prepared and tested for the presence of organic substances. Finally, mass spectrometry and High-performance liquid chromatography (HPLC) were employed to investigate the metabolite's chemical structure and approximate formula.

Results : Results: The isolate (S921) and Streptomyces alboflavus had 99 percent sequence similarity. S921 strain exhibited broad-spectrum antibacterial activity against B. cereus ATCC11778, Escherichia coli ATCC 25922, Pseudomonas aeruginosa ATCC 27853, Klebsiella pneumoniae ATCC 700603, Salmonella Typhimurium ATCC 14028 and Shigella sonnei RI366. The antibacterial activity of metabolite was retained at 60 ° C and in the presence of proteinase K, with no visible changes in the growth inhibition zone against the tested microorganisms. Mass Spectra analysis of the supernatant from S921 isolate showed that it was very similar to C32H32O14.

Conclusion : Conclusion: As a result of this study, it has been concluded that strain S921 has a bioactive metabolite, which has broad antibacterial activity against a wide range of human pathogens.

Keywords : Keywords: Streptomyces alboflavus; antimicrobial activity; Soil microbiology; Bioactive metabolite

P158-507: the effect of personnel's knowledge in controlling the infection

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Background and Aim : Nosocomial infection refers to infectious that occurs while hospitalized patients in the hospital are affected, and the disease manifestations may occur during the hospitalization or after discharge. Nosocomial infections are undoubtedly the most critical problem in the health centers of the world, and their occurrence in each country is different. Due to the effects of losses in hospital infections on the individual and society, it is necessary to measure and control these infections. Since the healthcare team members have a unique role in preventing infections, they should have the correct scientific and sufficient information on the types of hospital infections and follow-up methods. Therefore, this study investigated the effect of personnel's knowledge in controlling the infection.

Methods : articles related to the subject of this review are extracted from google scholar, PubMed, Scopus, and Science direct from 2015 to 2022. To do this, the words hospital infection, infection control, hospital staff, and hospitalization were among the words that were searched.

Results : In all similar studies conducted on the effect of personnel's knowledge in controlling the infection, there is a consensus that there is a positive correlation between the prevalence of hospital infections and the level of the personnel's knowledge. The more conscious the personnel are, the more uncomplicated controlling hospital infections would become.

Conclusion : From significant points, the personnel's knowledge is the basis of infection control. Since the personnel plays an essential role in preventing infections, their consciousness significantly affects the reduction of these infections.

Keywords : hospital infection, infection control, hospital staff, hospitalization

P159-525: Essential Oils Composition and Antibacterial Activity and Antioxidant Activity of Stachys lavandulifolia Vahl from Alborz - Iran

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Background and Aim : Stachys lavandulifolia Vahl (Lamiaceae) is a native plant, which is known as Chay-e-kohi in Persian. In Iranian traditional medicine, it is used as the herbal tea in gastrointestinal disorders, inflammatory diseases, sedative, antispasmodic and ulcers. This project investigated the chemical composition, antioxidant activity and antibacterial activity of Stachys lavandulifolia Vahl. essential oils on human infectious bacteria.

Methods : The aerial parts of Stachys lavandulifolia Vahl. were collected from Alborz Province, Iran. The essential oils were extracted using Clevenger apparatus system by Hydro-distillation method.The antibacterial effect of essential oils was determined using the minimum inhibitory concentration (MIC), and minimum bactericidal concentration (MBC) method. Also, free radical scavenging activity by 2,2-diphenyl-1-picrylhydrazyl (DPPH0) was examined. Chemical composition was measured using the Gas Chromatography-Mass Spectrometry (GC-MS).

Results : The major constituents in Stachys lavandulifolia Vahl. essential oils were alpha & beta - Pinene, Germacrene,alpha & beta - Phellandrene and etc. The essential oils of aerial parts of Stachys lavandulifolia Vahl. exhibited good antibacterial potential against gram positive and gram negative bacterial strains.

Conclusion : The essential oil of Stachys lavandulifolia Vahl. are potential natural antibacterials to treat human pathogenic bacteria and can be used as alternatives to produce antimicrobial agents.

Keywords : Stachys lavandulifolia Vahl., Clevenger Apparatus, Antibacterial activity, GC-MS, Germacrene, Human Pathogenic Bacteria.

P160-530: Characterization of biofilm formation and virulence factors of Staphylococcus aureus isolates from paediatric patients in Tehran, Iran

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Background and Aim : Staphylococcus aureus can cause several infections. Its capability to form biofilm has been reported to be a vital property involved in the bacteria's pathogenesis. Various genes contributing to biofilm formation have not yet been completely clarified. This study was designed to evaluate the factors influencing adherence and biofilm formation in S. aureus isolated from paediatric patients.

Methods : One hundred and ninety-seven S. aureus isolates were obtained from pediatric patients and confirmed with phenotypic and molecular examinations. Antimicrobial susceptibility testing and biofilm formation were evaluated using standard methods. The genes encoding adhesion and virulence factors were investigated by the PCR method.

Results : The most efficient antibiotics against S. aureus isolates were vancomycin and linezolid. Approximately, 54.2% of MSSA and 85.6% of MRSA isolates were biofilm producers according to the microtiter test. Our analysis indicated that MRSA isolates are better able to form biofilm compared with MSSA isolates. All isolates harbored clfA, fnbpA, icaA, icaB, icaC, and icaD, while clfB, fnbB, hlg, and pvl were detected in 99.5%, 42.1%, 97.5%, and 5.6% of isolates, respectively. In addition, a significant difference was found in fnhB gene and biofilm formation.

Conclusion : Our findings showed a significant correlation between mecA and pvl genes and MRSA and biofilm formation in S. aureus isolates. Additionally, this study indicated the significant role of the fnhB gene as a major marker for S. aureus biofilm formation. Therefore, further experiments are warranted to exactly elucidate the function of the fnhB gene in the formation of biofilm.

Keywords : Biofilm, Fibronectin binding-proteins, MRSA, MSCRAMMs, Pediatric, Staphylococcus aureus, Virulence factors

P161-533: Surveying on biofilm-related virulence factors in Acinetobacter baumannii: A cross-sectional study, and molecular typing of isolates using the REP-PCR method

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Background and Aim : One of the significant properties of Acinetobacter baumannii, as a critical priority agent in healthcare-associated infections, is biofilm-producing. This ability led to the development of antimicrobial resistance mechanisms, subsequently failing treatment. This study aimed to determine biofilm-related genes' distribution and investigate the genotype-relatedness of isolates.

Methods : A total of 100 A. baumannii isolated from hospitalized patients in Nemazee hospital, in Shiraz, Iran, were subjected for biofilm-producing using the tissue culture plate (TCP) method. Continuously, eleven biofilm-producing related genes, comprising ompA, bap, csuE, epsA, blaper-1, bfmS, pgaB, csgA, fimH, ptk, kpsMII were sought in all isolates using PCR. Finally, the REP-PCR technique was used to investigate the genotype-relatedness of isolates.

Results : Regarding the OD values of ELISA-Reader analysis, 98% of isolates were biofilm producers, yet 30.5% were known as biofilm-producing strong isolates. The most frequency of biofilm-producing related genes was observed for csuE and pgaB (99%), bfmS (98%), ompA (97%). The REP-PCR analysis has discriminated the 97 A. baumannii isolates into 7 clusters and two singletons; three isolates were non-typeable.

Conclusion : In conclusion, it seems the high frequency of biofilm-producing and related genes among A. baumannii isolates is one of the most highlighted factors that result in the development of antimicrobial resistivity. Therefore, further investigation on how it is possible to either knock down expression or diminish the transferring of these genes could be promising for reducing antimicrobial resistivity.

Keywords : Acinetobacter baumannii, biofilm-producing, healthcare-infection, REP-PCR, Virulence-factors

P162-537: Characterization of Antibacterial and Antioxidant Properties of Flowers of Ziziphora clinopodioides

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Background and Aim : Plants with medicinal properties play an increasingly important role in food and pharmaceutical industries for their functions on disease prevention and treatment. The aim of this project was to characterization the antibacterial and antioxidant properties of methanolic extract of flowers of Ziziphora clinopodioides (Lamiaceae).

Methods : In this project, the flowers of Ziziphora clinopodioides were collected and methanolic extract prepared by microwave assisted extraction (MAE) method. Then, in vitro antioxidant activity of methanolic extracts were assayed by 1,1-diphenyl-2-picrylhydrazyl (DPPH0) free radical scavenging method of Blois. and antibacterial effect of Ziziphora clinopodioides extracts was evaluated against pathogenic bacteria associated with human infections viz. Staphylococcus aureus (PTCC 1113), and Shigella dysenteriae (PTCC 1188) by Disk diffusion test.

Results : The antioxidant activity of the investigated methanolic extract of flowers of Ziziphora clinopodioides was scavenging ability of DPPH0 radical scavenging activity (56.61%). Whereas, the IC50 of methanolic extract of flowers of Ziziphora clinopodioides for DPPH0 assay was (36.72±0.23) mg/ml respectively. The methanolic extract of flowers of Ziziphora clinopodioides showed significant antibacterial activity against both (Gram positive) and (Gram negative) bacteria.

Conclusion : Thus, the methanolic extract of flowers of Ziziphora clinopodioides would be helpful for the preparation of pharmaceutically useful drugs to destroy pathogenic microbes. Furthermore, in the present study the phytochemical evaluation of Ziziphora clinopodioides were found to be a powerful antioxidant, antibacterial agent and this study can be continued for their structural elucidation and pharmacological activity.

Keywords : Ziziphora clinopodioides, Pathogenic Microbes, DPPH0, Shigella dysenteriae, Disk diffusion, Pharmacological Activity.

P163-540: Phytochemical, Antibacterial Activity Screening of Methanolic Psidium guajava L. Leaves Extract

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Background and Aim : Phytochemical evaluation is very important for the confirmation of various naturally occurring bioactive secondary metabolites in plants. The aim of this study was to investigate the preliminary phytochemical screening and antibacterial activity of the leaves of Psidium guajava L. belonging to family Myrtaceae.

Methods : In this project, the leaves of Psidium guajava L. were collected and subjected to successive extraction by microwave assisted extraction (MAE) method. The present study for phytochemical screening method of phytoconstitute by Trease and Evans, Sofowara and Harbone were followed. Later, the antibacterial activity of the methanolic extract of leaves of Psidium guajava L. was tested using both gram positive as well as gram negative bacteria i.e. (Bacillus subtilis and Escherichia coli) respectively using minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) methods.

Results : The results of the phytochemical screening of methanolic extract of leaves of Psidium guajava L. were (terpenoids, flavonoids, saponin, tannins, phlobatannins and cardiac glycosides) presented. The methanolic extract of leaves of Psidium guajava L. exhibited good antibacterial potential against gram positive and gram negative bacterial strains.

Conclusion : The findings of the present study demonstrated the potential of phytochemicals from Psidium guajava L. leaves, a natural source, in the pathway of developing a novel antibacterial agent able of treating bacterial infections.

Keywords : Psidium guajava L., Methanolic Extract, Phytochemical Screening, Escherichia coli, MIC, Terpenoids.

P164-547: Evaluation of Surgical Antibiotic Prophylaxis and Microbial Spectrum in Patients with Surgical Site Infection

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Background and Aim : Surgical Site Infections (SSIs) are among the most common Healthcare-associated Infections (HAIs). They can result in increased antibiotic use, additional cost of illness, prolonged hospitalization, and increased patient morbidity and mortality. The goal of this study is to evaluate the appropriateness of surgical antibiotic prophylaxis (SAP) and the microbial spectrum of SSIs in one of the biggest teaching hospitals in northeastern Iran.

Methods : A hospital-based retrospective cross-sectional study was performed on all patients admitted to Imam Reza Hospital, Mashhad from September 2018 to September 2019, for whom at least one event of SSI was recorded according to CDC criteria. Data obtained through chart review included demographic information, operative details (indication, site, technique, type), surgical wound classification, surgical antibiotic prophylaxis (regimen, timing) and microbial spectrum.

Results : A total of 82 patients were included (mean age 43.2±15.5). 61 (74.4%) were female. Most SSI cases were seen in obstetrics and gynecology patients (39.0%). The surgical site most commonly associated with SSIs was the abdomen (73.2%), where the highest incidence of infection was seen with incisions below the umbilicus (61.7%). Cesarean section (34.1%) was the procedure type most commonly complicated by an SSI. Most cases were seen with surgical wounds classified as Clean (62.2%). The most commonly prescribed regimen was a combination of ceftriaxone and metronidazole (40%). Choice of antibiotic regimen and antibiotic dosage were compatible with reference protocols in only 40.2% and 19.5% of cases, respectively. 42.7% of patients had received preoperative antibiotic prophylaxis, most of whom received antibiotics more than 120 minutes before surgical incision (54.3%). None of the patients who underwent cardiovascular surgery, and only 16.9% of the patients who underwent other surgeries, received postoperative antibiotic

prophylaxis at the appropriate time. The organism most commonly cultured from the wound site was Staphylococcus epidermidis (25.8%).

Conclusion : The present study demonstrates surgical antibiotic prophylaxis (SAP) in one of the largest teaching medical centers in northeastern Iran to be in low compliance with reference protocols, suggesting the potential prevalence of the problem and the need for greater stewardship and design of standard and reasonable local guidelines.

Keywords : antibiotics, prophylaxis, surgical site infection

P165-556: an experimental study on the feasibility of ozonation and ultraviolet radiation for decontamination of infectious waste

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Background and Aim : Nowadays, high production of waste has become a global concern. Among different types of waste, infectious waste is one of the most hazardous types requiring complete decontamination with a high safety factor before disposal. The high volume of waste produced by healthcare centers in Tehran has reached 80 to 110 tons per day. Also, the emergence of Covid-19 has increased this amount significantly. The lack of administration of adequate and cutting-edge technologies for complete and safe decontamination and sanitary disposal of infectious waste could pose a serious threat to public health as well as the environment. The administration of novel and environmental-friendly methods such as advanced-oxidation processes can treat infectious waste and prevent the occurrence of hospital-acquired infections significantly. The current study aims to evaluate the efficacy of administration of ozonation and UV radiation in the decontamination of solid wastes contaminated with Bacillus subtilis ATCC6633, Pseudomonas aeruginosa ATCC27853, and Staphylococcus aureus ATCC25923

Methods : An insulated apparatus capable of emission of different volumes of ozone and UV was designed and produced for the current research. Artificial solid wastes were prepared using 100 grams of sterile cotton as a solid waste model. Then, different portions were contaminated separately with bacterial suspensions (adjusted with 0.5 McFarland turbidity standard in 100ml), including B. subtilis, S. aureus, and P. aeruginosa. The wastes were treated using UV, ozonation (5000, 10000, and 15000 ppm), and UV+ozonation at different times, including 1, 3, 5,10, 20, 30, 60, 120, and 180 mins. For contamination evaluation, 10 grams of wastes were added to 90 ml of sterile normal saline, and serial dilutions were prepared. The samples were cultured on Trypticase soy agar and after 48 hours incubating(37c°) a colony count was performed.

Results : The optimum elimination (zero counts) of each bacterium was observed as follows: A) 15000 ppm ozonation+UV in 3 mins for B. subtilis. B) 5000 pmm ozonation+UV in 30 mins for P. aeruginosa. C) 5000 pmm ozonation in 180 mins for B. subtilis

Conclusion : Our results represent the practicability of the designed apparatus in the decontamination of infectious wastes as an cost-effective apparatus.

Keywords : Infectious waste, hospital-acquired infections, disinfection, ozone, UV

P166-569: The antibacterial activity of bacteriocin-like inhibitory substances (BLISs) extracted from clinical Pseudomonas aeruginosa strains

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Background and Aim : The emergence of pan-drug resistant strains (PDR) of bacteria has led to renewed efforts to identify alternative agents, such as bacteriocins and bacteriocin-like inhibitory substances (BLISs). In recent years, Bacteriocins have been recognized as natural preservatives in food and drug industries, also, nowadays, they are used as substitutes of chemical antibiotics for treatment of infections.

Methods : In a cross-sectional study, 150 Pseudomonas aeruginosa strains were isolated from different Iranian clinical sources (patients with burns, wound and skin infections, UTI, diarrhea, eye infections, human skin wounds, and soft tissue infections) during a 6-month period. isolates were investigated by Spot test and Well diffusion test for their ability to produce compounds exhibiting antibacterial activity. BLISs production was induced by mitomycin C (2 g/mL) in S. epidermidis.

Results : 23 isolated from the P. aeruginosa had potent activity against Staphylococcus epidermidis, Bacillus cereus, Listeria monocytogenes, Klebsiella spp., Staphylococcus aureus, Proteus spp. and Vibrio parahaemolyticus. The BLIS was heat-stable (up to 100°C for 15 min) and active within a pH range of 3 - 9.

Conclusion : The produced bacteriocin had a wide antibacterial activity spectrum against the gram-positive and negative bacteria, particularly pathogenic bacteria, and was also resistant to heat and pH ranges. As a result, the use of bacteriocin in the food and drug industry, as animal feed, and as a substitute for chemical antibiotics is recommended.

Keywords : BLISs, Bacteriocin, Pseudomonas aeruginosa, Antibiotic, Drug resistant.

P167-574: The prevalence of coinfections and antibiotic-resistant strains among hospitalized Covid-19 patients in Mashhad, Iran

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Background and Aim : Patients with viral respiratory infections are prone to bacterial coinfections, and such coinfections have a strong correlation with the severity of the complications caused by viral infections. Limited information is available on the prevalence of bacterial coinfections among individuals infected with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Furthermore, the management of empirical antibiotic guidelines could be significantly influenced by the determination of the incidence of bacterial coinfections in Covid-19 patients. Therefore, we aimed to evaluate the prevalence of bacterial coinfection among Covid-19 patients and to determine their antibiotic sensitivity profiles. Infection with Candida was also assessed.

Methods : This retrospective study includes the results of the evaluation of blood, respiratory, and urine samples that had been collected from 4609 Covid-positive patients admitted to Imam Reza hospital of Mashhad, Iran, in 2020 and 2021. A positive PCR test, as well as clinical determination of infection with Covid-19 by a physician, were the inclusion criteria for these infected patients.

Results : Out of a total of 11590 samples, 6506 samples had been collected from men and 5084 from women. Based on the assessment of the culture of the specimens, 3694 samples (32%) were determined to have coinfections. 444 samples were infected with Acinetobacter, 412 with Enterococcus, 375 with Klebsiella pneumoniae, 353 with Escherichia coli, and 1014 with Candida. 316 samples contained multidrug resistant-Acinetobacter, 187 contained multidrug resistant-Klebsiella pneumoniae, 224 had ESBL-producing E. coli, and 214 had vancomycin-resistant Enterococcus.

Conclusion : According to our findings, the prevalence of bacterial and Candida coinfection was high among Covid-19 patients. The majority of the identified bacterial coinfections were related to gram-negative bacteria, including K. pneumoniae, which could have valuable implications in developing appropriate treatment plans. Moreover, the significant number of resistant bacterial strains that were found among our samples shows the critical need for

establishing a suitable antibiotic stewardship program. Given that the presence of coinfecting pathogens and resistant strains contributes to morbidity and mortality rates among Covid-19 patients, constant surveillance of bacterial resistance and microbial coinfections is critical in controlling the pandemic.

Keywords : Coinfection, Bacterial coinfections, Covid-19, Antibiotic resistance

P168-588: Emergence of OXA-10 and OXA-48 like carbapenemases among Enterobacter isolates from inpatients in southern Iran

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Background and Aim : The global spread of carbapenemase-producing Enterobacteriaceae represents a public health concern. The aim of this study was to investigate prevalence of carbapenem resistance, oxacillinase types and the presence of class 1–3 integrons among Enterobacter clinical isolates from an Iranian inpatients' population.

Methods : Ninety Enterobacter isolates recovered from hospitalized patients were diagnosed by the standard microbiological methods. Antibiogram pattern was also determined. The presence of class 1–3 integrons and four types of oxacillinase genes were assessed using PCR.

Results : Of the 90 Enterobacter isolates, the most common species was identified as E. aerogenes, (45.6%), followed by E. cloacae (30%). The highest resistance rate was against to ampicillin (96.7%). Multi-drug resistance (MDR) was substantial (93%). Carbapenemase producers were detected in 96% of carbapenem resistant isolates by mCIM test. The frequency of evaluated genes was as follows: intI1 = 50 (55.6%), intI2 = 12 (13.3%), blaoxa?1 =6 (6.7%), blaoxa?2 =5 (5.6%), blaoxa?10 =18 (20%), and blaoxa?48 =18 (20%).

Conclusion : The determinants of class 1 integron with OXA-10 and OXA-48 like carbapememases have been responsible of relatively considerable of carbapenem resistance among isolates. This is the first OXA-10 and OXA-48-producing Enterobacter spp. in Iran, indicating that the prevalence of oxacillinases might be on the rise in country.

Keywords : Enterobacter, Carbapenemase, Oxacillinase, Integron, Iran

P169-604: Spectroscopic Determination of Total Phenol, Flavonoid Contents and Antibacterial Activity of Polylophium involucratum (Pall.) Boiss.

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Background and Aim : Medicinal plants can be valuable therapeutic resources. The treatment of infections with plant-derived compounds is an age-old practice that is employed throughout the world, especially in developing countries where traditional medicines are used to treat a variety of diseases. Interest in plants with antibacterial properties has been revived as a result of current resistance profiles associated with over- and inappropriate use of antibiotics. The objective of the present study was to evaluate content of phenolic compounds, flavonoids and the antibacterial activity of the seeds extracts of Polylophium involucratum (Pall.) Boiss. using spectrophotometric method.

Methods : The seeds of Polylophium involucratum (Pall.) Boiss. were collected from Ramsar, Iran and hydroalcohlic extract prepared by microwave assisted extraction (MAE) method. Then total flavonoids and total phenolic content of methanolic extracts were determined by the Aluminium Chloride Colorimetric and Folin-Ciocalteau method, respectivly. The antibacterial activity was determined by (Disk Diffusion Method) against three strains of (Gram-positive and Gram-negative) bacteria.

Results : Our data showed total phenolic content of hydroalcohlic extracts of Polylophium involucratum (Pall.) Boiss. seeds was 12.93±2 mg GAE/g dry plant material. Also, total flavonoid content of hydroalcohlic extracts was 7.58±7 mg QE/g dry plant material. The hydroalcohlic extract of seeds of Polylophium involucratum (Pall). Boiss. exhibited good antibacterial potential against gram positive and gram negative bacterial strains.

Conclusion : Therefore, Polylophium involucratum (Pall.) Boiss. Seeds, a natural source, in the pathway of developing a novel antibacterial agent able of treating bacterial infections, Also a source of important phytochemicals (mainly flavonoids and phenolic acids) with bioactive properties to be explored for pharmaceutical applications.

Keywords : Polylophium involucratum (Pall.) Boiss., Folin-Ciocalteau method, Antibacterial activity, Disk Diffusion Method, Pharmaceutical Applications.

P170-605: The evaluation of the antibacterial and antibiofilm activity of phycocyanin pigment & clindamycin antibiotic in liposomes against Staphylococcus aureus isolates

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Background and Aim : Staphylococcus aureus and Methicillin Resistant Staphylococcus aureus (MRSA) are two major causes of nosocomial and community-acquired infections and represent a significant burden on the healthcare system. The formation of a biofilm decreases the susceptibility to antimicrobials and immune defenses, making these infections difficult to eradicate. The goal of this study was to evaluate the effect of clindamycin eluting liposome nanoparticles, phycocyanin eluting liposome nanoparticles, and clindamycin and phycocyanin eluting liposome nanoparticles against biofilm of MRSA and S. aureus isolates.

Methods : The fifty clinical isolates of MRSA and S.aureus were collected from patients with bedsores at Loghman Hospital of Tehran-Iran. The biochemical and molecular tests were used to detect S. aureus and MRSA. Liposomes were synthesized using the thin film hydration method and were characterized by X-ray diffraction, Zeta potential measurement, SEM, and TEM. The encapsulation of clindamycin and phycocyanin was determined. The effect of the clindamycin eluting liposomes, phycocyanin eluting liposomes, and clindamycin and phycocyanin eluting liposomes was evaluated against one, three, and five-day-old biofilm of MRSA and S.aureus isolates using TTC method and then evaluated with Confocal laser scanning microscopy (CLSM).

Results : The round-shaped nanoparticles of clindamycin and phycocyanin eluting liposome were 230 nm and had -22 zeta potential. The encapsulation of clindamycin and phycocyanin in the liposome was 98% and 89%, respectively. Clindamycin and phycocyanin eluting liposomes removed one, three, and, five-day old biofilms of S. aureus and MRSA at the concentrations of 125 µg/mL, 250 µg/mL, and 250 µg/mL, respectively. The vesicular structure of liposomes seems to enhance antimicrobial activity by improving drug performance compared to free drugs and eliminating S. aureus biofilm.

Conclusion : Nanoparticles of antibiotics eluting liposomes can be promising for the treatment of MRSA and S. aureus biofilms related infections. The phycocyanin pigment with antibiotics eluting liposome can duplicate the effect of antibiotics eluting liposome.

Keywords : Nanoliposome, Phycocyanin Pigment, Biofilm, Bedsores, S.aureus, Methicillin Resistant S. aureus (MRSA)

P171-613: Evaluation of Antibacterial Activity of Essential Oils of Aerial of Heracleum persicum L. from Ramsar - Iran

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Background and Aim : Essential oils of the aromatic plants are compounds with different therapeutic characteristics, including antimicrobial effects. Besides, essential oils have also shown to exert antiviral, anti-toxigenic, anti-parasitic, and insecticidal activities, which are attributed to the function of their special compounds. Heracleum persicum is a flowering plant and native to Iran that commonly known as (Golpar) and it belongs to Apiaceae family. In this project the evaluation of antibacterial activity of essential oils of aerial of Heracleum persicum L.

Methods : The aerial parts of Heracleum persicum L. were collected from Ramsar, Iran. The essential oils were extracted using Clevenger apparatus system by Hydro-distillation method. Chemical composition was measured using the gas chromatography-mass spectrometry (GC-MS). The antibacterial activity of essential oils was determined using the disk diffusion method.

Results : The major constituents in Heracleum persicum L. essential oils were Hexyl butyrate, α-terpineol, octyl acetate, p-cymene and etc. The essential oils of aerial parts of Heracleum persicum L. exhibited good antibacterial potential against gram positive and gram negative bacterial strains.

Conclusion : Thus, the results of useful bioactive compounds aerial parts of Heracleum persicum L., making it a promising candidate for further studies.

Keywords : Heracleum persicum L., Hydro-Distillation Method, Essential Oils, Chemical Composition, Disk Diffusion Method.

P172-614: Bioactive Compound, Radical Scavenging and Antibacterial Activity of Aqueous Extract of Flowers of Echium amoenum Fisch. & C.A.Mey. from Guilan – Iran

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Background and Aim : Natural products have been a major source of new drugs. Plant used for traditional medicine contains a wide range of substances that can be used to treat chronic as well as infectious diseases. This research set to assess phytochemicals in the aqueous extracts of Echium amoenum Fisch. & C.A.Mey. flowers by qualitative and quantative screening procedures.

Methods : The Echium amoenum Fisch. & C.A.Mey. flowers were collected, and the extract was provided from aqueous by maceration method. The phytochemical assessment was done applying standard methods. Later, in vitro antioxidant activity of aqueous extracts were assayed by 1,1-diphenyl-2-picrylhydrazyl (DPPH0) free radical scavenging method. Then, the in vitro antibacterial activity of the aqueous extract of flowers of Echium amoenum Fisch. & C.A.Mey. against Staphylococcus aureus (PTCC 1113) and Escherichia coli (PTCC 1399) determined by the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) assay.

Results : The results of the phytochemical screening of aqueous extract of flowers of Echium amoenum Fisch. & C.A.Mey. were (Flavonoids, Quinones, Saponins and Phenols) presented. The value IC50 of aqueous extract determined 18.95 mg/ml. Also, the aqueous extract of flowers of Echium amoenum Fisch. & C.A.Mey. showed significant antibacterial activity against both gram positive and gram negative bacteria.

Conclusion : Thus, the aqueous extract of flowers of Echium amoenum Fisch. & C.A.Mey. would be helpful for the preparation of pharmaceutically useful drugs to destroy pathogenic microbes.

Keywords : Echium amoenum Fisch. & C.A.Mey., Maceration Method, Saponins, Staphylococcus aureus, Infectious Diseases.

P173-623: Immunogenicity of the combination of two outer membrane proteins, Oma 87 and BauA against Acinetobacter baumannii infection in a murine model

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Background and Aim : Acinetobacter baumannii is a mortal nosocomial pathogen. Outer membrane proteins (OMPs) of gram-negative bacteria are known as powerful strong immunogens.BauA is the corresponding siderophore receptor of A. baumannii. In addition to antibacterial and opsonizing activity, monoclonal antibodies produced against IROMP can also block the in vitro iron absorption system. Oma87 has been stated introduced as an immunogenic outer membrane protein per via contrary reverse vaccinology. In this study, After purification, they were injected in combination to create immunity in mice. After that, the level of IgG in them was evaluated by ELISA method and the established safety was evaluated. As a result, the administration of combination antigens provides better protection than individual antigens.

Methods : In this study, both Oma87 and BauA proteins were cloned into the plasmid pET28a. After purification of proteins, dialysis was performed by dialysis membrane. they were injected in combination to create immunity in mice. Blood samples were taken from mice at least once every 15 days and combined injections were performed. After that, the level of IgG in them was evaluated by ELISA method and the established safety was evaluated.

Results : The combination of the two antigens led to significant protection against A.baumannii in comparison to the single antigens. As a result, the administration of combination antigens provides better protection than individual antigens. The ELISA results showed maximum antibody titer after the third booster injection in mice. Difference in antibody titer between first and second doses of immunization was statistically significant. The rise in antibody titer after third immunization was also significant while there was no statistically significant rise after third dose.

Conclusion : Protective effect of A. baumannii receptor protein (BauA), a cross-antigen that is a key protein in the iron uptake process and its combination with Oma87, a protein that folds membrane proteins, against bacterial infection in the animal model evaluated And showed better immunity than previous single protein vaccines. Productionof vaccines that

could effectively prevent bacterial colonization could significantly aid diagnostic and therapeutic aspects of nosocomial infections caused by this bacterium.

Keywords : Acinetobacter baumannii, Vaccine, Oma87, BauA

P174-629: Antibacterial effects of silver nanoparticls nursing gowns on geram- positive bacterial

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Background and Aim : Background and Objective: Nosocomial infection is a major challenge in health care system. In fact, it is regarded as one of the risk factors in hospitalized patients. The aim of this study was to determine the antibacterial effect of silver nanoparticles (AgNPs) nursing gowns on germs-positive bacterial.

Methods : Method: this descriptive and analytical study was done on 200 nurses gowns were surveyed in two hospitals of Sirjan city in Kerman Province central area of Iran. At first, antimicrobial activity of silver nano fabrics on Staphylococcus aureus bacteria was confirmed by examining the optical density OD (0.325) medium. Sampling was gathered into the two mods, before using nano gowns and after using nano gowns by using wet sterile swabs. The sample collected were cultured and the formations of colonies were examined and biochemical tests were used to identify isolated bacterial.

Results : Results: the most commonly isolated gram- positive bacterial from normal gowns were Staphylococcus epidermidis (43%) and the lowest pathogen was Streptococcus (1%). In these hospitals, after using nano silver gowns, the amount of microbial load on the clothes were determind zero.

Conclusion : Conclusion: This study showed that gram- positive bacterials of nursing gowns after contact with silver nanoparticles were eliminated.

Keywords : Silver nanoparticle, Gram- positive bacterial, Gown, Antibacterial, Nurs.

P175-643: Determination of Minimum Inhibitory Concentration (MIC) and Minimum bactericidal Concentration (MBC) of Copper (Cu) and Silver oxide (AgO) Nanoparticles against Actinomyces viscomus

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Background and Aim : Human societies are still in difficulty encounter with human pathogens, despite advances in personal health and control of various diseases. One of these problems is tooth decay, which causes annoyingly high mortality and financial losses in human societies. In recent years, nanotechnology has been able to make profound developments in the research and production of various products. Therefore, in this study antibacterial effects of Silver oxide (AgO) and Copper (Cu) nanoparticles are investigated through various microbial tests on Actinomyces viscomus, which act as primary colonizers in the formation of dental plaque.

Methods : In each tube 1 ml bacterial suspension and 1 ml nanoparticles suspension added relatively. In this case, the final volume in each well was equal to 2 ml and the final concentration of the bacterium was equal to 5 ×105. Incubated at 37 °C for 18 h. To determine the minimum bactericidal concentration (MBC), 100 µl of the tubes were taken and streaked on plates with a Muller Hinton Agar. Then they examined for bacterial growth and colony formation. For the study of Effect of nanoparticles in 24-hour culture, is done in the same way as above. Recap the tubes and incubated at 37 °C for 24 h. Result observed spectrophotometer at 600 nm wavelength.

Results : the minimum inhibitory concentration (MIC) of Copper nanoparticles for Actinomyces viscomus was 78.125 ppm, and the Minimum bactericidal concentration (MBC) was obtained 156.25 ppm, though for the Silver oxide nanoparticle, the MIC was 156.25 ppm and MBC was 312.5 ppm. The growth of bacteria in the presence of nanoparticles has declined after 24-hour incubation.

Conclusion : Based on the data obtained in this test, Copper nanoparticles were detected more fatal and antibacterial than Silver oxide nanoparticles. It was also found that by increasing the concentration of nanoparticles, their fatal rate increased significantly. According to other studies carried out in this area, which all prove antibacterial properties of these nanoparticles at low concentrations, these nanoparticles can be used as antibacterial agents in combination with mouthwashes and toothpastes in the market.

Keywords : Copper, Silver oxide, Nanoparticles, Actinomyces viscomus.

P176-647: Frequency distribution of secondary bacterial infections (aerobic and anaerobic) in patients admitted to the dermatology ward of Alzahra Hospital, Isfahan University of Medical Sciences

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Background and Aim : The prevalence of bacterial infections in hospitalized patients has increased dramatically in recent years. Antibiotic resistance also increases the importance of recognizing the abundance of bacteria associated with secondary bacterial infections. Therefore, the aim of this study was to investigate the frequency distribution of secondary bacterial infections (aerobic and anaerobic) in patients admitted to the dermatology ward of Al-Zahra Hospital, Isfahan University of Medical Sciences.

Methods : This analytical descriptive study was performed on 200 dermatological patients admitted with secondary bacterial infection in the dermatology ward of Al-Zahra Hospital who underwent smear and culture. Patients' file information was reviewed and information including patient's sex, patient's age, type of bacteria, type of skin disease, type of underlying disease was prepared. After collecting data using frequency, percentage and paired t-test, the results were analyzed using SPSS software version 21.

Results : 77 women (38.5%) and 123 men (61.5%) had secondary bacterial infection. The minimum age of patients was 7 and the maximum was 93 years with a mean age of 48.97 20 20.075 years. Also, the patients were hospitalized for a minimum of 2 and a maximum of 32 days, with a mean hospital stay of 11.33 6. 6.1 days. 166 cases (83%) of the samples were cultured in the laboratory and 34 cases (17%) were smeared. Staphylococcus species included a total of 107 cases (53.5%) of the total bacteria involved in the development of secondary bacterial infection.

Conclusion : The main bacterial agent in secondary infections in patients admitted to the dermatology ward of Al-Zahra Hospital of Isfahan University of Medical Sciences is Staphylococcus aureus.

Keywords : secondary bacterial infections, Skin disease, Systemic disease

P177-658: The comparison of the antibacterial and antibiofilm activities of Zingerone and Niosome containing Zingerone against Methicillin- Resistant Staphylococcus aureus (MRSA) isolates, isolated from diabetic ulcers

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Background and Aim : Introduction Methicillin Resistant Staphylococcus aureus (MRSA) is major cause of nosocomial and community acquired infections and represent a significant burden on the healthcare system. The formation of biofilm, decreases the susceptibility to antimicrobials and immune defence, making these infections difficult to eradicate. Zingerone (the active ingredient of ginger root) is a nontoxic and inexpensive compound with varied pharmacological activities. The goal of this study was to evaluate the effect of antibacterial and antibiofilm activities of Zingerone and Niosome containing Zingerone, against pre-formed biofilm of MRSA isolates, isolated from diabetic ulcers.

Methods : Materials & Methods About 62 MRSA isolates were collected from patients with diabetic ulcers who were referred to Loghman Hospital of Tehran, Iran. Niosome containing Zingerone were synthetized using thin layer hydration method and were characterized using X- ray diffraction, Zetapotential measurement and SEM. The effect of the Zingerone and Niosome containing Zingerone was evaluated against one, three and five day old biofilm of MRSA isolates using Crystal violet method.

Results : Results The round-shaped Niosome containing Zingerone had a diameter of 196.1 nm and a -37.3 mV zeta potential. Zingerone removed one, three and five day old biofilms of MRSA at the concentrations of 1000 µg/mL, 1000 µg/mL and 2000 µg/mL while the Niosome containing Zingerone removed 1, 3 and 5 day old biofilms at the concentration of 250 µg/mL, 250 µg/mL and 500 µg/mL.

Conclusion : Conclusion Niosomes containing Zingerone is a promising treatment to combat MRSA and its Biofilms.

Keywords : Key words: Niosomes containing Zingerone, Biofilm, Methicillin Resistant Staphylococcus aureus (MRSA).

P178-665: Synthesis and investigation of antibacterial properties of nanosheet carbon nitride

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Background and Aim : Bacterial infections and their transmission are a significant threat to human health, and controlling the harmful effects of microorganisms in recent years has become unavoidable. Currently, the treatment of these infections is mainly limited to the use of antibiotics, which has inevitably led to the rapid emergence of antibiotic-resistant bacterial species in the past few decades. Therefore, developing a new strategy to inactivate bacteria is necessary and of great importance. One of the materials that has attracted the attention of many scientists in recent years due to its similarity to graphene as a non-metallic material is nanosheet carbon nitride (g-C3N4 Nanosheet). The purpose of this study is to synthesize and investigate the antibacterial properties g-C3N4 Nanosheet.

Methods : In order to synthesize carbon nitride nanosheets, the melamine precursor was subjected to heat treatment in an electric furnace. Then, XRD, FE-SEM, BET, FTIR and UV-VISIBLE characterization tests were used to identify and check the properties of nanomaterials. Finally, the antibacterial properties of g-C3N4 Nanosheet against Gram-positive and Gram-negative bacteria were evaluated using the Colony Count method, and MIC and MBC method.

Results : The analyzes performed while confirming the size and structure of the synthesized nano material showed the separation of the carbon nitride plates. Also, the results of the Colony Count test showed that the colony density of both bacterial strains decreased after treatment with nanomaterials. In addition, the minimum bacterial growth inhibition concentration (MIC) and minimum bactericidal concentration (MBC) of carbon nitride nanosheets for each of bacteria was equal to 25 µg/mL.

Conclusion : One of the reasons that g-C3N4 Nanosheet can destroy bacteria is that the sharp edges of the nanomaterial lead to the rupture of the bacterial membrane and its death. The carbon nitride nanosheets synthesized in this study can be mentioned as a nano material with unique features such as high biocompatibility, low cost and simple synthesis, and high speed of the process.

Keywords : Antibiotic Resistance, nanosheet carbon nitride, Antibacterial property

P179-685: Synthesis and investigation of antibacterial carbon nitride

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Background and Aim : Nosocomial infections have a high prevalence and are a serious problem for health care centers and they impose a lot of costs on patients and health care centers every year. The emergence of multi-drug resistant microorganisms as a result of hospital infections and bacterial resistance to antibiotics, is one of the most important health problems around the world and threatens human health in the modern era. Therefore, it is of great importance to develop a new strategy to inactivate bacteria. Graphite carbon nitride (g-C3N4) as a new class of two-dimensional non-metallic semi-conducting nanomaterials whose structure is close to graphene in terms of being planar has recently attracted the attention of many scientists. Our aim in this study is to synthesize and investigate antibacterial properties. of Carbon nitride.

Methods : For the synthesis of graphite carbon nitride, raw materials such as melamine are subjected to heat treatment using a Muffle furnace. SEM, EDS, MAP, XRD, UV-VIS, FTIR characterization tests are used to check carbon nitride characteristics such as particle size and structure, and to evaluate the number of Gram-positive and negative bacteria colonies or the diameter of the non-growth halo in order to determine the properties. Antibacterial MIC and MBC tests are used

Results : Characterization analyzes were performed to confirm the particle size and structure. Also, the colony count results of the experiment showed that the colony density of both bacterial strains decreased after exposure to the nanomaterial. In addition, the minimum bacterial inhibitory concentration (MIC) and the minimum lethal concentration (MBC) of graphite carbon nitride for each of the bacteria. It was equal to 25 micrograms per milliliter.

Conclusion : Graphite carbon nitride nanomaterial, due to their unique physical, chemical and mechanical properties, especially the high specific surface area and the very sharp edges

of these two-dimensional materials that can damage the outer membrane of bacteria and because of biocompatibility High, low cost and quick and easy synthesis are more important compared to other nanomaterials.

Keywords : Antibiotic Resistance, Carbon nitride, Antibacterial property

P180-703: In-vitro activity of antibiotics combination against carbapenem resistant Acinetobacter baumannii

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Background and Aim : The present study was performed to investigate in-vitro effect of antimicrobial agent's combination against carbapenem-resistant Acinetobacter baumannii.

Methods : Ten carbapenem resistant A. baumannii isolates were collected from different specimens. The resistance to meropenem were detected by the phenotypic and PCR methods. The antimicrobial effect of antimicrobial agents was determined by the micro broth dilution method according to the CLSI guideline. To synergetic effects of the drugs combinations, the checkerboard assay was used for fractional inhibitory concentration (FIC) determination

Results : The highest synergic interaction was observed in colistin/meropenem and amikacin/meropenem (8 of 10 isolates), and the lowest synergic interaction was observed in colistin/amikacin and colistin/ciprofloxacin (2 of 10 isolates).

Conclusion : Distinct and standard testing of inhibitory activity of the antimicrobial agent's combination is required for treatment of high level resistant pathogens. Colistin/meropenem and amikacin/meropenem were more effective against carbapenem resistant A. baumannii.

Keywords : Acinetobacter baumannii, Antimicrobial Combination, Carbapenem-resistant

P181-748: Multidrug - resistant pathogens in burn wound and using nanoparticles as advanced therapeutic strategies

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Background and Aim : In the early days of admission to burn patients, gram-positive bacteria were the dominant isolates with a more sensitive antibiotic pattern. However, the emergence of gram-negative bacteria that are more resistant later occurs

Methods : In this review article, we will discuss about different aspects of multidrug resistant pathogens in burn wounds, in addition to emphasizing on the full role of these pathogens in burn patients, to mention the importance of nanotechnology in dealing with them

Results : An effective way to avoid antibiotic resistance and survival of burn patients is using a multidisciplinary therapeutic approach that involves the participation of infectious disease specialists and pharmacists in addition to burn surgery. The need to discover new antibiotics and hyperdynamic state fore severe burn patients has challenged the treatment of multi-drug resistant infections, and the use of nanoparticles is a suitable alternative.

Conclusion : Preventing the outbreak of MDR bacteria in this population requires a multi-step approach including hand hygiene, antimicrobial care, operation optimization, careful use of medical equipment, and environmental controls. Given the many individuals, social and economic consequences of burn wounds and that treatment of multidrug-resistant infections caused by these wounds have always been a controversial issue among physicians, the development of new and efficient methods is essential. Nanotechnology has brought about wide-ranging changes in various industries, especially pharmaceuticals, and recently the use of nanoparticles with antibiotics has received more attention due to many characteristics such as surface properties, drug delivery, minimizing systemic exposure to drugs and especially more antimicrobial effects.

Keywords : Burn wounds, Multidrug-resistant, Nanoparticles, Treatment

P182-11: Molecular Identification of Mycoplasma¬ Hominis in Vaginal Sample of Women Referred to the Infertility Center of Fatemieh Hospital in Hamadan

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Background and Aim : Mycoplasma hominis is one of the smallest bacteria that isolated from natural source and sometimes found as pathogenic flora in plants, animals, and humans. The aim of study was molecular identification of M.hominis in vaginal sample of women referred to the infertility center of Fatemieh Hospital in Hamadan.

Methods : In this Cross-sectional study, vaginal swab samples from symptomatic females were collected and M.hominis identified by PCR and Real-Time PCR. DNA was extracted using extraction kit. M.hominis strains were identified using 16 S rRNA gene. Finally, Statistical analysis was performed using SPSS 21 software.

Results : A total of 234 vaginal samples were studied in women with a mean age of 39.8 years. The results showed that M.hominis was identified by PCR (13%) and Real-time PCR (15%) methods, respectively. There was a significant relationship between PCR and Real-Time PCR methods ($P \leq 0.05$).

Conclusion : Real-time PCR was successfully used for rapid and accurate diagnosis of M.hominis. This method, compared to the PCR has significant potential for rapid, accurate and highly sensitive molecular detection of M.hominis

Keywords : Mycoplasma hominis, Infertile women, PCR, Real-Time PCR

P183-15: An electrochemical DNA biosensor based on a gold nanostructure for the detection of Enterococcus faecalis gene sequence

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Background and Aim : Bacteria, viruses and parasites are potential pathogens and can be a source of infection and sepsis. Therefore, detection of pathogenic bacteria is a key step toward preventing problems related to the human's health and safety. The enterococci, especially Enterococcus faecalis (EF) can act as agents of infections, particularly in elderly patients with serious underlying diseases and other immunocompromised patients who have been hospitalized for prolonged periods, treated with invasive devices and/or have received broad-spectrum antimicrobial therapy.

Methods : In the present study, we report the fabrication of a novel electrochemical DNA biosensor based on electrodeposited gold nanostructures as a transducer substrate combined with toluidine blue (TB) as a redox marker. A specific thiolated ssDNA sequence was immobilized on the transducer substrate, and DNA hybridization was followed by differential pulse voltammetry.

Results : DNA biosensor had a long-time stability, good fabrication reproducibility and good regeneration ability. The DNA biosensor showed excellent performances with high sensitivity and good selectivity. The DNA biosensor was applied to detect a synthetic target in a line arrange of 1.0 × 10?17-1.0 × 10?10 mol L?1with a limit of detection (LOD) of 4.7 × 10?20 mol L?1. In addition, LOD of the DNA biosensor for the detection of genomic DNA was found to be 30.1 ng µL?1.

Conclusion : The developed biosensor can be employed as an alternative method for EF detection without using PCR amplification in clinical samples for positive/negative diagnosis.

Keywords : E. faecalis, DNA biosensor, Genosensor, Detection

P184-16: DNA electrochemical biosensor for the detection of 16s rRNA gene sequence related to the Enterococcus faecalis

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Background and Aim : Some of microorganisms are potential pathogens that can be infectious agents under some circumstances. From enterococcal species, Enterococcus faecalis (E.faecalis) and Enterococcus faecium commonly colonize and infect human in detectable numbers. They are a cause of bacteremia, bacterial meningitis, urinary tract infections, endocarditis, wound infections, and various other infections in human. Enterococcal infections now roughly account for 12% of nosocomial infections in US with a major cause by E. faecalis (> 80%) and Enterococcus faecium being major reason of the remaining Infections.

Methods : In the present study, an Enterococcus faecalis (E. faecalis) DNA biosensor (ef-biosensor) was fabricated to quantify the bacterium genome. A specific E. faecalis DNA probe was selected from 16S rRNA sequence of E. faecalis and immobilized on a gold electrode surface in an optimized time to fabricate the ef-biosensor.

Results : The ef-biosensor detected a synthetic target of the probe with a detection limit of 3.3 amol L-1 and with a nice selectivity to resolve from one-, two- and three-base mismatched sequences. In addition, the bacterium genomic DNA was quantified with a detection limit of 7.1×10-9 ng mL-1 in a concentration range of 1.1×10-7 to 1.1 ng mL-1. The ef-biosensor had a long-time stability, good fabrication reproducibility and good regeneration ability.

Conclusion : The ef-biosensor was successfully applied for E. faecalis detection in human samples.

Keywords : E. faecalis, Pathogen, Genosensor, Electrochemical biosensora

P185-61: Oral Microbiota Dysbiosis as a Prognostic Biomarker for Colorectal Cancer

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Background and Aim : Colorectal cancer rates are growing around the world. In terms of diagnosis this disease is in the fourth place. In the recent years, the roles of symbiosis microbes, which live in the human body especially in the oral cavity, and their indirect role in colorectal cancer development have received much scientist's attention. These microbes have a critical role in metabolism and homeostasis of the body through secretion of immune molecules, signaling pathways modulators and cell cycle intermediates. Recent studies showed that oral bacteria have found in tumor tissues in patients with diagnosed colorectal cancer.

Methods : Literature review

Results : With advance in metagenomics technology, it is possible to detect and compare more precisely the symbiotic microbe's communities that live in oral and digestive tract of human. Studies showed that detection of symbiosis bacteria in the oral cavity, which could be find in colorectal tumor tissue, might be consider as a prognostic factor for further therapeutic purposes. In this review, with an eye on future applications, we intend to consider metagenomics studies in oral cavity for introducing novel prognostic biomarkers for disease detection, control and management.

Conclusion : Bacterial species, which have been found in tumor tissue of patients with colorectal cancer, have an equal frequency in the oral cavity. Metagenomics studies show some of the particular bacterial species of the oral cavity such as Porphyromonas spp., Peptostreptococcus spp., Prevotella spp., Parvimonas spp. and Gemella spp. are associated with colorectal cancer development.

Keywords : Oral Microbiota, Colorectal Cancer, Prognostic Biomarker, Metagenomics

P186-75: Diagnosis and treatment of Merkel cell polyomavirus

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Background and Aim : Merkel cell polyomavirus (MCPyV) causes a very aggressive and relatively rare skin cancer called Merkel cell carcinoma (MCC). Diagnosis of the virus is still at a research phase and is generally not available as a clinical test. Diagnosis of viral DNA is performed using PCR or by Southern blot. Care should be taken when interpreting PCR results, as PCR results are susceptible to false-positive contamination and a significant proportion of healthy skin samples can indicate low levels of infection.

Methods : Antibodies have been developed to stain T antigens in tumor tissues and seems to be specific for MCV-infected tumor cells. Blood tests have also been developed which suggest that the majority of adults have been exposed to MCV and may continue to carry it as an asymptomatic infection. Treatment guidelines are not different for Merkel cell carcinoma with or without MCV.

Results : A recent nationwide study in Finland found that MCV-positive tumors had a better prognosis than uninfected tumors. If confirmed, routine virus detection could benefit future medical guidance. The virus itself is not known to be susceptible to current antiviral drugs.

Conclusion : Recent studies suggest that survivin oncoproteins activated by MCV large T proteins that target retinoblastoma proteins and that survivin inhibitors can delay tumor progression on animal model. MCVs are targets for cell-mediated immune responses, and therefore important research efforts focus on immunotherapies that may benefit MCC patients.

Keywords : Merkel cell polyomavirus (MCPyV), Merkel cell carcinoma (MCC), T antigens, survivin oncoproteins, immunotherapies

P187-115: Comparison of Penicillinase and β–lactamase enzymes in validation of sterility test in some of injectable β–lactam antibiotics

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Background and Aim : Sterility test is an essential test for injectable products in pharmaceutical industries. In this test, inhibition effect of materials must be neutralized. β-lactamases break β–lactam ring of some antibiotics such as Cephalosporins, Carbapenems, etc. The aim of this study was to apply penicillinase and LacbusterTM-S (betalactamase) enzymes in sterility test and their validation in some of injectable β–lactam antibiotics such as Cefazolin Sodium, Ceftriaxone Sodium, Ceftazidime Sodium Carbonate, Cefotaxime Sodium, Imipenem-Cilastatin and Meropenem with Sodium Carbonate.

Methods : One gram/L peptone from meat (fluid A) including different dilutions of enzymes were inoculated with S. aureus, P. aeruginosa, B. subtilis, C. sporogenes, C. albicans and A.niger separately. Then, above mentioned antibiotics were solved in prepared fluid A, filtered and washed with the same dilution of Fluid A. Filters put in FTM and TSB with the same dilution of enzymes. Media were incubated 3 days for bacteria at 30-35 ºC and 5 days for mold and yeast at 20-25 ºC.

Results : Our results showed growth of mold and yeast were seen in enzyme free media containing antibiotics. In this study we found that 14286 Unit/ml of penicillinase were needed to break Cefazolin (0.5gr), Ceftriaxone, Ceftazidime and Cefotaxime (1gr), while, sterility test of Imipenem-Cilastatin validated with 85741 Unit/ml penicillinase concentration in solvent, washing fluid and media. Furthermore, there were 3× 106 Unit/ml in solvent, washing and 2 × 105 Unit/ml in media for meropenem, but these amount were decreased to 200IU for β–lacII (Lacbuster).

Conclusion : Lesser use amount and long lasting form of enzyme (freeze dried power) are two advantages of LacbusterTM-S.

Keywords : β–lactam, β- lactamase, Sterility test, Validation

P188-139: Designing a non-enzymatic system at constant room temperature as a signal amplification technique for the detection of Klebsiella pneumoniae

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Background and Aim : Encapsulated, gram negative, and non-motile bacilli Klebsiella pneumoniae is one of the most common secondary infection agents enlisted as a serious threat by the CDC according to its wide-range drug resistance. Amid vast molecular diagnostic tools, nano-biosensing is a proper candidate to provide simplicity and accuracy simultaneously. Herein, a signal amplification autonomous enzyme-free machinery was designed to sense a virulent gene in Klebsiella pneumoniae specifically.

Methods : A target gene in Klebsiella pneumoniae, responsible for the capsule diversity, was selected. Two oligonucleotides as the main components of the system were created and verified by particular online tools. The gene was added to the reaction mixture as a trigger. The signal amplification process was conducted at a constant room temperature. During a one-hour incubation at 25 ℃, color differentiation between the positive and the negative samples was monitored. The distance between nanostructures was measured by TEM imaging.

Results : The results demonstrated that the nanostructures were more aggregated when the target gene was absent. However, a step-by-step reaction cascade was conducted in the presence of the target, leading to more relative stability in the solution, which was caused by the further distance between the secondary structures (that are only formed when the amplification is implemented). The visually detectable more-reddish color of the positive samples was interpreted as a result of the abovementioned stability, which was confirmed by TEM images.

Conclusion : The selected gene, which is only present in K. pneumoniae, plays a role in its pathogenicity and antigenicity, meaning that the gene is worth diagnosing and it guarantees the specificity of the method. The developed technique could specifically sense the pathogenic nucleo-biomarker and amplify the signal at room temperature, needless of any enzyme and sophisticated instrumentation. The fact was confirmed by both in-silico and in-vitro analyses.

Keywords : Signal amplification, Nucleo-biomarker, Direct diagnosis, Klebsiella pneumoniae

P189-242: Detection of Chlamydia abortus sheep abortion specimens by Nested PCR

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Background and Aim : From a long time ago up to the present time, sheep abortion has been considered as one of the most important problems in the sheep industry in many sheep-breeding countries, including Iran and it causes heavy damages to the livestock economy of countries every year. Chlamydia abortus is one of the most important infectious agents that can cause abortion in ruminants. This microorganism causes ovine enzotic abortion in sheep and goats, but is less important in cattle. Chlamydia abortus usually affords to abortion in late pregnancy. In addition, infection with this microorganism may lead to stillbirth or the birth of weak lambs. This project was implemented with the aim of investigating the rate of chlamydial abortion in sheep farms around Tabriz.

Methods : In this project, 48 cases of aborted embryos (late in pregnancy) referred to Majid Laboratory from September 2020 to May 2021 were randomly selected. In the laboratory, after necropsy, using aseptic techniques samples were taken from liver, spleen, lung, heart, brain and abomasum contents and were kept at -20 ° C until DNA extraction. After DNA extraction, presence of Chlamydia abortus was examined by a Nested PCR in the samples.

Results : According to the results, 2 samples out of 48 (4.17%) was positive for Chlamydia abortus.

Conclusion : Isolation of Chlamydia abortus as one of the most important causes of abortion from the reference samples around Tabriz indicates that special attention should be paid to expanding researches and implementing preventive and control measures in the province.

Keywords : Chlamydophila abortus, abortion, sheep, Nested PCR

P190-346: In silico analysis and experimental study on Bst DNA polymerase 1 Large fragment (Bst pol 1 L.F) in E.coli

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Background and Aim : Nowadays, isothermal amplification techniques like loop mediated isothermal amplification (LAMP), are getting more attention in comparison to other common DNA amplification methods same as PCR, due to their benefits. LAMP's enzyme is a type of DNA polymerase1 which was extracted from Geobacillus stearothermophilus strains and termed Bst pol 1. This paper is aimed to study in silico analysis in order to clone and to express Bst pol1 large fragment (Bst pol1 L.F) in E.coliBL21 (DE3) plysS.

Methods : The nucleotide sequence encoding Bst pol1 L.F was obtained from NCBI. Secondary structure consensus prediction was performed using the SPOMA method, PSIPRED, ProtParam, Pepstats, Scratch Protein Prediction, and Recombinant Protein Solubility Prediction. Moreover, two strains of Geobacillus stearothermophilus PTCC1713 and IBRC-M10771were obtained from internal resources, and three pairs of primers were designed including diagnostic primers and cloning primers. They degenerated primers to investigate the Bstpol1L.F gene in Iranian native stains.

Results : The codon usage bias in E. coli was upgraded the CAI from 0.71 to 0.87, and GC content was optimized to increase the half-life of the mRNA. A secondary structure study showed Bst pol1 L.F is a hydrophobic protein and its solubility upon overexpression with a probability of 0.882074 and possibility of expression in inclusion bodies of 0.798. The aliphatic index computed by ExPasy's ProtParam showed that mRNA was efficiently stable for translation in the host. The encoding sequence was optimized and synthesized, and a pET-28a (+)-Bst pol1 L.F (pEBpol1 L.F) recombinant vector was produced. The cloning was confirmed by PCR and double digestion techniques. The accuracy of expression in transformants was analyzed by applying SDS-PAGE and Western blotting which showed a band around 66.62 kDa associated with Bst pol1 L.F protein.

Conclusion : No gene was detected using designed primers in native strains, indicating that maybe there is some difference between the Bst pol1 L. F gene sequence in native strains versus the gene submitted in NCBI data bank.

Keywords : cloning and expression, Bst pol1 L. F, Geobacillus stearothermophilus, Loop mediated isothermal amplification (LAMP), in silico

P191-380: The effect of Bacillus subtilis natto on the gene expression level of E-cadherin in colonic carcinoma cell line Caco2

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Background and Aim : Gut microbiota and host genetic alterations, such as downregulation of E-cadherin expression in the gastrointestinal tract, are tightly associated with the development of colorectal cancer. Bacillus subtilis natto is an effective treatment probiotic supplement for various diseases including colon cancer. In this study, we investigated the gene expression of E-cadherin in Caco-2 cell line treated with B. subtilis natto.

Methods : The lyophilized powder of B. subtilis natto (ATCC 7059) was cultured in BHI broth under facultative anaerobic conditions and placed in a shaker incubator for 24 hours. Th colonic carcinoma cell line Caco-2 was treated with different MOIs of live bacteria. MTT assay was used to assess the viability of Caco-2 cells upon treatment. The effect of B. subtilis natto on the gene expression level of E-cadherin was examined by RT-qPCR.

Results : Based on the results obtained in this study, B. subtilis natto significantly increased the gene expression level of E-cadherin in Caco-2 cells compared to untreated control.

Conclusion : The results of this study showed that probiotic B. subtilis natto can increase cell-cell adhesion through E-cadherin in Caco-2 cells. Taken together, probiotic B. subtilis natto can be regarded as an effective supplementation in the treatment of colorectal cancer.

Keywords : Bacillus subtilis natto, Probiotic supplementation, E-cadherin, RT-qPCR, Caco-2 cells

P192-390: A novel electrochemical biosensor for detection of Streptococcus penumoniae

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Background and Aim : We have constructed a novel electrochemical biosensor for detection and quantification of the Streptococcus Pneumoniae bacteria (SPB) based on change in electrochemical impedance spectroscopic (EIS) responses of the biosensing system.

Methods : A glassy carbon electrode (GCE) was chosen as the platform of the biosensor and it was modified with lead nanoparticles (Pb NPs) and then, DNA-[FAM]CGC AAT CTA GCA GAT GAA GCA GGA AAA AAA AAA [Thiol] (DNA-FAM-S) was loaded onto Pb NPs as a selective probe for sensitive and selective deter- mination of the SPB. After electrochemical and microscopic characterization of the modifications applied to the GCE, analytical characterization of the biosensor was performe.

Results : The biosensor had a limit of detection of 0.0022 ng/ml ~ 622 SPBs and a sensitivity of 3432.9 ? (ng/ml). The biosensor response was selective, sensitive, stable, repeatable and reproducible in determination of the SPB. The biosensor performance for determination of the SPB was comparable with the NanoDrop method which encouraged us to recommend it for practical purposes.

Conclusion : This paper was very interesting from experimental point of view which developed a novel electroanalytical method for determination of the SPB which showed a comparable performance with a reference method. Interesting results were obtained from different sections of this study and we justified them. Structure of the biosensor was efficiently engineered whose selectivity was guaranteed by the presence of the DNA-FAM-S while its sensitivity was supported by the presence of PbNPs and using the EIS as a sensitive electroanalytical method. The biosensor showed good stability, repeatability and reproducibility as well. After calibration of the biosensor response towards determination of the SPB, its performance was statistically and graphically compared with the NanoDrop as a reference method which confirmed a good practical performance for the biosensor for detection and determination of the SPB.

Keywords : Biosensor, Streptococcus Pneumoniae, Electrochemical impedance spectroscopy

P193-397: Biotransducer-conjugated nobel metal nanomaterials as nanobiosensors for pathogenic organisms

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Background and Aim : Pathogenic organisms are a threat to public health, so their quick and timely diagnosis increases the quality of treatment and public health. Noble metal nanomaterials (NMNs) due to their unique physicochemical properties, high surface area, diverse shapes, size, and composition-dependent features such as surface plasmon resonance and quantum confinement take part in the designing of biosensing nanoplatforms with high sensitivity and performance. NMNs are conjugated with biotransducers (like the DNA, enzymes, antibodies, aptamers, etc) and generate nanobiosensors that possess signal amplifying ability, high specificity, and low concentration-diagnosis ability of biomarkers. According to the physicochemical features of NMNs, biosensing of approaches of NMNs are including localized surface plasmon resonance (LSPR), fluorescence enhancement/quenching, surface-enhanced Ramman spectroscopy (SERS), chemical activity, etc. This review examines biosensors based on biotransducers conjugated to NMNs for biosensing of pathogenic organisms.

Methods : In order to select the articles, the papers of the years 2010-2022 were examined in the Google Scholar, PubMed, and Scopus databases with the keywords of metal nanoparticles, biosensors, transducers, and biomolecules. And information extraction from basic studies has been done. The keywords were selected by the MeSH browser.

Results : Gold nanoparticles (AuNPs)-conjugated polyclonal antibodies are effective for rapid and sensitive sensing of Escherichia coli. Silver nanoclusters(AgNCs) and cystine-rich signal probe DNA conjugated with AuNPs as electrochemical DNA biosensors showed enhanced selectivity and proper stability for sensitive determination of Salmonella. Anti-RSV polyclonal antibody conjugated to metallic nanoparticles (Cu, Ag, and Au) as LSPR-based biosensors, especially functionalized copper (Cu) nanoparticles, have high specificity for the diagnosis of Respiratory syncytial virus (RSV).

Conclusion : Biotransducer-conjugated NMNs can act as nanobiohybrides platforms for high sensitive detection of pathogenic organisms with high specificity and selectivity.

Keywords : Metal nanoparticles, Biosensors, Transducers, Biomolecules

P194-462: Aptamer-based nanobiosensors for the detection of E.coli

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Background and Aim : Escherichia coli (E.coli) is a pathogenic bacterium that is transmitted to humans through food. There are many conventional methods for detecting the presence of E. coli, which usually take two to three days. But nanotechnology and new methods have made this diagnosis easier. A simple, fast and environmentally friendly method to detect this pathogen is using aptamer-based nanobiosensors. Aptamers refer to single-stranded nucleic acids (single-stranded DNA or RNA) or oligopeptides capable of binding to a target specifically with high affinity.

Methods : Keywords of aptasensor, nanobiosensor and E.coli were searched in PubMed and Google Scholar databases between 2009 until 2022.

Results : Aptamer-based optical sensors, including visible light, ultraviolet, and fluorescent sensors, have been developed and widely used. Compared with visual detection and colorimetry, E.coli aptasensors based on fluorescence measurement have many advantages of the opinion of detection sensitivity, feature selection, etc.. In the construction of a aptasensor, the target E.coli was captured by antibody-conjugated magnetic beads. Second, RNA aptamers were sandwiched onto the surface of captured E.coli. Finally, heat-released aptamers were amplified using real-time reverse transcription-PCR (RT-PCR). Developed aptamer-based biosensors (aptasensors) based on label-free aptamers and gold nanoparticles (AuNPs) for the detection of E. coli. Aptamers binding to target bacteria are adsorbed on the surface of unmodified AuNPs to attract target bacteria, and detection was performed by aggregation of the aptasensor induced by target bacteria, which is correlated as a red-to-purple color change under high-salt conditions. This aptasensor could detect less than 105 colonies forming units (CFU)/mL of the target bacteria in 20 min or less, and the specificity was 100%.

Conclusion : This review presents new developments in the development of aptamer-based sensors for the diagnosis and treatment of E.coli. Due to the current limitations of common detection techniques in the early diagnosis of infectious diseases, researchers have turned their attention to the development of aptamer-based diagnostics for rapid and efficient non-invasive diagnosis of diseases. Aptamer-based biosensors are gaining importance due to their many advantages over other biosensors. However, the development of biosensors for the diagnosis of several diseases is still a great challenge for scientists and researchers.

Keywords : aptasensor, nanobiosensor, Escherichia Coli

P195-512: Introduction of a novel tellurite-containing selective medium for the rapid phenotypic identification method of hypervirulent Klebsiella pneumoniae isolates

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Background and Aim : Klebsiella pneumoniae has two pathotypes circulating worldwide: classic K. pneumoniae (cKp) and hypervirulent K.pneumoniae (hvKP) strains. hvKps due to the expression of multiple virulence factors has increased the mortality and complications of K.pneumoniae infections. So far, the string test method used for phenotypic identification of hvKps showed low sensitivity and accuracy. Therefore, the aim of this study is to use a method based on the resistance of hvKps to potassium tellurite to design a rapid screening method that has higher accuracy and sensitivity than the string test.

Methods : we collected 477 non-repetitive K.pneumoniae as clinical isolates from two educational hospitals. The hypermucoviscous phenotype of the hvKp isolates was examined by the string test. Since most hvKp isolates carry tellurite resistance genes located on virulence plasmid, they are able to reduce tellurite and form a black colony. Therefore, in this study, we used tellurite-containing selective medium as a rapid screening test. Finally, we evaluated and compared two phenotypic methods using the hvKp molecular identification marker (PCR the aerobactin gene iuc, and iut).

Results : In this study, out of 477 K. pneumoniae isolates, 163 isolates (34.2%) were tellurite-resistant K. pneumoniae isolates, while 62 of the 477 K. pneumoniae isolates (13%) were reported with positive string test and hypermucoviscous phenotype. So they were selected for the molecular identification test. In the PCR method 62.6% (102/163) of tellurite-resistant were hvKp and 48% (49/102) hvKp isolates showed string test positive.

Conclusion : This study showed that resistance to tellurite is strongly associated with hvKp isolates. It seems that most of the large virulence plasmids in hvKps carry tellurite resistance genes. Therefore, this method was found to be superior to the string test for rapid phenotypic hvKp detection

Keywords : Hypervirulent Klebsiella pneumonia, rapid phenotypic identification method, tellurite-resistant, string test, PCR

P196-527: A comparison between a colorimetric and a fluorescent dye in a SARS-CoV-2 reverse transcriptase-loop-mediated isothermal amplification (RT-LAMP) assay

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Background and Aim : Loop-mediated isothermal amplification (LAMP) as a new molecular technique in the third millennium which has a broad application in detection of infectious diseases including emerging contagious disease such as viruses including influenza, Ebola, HIV, Zika. This method also has been wildly used in detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). This virus causes COVID-19 disease and after more than 2.5 years it is still an ongoing pandemic when it was first reported in December 2019. Reverse transcriptase-loop-mediated isothermal amplification (RT-LAMP) is able to amplify the viral gene with 6 primers targeting eight regions of the gene and to detect the infectious agent in less than one hour without any needs for complicated equipment and highly trained staff. This technique uses different ways for reading the results and data interpretation. One of the approaches is using different dyes including colorful and fluorescent dyes. The aim of this study is to compare the efficiency and simplicity of a a pH sensitive dye with a fluorescent dye in an RT-LAMP assay.

Methods : In this study, hydroxy naphthol blue (HNB) as a pH sensitive coulometric dye was compared with SYBR Gold fluorescent intercalating dye in an RT-LAMP reaction. After validation of an optimum dye concentration, the time for reaction end point as well as ease of their applications were evaluated.

Results : The results show that HNB is simpler and more quick dye of choice for RT-LAMP results read when compared with SYBR Gold. From RT-LAMP reaction to the result being read, the tubes with HNB have no need for the tubes to be opened while for SYBR Gold application, it is needed that the fluorescent dye to be applied after the reaction was finished by opening the tubes and observing the fluorescent color in a separate tube which caused high cross contamination.

Conclusion : Here, we showed that in a comparison between HNB as a pH-sensitive dye and the SYBR Gold fluorescent dye in an RT-LAMP assay, the former one not only gave an easier way for reading the results to be recorded with naked eyes but also prevents the pre-amplification sample cross contamination.

Keywords : Viral detection, Loop-mediated isothermal amplification, pH-sensitive dye, Fluorescent dye, RNA viruses, Molecular technique

P197-534: Title of the article: Investigation of new methods for detecting microbes (Batakid comparing two methods, PCR and LAMP)

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Background and Aim : In this article, by recalling some new methods of detecting microbes that are being investigated in immunology, two very suitable and proven new methods that are being used to detect microbes and viruses have been investigated and researched. One of the advantages of this research is familiarizing with the types of methods and also focusing on two very important PCR methods, which are currently providing a great service to society by using them in the diagnosis of the corona virus, and molecular diagnosis by the LAMP method. .

Methods : In this article, using the research done by the researchers, descriptive library method is used.

Results : In this article, looking at the types of virus detection methods, two new methods, PCR and LAMP, were compared. The LAMP method is used to detect microorganisms because due to the conditions of low permeability, low temperature and constant temperature, this method causes less damage to the bacteria than the PCR method. It is done at a temperature of 60 to 65 degrees. The sensitivity of the LAMP method is higher than the PCR method in some amounts of DNA. Researchers' research shows that in the LAMP method, it shows about 10 times more sensitivity than PCR. The PCR method has a much higher price than the LAMP method due to the thermocycler and the need for an equipped laboratory. The LAMP method is faster and cheaper. Considering these differences, the LAMP method can be used to detect a wide range of pathogens.

Conclusion : The LAMP method is faster and cheaper. Considering these differences, the LAMP method can be used to detect a wide range of pathogens.

Keywords : New methods of detecting microbes, PCR, LAMP

P198-601: Limit of detection evaluation of a synthetic SARS-CoV-2 RNA by RT-LAMP and Real-time PCR

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Background and Aim : Molecular techniques have advantages over antigen-antibody based techniques in detection of microorganism including viral diseases such as COVID-19 caused by SARS-CoV-2. Recently, two molecular methods including reverse transcriptase-loop-mediated isothermal amplification (RT-LAMP) and Real-time PCR are mainly used in detection of SARS-CoV-2. The former one uses 6 primers targeting eight regions of the gene and to detect the infectious agent in less than one hour without any needs for complicated equipment and highly trained staff. The second method which is a gold standard is routinely used in diagnostic laboratories. These techniques are both very sensitive to detect as little as 1 copy number of RNA molecules. RT-LAMP can also be performed for large sample scales so it can be a supportive choice during a pandemic when the capacities of the diagnostic laboratories are out of their capacities.

Methods : Of around 30Kb reference genome of SARS-CoV-2, bioinformatics analysis were performed using different softwares. Then a short fragment of the genome was synthesized artificially as RNA. Specific primers then designed for the target region. After determining the RNA concentration with nanodrop, a serial dilution was prepared to be applied for detection via RT-LAMP and Real-time PCR in triplicates. The results were read by naked eye and machine respectively.

Results : The results showed that RT-LAMP and Real-time PCR can detect as little as 25 and 10 copies of synthetic SARS-CoV-2 RNA number in the samples respectively. The reaction for RT-LAMP was very shorter than RT-PCR completed in less than one hour. The results were read using dye and also gel electrophoresis.

Conclusion : Here, we showed that both RT-LAMP and Real-time PCR are very sensitive methods for detection of SARS-CoV-2 RNA. The former one is simpler, quicker and easier for a field work application required minimum equipment and trained staff. RT-LAMP is also under the Food and Drug Administration's Emergency Use Authorization and can support the society health by higher diagnostic and detection tests for cutting off the transmission chains of virus.

Keywords : SARS-CoV-2, Loop-mediated isothermal amplification, Real-time PCR, Limit of detection

P199-1: Zoliflodacin: A Hope to Treat Antibiotic-Resistant Neisseria gonorrhoeae

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Background and Aim : Neisseria gonorrhoeae is a gram-negative diplococcus that leads to sexually transmitted infection. N.gonorrhoeae is an obligate human pathogen that causes infection to the mucus-secreting epithelial cells both in males and females. In 2017 the center for disease control and the World Health Organization published the list of global priority pathogens-12 with denting therapeutic options, including antibiotic-resistant N. gonorrhoeae.

Methods : We characterized thoroughly zoliflodacin antibiotic, its clinical trials, and its effect on human health by using different keywords like “moxifloxacin”, “covid-19”, and “clinical trials” from different data sources like Pub-Med, Google-Scholar, and Science-Direct.

Results : Zoliflodacin targets antibiotic-resistant gonorrhoeae. Zoliflodacin shows a therapeutic approach against N. gonorrhoeae. It acts by inhibiting bacterial type 2 topoisomerase with the binding site in bacterial gyrase. It shows promising results against N. gonorrhoeae. Zoliflodacin is effective in treating gonococcal urogenital and rectal infection. Discussion: Antibiotic is the only option to treat N. gonorrhoeae. There is no vaccine available to treat gonorrhea. The new drug, zoliflodacin, specifically targets antibiotic-resistant gonorrhea. This is giving hope to researchers. In this study, we elaborate on the discovery of zoliflodacin, its mechanism of action, the current clinical trials, and the effectiveness of moxifloxacin

Conclusion : Antibiotic is the only option to treat N. gonorrhea. There is no vaccine available to treat gonorrhoeae. The new drug, zoliflodacin, specifically targets antibiotic-resistant gonorrhea. This is giving hope to researchers. In this study, we elaborate on the discovery of zoliflodacin, its mechanism of action, the current clinical trials, and its effectiveness of zoliflodacin.

Keywords : Neisseria gonorrhoeae; Zoliflodacin; Covid-19; Antibiotic-resistance; Treatment

P200-38: Simultaneous Molecular identification Mycoplasma and Ureaplasma in women with vaginosis

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Background and Aim : Genital Mycoplasmas are the cause of genito-urinary tract infection. These organisms are associated with bacterial vaginosis, pelvic inflammatory disease, endometritis, cervicitis, non-venomous urethritis, spontaneous abortion, preterm labor, pneumonia, and neonatal meningitis. Therefore, this study was designed to detect Mycoplasma hominis, Mycoplasma genitalium and Ureaplasma urealyticum in women with vaginosis using multiplex-PCR method.

Methods : In this cross-sectional study, a total of 120 vaginal swab samples were collected from non-pregnant women (60 women with vaginosis and 60 healthy women). Demographic data was obtained during the admission process by a gynecologist. After DNA extraction, Multiplex-PCR was performed for simultaneous detection of M. hominis, M. genitalium and U. urealyticum. The results were analyzed by Chi-square test.

Results : The age range of patients was 21-72 years old with a mean of 33.5 ± 10.23 and healthy subjects of 18-69 years with an average of 43 ± 8.4 years. The prevalence of U. urealyticum and M. hominis were 28.3% and 18.3%, respectively. All specimens were negative for M. genitalium.

Conclusion : Considering the potential effects of mycoplasmas on the complications of vaginosis and colonization in women, the mortality of infants, as well as the isolation of M. hominis and U. urealyticum in patients with genital infections, the need for diagnosis and treatment of these patients is urgently needed.

Keywords : Mycoplasma - Ureaplasma - vaginosis - Multiplex-PCR

P201-52: Phylogroup classification and investigation the relationships between phylogroups and antibiotic resistance patterns of uropathogenic E. coli isolated from pediatric urinary tract infection

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Background and Aim : One of the most challenging therapeutic fields in Pediatrics is treating urinary tract infection (UTI) caused by the most common pathogen, uropathogenic Escherichia coli (UPEC), with a different distribution of phylogenetic groups that acquired a variety of antibiotic resistance phenotypes. The aims of this study were to determine the prevalence of phylogroups and find out the relationship between resistance induced and phylogroup dominance among children with UTI in Hamadan, Iran.

Methods : In this cross-sectional study, 140 uropathogenic E. coli isolates from children with UTI were investigated. Antimicrobial susceptibility testing against 6 antibiotic classes was performed by the disk diffusion method. Isolates were subjected to phylogenetic typing using the quadruplex polymerase chain reaction (PCR) method.

Results : Antibiogram results indicate that the highest and lowest resistance were against co-trimoxazole (64.3%) and meropenem and imipenem (0%), respectively. Phylogroup B2 (27.9%) was predominant followed by E (26.4%), A (16.4%), Clade1 (10.7%), B1 (5.7%), C (5.0%), F (4.3%), D (2.9%) and unknown (0.7%) phylogroups. 42.1% of E. coli bacteria were multi-drug resistant (MDR) with most belonging to phylogroups E (30.5%) and B2 (27.1%).

Conclusion : Besides phylogroup B2, phylogroup E is also dominant and a cause of much antibiotic resistance in our study population.

Keywords : Pediatrics' UTIUropathogenic E. coliPhylogenetic typingQuadruplex PCRMultiple-drug resistance

P202-80: Antimicrobial Resistance Pattern and multi drug resistance frequency in Escherichia coli Strains Isolated from Patients Referred to Teaching Hospitals in Mazandaran Province, Iran

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Background and Aim : Urinary tract infections are among the most common infections in both outpatients and inpatients worldwide. Due to the widespread empiric antibiotic treatment used, the resistance of common microorganisms to antibiotics has significantly increased. The present study was designed to investigate the pattern of drug resistance in Escherichia coli strains isolated from patients.

Methods : In this cross-sectional study, 100 urine samples completely randomly were taken from inpatients (more than 48 hours) and outpatients. After confirmation of E. coli strains, Susceptibility patterns of isolates were assessed by disc diffusion methods according to the Clinical Laboratory Standard Institute (CLSI) guidelines.

Results : Based on the antibiogram results, the resistance of isolated isolates was reported as ampicillin (66.6%), ampicillin-sulbactam (62.8%), Cotrimoxazole (60.7%), Cefazolin (52%), Cefotaxime (38.6%), Tetracycline (35.5%), Ceftazidime (34.8%), Ceftriaxone (33.75%), Nalidixic acid (33.4%), Ciprofloxacin (33.2%), Piperacillin (33%), Amoxyclav (27.6%), Nitrofurantoin (19.8%), Gentamicin (1.7%), Cefoxitin (1.2%) and imipenem (1%) while resistance to amikacin and tobramycin was not found. Between outpatients (53%) and inpatients (47%), The most resistant antibiotics in outpatients were ampicillin (65%) and ampicillin-sulbactam (55%) and the lowest resistance was to Cefotaxime (31/1%). The highest resistance of isolated isolates reported in inpatients was Cefotaxime (68.9%), Ceftriaxone (66.6%), Ceftazidime (60.2%) and the lowest resistance rate is ampicillin (35%). Among all the 100 isolates, the frequency of MDR E.coli was 44% in urinary culture samples, while 56% non-MDR were found, and (45.42%) were not resistant to any antibiotics. 28.57% and 25% among them, were resistant to one or two antibiotics respectively. Based on 44 cases of MDR E.coli, 72.7% were women and 27.3% were men. Resistance rates of MDR E.coli isolates from inpatients (56.8%) were significantly higher than outpatients (43.2%). Moreover, the higher levels of MDR E.coli was reported based on the age of 65-80 were (22.72%) and 25-45 were (15.9%), and the lowest levels of MDR E.coli in 10-25 (9%) was reported.

Conclusion : Carbapenems and aminoglycosides, especially amikacin and gentamicin, due to their high sensitivity, can be one of the treatment lines for the treatment of urinary tract infections in hospitalized patients.

Keywords : Escherichia coli - Urinary Tract Infection – Antibiotic Resistance

P203-113: Necessity of Laboratory Screening for Bacteriuria in Elderly Population

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Background and Aim : Bacteriuria is common in functionally impaired elderly patients .Asymptomatic bacteriuria (ASB) is the presence of bacteria in the properly collected urine of a patient with no signs or symptoms of urinary tract infection (UTI). Bacteriuria is common in the elderly, especially among institutionalized or hospitalized patients. Risk factors include impaired immune system, diabetes mellitus, structural urinary tract abnormalities and indwelling catheters. Its incidence increases with age and is usually caused by ascending of normal flora of the gut. Differentiating between ASB and UTI in this population is challenging. Identifying subpopulations with low or high risks for asymptomatic bacteriuria could help to guide the decision to initiate or withhold antibiotic therapy.

Methods : This review article aims to discuss the benefits and harms of screening for and treatment of ASB in elderly patients. PubMed and the Infectious Disease Society of America (IDSA) guideline were the sources of search in this article.

Results : Most patients with ASB, specifically older patients, will have no adverse consequences from asymptomatic bacteriuria. Treatment in these patients does not decrease the incidence of ASB or improve survival, but it will increase the adverse effects from antibiotics and the development of antibiotic-resistant bacteria.

Conclusion : In the absence of symptoms or signs of infection, routine screening and subsequent antimicrobial therapy is not recommended. It is not appropriate to routinely order a urinalysis and urine culture and sensitivity test on every patient admitted to the hospital unless there is a clinical reason to suspect a symptomatic or an occult urinary tract infection.

Keywords : elderly, asymptomatic bacteriuria, screening, UTI

P204-120: Antimicrobial Efficacy and Prevalence of Microcins among Escherichia coli isolates

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Background and Aim : Bacteriocin is defined as an antibacterial protein with bactericidal activity. Microcins are a diverse group of low-molecular-weight antibiotics produced by several Enterobacteriaceae, mainly strains of Escherichia coli. The objective of this study was to detect and evaluate the wide range of antimicrobial activity of Microcins produced by the bacteriocinogenic Escherichia coli.

Methods : In this experimental study, 125 clinical isolates were selected from private diagnostic laboratories at Isfahan during the year 2021. They were cultured and incubated at 35°C for 18 - 24 hours. Antagonistic activity of isolates was tested by adopting agar plug method. Total DNA was extracted from clinical specimens and PCR was optimized using specific primers for the amplification of the complete sequence of some Microcin genes.

Results : 125 isolates of Escherichia coli were isolated from clinical samples. It was shown that the antibiotic activity of this peptide is mainly directed to Enterobacteriaceae, including several pathogenic E. coli strains. Out of 125 isolates, 36% (n=45) isolates had positive well assay samples. Based on the obtained results by the PCR analysis 40%, 33.3% and 8.8% of the isolates were positive for Mcc J25, Mcc M and Mcc B17 genes respectively. four isolates were Double-producers. (Mcc J25 and Mcc M)

Conclusion : The objective of the present study was to evaluate the inhibitory activity of microcins, particularly J25 and M, against clinical strains of several Enterobacteriaceae. Our results showed that most strains tested were inhibited by at least two microcins. This property can be useful for antibacterial trials.

Keywords : Antimicrobial peptides, Microcins, Escherichia coli

P205-125: Evaluation Antibacterial behavior of Silver nanoparticles on general escherchia uropathogenic

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Background and Aim : Urinary tract infection (UTI) is a big problematic issue in Health Systems. Members of Enterobacteriaceae family are the main causes of UTIs and Escherichia coli has been reported as the most important involved microorganism,. Escherichia coli , a rod-shaped Gram-negative bacterium is the causative of 80- 90 percent cases of UTIs. Antibitic resistance phenotypes amongst the uropathogenic strains of E,coli makes it difficult to cure UTIs. This study was conducted to investigate the influences of Silver nanoparticles to prevent and combat antibiotic resistance in E. coli.

Methods : In this study silver nanoparticles with an approximate size of 5 nm was prepared by the Chemistry Department. Serial dilutions of nanoparticles were prepared in Nutrient broth medium and 10 microbial suspension equal to 0.5 McFarland, was added to it. A5er 24 hours of incubation at temperature of 37°C was transferred to Mueller- Hinton agar,trough dilution and with second incubation(24 hours,37 degrees centigrade),intended colonies are counted for determination of MIC and MBC. Also bacterium sensitivity to silver nanoparticles is studied by disc diffusion and well diffusion methods.

Results : According to the result of this study ,MIC and MBC amounts for 5 nm silver nanoparticles are determined az 12500 ppm and 25000ppm.Also disc diffusion method can make zone of (growth) inhibition with size of 8-10 milimeters,for E.coli from 5nm silver nanoparticles ,using 20 µL fron the 25000ppm concentration in every disc

Conclusion : The results show E,coli is sensitive to silver nanoparticles and there is no resistance for silver nanoparticles in resistant Pathogen microbes against drugs

Keywords : E.coli,silver nanoparticles.MIC and MBC

P206-166: The association between microbial and viral infectious agents with ulcerative colitis

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Background and Aim : Inflammatory bowel disease (IBD), a general term for ulcerative colitis and Crohn's disease, is a chronic immune-mediated disease of the gastrointestinal tract that occurs in genetically predisposed individuals. Over the years, the role of infection by many pathogenic agents in the development and exacerbation of inflammatory bowel disease has been widely studied, such as; Mycobacterium paratuberculosis, E.Coli, Clostridium difficile, Listeria monocytogenes, Chlamydia trachomatis, and Campylobacter concisus as well as viruses such as rubella, Epstein-Barr virus, Measles, Mumps, and Cytomegalovirus.

Methods : In this systematic review, the desired information was searched from Google Scholar, SID, Pubmed, Scopus, and Science Direct databases with keywords IBD and pathogenic factors in the period 2012-2018. According to Jadad criteria, studies that scored 3 or more were included in the study. Data analysis was done qualitatively.

Results : Finally, 25 trials that met the inclusion criteria were reviewed. According to research, overexposure of the immune system to the presence of bacterial substances can lead to the loss of immune tolerance to bacteria that are usually considered normal flora in the gut. Also, it may subsequently cause intestinal inflammation and the spread of IBD.

Conclusion : Considering all the available information, more research and studies in animal models and clinical trials are needed to draw accurate conclusions about the role of microbes and viruses in the development of IBD. Antibiotic therapy against specific organisms or fecal microbiota transplantation (FMT) could be a promising prospect for the prevention and treatment of IBD.

Keywords : Inflammatory bowel disease (IBD), Ulcerative colitis, Pathogenic factors

P207-315: Non-antibiotic methods in the treatment of urinary tract infection

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2. -

Background and Aim : Urinary tract infection is one of the most common of infections that can occur in humans. Women due to the anatomical conditions of their urinary tract ،elderly people with underlying diseases and patients admitted to hospital or nursing homes who use catheters are more exposed to this infection. Frequent burning of urine is the most clinical symptom of this infection, although fever and loss of appetite also occur in children. This infection can occur in the form of bacteriuria that will heal by itself or uncomplicated type that treats by usual antibiotics, or a complicated infection that leads to pyelonephritis or cystitis. Common first-line antibiotics in the treatment of urinary tract infections include nitrofurantoin, cotrimoxazole, trimethoprim, and ciprofloxacin. Our goal in this article is to investigate ways to The patient recovers without long-term use of antibiotics .

Methods : this article, discuss other methods besides antibiotic treatment. One of these methods is the use of ibuprofen, that shortens the treatment period and sometimes improves the symptoms.Another method is to use the adhesin metabolite of the gene FimH that Competitive with the main gene in E.coli, it reduces the microbial load and controls the infection.Another method is to use a device(Utipro plus) that is mechanically placed in the intestine and prevents the invasion of bacteria. Afurther method is to use Conferon which is a type of traditional plant and use as an auxiliary treatment in urinary tract infections. Other methods can be the use estrogen in postmenopausal women ،blueberry products, ،Ecoli om-89 bacterial lysis vaccine

Results : The results obtained from the use of non-antibiotic treatment, show that these methods are effective for the recovery of urinary infection. By conducting extensive tests and research, we can hope that these methods will replace antibiotic in the treatment of uncomplicated urinary tract infections.

Conclusion : Considering that urinary tract infection is one of the most common infections in today's world and antibiotic resistance is one of the problems in the medical world, so،the use of alternative antibiotic treatments can solve the problem of antibiotic resistance and prevent extra costs to the society.

Keywords : urinary tract infection,antibiotic resistance, non-antibiotic,treatment,new method

P208-451: Prevalence of blaTEM gene among Escherichia coli strains isolated from Tabriz hospitals

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Background and Aim : Escherichia coli (E.coli), which produces extended spectrum β-lactamases (ESBLs), has become a significant issue on a global scale in recent years. The TEM family includes the majority of β-lactamases. This study's primary goal was to determine how frequently the blaTEM β-lactamase gene was found in E. coli isolates from Tabriz, Iran.

Methods : A total of 232 E. coli strains recovered from clinical samples in Tabriz hospitals were the subject of this cross-sectional study. By using the disc diffusion approach, the antibiotic susceptibility pattern of each isolate was identified. After that by using a combined disk test in the presence of cefotaxime and clavulanic acid, the ESBL-producing strains were identified. Using the PCR technique, the TEM gene's existence in ESBLs was evaluated.

Results : The prevalence of ESBL-producing E. coli was 33%, according to the combined disk-test results. 27 percent of the ESBL-producing E. coli tested positive for the TEM gene. Tazocin (91%) and aztreonam (90%) had the highest rates of sensitivity, although they were resistant to cefuroxime (57%).

Conclusion : Most ESBL-producing E. coli bacteria recovered from Tabriz hospitals share the TEM gene. Monitoring the ESBLs producing E. coli in hospitals requires ongoing surveillance. The therapy of ESBL infections is greatly hampered by resistance to β-lactam medicines.

Keywords : E-coli, Extended-spectrum beta-lactamase (ESBL), TEM gene

P209-532: Distribution of virulence genes among Staphylococcus saprophyticus isolated from patients with UTI

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Background and Aim : Urinary tract infection (UTI) is one of the most common bacterial infections caused by gram-positive and gram-negative factors. Staphylococcus saprophyticus is a common gram-positive agent that causes uncomplicated UTI in women.The present study aimed to determine detect genes encoding surface proteins Aas,SdrI,Ssp,Uaf that play a role in the infections.

Methods : This study was financially supported by a grant from Golestan University of Medical Sciences, Gorgan, Iran. (IR.GOUMS.REC.1401.061).A total of 35 S. saprophyticus isolates were obtained from female patients with UTI. All the strains were identified by PCR for 16S rRNA Gene.For the amplification of the virulence genes the primers were designed in this study.

Results : The distribution of the virulence genes in Clinical Isolated was evaluated . Distribution of virulence genes encoding the surface proteins Aas,Ssp UafA were %98 ,92% and 84% respectively. In contrast, the gene encoding SdrI was not detected in any of the strains of S.saprophyticus.

Conclusion : These results provide a new insight of the characteristics of S. saprophyticus strains and it shows that all this surface proteins necessary to colonize the urinary tract.

Keywords : Staphylococcus saprophyticus, virulence genes , Urinary tract infection

P210-548: Comparative study of antifungal effect of different active herbal compounds

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Background and Aim : The use of medicinal plants as antifungal agents in the diagnosis, prevention, and treatment of disease has a long history. Candida spp. is part of the natural microflora of the human body and is the most common cause of fungal infections worldwide. Although Candida species are part of the normal flora of the skin and mucous membranes, they can cause a wide range of infections, especially in people with immunodeficiency. Due to the increase of resistant species to antifungal drugs and the side effects observed with the use of chemical drugs, therapeutic agents derived from plants have been introduced as suitable alternatives against microbial pathogens. This study aims to investigate the antifungal activity of three plant-derived agents, including tannic acid, hesperidin, and piperine, and to compare their ability to reduce the growth of Candida albicans.

Methods : The standard strain of Candida albicans fungus was cultured, and then the minimum inhibitory concentration (MIC) for each of the effective plant compounds was investigated by the broth microdilution method.

Results : The results showed that the fungus could not grow in the case of tannic acid and piperine at all tested concentrations, but the MIC in the presence of hesperidin was measured at 31.25 µg/ml.

Conclusion : According to the results of this study, all three substances have outstanding antifungal potential and can be proposed as alternatives to chemical drugs

Keywords : Tannic acid, Hesperidin, Piperine, Candida albicans, Minimum inhibitory concentration.

P211-550: Blue light irradiation inhibits bacterial growth

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Background and Aim : In addition to antibiotic therapy, there have been various types of therapeutic methods developed to deal with bacterial infections. Nowadays, irradiation has been introduced as one of the therapeutic strategies in the treatment of various diseases and has attracted a lot of attention in research. Due to the growth of infectious diseases, it is necessary to provide a valuable and non-invasive treatment method that can overcome the limitations of other methods and be a suitable alternative to them. In this regard, the use of irradiation to destroy bacteria has been suggested, which can achieve this goal by producing free radicals and changing the bacterial cell structure. The purpose of this study is to investigate the effect of blue light irradiation on the growth of Gram-positive and Gram-negative bacteria.

Methods : Staphylococcus aureus and Escherichia coli bacteria were spread on solid medium plates. The plates were exposed to light-emitting diodes with wavelengths of 435 nm with an energy dose of 37 J/cm2

Results : The results showed that irradiation had a significant effect in reducing the growth and number of colonies in both strains compared to the plates without the presence of irradiation.

Conclusion : According to the conducted study, it is possible to suggest the irradiation method to inhibit bacterial growth, and this solution can help in the treatment of infectious diseases along with other treatment methods.

Keywords : Irradiation, Gram-positive bacteria, Gram-negative bacteria

P212-591: Investigation of virulence factors and their association with antimicrobial resistance among uropathogenic Escherichia coli strains isolated from patients in Basra city; Iraq

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Background and Aim : The aim of present study was to investigate the antimicrobial resistance (AMR) pattern, the frequency of some virulence genes (VGs) in UPEC strains and the association of AMR with VGs.

Methods : Current study was conducted at the AL Zubair Hospital and Dar AL Shifaa Investment Hospital in Basra- Iraq, during the period from November 2020 to March 2021. A total of 300 urine samples was collected from patients suspected to have UTI according to the clinical manifestations diagnosed by the examining physician. Antimicrobial resistance pattern and virulence genes (papAH, papC, papEF, papG, fimH, and fyuA) profile of these isolates were investigated by Kirby-Bauer disc diffusion method and polymerase chain reaction, respectively.

Results : Among these samples, 201 (67%) exhibited a positive growth on culture media. Out of these 201 isolates, 38 (18.9%) were Gram-positive, while 163 (81.1 %) were Gram-negative bacteria. In addition, the positive cultures for women and men were 152 (75.62%) and 49 (24.37 %), respectively. E. coli was found in 60 (29.85 %) specimens compared with Klebsiella pneumonia 42 (20.89%), Staphylococcus aureus 38 (18.9%), Enterobacter spp 29 (14.42%), Pseudomonas aeruginosa 10 (4.97%), Proteus mirabilis 15 (7.46%), others about 7 (3.48 %) isolates.Antibiogram results of 15 antibiotics examined showed that all E. coli isolates were Multidrug resistant (MDR). The frequency of resistance against antimicrobial drugs was as follow: Streptomycin (100%), Kanamycin (98.3%), Ampicillin (96.7%), Ceftazidime (95.0%), Amoxicillin-clavulanate (88.3%), Cefotaxime (86.7%), Amikacin (85.0%), Gentamycin (43.3%), Nalidixic acid (58.3%), Ciprofloxacin (55.0%), Tetracycline (58.3%), Meropenem (6.7%), Trimthoprim-sulphametoxazole (71.7%), Nitrofuranation (15.0%), and Imipenem (36.7%). VGs detected among E. coli isolates were papAH (85%), papC (85%), papEF (60%), papG (80%), fimH (88.3%), and fyuA (80%). Moreover, these results alleged a no connection between virulence factors and antimicrobial resistance in E. coli strains. Only, it was found an association between fimH gene and antimicrobial resistance against nitrofurantoin (P-value 0.028).

Conclusion : The bacterial VFs that were investigated in this study could not serve to predict the potential for E. coli to cause antibiotic resistance in UTI. However, based on the results of this study virulence genes and antimicrobial resistance are independent properties and can transfer to other bacteria separately.

Keywords : Antimicrobial resistance; Urinary tract infection; uropathogenic Escherichia coli; virulence factors

P213-637: New findings from diagnostic methods of urinary infections in children

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Background and Aim : Urinary tract infection is a common cause of referrals to emergency units and hospitalization may be needed in some cases particularly in very young patients. Diagnoses of urinary tract infections in children are challenging because symptoms and signs are often non-specific especially in too young children. Although urine culture test is considered the gold standard for the diagnosis of UTIs, but this test may be affected by false negative and false positive results. Sample collection in children is challenging and urine contamination is frequent and can obscure true positive infections, resulting in incorrect treatment. The aim of this study was to explore about new findings from diagnostic methods of urinary infections in children

Methods : In this study various databases used to select articles including Google Scholar, PubMed, Scopus, Web of Science. The applied keywords included urinary infections, children and new diagnostic methods

Results : Recent literature recommended updated diagnostic strategy including 1)Ultrasound: bladder and renal ultrasound within 24 h is an advised method in infants with febrile urinary tract infection. 2) Voiding cystourethrography / urosonography is gold standard test for vesico-ureteral reflux 3) nanomaterials are strong potential for diagnosis UTIs via controlled delivery of antimicrobials upon stable, effective and sustained drug release. 4) causal Bayesian networks and directed acyclic graphs explicitly outline the contamination and diagnostic processes, underlying disease, and make quantitative inference, thus act as a tool for decision support. 5)Urinary neutrophil gelatinase-associated lipocalin show highly accurate to diagnosis UTIs when specimen obtained via catheterization. 6)Leukocyte Esterase enzyme is a diagnostic tool for screening of UTIs. 7)Urinary angiotensinogen is a new biomarker in many renal diseases

Conclusion : Children are sensitive patients due to their age and low immune system, and urinary tract infections are multifactorial diseases, so the latest and highest quality laboratory methods should be used in order to obtain accurate and correct results to help physicians for best treatment protocol

Keywords : urinary tract infections, children, new diagnostic methods

P214-662: Study of biofilm formation among S.saprophyticus isolated from patients with UTI

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Background and Aim : Urinary tract infection (UTI) is the most frequent bacterial infection following respiratory tract infections. Gram-negative bacteria, such as Escherichia coli, are the main causative etiologic agents of UTI that accounts for up to 80% of community-acquired uncomplicated UTIs, followed by Klebsiella spp., Enterobacter, and Proteus species. Staphylococcus aureus, Enterococcus spp., and coagulase-negative staphylococci (CoNS) are the most common gram-positive etiologic agents of UTI. Staphylococcus saprophyticus is the most common CoNS which causes uncomplicated urinary tract infections after Uropathogenic Escherichia coli (UPEC). The present study aimed to determine biofilm formation in S. saprophyticus strains that cause UTIs in women in Golestan, Iran.

Methods : This study was financially supported by a grant from Golestan University of Medical Sciences, Gorgan, Iran. (IR.GOUMS.REC.1401.061).A total of 35 S. saprophyticus isolates were obtained from female patients with UTI. The biofilm formation of S.saprophyticus isolates was carried out using the conventional method (microtitre plate).

Results : Generally, 21(60%) S.saprophyticus isolates were biofilm positive, and among them (29%) isolates showed strong biofilm formation. (18%) showed moderate biofilm formation.

Conclusion : In some countries, including Iran, the pathogenicity of S.saprophyticus, is less studied. The goal of the present study was to investigate the pattern of biofilm formation among S.saprophyticus isolated from patients with UTI.

Keywords : Staphylococcus saprophyticus ,urinary tract infection ,biofilm formation

P215-702: Investigation of the antibacterial effect of IDR-1018 peptide and chitosan nanoparticles on resistant Pseudomonas aeruginosa isolated from patients with urinary tract infections

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Background and Aim : Pseudomonas aeruginosa strains are among the most common causative agents of urinary tract infections in the hospitals. The excessive use of antibiotics has significantly increased resistance to antibiotics in the treatment of UTIs caused by Pseudomonas aeuroginosa. Peptide IDR1018 and chitosan nanoparticles (CNs) have antimicrobial and anti-biofilm activity against bacteria. Therefore, in the present study, antibacterial efficacy of chitosan nanoparticles and peptide IDR-1018 was evaluated against collected P. aeruginosa isolates.

Methods : In this study, 20 resistant and 20 sensitive P. aeruginosa isolates to imipenem were collected from patients with urinary tract infections. The ability of biofilm formation and the presence of three genes involved in biofilm production including algD, pslD and pelF in the isolates were determined by crystal violet and PCR methods, respectively. The anti-bacterial effect of imipenem, antimicrobial peptide IDR-1018 and chitosan nanoparticles was evaluated by determining the MIC by microdilution broth method.

Results : The ability of biofilm formation in the isolates was weak (10%), moderate (35%) and strong (55%). The frequency of presence of three genes related to biofilm formation including algD, pslD and pelF was 90%, 80% and 75%, respectively. MIC values for the isolates were 16-168 µg/ml for imipenem, 40 and 80 µg/ml for peptide IDR-1018, 750 and 375 µg/ml for chitosan nanoparticles, respectively.

Conclusion : Finding alternative approaches such as antimicrobial peptides and nanoparticles can be effective in treatment of P. aeruginosa infections. The results of our study showed that peptide IDR-1018 and chitosan nanoparticles alone or in combination with imipenem can be considered as a treatment strategy.

Keywords : Urinary tract infection, Pseudomonas aeruginosa, Antibiotic resistance, Chitosan nanoparticles, Peptide IDR-1018

P216-705: Expression of a hybrid protein composed of several antigens from uropathogenic Escherichia coli in Lactococcus lactis and confirmation of its expression on the surface of the bacteria

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Background and Aim : Uropathogenic Escherichia coli (UPEC) are the most frequent pathogen causing urinary tract infections (UTIs). Nowadays, emerging of antibiotic resistance among UPEC isolates is considered as an important challenge, making the development of an efficacious vaccine against these infections more urgent. Lactic acid bacteria (LAB) such as Lactococcus lactis by induction the humoral response especially induction of mucosal antibody against the applied antigen can be used as the carrier in the vaccine combinations. Therefore, in the current study, we expressed a hybrid protein composed of virulence factors of UPEC including FimH adhesin of type 1 pili, cytotoxic necrotizing factor type 1 (CNF1) and iron scavenger receptor FyuA in lactococcus system and then confirmed its expression on the surface of bacteria by different methods.

Methods : In this study, a multi-epitope composed of proteins FimH, FyuA and CNF-1 was designed. The synthesized gene was ligated into the pT1NX plasmid and then recombinant plasmids were transformed into the Lactococcus lactis MG1363 strain. The recombinant plasmids were screened using PCR, enzymatic digestion, and sequencing. The expression of the hybrid in Lactococcus lactis was evaluated by SDS-PAGE and Western blot. Immunofluorescence microscopy and whole-cell ELISA were used to confirm cell surface display of the multi-epitope on L. lactis.

Results : After synthesis of the hybrid gene, its transformation into the Lactococcus lactis were performed. After culture on M17 medium, the recombinant clones containing the gene were selected. Analysis of protein expression by SDS-PAGE and western blot showed the expression of this protein with a size of 66 KD. Evaluation of protein expression on the surface of Lactococcus lactis by immunofluorescent showed strong fluorescent on the surface of recombinant bacteria. The results of the ELISA method based on the whole bacterial cell showed that the recombinant bacteria expressing the protein showed a higher absorption rate at OD450nm compared to the Lactococcus lactis carrying the vector alone.

Conclusion : Despite the expression of the hybrid protein on surface of Lactococcus lactis, it is able to induce the immune response against the designed protein. Thus, we are going to evaluate the immunogenicity of the induced responses in animal model.

Keywords : Lactococcus lactis, Uropathogenic Escherichia coli, urinary tract infections, immunofluorescent, ELISA

P217-36: Evaluation Human Papillomavirus infection and Correlation with H.Pylori infection in Adenocarcinoma gastric cancer

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Background and Aim : Gastric cancer is one of the most common causes of cancer deaths worldwide. Every year. Gastric cancer is the first most common cancer in men and the third most common cancer in women. New studies suggest the role of the HPV virus in the risk of co-infection with H. pylori infection. In this study, we determined the severity of H. pylori and HPV infection simultaneously and the relationship between these infections and tumor size and grade, lymph node involvement and the depth of tumor penetration in patients with gastric and their effect on pathological symptoms.

Methods : Samples were taken from healthy cell and gastric tumor from patients referred to the hospital and transferred to the laboratory. DNA extraction was performed using a biogenic kit. After confirming the concentration and quality of DNA, the severity of viral-bacterial infections and Helicobacter pylori were assessed by real-time PCR. The mean age of patients and controls was 61.1±9.2 and 58/2±7.6 respectively, there was no statistically significant difference (student test).. 8 patients were female and 24 patients were male.

Results : 8 patients (61.5%) under 60 years of age were positive for H. pylori infection and 5 patients (38%) were negative for H. pylori infection. Also, 18 patients (94.7%) were positive for H. pylori infection for more than 60 years and 1 patient (5.3%) was negative for H. pylori infection. Other findings did not show significant results in the number of lymph nodes involved (N), tumor staging and grading in HPV infection in patients with concomitant H. pylori infection.

Conclusion : It is suggested that more biological and molecular research be conducted in this area to determine the role of human papillomavirus in the development of various malignancies, including gastric cancer.

Keywords : : Human Papilloma Virus, Real Time, Cancer, H.Pylori

P218-37: Evaluation of severity persistent asthma with Hemophilus influenza Type A infection in sputum of patients based on Real time PCR

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Background and Aim : Asthma is one of the most common non-communicable diseases characterized by reversible obstruction of airflow. It poses many problems for all age groups from infancy to old age. Severe persistent asthma is a severe disease that is accompanied by persistent daily and frequent nighttime symptoms. Various studies have shown that the occurrence of viral infections is associated with the severity of asthma symptoms, so that its progression can be prevented by controlling viral agents. In this study, the severity of symptoms of severe persistent asthma with Haemophilus influenzae type A infection was investigated.

Methods : 31 patients with asthma with different degrees of disease were studied in this study. First, patients' sputum samples were taken. After purification, the DNA extraction kit was performed. The severity of Haemophilus infection was then assessed by the microbial panel kit by real-time.

Results : The results showed that in patients with asthma, the percentage of people with Haemophilus influenzae was 77.4% and in 22.6% of other asthma cases, Haemophilus influenzae virus was not observed. The relationship between the severity of asthma, cough and shortness of breath with Haemophilus influenzae infection showed that with increasing asthma symptoms, the severity of infection increases Therefore, the results of this study show that Haemophilus influenzae virus worsens asthma symptoms in patients. The relationship between asthma severities, ACT.Score, FEV.pre, FENO pre, 0% Lym, % Mq, % Neu and %EO with Haemophilus influenzae type A infection was also studied. The results of this study showed that there was a significant relationship between ACT.Score and Haemophilus influenzae type A.

Conclusion : It is suggested that the effect of Haemophilus influenzae type A on the severity of symptoms of other lung diseases be studied.

Keywords : Haemophilus influenzae, severity persistent asthma, Real time-PCR

P219-77: Therapeutic Potential of Gut Microbiota in Colorectal Cancer

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Background and Aim : The numerous bacteria, fungi, protozoa, and viruses are associated with gut microbiota diversity and obviously, the gut microbiota's composition has strongly impacted the development of colorectal cancer (CRC). Bacteria, among gut microbiota's composition, provide metabolites with antioxidant and anti-inflammatory properties which is modulated the host's and gut's homeostasis. Aside from gene mutation and hereditary variables, the loss of gut micro-ecological equilibrium offers a novel approach to treating CRC.

Methods : We searched the keywords "Gut microbiota," "Colorectal cancer," and "Treatment" in PubMed, NCBI, Scopus, and Google Scholar for updated articles.

Results : Modulating gut microbiota composition has been recently discussed as a promising technique for improving tumor response to chemotherapy drugs. Meanwhile, the elimination of gut microbiota provides clinical advantages to CRC patients by overcoming chemotherapy resistance. The gut microbiota, especially intratumor bacteria, contribute to inducing gemcitabine resistance through enzymatic inactivation of the medication. In contrast, a gemcitabine-ciprofloxacin combination therapy reverses resistance. Indeed the impact of gut microbiota's makeup and activity have demonstrated the improvement of colorectal carcinogenesis treatment and anticancer therapy's efficacy. CRC-associated pathogens are known as a possible colorectal cancer screening tool due to gut microbiota development. The fecal microbiota can use to create non-invasive colorectal cancer indicators. Also, the gut microbiota has been shown to impact chemotherapy and immunotherapy effectiveness by influencing immunity. Cyclophosphamide, used in chemotherapy and immunotherapy, has been demonstrated to trigger the translocation of specific Gram-positive bacteria (Lactobacillus johnsonii, Lactobacillus murinus, and Enterococcus hirae) into secondary lymphoid organs.

Conclusion : Little information is available on the microbiome that affects tumor regression or resistance to cancer treatment; Because intestinal microbiota is still a new field in treating

CRC, and more research is needed. On the other hand, we found that controlling the gut microbiota population positively affects CRC. So it is better to focus on the relationship between gut microbiota and immunotherapy or chemotherapy.

Keywords : Gut microbiota, Colorectal cancer (CRC), Treatment

P220-82: Anticancer Effects of Caffeic Acid on A549 Non-small Cell Lung Cancer Cells

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Background and Aim : Cancer is a major threat to human health and a global problem, and lung cancer is the most common type of malignant tumor. Caffeic acid is one of the known phenolic compounds. The beneficial effects of Caffeic acid, including its anti-inflammatory, anti-viral, immune-boosting, antioxidant and carcinostatic and anticarcinogenic properties have been confirmed in several studies. The aim of this study was to evaluate the induction of apoptosis in lung cancer cells by Caffeic acid (obtained from propolis).

Methods : Cultured lung cancer cell lines (A549) were treated with Caffeic acid then the treated cells were examined by flow cytometry after preparation.

Results : The results showed that Caffeic acid has effective roles in inducing apoptosis and has caused significant changes in the percentage of living cells and the percentage of cells in the early and late phase of apoptosis.

Conclusion : Caffeic acid has significant apoptotic effects on lung epithelial cancer cells and has an effective role in inhibiting lung cancer cells, so it can be considered as an effective substance in the treatment of cancer.

Keywords : A549; Apoptosis; Caffeic Acid Phenethyl Ester; Flow cytometry; Lung Cancer

P221-85: Epidemiology of Merkel cell carcinoma

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Background and Aim : Merkel cell carcinoma (MCC) is a rare but invasive skin cancer that occurs in about 3 out of every 1,000,000 population. Factors involved in the development of MCC contain the Merkel cell polyomavirus (MCPyV or MCV), a weakened immune system, and exposure to ultraviolet light. Merkel cell carcinoma usually occurs in the head, neck, limbs, perianal area, and eyelids. It is common in people over the age of 60, whites, and men. MCC is less common in children.

Methods : MCCis a rare type of skin cancer, with an incidence of only 0.7 per 100,000 in the United States in 2013. Since 2005, about 2,500 new MCCs have been newly diagnosed each year in the United States, with about 60,000 malignant melanomas and more than 1 million non-melanoma skin cancers. Like melanoma, the incidence of MCC is increasing rapidly in the United States.

Results : Globally, MCCs are most commonly found in areas of increasing sun exposure. Australia has the highest incidence of MCC, but the incidence of MCV-positive MCC is lower than in other countries.

Conclusion : Since 2006, other primary cancers have been known to significantly increase the risk of MCC, especially in patients with previous multiple myeloma, chronic lymphocytic leukemia, and malignant melanoma.

Keywords : Merkel cell carcinoma (MCC), Merkel cell polyomavirus (MCPyV or MCV), skin cancer, sun exposure

P222-88: The evaluation of bacterial infection in patients with acute Lymphoblastic leukemia in induction phase of treatment with Hyper CVAD regimen

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Background and Aim : Acute Lymphoblastic Leukemia is one of the lethal disease in adult population. The most common cause of death especially in induction phase of treatment is infection, and majority of cases experienced neutropenia and fever. The most important complication in this situation is bacterial infection. The aim of this study is the evaluation of bacterial infection in induction phase of newly cases with Acute lymphoblastic Leukemia.

Methods : In this prospective single center study, 39 cases of acute lymphoblastic leukemia entered.The primary disease confirmed with blood film, bone marrow exam, flowcytometery. 30 cases was male. All cases had daily physical exam, check of vital sign and inserted central vein pressure line, complte blood cell. If the patients experienced fever, culture of blood, urine and other suspicious sites were done. Emperical antibiotic therapy started after full evaluation as above.

Results : In our study 35 cases experienced fever and neutropenia. For all cases, chest x ray, complete blood count, blood and urine culture were done. After these procedures , we started empirical therapy as ward policy. Of 35 cases with fever and neutropenia, only 2 cases had blood culture positive. These 2 cases were positive for gram negative pathogen. We didn't have any cases with overt invasive fungal infection except mild local oropharyngeal candidiasis. In our study mortality due to infection in induction phase of treatment was zero percent.

Conclusion : Fever and neutropenia are the very common manifestation in acute lymphoblastic leukemia, but culture positive has very low incidence. The causes of this low prevalence may be due to prior prophylactic therapy and lack of specific and sensitive culture instrument.

Keywords : Acute lymphoblastic leukemia, Neutropenia, Fever

P223-93: Invasive Aspergillosis in post-liver transplant patients

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Background and Aim : Aspergillosis is a severe and fatal complication that causes infection in transplant recipients and patients with immunodeficiency syndrome, neutropenia, chronic granulomatosis, and hematologic malignancies. Invasive Aspergillosis has been reported as one of the fungal infections with high mortality in transplant recipients. This study aimed to evaluate the manifestations of Aspergillosis fungal infections in liver transplant patients

Methods : This Descriptive cross-sectional study was conducted on Ten case of 86 patients with liver transplantation who were infected with Aspergillosis fungal infections. Data were gathered from the medical records of the archive of Montasryieh Hospital, Mashhad, Iran, between August 2019 and August 2020.

Results : In general, 11.6% (n=10) of the patients who had liver transplantation from August 2019 to August 2020 had been infected with Aspergillosis. Only 6.7% of the patients were categorized under the late-onset (>90 days after liver transplantation), and 93.3% of them were early-onset (<90 days after liver transplantation). Aspergillosis fungal infections were suspected on the basis of clinical or radiological signs (possible in 30% of cases; n=3). The probable diagnosis was reported in 60% (n=6), and the proven diagnosis was observed only in one patient. Moreover, 80% of the patients were diagnosed with Pulmonary Aspergillosis, and two patients had pulmonary Aspergillosis in combination with the central nervous system and cutaneous Aspergillosis. A correlation was reported between a comorbid disease and type of Aspergillosis (r=0.69; P=0.02). Voriconazole was effective to treat invasive Aspergillosis in all patients.

Conclusion : The prevalence rate of Aspergillosis is relatively high among liver transplant recipient populations (11%). All recipients infected with Aspergillosis had at least one risk factor, including an underlying disease. It seems that therapy is effective using Voriconazole among transplant patients with pulmonary Aspergillosis.

Keywords : Aspergillosis, Fungal Infections, Transplant Patients, Voriconazole

P224-94: Critical COVID 19 in Solid Organ Transplatation

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Background and Aim : Considering the importance of assessing solid organ transplant, infected individuals with coronavirus disease 2019 (COVID-19), and the lack of information in this regard, this descriptive study aimed to investigate the clinical features, immunosuppressive agents, and outcomes of liver transplant patients in the critical phase of infection with COVID-19.

Methods : This descriptive cross-sectional study was conducted on 12 critically ill liver transplant recipients referred to Imam Reza and Montaseriyeh hospitals affiliated to Mashhad University of Medical silences, Mashhad, Iran, within 2020-21. This study was extracted from a thesis to obtain a specialist MD degree in infectious diseases (Code: 981818). The required data, including demographic and clinical information, were gathered and recorded in a checklist, and the correlations between variables were assessed in SPSS software (version 24).

Results : Hypertension, diabetes, and chronic kidney disease were reported in 83.3% (n=10), 58.3% (n=7), and 41.6% (n=5) of patients, respectively. The administration of Mycophenolic acid was correlated with conjunctivitis (r=-0.67; P=0.02), weakness (r=0.77; P=0.006), and sore throat (r=-0.67; P=0.02). Ground glass opacity was reported in all patients, which was along with consolidation in 90.9% of the cases, and acute pulmonary embolism was found in 36.3% of the subjects. Finally, 66.7% (n=8) of patients passes away. Among immunosuppressive agents, only the use of Mycophenolic acid was correlated with outcome (r=-0.77; P=0.006).

Conclusion : Due to the high rate of mortality among liver transplant recipients in the critical phase of COVID-19, earlier and more aggressive treatment with antiviral and antibacterial agents should be performed in this group of patients.

Keywords : COVID- 19; Immunosuppressive; Liver Transplantation; Mortality

P225-213: Cancer and Coronavirus Disease (COVID - 19) : Comorbidity , Mechanical Ventilation , and Death Risk

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1. *andishesazan olom paye mazandaran*

Background and Aim : The presence of comorbidity poses a major clinical challenge in the care and treatment of COVID - 19 patients . Moreover , having one or more comorbidities could be a life - threatening situation in COVID - 19 patients . Cancer is substantially associated with significant morbidity and mortality in COVID - 19 patients . However , there is not sufficient data to conclude that cancer patients have a higher risk of COVID - 19 infection . In this study , we reviewed cancer comorbidity and risk of mechanical ventilation or death in patients with confirmed COVID - 19 .

Methods : A comprehensive systematic search was performed on PubMed , scopus , Web of Science , SciELO , and CNKI , to find articles published until August 01 , 2020 . All relevant case series , case reports , systematic and narrative reviews , meta - analyses , and prospective and retrospective studies that reported clinical characteristics and epidemiological information of cancer patients infected with COVID - 19 were included in the study .

Results : A total of 12 cohort studies exclusively on cancer patients with confirmed COVID-19 were selected. Initially , our search strategy yielded 358 possibly relevant articles . Of them , 269 publications were removed due to duplication , or were not human research . Finally , a total of 12 cohort studies exclusively on cancer patients with confirmed COVID - 19 were included in the review . Of note , most of cohort studies were published in Chinese , English , and French . Most of the cancer cases with confirmed CPVID - 19 originated from East Asian and Europe .

Conclusion : This study found that cancer was not among the most prevalent underlying diseases among patients with confirmed COVID - 19 . In addition , cancer patients with confirmed COVID - 19 had a lower risk of mechanical ventilation and death than those non - cancer - infected patients . Due to the limited data , it is critical that larger and well - designed studies in various malignancies from different centers are needed to confirm our data .

Keywords : COVID-19 . Cancer . Malignancy . Intensive care unit . Ventilation . Death

P226-255: Investigation of the frequency of Helicobacter pylori infection in tissue samples of gastric cancer in Tabriz hospitals

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Background and Aim : Gastric cancer is one of the most common cancers of the gastrointestinal tract and the second most common cause of cancer-related deaths worldwide, and various factors such as Helicobacter pylori (H. pylori)infection play a role in its occurrence. The purpose of this study is to investigate the prevalence of H. pylori in gastric cancer tissue samples in Tabriz hospitals.

Methods : In this descriptive cross-sectional study, 50 gastric cancer tissue samples were collected along with 50 non-cancerous samples as positive controls from Tabriz hospitals. The samples were examined using rapid urease test and culture and pathological examination for H.pylori. SPSS version 20 software was used for data analysis.

Results : In this study, 100 cancerous and non-cancerous samples were compared in terms of H. pylori prevalence. The prevalence of H. pylori was 60% in the cancer group and 30% in the non-cancer group. There was no significant relationship between age and gender in the prevalence of H. pylori ($p > 0.05$).

Conclusion : There is a direct relationship between gastric cancer and H. pylori. Identification of qualitative criteria for the diagnosis of Helicobacter pylori infection is required.

Keywords : Gastric cancers, infection, Helicobacter pylori

P227-284: Genotyping Helicobacter pylori and fgf7 Gene Expression in Gastric cancer

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Background and Aim : Helicobacter pylori as the causative agent of the most common chronic bacterial infectious disease in human still involves a range of clinical challenging complications. In this meantime, the survey of the interaction between H. pylori virulence genes expression and its consequences on gastric antral epithelial cells is Controversial. This study surveyed the correlations between H. pylori cag Pathogenicity Island and virulence factors , genes with Fgf7 gene expression as an angiogenic factor in developing gastric cancer in gastric antral epithelial cells of patients with H. pylori infection.

Methods : Gastric antral biopsy samples collected from patients out of exclusion criteria, including consumption of tobacco, alchohol and anti-H. pylori drugs, were categorized into gastric cancer (case group n:53) and gastritis (control group n:50) with and without H. pylori infection to detect changes in cDNA of fgf7 in gastric antral epithelial cells by using Real Time RT PCR. Extracted total RNA from gastric antral biopsy samples was used to synthesize cDNA for real time PCR. Furthermore, the cDNA of H. pylori cag Pathogenicity Island and other virulence factors , genes were detected by using specific designed primers and simple PCR.

Results : Fgf7 gene expression revealed a significantly increase in gastric antral epithelial cells of gastric cancer and H. pylori-positive patients in contrast with gastritis and H. pylori-negative patients ($p<0.05$). In the meanwhile, cag Pathogenicity Island and hopQ genotypes showed a positive correlation with Fgf7 gene expression (fold changes of cDNA) in gastric antral epithelial cells ($p<0.05$).

Conclusion : This study revealed an obvious correlation between Fgf7 gene expression in gastric antral epithelial cells of patients with H. pylori carcinogenic genotypes infection and some host factors including age.

Keywords : Fibroblast Growth Factor 7 gene, Helicobacter pylori, Gastric cancer

P228-342: Bacteria-cancer interactions: bacteria-based cancer therapy

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Background and Aim : Bacteria accumulating (colonizing the tumors) and proliferating within tumors can initiate anti-tumor immune responses. Using tumor-targeting bacteria as delivery vectors improve chemotherapeutic drugs' activities while reducing systemic toxicity to the host. Bacterial-based cancer therapy (BBCT) can be either used as a monotherapy or in combination with other anticancer therapies for better clinical outcomes.

Methods : We searched the keywords "cancer therapy," "(BBCT)," and "Bacterial anticancer agents "In google scholar, NCBI and Scopus for updated articles.

Results : The TME's (Tumor microenvironment) condition can be reversed, and the anti-tumor immune response can be triggered using bacteria. Bacterial vectors can transport, produce, and deliver anticancer agents in medicines, therapeutic DNA, microRNA, shRNA, siRNA, cytotoxic chemicals, and enzymes that turn prodrugs into anticancer drugs. Therefore, Bacterial anticancer agents such as antibiotics, toxins, etc. Many action strategies have been utilized to eliminate cancer cells, including apoptosis, necrosis, decreased angiogenesis, suppression of translation and splicing, and blocking crucial signaling pathways. The tumors or tumor-driven lymph nodes can be colonized selectively by live tumor-targeting bacteria. It is possible to use bacteria as a cancer treatment. Even if bacteria may not have the full therapeutic potential by themselves, their alterations as anti-tumor agents, oncogènes, or immunogenic antigens, as well as their conjunction with other therapeutic processes, will increase their potential for cancer therapy.

Conclusion : To summarize, although still in their infancy, bacteria-based treatments have immense potential. We discovered that Bacteria can be genetically modified to have less innate virulence without changing how well they target tumors. Therefore, BBCT is a good way of cancer therapy by using Bacterial anticancer agents. In addition, we found that various strains of Salmonella, Bifidobacteria, and Clostridia can colonize the hypoxic region of a tumor and kill the tumor cells. They are therefore prospective strains for targeted therapies

that specifically target tumors. The results indicated that these "smart" bacteria may soon establish this strategy as a potent weapon in the fight against cancer.

Keywords : (BBCT), cancer therapy, anticancer agents

P229-455: Cytotoxic activity of exosomes carrying gold nanoparticles produced by Micrococcus yunnanensis strain J2

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Background and Aim : Exosomes derived from stem cells exhibit actions similar to those of mesenchymal stem cells, such as repairing tissue damage, inhibiting inflammatory responses, and regulating the immune system. The use of exosome does not have risks, such as aneuploidy and transplant rejection, and can be a suitable alternative for the treatment of various diseases. Also, exosome can play a role in examining the treatment process of diseases such as cancer. Nowadays, treatment with antioxidants is a way to prevent the occurrence of cancer. Nanoparticles are among the substances whose antioxidant properties have been proven. Gold nanoparticles are used in drug delivery for cancer treatment. The aim of this study was to isolate exosome derived from stem cells and use them as carriers of nanoparticles synthesized by bacteria in the treatment of breast cancer.

Methods : In the present study, the capability of Micrococcus yunnanensis J2 (isolated from Sarcheshme mine soil samples and identified by 16S rDNA sequencing) for biosynthesis of gold nanoparticles (Au NPs) was evaluated. Then gold nanoparticles were prepared by HauCl3 solution and used for identification by electron microscope. A kit was used to prepare exosomes and finally the effect of exosomes containing gold nanoparticles on mcf7 cells was investigated

Results : Cytotoxic activity of exosomes containing gold nanoparticles (assisted by MTT-based colorimetric assay) revealed IC□50 (μg/mL) of 88.4±2.1 against cancer cell line of MCF7.

Conclusion : we propose that targeting the exosome represents a novel strategy for cancer therapy.

Keywords : Gold nanoparticles, Cytotoxic, exosome, Green synthesis

P230-461: Review of Handrab and Handwash by scrub method In the first surgery And the second operation Doctors and Oncology operating room working personnel in Mashhad-spring1401

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Background and Aim : Title: Review of Handrab and Handwash by scrub method In the first surgery And the second operation Doctors and Oncology operating room working personnel in a private hospital in Mashhad In the spring of 1401 Writers:Zohreh Rokni-Zahra Askari hosini-Mahbobe Mokhtarpoor-Sedighe Mohamadnegad Ostad. Introduction: Viruses and bacteria are important factors in chronic and acute infections in the hospital environment so that it leaves irreparable side effects to the patients. To reduce these infections .The best, simplest and least expensive way is to observe hand hygiene by medical personnel ,And because the infection spreads easily in the operating room and operation site .Therefore, the duration of hospitalization and re-hospitalization of the patient increases , which imposes a financial burden on the patient and the treatment system. Therefore, hand hygiene in the operating room is important in preventing hospital infections. Target: From this study, the hand hygiene index of Hendrab and Handwash by scrub method is in the oncology operating room in a private hospital in Mashhad.

Methods : A study of hand hygiene in two scrub methods in oncology operating room personnel is in a private hospital in Mashhad which includes 102 cases of indirect observation by the infection control supervisor is by the method of Handrab and Handwash which used to collect checklist information Approved by the World Halth Organetion .

Results : Average scores of hand hygiene in surgeons in the first operation is handrab78%and handwash22% -in operating room personnel in the first operation is handrab9% and handwash91% , While in the second surgery of the surgeons is handrab 89% and handwash 11%. in operating room personnel in the second surgery is handrab13% and handwash87%.

Conclusion : It was observed in this review The percentage of hand hygiene is decreasing in the scrub of surgeons and significant difference With handwash scrub can be seen in the operating room personnel. Non-observance of handwash scrub by surgeons is contrary to the guidelines for safe surgery. Therefore, more emphasis on handwash scrub in patient safety indicators have according to the defect of the immune system of cancer patients.

Keywords : infection control- Handrab-handwash-scrub- operating room.

P231-472: Examination of handrub and hand wash scrub on first and second operation in doctors and oncology operating room personnel in the private hospital of Mashhad in the spring of 1401

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Background and Aim : Viruses and bacteria are important factors in chronic and acute infections in the hospital environment, so they cause irreparable effects on the patient. To reduce these infections, the simplest, cheapest and best way is to observe hand hygiene by medical personnel and because the infection spreads easily in the operating room and the surgical site, the length of the patient's hospitalization and re-hospitalization increases, which imposes a heavy financial burden on the patient and the system. Therefore, observing hand hygiene in the operating room is important in preventing hospital infections. Objective: This study investigates the index of hand hygiene using the hand rub and hand wash scrub method in the oncology operating room of a private hospital in Mashhad.

Methods : Study of hand hygiene using two scrub methods on oncology operating room personnel in Mashhad private hospital, which includes 102 cases of indirect observation by infection control supervisors using hand rub and hand wash methods which was organized to collect information from a checklist approved by the World Health Organization, and each member of the research community was observed.

Results : The average score of hand hygiene among first-operating doctors in Hand rub is 78% and hand wash scrub is 22% and in first-operating operation room personnel, Hand rub is 9% and hand wash scrub is 91% whereas The average score of hand hygiene among second-operating doctors in Hand rub is 89% and hand wash scrub is 11% and this average score for operating room personnel were 13% hand rub and 87% hand wash, which can be seen between the attitude of doctors and operating personnel in compliance with the global guidelines for safe surgery.

Conclusion : Therefore, regarding the importance of hand hygiene in the patient’s safety indicators, doctors should put more emphasis on the hand wash scrub considering the deficiency of the immune system of cancer patients.

Keywords : infection control, hand rub, hand wash, operating room

P232-477: HTLV-1–Cell Interactions in the Development of Adult T-Cell Leukemia

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Background and Aim : Human T-cell lymphotropic virus type 1 (HTLV-1) is a human retrovirus that causes a lifelong infection. HTLV- infections such as leukaemia, progressive neurological disorder, ropical Spastic Paraparesis and HTLV-1 Associated Myelopathy (TSP/HAM), directly are associated to the most aggressive T cell malignancies. Most HTLV-1-infected individuals remain asymptomatic for life. The factors that cause different manifestations of infection are not fully understood, and accumulating evidence suggests that the complex virus-host interactions, as well as the host immune response against HTLV-1 infection, appear to regulate the development of HTLV-1-associated diseases. The aim of this study was to evaluate the progress made over the last years in the recognition of HTLV-1 infection, cloning, gene expression, and its resulting cell transformation, as well as methods to prevent human T-cell lymphotropic virus infection and cellular lymphoma/leukemia T cells.

Methods : This review was conducted using keywords such as liver cell cancer, treatment, Crisper technology, and HCC in PubMed, Springer, Scopus, Medline, Google Scholar, Science Direct, and Web of Science based on Cochrane Highly Sensitive Search Strategy.

Results : HTLV- infections are considered a neglected disease nowadays, and despite recent advances in chemotherapy, allogeneic hematopoietic stem cell transplantation (alloHSCT), and supportive care, the prognosis of patients with ATLL is one of the weakest among hematologic malignancies. Prenatal screening for HTLV-1 should be performed in endemic areas with accurate information and advice. The development of a safe and effective vaccine can be an important tool in protecting vectors against ATLL. Therefore, the aim of vaccination should be to enhance HTLV-1-specific T-cell responses in asymptomatic carriers and enhance clearance of infected and altered cells, thereby protecting against ATLL.

Conclusion : Vertical transmission, high provirus count, and suppression of T-cell immune responses in HTLV-1 are important risk factors for the development of ATLL. Vaccination of uninfected individuals against HTLV-1 is a complex practical strategy to prevent ATLL. However, there are several hurdles that need to be overcome before clinical application. In this article, we provide a comprehensive overview of recently uncovered information on the molecular basis of leukemogenesis in ATLL and HTLV diseases.

Keywords : Leukemia; Lymphoma; HTLV-1; Sexual Transmission.

P233-515: Mutations in HBV- S gene and overlapping RT region in association to hepatocellular carcinoma

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Background and Aim : Background: Chronic hepatitis B virus (CHB) infection is a major health problem and leading cause of hepatocellular carcinoma (HCC) worldwide. Among the viral risk factors of HCC, variations within HBsAg coding region has been recently considered with HCC. Mutations in RT are dominant treatment responsive factor that is associated to replication rate and liver disease progress. So, we aimed to investigate the mutation profile of s and RT gene of HBV in the liver tissue of patients with HCC from Iran.

Methods : Method: This was a cross-sectional work performed from 02/2018 to 03/2020, among Iranian patients with HCC, liver cirrhosis and normal liver (LC). Preserved FFPE samples and fresh Needle biopsies were collected from liver tissues with HCC. Tissue samples were subjected for DNA extraction, next PCR test was performed to amplify HBV S gene. Mutations were detected by direct Sanger sequencing.

Results : Results: In overall there were 79 samples positive for HBsAg, among which 68 cases were positive for HBV-DNA including HCC (n: 39), LC (n: 18) and normal (n: 11). The mean intrahepatic viral load was 9×105 ± 6×106 copies/µl, and the HBV genotype was D among the all samples. In S gene Q30E, P120S, Q129H, T126I/S, D144E, V190F, W201L and P203L were predominant mutation. The observance of P120S and D144E were significantly associated with HCC. In RT region G26R, P34L/S, A38G, V142L, R152G/W and C198F were prominent mutations. Among mutations of RT, V142L and R152G/W were seen mostly in HCC group that were associated with higher viral load.

Conclusion : Conclusion: We detected 23% amino acid changes in S region. Two mutation at amino acid 120 and 144 on S gene were associated with HCC. Further investigations are recommended to further clarify the relationship and interaction between mutations in HBV genome and HCC progression.

Keywords : HBV, S gene, HBsAg, RT, mutation, HCC, liver cirrhosis, Iran

P234-582: Bacterial etiology and antibiotic resistance pattern of bacteremia in patients with hematologic malignancies admitted to Imam Reza Hospital, Mashhad: an 8-year retrospective study

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Background and Aim : Identification of disease causing organisms, and their antimicrobial resistance patterns, is essential for appropriate empiric therapy. Patients afflicted with a variety of hematologic malignancies are especially at risk of infection with drug resistant organisms, owing in part to recurrent infections and repeated courses of antibiotics therapy. This study aims to investigate the bacterial etiology and antibiotic resistance patterns of organisms isolated from the blood of bacteremic patients admitted to the Hematology and Oncology ward of Imam Reza Hospital, Mashhad.

Methods : In this retrospective cross-sectional study, we reviewed the medical records of all patients admitted to the Hematology and Oncology ward of Imam Reza Hospital from March 2010 to March 2017, for whom at least one positive blood culture was recorded. Obtained data included demographic information, blood culture and antibiogram results, and outcome.

Results : A total of 107 patients were included (mean age 43.8±1.8). 60 (56%) were male, and 47 (44%) were female. The organisms most commonly isolated from the blood were, in order, Staphylococcus aureus (15.9%), Acinetobacter (15%), Enterococcus (13.1%), and Staphylococcus epidermidis (12.19%). 68 (63.5%) patients survived the episode of bacteremia, while 39 (36.44%) died. The highest rates of antimicrobial susceptibility were seen in S. epidermidis treated with vancomycin (92.3% of isolates), and S. aureus treated with vancomycin or ciprofloxacin (82.35% and 52.9% of isolates, respectively).

Conclusion : The most common cause of bacteremia was Staphylococcus aureus, followed closely by Acinetobacter. The results of the present study should be considered in the management of patients with hematologic malignancies in the region.

Keywords : bacteremia, antibiotic resistance, hematologic malignancy

P235-620: Evaluation of antibacterial resistance pattern of Helicobacter pylori isolated of Patient with suspected gastric cancer

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Background and Aim : Gastric cancer is the 5th most common malignancy and the third most common cause of death from cancer worldwide. There is increasing evidence from epidemiological studies of the association of H. pylori infection and gastric cancer. Also, eradication of H. pylori infection has shown positive effects on decreasing the risk of gastric cancer, but this has become a challenge due to the development of antibiotic resistance in H. pylori against the antibiotics of choice. This research studied antibiotic resistance pattern of H. pylori associated with increased risk of gastric cancer.

Methods : it was used routine diagnostic isolates of H. pylori that were cultured from single gastric (antral) biopsies. The patients were from consecutive endoscopy lists and were undergoing routine investigation at the Institute of Oncology, Istanbul University, Istanbul, Turkey, for a variety of upper gastrointestinal tract symptoms. Isolates Identity as H. pylori was confirmed by transported in a special medium that comprised selective antibiotic supplement, subcultured on Columbia agar base with defibrinated horse blood at 37 °C under microaerobic conditions, Gram's stain, urease, catalase and oxidase. Used antibiotic discks included metronidazole, clarithromycin, levofloxacin, amoxicillin, tetracycline, furazolidone, and rifabutin.

Results : During 4 months a total of 15 H. pylori isolates meeting the inclusion criteria were identified. Rates of H. pylori antibiotic resistance were 46.67% for metronidazole, 20% for clarithromycin, 20% for levofloxacin, and 14.67% for amoxicillin, 11.70% for tetracycline, 14.67% for furazolidon and 6.67% for rifabutin.

Conclusion : Gastric cancer is a highly lethal disease and H. pylori as a risk factor for this malignancy is extremely common. Monitoring of resistance to antimicrobial agents is important for H. pylori infections therapy in medical practice. Resistance to antimicrobial agents creates at risk H. pylori eradication in the world.

Keywords : Antibacterial resistance pattern, Helicobacter pylori, Gastric cancer

P236-622: CAR-T Cells & Oncolytic Viruses against Solid Tumors

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Background and Aim : Adoptive transfer of chimeric antigen receptor (CAR) modified T cells has resulted in unprecedented rates of sustained complete response in leukemia and lymphoma patients.

Methods : However, despite significant results in patients with hematological malignancies, CART cells display limited effect on solid cancers. New approaches must simultaneously overcome many of the challenges faced by CART cells in solid tumours, containing the immunosuppressive tumor microenvironment and the heterogeneity of antigen expression.

Results : Oncolytic viruses are lytic and immunogenic anti-cancer agents that have the potential for synergism with CAR-T cells to treat of solid tumor.

Conclusion : In addition, viruses can be modified to deliver therapeutic transgenes selectively to the tumor microenvironment, which can enhance the effective functions of tumor-specific T cells.

Keywords : chimeric antigen receptors (CAR), oncolytic viruses, solid tumors, immunosuppressive tumor microenvironment, tumor-specific T cells

P237-625: Molecular characterization of virus-positive and virus-negative in Merkel cell carcinoma

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Background and Aim : Merkel cell carcinoma (MCC) is a highly invasive neuroendocrine carcinoma of the skin. Risk factors for developing MCC contain advanced age, light skin associated with over exposure to sunlight, and a variety of immunodeficiency conditions. In 2008, Merkel cell polyomavirus (MCPyV) was first identified by Southern blot in some but not all MCC tumors with integration of viral DNA that occurs at several different chromosomal sites.

Methods : Importantly, a pattern of identical clonal integration was identified in one primary tumor and corresponding metastatic lymph node. This important insight suggested that integration of the viral DNA was an early event in virus-positive MCC oncogenesis. MCPyV usually infects most people at young age and leads to asymptomatic and lifelong infection, which is manifested by the persistent presence of antibodies to the VP1 viral envelope protein. MCPyV DNA is easily detected in the skin, but the cell type in which the virus replicates in vivo has not been identified. Since the initial discovery of MCPyV, it has become increasingly clear that virus-positive MCC has a different cause than virus-positive, UV-associated, MCC.

Results : Virus-positive MCC expresses the viral oncogenes large T antigen (LT) and small T antigen (ST) and the tumor genome usually includes very few mutations in cellular oncogenes and tumor suppressor genes. In contrast, studies using whole exome or targeted hybrid capture sequencing have showed that virus-negative MCC has an exceptionally high somatic mutation load predominated by UV-mediated mutations with frequent mutations in RB1, TP53, NOTCH1, and FAT1.

Conclusion : Whole genome sequencing (WGS) of MCC confirmed virus-positive MCC shows a globally lower, non-UV-mediated, mutation burden as well as few somatic copy number amplifications, deletions, and rearrangements compared to virus-negative MCC, while offering new insights into virus integration structure and mechanism.

Keywords : Merkel cell carcinoma (MCC), Merkel cell polyomavirus (MCPyV), virus-positive, virus-negative, virus integration

P238-635: Study of probiotic effect of Bifidobacterium bifidum on CacoII cancer cell line

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1. *Dr.mirpour*

Background and Aim : Probiotics are live microbial supplements with a wide range beneficial in human life.Effect of probiotic microorganisms on human cancer is a controversial issue.

Methods : In this work the inhibitory effect of the supernatant of an autochthonous isolate of bifidobacterium bifidum on the CacoII cells of human colonic carcinoma was investigated. Different concentration of 100,200, and 300 µl/ml of the supernatant of the probiotic bacteria harvested at 24,48 and 72 hours of bifidobacterial growth in MRS media were applied in to the 96 well microplates each containing 8000 cells of CacoII after neutralization of the pH with 1N NaOH

Results : The percentage of cancer cells inhibition observed ranged from 55% to 82% which obtained from 100 µl/ml (24h)and 300 µl (72h) supernatants.

Conclusion : The inhibitory effect of the probiotic bacteria on human cancer cells seems to be concentrated dependent and not affected by neutralization.

Keywords : Probiotic, Bifidobacterium bifidum, colon cancer, CacoII cells

P239-686: Prevalence of hepatitis B Virus Infection Among HIV positive patients in Zabol city(iran)

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Background and Aim : Today, due to the increase of life expectancy in HIV-infected patients, the incidence of related diseases such as hepatitis B and C due to similarity in transmission routes has become a major concern of the health community. Therefore, this study was performed to determine the prevalence of hepatitis B among HIV + patients in Zabol.

Methods : This descriptive cross-sectional study was performed on 37 HIV-infected patients in the Zabol city (2021-2022). In the present study, HIV-infected patients were screened for hepatitis B by measuring serum levels of HBC Ab and HBs Ag. Finally, the data in SPSS V21 software were analyzed.

Results : In the present study, a total of 37 HIV-infected patients with a mean age of 40.81-11.64 years were evaluated. In the present study, the prevalence of HIV and HCV coinfection was 21.6%. Also, 13.5% of HIV patients had HBV and HCV simultaneously. Examination of risk factors for viral hepatitis in HIV-infected patients showed that unprotected sex (100%), injecting drug use or IDU (87.5%), dental procedures (75%), history of imprisonment (62.5%) and tattooing (50.5%) were the most common factors in HIV patients. Family history of hepatitis B (12.5%), alcohol (12.5%), transfusion (12.5%) and cupping (25%) were among the lowest cases in these patients.

Conclusion : the frequency of HBV infection and co-infection with HCV and HBV in HIV-positive patients were relatively high. Except for the history of tattoos, there is no significant relationship between other risk factors and hepatitis B among HIV-positive patients.

Keywords : HIV, HBV, prevalence

P240-687: Prevalence of Extended-Spectrum Beta-Lactamase Producing Escherichia coli Causing Bloodstream Infections in patients with leukemia undergoing levofloxacin prophylaxis

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Background and Aim : Bloodstream infections (BSIs) are severe complications in patients with leukemia undergoing levofloxacin prophylaxis during chemotherapy. extended-spectrum beta-lactamase (ESBL) producing Escherichia coli are rising worldwide, resulting in increased morbidity, mortality, and healthcare costs, This study aimed to evaluate the frequency rate of extended-spectrum beta-lactamase-producing Escherichia coli causing bloodstream infections (BSIs) in leukemia patients referred to referral hospitals in Tehran, Hamadan, and Rasht, Iran.

Methods : in a cross-sectional study, 64 blood cultures were collected from leukemia patients suspected to have BSI from July 2021 to February 2022. The blood culture bottles were incubated aerobically at 35–37ºC for 24 hours and then sub-cultured on routine microbiology culture media. The bacterial colonies were identified using microbiological tests. Antibiotic susceptibility tests were performed by the Kirby-Bauer disc diffusion method. The phenotypic detection of ESBLs was carried out by the combination disc-diffusion test (CDDT).

Results : according to the results of this study.The rate of resistance of 64 E. coli isolates against the nine antibiotics was as follows: Amoxicillin-clavulanic acid 95%, Ampicillin 93%, Cefepime 57.8%, cefixime 57.8%, Ceftazidime 59.3%, ceftriaxone 64%, imipenem 6.2% ciprofloxacin 56%, to levofloxacin 54%. The production of extended-spectrum beta-lactamases (ESBL) in E. coli strains was reported in 56.2%

Conclusion : The results of this study show a high prevalence of resistance to beta-lactam and fluoroquinolone antibiotics in patients with leukemia undergoing levofloxacin prophylaxis. Therefore, surveillance and antibiotic stewardship programs should be implemented in leukemia patients to prevent spreading and outbreaks of more ESBLs with limited therapeutic choices.

Keywords : Leukemia, Levofloxacin, Extended spectrum beta-lactamase-producing, Escherichia coli

P241-694: intertumoral microbiome and their effect on tumors

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Background and Aim : Microbiomes are bacteria that normally live in different parts of the human body. So far, it has been thought that bacteria are only present in limited parts of the body, and organs such as the pancreas and lungs are sterile which is not true. One of the sites where bacteria have been found in the human body is cancerous tumors. These tumors have their own microenvironment, which includes cancer cells, fibroblasts, T-cells, NK-cells, macrophages, and dendritic cells in addition to bacteria.

Methods : Our method was searching in online databases such as google scholar, PubMed, etc. the search was limited to the English language and time-limited from 2020 to 2022 due to the subject's novelty and history. Then we filtered 30 primary articles by reviewing their titles and abstracts and removed irrelevant and nun useful ones through the PRISMA chart and eventually used 11 as references.

Results : the tumor microbiome can help cancer to grow or stop its progression through following ways: 1. Inhibiting the immune system and immune responses 2. Direct effect on the cancerous tumor by damaging DNA, increasing mutations, activation of oncogenic pathways, and regulation of oncogene compounds 3. Effect on response to cancer treatment by metabolizing the compounds used in chemotherapy and inhibiting them 4. Impact on the spread and metastasis of cancer

Conclusion : The purpose of identifying and investigating the characteristics of these bacteria is to use them in the prevention and treatment of cancers. After knowing the genus and species, the characteristics, and their function, we can prevent cancers or reduce their progression if the bacteria that cause pre-cancerous inflammation are observed and detected. It is also possible to prevent further growth and spread of cancer by targeting bacteria that help in the growth and development of cancer, which can be through target therapy or by using antibiotics. A series of treatments such as biliary stent placement or neoadjuvant treatment can increase the tumor microbiome, which knowing these can be effective in choosing the best treatment. Another method of using these bacteria in the treatment is to replace the tumor microbiome with helpful bacteria.

Keywords : cancer, tumoral microbiome, chemotherapy

P242-232: Survey on Prevalence of Antibiotic Resistance in Anaerobic Bacteria Isolated from Oral Infections

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Background and Aim : Since the obligate anaerobic bacteria are the most common causes of oral infections such as periodontitis, it is important to investigate their prevalence in patients with oral infections. Also, antibiotic-resistance in anaerobic bacteria have been reported in recent years, therefor, the aim of this study was to investigate the antimicrobial resistance profile in anaerobic bacteria isolated from oral infections (periodontitis) in Shahid Sadoughi University, Yazd.

Methods : A total of 96 oral specimens were collected from patients with periodontitis and cultured onto anaerobic blood agar and kanamycin-Vancomycin-Laked Blood agar. After incubation at anaerobic condition, isolates were identified by gram-staining and biochemical tests such as esculin hydrolysis test, catalase, indole, kanamycin (1 µg)/vancomycin (5 µg)/colistin (10 µg) diagnostic disks and aerotolerance tests. Finally, the isolates were verified with a 16S rRNA-based PCR assay. Minimal inhibitory concentration (MIC) of metronidazole and tetracycline were determined by agar dilution method according to CLSI protocols.

Results : In this study, the most common isolates were belonged to gram-negative anaerobic rods included Porphyromonas gingivalis (66.7%) and Prevotella intermedia (8.3%). The most common gram-positive bacilli were Cutibacterium acnes (19.8%), Eubacterium, (4.2%) and Lactobacillus (1.04%). Also, 16.7% of isolates were resistant to metronidazole (MIC?64 µg/ml) and All of the isolates were susceptible to tetracycline (MIC?4 µg/ml).

Conclusion : According to the results, the antibiotic resistance of anaerobic gram negative rods specially P. gingivalis and P. intermedia against metronidazole is increasing, it is recommended to determine the antibiotic resistance pattern of anaerobic bacteria to common antibiotic in the treatment of oral infections, periodically and annually and the results should be reported to dentists.

Keywords : Anaerobic Bacteria; Antibiotic Resistance; Oral Infections

P243-283: Frequency of virulent Legionella pneumophila in hospital water supply systems in the west of Iran

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Background and Aim : Legionella pneumophila as a fastidious rod-shaped aerobic and Gram-negative bacterium causes hospital-acquired pneumonia. Hospital water supply systems are known as long-term and critical reservoirs in the human infectious cycle. This study aims to detect the frequency of L. pneumophila. in water supply systems of hospitals of Sanandaj city in the west of Iran.

Methods : In a cross-sectional study, 100 water samples (50-1000 cc) were collected from 100 different sites of hospital water supply systems. Following separation of sediments of water samples by using centrifuge machine and heat treating, the sediments were processed by using culture and direct PCR methods to detect Legionella spp.

Results : The frequency of Legionella spp. isolated from the water samples by using culture on BCYE agar and PCR method (16s rDNA gene specific primers for Legionella spp.) was 12% and 16%, respectively. The most isolates of Legionella spp. were detected by using direct PCR on the water samples collected from shower head (n 7) and water pond (n 4) ($p<0.05$). In this meanwhile, the frequency of mip and rtxA virulence genes by using direct PCR was 25% (4/16) and 25% (4/16), respectively. Based on the results of Hippurate hydrolysis tests and 16s rDNA gene sequencing, 4 isolates grown on the BCYE were L. pneumophila which showed frequency 100% of mip and rtxA virulence genes (4/4).

Conclusion : This study showed the high frequency of virulent L. pneumophila and its virulence genes in water supply systems of hospitals in the west of Iran.

Keywords : Legionella, mip, rtxA,

P244-334: Molecular detection of Brucella spp. in the population of vaccinated and non-vaccinated sheep against brucellosis in Yazd Province of Iran.

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Background and Aim : Brucellosis is a common disease between humans and animals, which has great global importance. Brucellosis is endemic in Iran and has been reported with different prevalence in livestock and human population from different parts of the country. In Iran, sheep have a higher percentage of brucellosis than cattle. Timely and accurate diagnosis of this disease is the starting point of any effective program to control it in animals and humans. Therefore, the purpose of this study is to investigate the status of Brucella infection in the sheep population of Yazd city with the help of molecular PCR technique.

Methods : To carry out this research, after clinical examinations and Rose Bengal test, blood was taken from 50 healthy non-vaccinated sheep, 25 sheep vaccinated with Rev-1 vaccine and 25 sheep infected with brucellosis. For this purpose, blood was taken from the vein of Vadaj (a tube containing an anticoagulant). Subsequently, DNA extraction was performed using a commercial kit. Then, the PCR technique was used to detect Brucella bacteria. Finally, the PCR product was electrophoresed to evaluate the target gene.

Results : Out of 50 healthy samples, 8 samples (16%) were found to be infected with Brucella bacteria. Also, among 25 patient samples and 25 vaccinated samples, seventeen samples (68%) and nineteen samples (76%) were infected with Brucella bacteria, respectively.

Conclusion : Considering the prevalence of this disease in sheep and the high population of sheep in Yazd and the large slaughter of this type of animal in the slaughterhouse, as well as the consumption of its milk by citizens and villagers in raw and unpasteurized form, it is necessary to take a series of measures. Obviously, breaking the chain of transmission of disease to humans depends on the health of animals and compliance with health standards. Inter-departmental coordination and implementation of care policies, effective vaccine production, community education, identification and removal of diseased livestock, etc. are considered as the main solutions in controlling and preventing this disease. It is also

recommended to perform molecular tests in parallel with serological tests for more accurate diagnosis.

Keywords : Sheep, Brucella, PCR

P245-356: Cloning and sequencing of the etx gene from Clostridium perfringens type D strains isolated from patients with antibiotic-associated diarrhoea (AAD)

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Background and Aim : C. perfringens is divided into seven types (A, B, C, D, E, F, and G) based on the production of different toxins (alpha, beta, epsilon, iota, enterotoxin, necrotic enteritis toxin B-like). Of these, alpha, beta, and specially enterotoxin are of major importance in human medicine, and the others are commonly involved in veterinary medicine. The epsilon toxin (ETX) of type D, hitherto unknown association with human disease, is mainly responsible for enterotoxemia in small ruminants. This study was performed to characterize the etx gene sequence of the recently C. perfringens type D strains isolated from Iranian AAD cases.

Methods : C. perfringens type D isolates (N= 15), recently recovered from human AAD patients, were used in this study. Plasmid DNA of the isolates was extracted. For genetic analysis of the etx gene, its entire sequence was synthesized with the designed specific primers. The amplified gene was digested with EcoRI and XhoI, then ligated into pET-26b(+), and electroporated into E. coli DE3 strain. The recombinant strains were obtained by screening the Kanamycin-resistant clones and investigated for the presence of etx gene by PCR and sequencing. The etx gene sequences were manually aligned according to their nucleotides and the deduced amino acid sequences. Phylogenetic analyses were conducted using MEGA X, and the phylogenetic tree was generated using the maximum likelihood (ML) approach.

Results : The etx gene from human type D isolates was synthesized. The expected size of the amplified fragment corresponded to 1006 bp. These were cloned in the pET-26b(+) vector and the pET-26b-? plasmid (6227 bp) was constructed. These results illustrated that this plasmid had been constructed successfully in E. coli.

Conclusion : The present study reports the first sequencing analyses of the etx-positive C. perfringens type D isolates associated with AAD disease. The etx sequences showed high similarity, with >97-99% identity to sequences available in the GenBank database and the etx sequence from C. perfringens type D vaccinal strain (CN409).

Keywords : Cloning; Sequencing; Clostridium perfringens Type D; etx Gene; Antibiotic-associated diarrhoea (AAD)

P246-370: Impact of Pepsin on Transcriptional Alteration of Helicobacter pylori Virulence Genes

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Background and Aim : Helicobacter pylori could survive in the stomach and infect the epithelial cells. Its pathogenicity depends on the bacterial virulence factors that upon interaction with the host are associated with histological changes, inflammatory response and carcinogenesis. Although it is known that acidity of the stomach could affect the pathogenicity of H. pylori, there is a lack of data to indicate its interaction with gastric proteolytic enzymes. The current study aims to shed light on the function of pepsin as the most important proteolytic enzyme of gastric tissue in the pathogenicity of H. pylori.

Methods : Clinical isolates of H. pylori were provided using the culture method from the gastric biopsies of patients subjected to endoscopy. A polymerase chain reaction was done to confirm the isolates and their virulence potential. Well-defined isolates with ureB+/flaA+/cagA+ genotype were selected for in vitro transcriptional analysis. Accordingly, the selected isolates were treated with 0.5 and 1 mg/mL pepsin for 30 and 90 min and relative changes in the transcription of ureB, flaA and cagA genes were measured using real-time PCR compared with the untreated counterparts.

Results : Out of 46 H. pylori isolates from 168 biopsy samples, 17 isolates with optimum growth in broth culture medium were screened for ureB, flaA and cagA genes. All the strains were ureB positive, while 94.1% and 82.3% of them carried flaA and cagA genes, respectively. Transcriptional analysis showed down-regulation of ureB and flaA (Ranges between 0.2 to 0.008 folds) and up-regulation of cagA (Ranges between 3 and 9 folds), while the strains sustained their survival. No significant diversity in transcriptional levels was detected among the three tested strains in response to different concentrations of pepsin.

Conclusion : Results of our study showed induction of cagA and suppression of flaA and ureB transcription in response to regular pepsin concentrations in the gastric juice. Further studies are needed to show possible outcomes of this interplay on the H. pylori pathogenesis.

Keywords : Helicobacter pylori; Pepsin; Gene expression; ureB; flaA; cagA.

P247-371: A study of the prevalence of Neisseria gonorrhoeae and its molecular characterization in Tehran, Iran

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Background and Aim : Neisseria gonorrhoeae is an important global public health concern due to increasing rates of diagnosis. Molecular epidemiology data is used to understand the distribution and spread of N. gonorrhoeae as well as the relationships between cases in sexual networks. This study was performed to prevalence and molecular epidemiology of N. gonorrhoeae isolates in Tehran, Iran.

Methods : We collected 500 urogenital swabs (468 endocervical, 32 urethral) from patients presenting to two women's hospitals and one health center in central and south Tehran with signs and symptoms of genitourinary infections between 1 July 2018 and 30 July 2020. A culture of the specimens was performed, and the isolates were analyzed for the presence of N. gonorrhoeae isolates by biochemical tests. NG-MAST (Neisseria gonorrhoeae multiantigen sequence typing) was also performed.

Results : Patient data: The most common clinical symptoms in females were vaginal discharge (276/ 468, 58%), and nearly a quarter (7/32, 21.8%) of males had dysuria. Isolation of Neisseria gonorrhoeae: A total of 38 N. gonorrhoeae isolates were identified. The patients from which the isolates were cultured comprised 1/32 (3%) male patients and 37/468 (7.69%). Neisseria gonorrhoeae multiantigen sequence typing (NG-MAST): A total of 25 NG-MAST sequence types (STs) were identified. There were 1–4 isolates in each ST, and ST266 (n = 4) was the most prevalent ST. Overall, one ST was represented by four isolates, one ST by three isolates, eight STs by two isolates, and 15 STs by single isolates. Out of 38 STs, 11 (29%) novel STs were identified.

Conclusion : These findings suggest a high prevalence of gonorrhoea in at-risk patients visiting our hospitals and health centers. Our study reflects a highly diverse gonococcal population in Tehran. Combining molecular and epidemiological data provides insight into the spread of this pathogen.

Keywords : Neisseria gonorrhoeae, Neisseria gonorrhoeae multiantigen sequence typing, sexually transmitted infections

P248-404: Comparison Specificity of Invasive and Serologic Methods in the Diagnosis of Helicobacter pylori in Khorrmabad City, Iran

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Background and Aim : Helicobacter pylori is a gram-negative bacterium that is the main etiology of peptic ulcers and chronic gastritis. The prevalence of this bacteria is typically high in developing countries. This study aimed to compare the specificity of invasive pathological and serologic methods in diagnosing Helicobacter pylori in hospitals in Khorramabad city.

Methods : This study was performed on 100 samples of Shohadaye Ashayer & Shahid Rahimi hospitals in Khorramabad city, Iran. The gastric antrum and duodenal biopsies were done to detect H. pylori by pathological methods and determine if the Antibody was done by the ELISA method.

Results : The number of positive results obtained in this study was 60% by pathology and 33% by serology. The number of women with infections was higher than that of men. The highest rate of infection was between the ages of 30 and 40 years

Conclusion : In this study, the pathology method was more accurate than the serologic method in detecting Helicobacter pylori H. pylori infection. So, antibody titration alone is not sufficient for definitive diagnosis and requires invasive pathological methods such as biopsy

Keywords : Helicobacter pylori, invasive pathology, noninvasive, serology

P249-408: spoT gene is involved in biofilm formation and antibiotic resistance of Helicobacter pylori isolates

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Background and Aim : Antibiotic resistance decreases the eradication rate of Helicobacter pylori (H. pylori). Biofilm formation on the surface of gastric mucosa is a reason to surpass eradication therapy. Most of the clinical isolates carry spoT gene which is considered as the major gene of biofilm formation in this pathogen. So, this research was designed to study presence of spoT gene in H. pylori isolates, and their association with antibiotic resistance and biofilm formation.

Methods : Microplate method was used for obtaining MICs of amoxicillin, and clarithromycin for 72 isolates of H. pylori. Also, the ability of H. pylori strains for forming biofilm was analyzed. The presence of spoT gene was detected by PCR method and their association with biofilm formation and antibiotic resistance was investigated.

Results : The spoT gene were detected in 66(91.6%) of 72 isolates, respectively. Out of 66 spoT- positive isolates, 52 were able to form biofilm and none of 6 spoT- negative isolates were able to form biofilm. The frequency of resistance to amoxicillin, and clarithromycin in spoT+ H. pylori were, 24 (36%),and 44 (66.66%), respectively.

Conclusion : The study showed that resistance of H. pylori to conventional antibiotics is high in this region. Hence, there is need for antibiotic susceptibility testing in order to select drug regimens. Additionally, biofilm production and antibiotic resistance of H. pylori was associated with harboring of spoT gene , so could be served as a therapeutic target and genetic markers of antibiotic resistance.

Keywords : Helicobacter pylori, antibiotic resistance, biofilm, spoT gene

P250-418: Decolorization of textile wastewater using thermophilic bacteria isolated from the wastewater and returned to the production line

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Background and Aim : Materials and Methods: From a wastewater treatment plant (wastewater) 1 * in Kashan, samples were taken and bacteria that decompose the existing dyes of the wastewater were isolated. TSB, effluent, modified M9, TSA and agar effluent were used to enrich and screen the bacteria that degrade wastewater dyes.

Methods : Using M9 medium containing dye at 26 to 53 ° C, different strains (temperate, thermophilic, salt-loving) of the dye decomposer were selected from among the primary isolated bacteria. Identification of the selected bacterial strain was performed by sequencing the 16S rRNA gene.

Results : 47 bacterial strains were isolated using culture media containing degradable dyes in wastewater. The decolorization ability of these strains was observed from 22 to 78.5% during three days of incubation at a temperature of (263-37-37-42-48-53 ° C). Among these strains, 3 strains in the consortium had the ability to grow well in the environment containing dye and remove dye by 95.5%. The optimum conditions for dye removal by response procedure (RSM) are 42 ° C, 1% salt concentration, 50 mg / l dye concentration and pH 7.

Conclusion : The amount of decolorization of SN7, SN10 and SN5 strains in aerated (on shaker) and static (anoxic) conditions indicates more paint removal in static state. Better decolorization was observed using two-stage aeration method and then static conditions. Industrial use of this strain in textile wastewater treatment has been suggested.

Keywords : various bacteria (moderate, thermophilic, halophilic), color analysis, azo and reactive dyes

P251-464: New toxinotyping of clostridium perfringens isolates based on molecular characterization of netB and cpe genes

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Background and Aim : Clostridium perfringens (C. perfringens) belongs to the family of Clostridiaceae and produces a wide range of toxins (four major and a variety of minor toxins). C. perfringens is divided into five toxinotypes (A-E), according to the presence and combination of the four major toxins: alpha (CPA), beta (CPB), epsilon (ETX), and iota (ITXA and ITXB). This traditional classification has been changed and updated toxinotyping scheme that suggested strains, producing CPA-toxin, as well as CPE are determined as type F, whereas those producing CPA and NetB toxins are categorized as type G.

Methods : 22, 19, 22, and 21 C. perfringens isolates that were designated as toxinotype A, B, C, and D, respectively that were identified by multiplex PCR amplifying multiple target genes encoding C. perfringens alpha, beta, epsilon, and iota toxins used in this research. isolates were provided by the microbial archive of Razi Institute (south-east branch). All isolates smeared on blood agar medium containing 5% defibrinated sheep blood in anaerobic condition then examined with single PCR assay to identify the cpe, and netB genes by using two pairs of specific primers. PCR reaction mixture was done in a final 25 µl reaction volumes, amplified bands were inspected under a UV transilluminator and photographed using the gel imaging system.

Results : Results showed that cpe gene was identified in 29 out of 84 (35%) which was higher in type A (68%) than the others. while it was not detected in any of type B isolates and the netB gene was not found in none of studied isolates. Based on the results, the first toxin types of isolates changed. Accordingly, 14 cpe positive isolates that were primarily classified into type A, will categorize as type F.

Conclusion : Because certain toxins are associated with specific hosts and diseases the accurate typing of C. perfringens isolates and classification into 7 toxin types is important for epidemiology and diagnosis and to differentiate the strains involved in enteric infection.

Keywords : C. perfringens, toxin types, PCR, gene

P252-466: Evaluation of toxin production power in different types of clostridium perfringens isolates

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Background and Aim : C. perfringens is a gram-positive, rod-shaped anaerobe bacterium that is one of the most common pathogens and causes a spectrum of human and veterinary diseases and has a prolific toxin-producing ability that produce an array of toxins. C. perfringens has five toxinotypes (A, B, C, D, E), according to the presence and combination of the four major toxins: alpha, beta, epsilon and iota. Serological methods such as ELISA are widely used to detect clostridial toxins, usually these methods are used to identify a specific toxin in intestinal contents or pure bacterial culture.

Methods : A total of 84 C. perfringens isolates which was obtained from the microbial archive of Razi Kerman Institute from various types that originated from sheep and goats used in this research that were identified as C. perfringens by microbiological, biochemical and toxin typed by PCR method.All isolates were evaluated for production of alpha, beta, and epsilon toxin by BIOX ELISA kit and the he frequency and distribution of toxins in different strains were evaluated.

Results : Out of 84, 64 isolates showed the presence of at least one toxin in ELISA test, 31, and six isolates were positive for only alpha and only epsilon toxin respectively, 17, six isolates show presence of both alpha and epsilon and both alpha and beta toxins respectively furthermore four isolates positive for the presence of all three toxins, meanwhile, 20 C. perfringens isolates didn't show none of the toxins. The results of this study show that type C isolates were the most positive cases of alpha and beta toxin while type B isolates were the most positive cases of epsilon toxin, which could be related to the pathogenicity of these types in the isolates studied

Conclusion : These findings indicated that the presence of a toxin-producing gene in an isolate is not directly related to the secretion of all the expected toxins in different types by ELISA test, and despite the confirmation of the isolates by PCR, in some cases, the desired toxin is not expressed and produced.

Keywords : Clostridium perfringens, toxin, serological,ELISA

P253-519: A study of prevalence of vacA d genotypes of Helicobacter pylori isolated from patients with gastrointestinal problems in Mashhad

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Background and Aim : Helicobacter pylori is a bacterium that resides in the human stomach, which is associated with gastric diseases. The vacA gene is one of the most virulence factors of H.pylori and associated with gastric pathology. Pathogenesis of vacA depends on polymorphic diversity within the signal (s), middle (m), intermediate (i), deletion (d) and c-regions.These regions show distinct allelic diversity. The present study aimed to investigate the prevalence of vacA d1, d2 genotypes in the H.pylori isolates from patients with gastric disease.

Methods : A total of 100 patients suffering from gastric diseases were enrolled. The presence of urease enzyme in the samples was checked by urease test and Detection of H.pylori infection and genotyping of vacA d region were carried out by PCR.

Results : Of the total of 66 H.pylori isolates, 22 contained the d1 allele and 29 were subtype d2. d2 allele was more prevalent among patients with gastric problems and a significant relationship was found between this allele and the development of gastritis.

Conclusion : Genotyping of vacA d region might be a reliable marker for the identification of vacA virulent strains that represent a high risk of developing gastric diseases.

Keywords : H.pylori, VacA gene, PCR

P254-701: Carbapenems resistance among Bacteroides fragilis isolated from skin and soft tissue infections

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Background and Aim : The carbapenem susceptibility pattern of Bacteroides fragilis isolated from skin and soft tissue infections were investigated.

Methods : Twenty- Six B. fragilis isolated was isolated from skin and soft tissue infections. The standard microbiological and biochemical tests were used for identification of isolates. Agar dilution methods were applied for determine the susceptibility to imipenem according to the clinical and laboratory standards institute (CLSI). The presence of Metallo-β-lactamase (MBLs) and efflux pump mediated resistance were detected by phenotypic methods.

Results : According to the minimum inhibitory concentration (MIC), 4 isolates were imipenem resistant (MIC ≥ 16 µg/mL). The imipenem MIC ranges were 2-64 µg/mL in bacterial isolates. The MIC50 and MIC90 of imipenem were 8 µg/mL and 16 µg/mL, respectively. The MBLs mediated resistance was detected in all imipenem resistant isolates. Efflux pump mediated resistance was detected in 1 isolates that was MBLs positive.

Conclusion : According to our results the incidence of carbapenems resistant B. fragilis is at a worrying level. The most common mechanism of carbapenems resistance among B. fragilis was carbapenemase production. The resistance to carbapenem may be multifactorial in some B. fragilis isolates. We propose reassessment in the controlling program of anaerobic pathogens in our health care centers.

Keywords : Bacteroides fragilis, Carbapenem, Metallo-β-lactamase, efflux pump

P255-29: The novel therapeutic strategy for obesity through the gut-brain axis

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Background and Aim : The interaction between commensal bacteria and the host is essential for health and the gut-brain axis plays a vital role in this regard. Obesity not only does disorder affects the health of the individuals, but also the economic and social aspects of communities are affected by it. The presence of any dysbiosis in the composition of the gut microbiota disrupts in the gut-brain axis, which in turn leads to an increase in appetite and then obesity. Because common treatments for obesity have several drawbacks, the use of microbiota-based therapy in addition to treatment and prevention of obesity can have other numerous benefits for the individual. In this review, we intend to investigate the relationship between obesity and the gut-brain axis as well as novel treatment strategies based on this axis with an emphasis on gut microbiota.

Methods : -

Results : -

Conclusion : -

Keywords : gut–brain axis; obesity; dysbiosis; gut microbiota; probiotics; prebiotics; FMT

P256-79: The Impact of the Gut Microbiome on Toxigenic Bacteria

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Background and Aim : A vast amount of evidence in recent decades has strongly indicated that human microbiota has vital function in the human condition by several mechanisms (3, 4). In addition, the microbiota can increase food energy extraction (5), raise nutrient yield (3),(6) and change the signaling of appetite (7),(8). Second, the human microbiota also develops a physical obstacle by production of antimicrobials and the competitive elimination which help to defendthe host against external pathogens (9)–(10) This article is based on how anti-infectious defense mechanisms interfere with host-microbiota interactions and also elucidate the direct conflict between pathogens or commensals in the body

Methods : The gut microbiota cells outnumber the somatic cells 10–100 times, but most of them can not be grown in vitro. Molecular technologies have shown that the healthy human flora comprises more than 99.1 percent of bacterial species and is primarily represented by four phyla, Bacteroidetes, Firmicutes, Proteobacteria, and Actinobacteria.The interaction between the gut microbiota and the organism may be symbiotic, cooperative, or commensal, thus allowing for colonization with protective species ("symbionts"), (24)The organism avoids enteric pathogens via an "intestinal barrier" consisting of three interdependent elements: the intestinal microbiota, the continuous intestinal epithelium covered by the mucus layer, and the mucosal immunity

Results : Whenever antibiotics are used regardless of targeting, we have calculated the collateral effects on the gut microbiome.Bacterial pathways or growth functions, biochemistry, and metabolism have been conserved. .(138) Intestinal microbiotaderived urinary biomarkers of colonization resistance in antibiotic-treated mice are identified in a targeted metabolomics method.(138) In comparison to antibiotic therapy, the elegance of CRISPR/Cas technology involves the delivery of bacterial strain-specific gRNA, exploiting the CRISPR/Cas framework of the target bacteria for accurate targeted treatment.

Conclusion : Many scientists believe that the human intestinal microbiome is a complex ecological group that influences normal physiology and disease susceptibility through consensual metabolism, immunology, and host interaction. In combination with animal studies, high-efficiency sequence, and computational techniques, therapeutic products' efficacy and toxicity at the population-level remained unclear. Although several studies have

shown a higher prevalence of food, nutrients, pharmacology [(144, 145) the impact of host genetic factors on intestinal microbiota cannot be ignored or excluded[25]

Keywords : Health, microbiota, toxigenic, Treatment

P257-84: Replacing Meal worm in aquatic diet to increase probiotic bacteria and reduce disease

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Background and Aim : Consumption of meal worm larvae powder can affect the microbial flora of different parts of the fish body, but in this article, the main focus has been on the microbiota of the gastrointestinal tract of trout fed with TM larvae powder. Therefore, a better understanding of host-symbiotic pathogen transplantation is essential not only for gaining insight into microbial involvement in fish diseases, but also for activating new antimicrobial and antimicrobial approaches to their treatment. The present study aimed to investigate the effects of using different percentages of TM larvae powder in the diet of rainbow trout (Oncorhynchus mykiss) on increasing the amount of beneficial bacteria and probiotic Bacillus safensis.

Methods : After adaptation of the fish and feeding with meal worm larvae powder and completion of the feeding period, the fish were randomly separated from 4 treatments and 3 replications and probiotic and beneficial intestinal bacteria were studied and compared with the control group. In addition, the effect of these bacteria on growth performance, survival and other factors affecting the immune system were evaluated.

Results : The results showed that Bacillus safensis bacterium had the highest number of beneficial bacteria and probiotics in the gastrointestinal tract of rainbow trout fed with TM powder, which was identified by culture, PCR and phylogenetic tree drawing. Data analysis also showed that the number of beneficial bacteria of Bacillus safensis for treatments that used TM larvae powder in their diet was significantly increased compared to the control group. As this increase in treatment showed the highest rate of 45%.

Conclusion : The gastrointestinal tract of all vertebrates contains a complex set of microorganisms (microbial communities) commonly known as intestinal microbiota. Intestinal microbiota is a research area of interest that is universally available to animals, but most studies on the composition and function of intestinal microbiota in vertebrates have been performed in mammals. There is relatively little information about fish gut microbiota and its response to nutritional and environmental conditions, despite the fact that fish make up almost half of the living vertebrate species and are of global economic importance.

Keywords : Meal worm , probiotic, Bacillus safensis, Gastrointestinal

P258-108: Evaluation of Lactobacillus brevis supernatant on Pseudomonas aeruginosa biofilm formation

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Background and Aim : Pseudomonas aeruginosa is one of the most causes of healthcare-associated infections, including urinary tract infections, nosocomial pneumonia, bloodstream infections, and skin infections. Unfortunately, Pseudomonas aeruginosa shows resistance to a variety of antibiotics. One of the most serious consequences of microbial biofilms is that the bacteria can tolerate and survive at high concentrations of antibiotics. According to this issue in our project, we evaluated the Lactobacillus brevis supernatant on Pseudomonas aeruginosa biofilm formation

Methods : In this assessment, MIC and Disk Diffusion techniques were used to evaluate the effect of Lactobacillus brevis on Pseudomonas aeruginosa strains. In this regard, Bacteria-free supernatant was obtained by centrifugation at 12000 rpm for 20 min. To ensure the cell-free status of bacterial cells, supernatants were passed through a 0.4 µm pore size filter. The effect of antibacterial activity of the supernatant of probiotic was evaluated after 24h at 37°C.

Results : The highest resistance was to Ciprofloxacin, Imipenem, Amikacin, Gentamicin, Tobramycin, and Cefotaxime. Lactobacillus brevis supernatant was used for MIC assay. The results show that MIC for all isolates was 50 µl against Pseudomonas aeruginosa.

Conclusion : Briefly, probiotics could affect biofilm formation of Pseudomonas aeruginosa and likely this issue is due to the effect on host cells through regulating the transcription of its virulence-associated factors. Probiotic bacteria have numerous effects on medical aspects. One of them is related to utilize for inhibition of biofilm. These days, due to the lack of proper antibiotics for several infections, probiotics could be highly useful.

Keywords : MIC, Lactobacillus brevis, Pseudomonas aeruginosa

P259-130: Postbiotics and Paraprobiotics: The New Scopes in Innovative Microbial Functional Foods and Neutraceuticals

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Background and Aim : Throughout the years, numerous researches were conducted to either showcase health-promoting features or prove potential characteristics of probiotics, prebiotics and the combination of the two (synbiotics). Although the science-based outcomes seem to be promising and reliable for human health but proposing new helpful options and alternative strategies are invariably appreciated. Due to concerns like safety issues and the risk of probiotic sepsis propagating infection and antibiotic development probabilities, the shortages on probiotics viability, shelf-life and preservation methods and also increasing demand for non-dairy bioproduct substitutions; introducing postbiotics and paraprobiotics is pivotally important. Postbiotics are biogenics (aka. metabiotics) consisting of either metabolites or byproducts derivating from the biogenesis of probiotic cells. Paraprobiotics are referred to the non-viable microorganisms, the inactivated probiotic microbial cells, cell-free supernatant or different cell residues and components. Since probiotics are living organisms mainly ingested orally to eventually affect the gut flora, they are required to endure surviving in great quantities after passing the gastrointestinal tract harsh pH and conditions. As postbiotics and paraprobiotics are considered non-living, they remain unaffected by the GI conditions and also potentially hold the beneficial goodness of probiotics to the consumer while effortlessly elevating viability control by keeping the effective desirable components intact, in order to be well-digested leading to gut microbiota safer enhancement. This study is intended to highlight a review on postbiotics and parabiotics, main categories, nutritional health benefits and conferring possible future prospects in industrial food biotechnology.

Methods : Thirty research studies were chosen and explored from GoogleScholar databases NCBI, ScienceDirect and Taylor&Francisonline (from year 2020 to July 2022) and the obtained data was remarked with commentary classificational view with a focus on nutritional health and innovations in modern biotechnology market.

Results : Studies and trials mark the considerable potential of paraprobiotics and postbiotics as the next-generation of new safe choices to be used in producing novel functional foods and nutraceuticals in nutribiotic industry via innovative scale-up biotechnological applications.

Conclusion : Functional products containing postbiotics and paraprobiotics improve the microbiota balance while also improving product safety, viability and shelf-life therefore

keeping up with the post- and para- new generation trends result in optimistic future industrial success.

Keywords : Functional foods, Postbiotics, Paraprobiotics, Health benefits, Innovative therapy

P260-149: Therapeutic potential of fecal microbiota transplantation in systemic lupus erythematosus

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Background and Aim : Systemic Lupus Erythematosus (SLE) is one of the chronic and autoimmune diseases that can involve and damage different body organs, including kidneys, bones, and skin. The prevalence of this disease in women is ten times more common than in men, and due to the high treatment costs and the problems it causes in daily life, it has become a severe problem for patients. Fecal microbiota transplantation (FMT) is one of the new, efficient, and available treatment options for this disease. In this method, the balanced bacterial population of a healthy person's intestine is screened during a process and transferred to the patient. A balanced microbial flora is one of the primary axes in body health, and this microbiota in people with SLE is out of balance and provides the basis for the development of subsequent disorders for the patient so that the FMT method can return the necessary balance to the patient's intestine and help to treat SLE faster.

Methods : This article is a review, and its documents were collected by searching the keywords "systemic lupus erythematosus," "fecal microbiota transplantation," and "treatment" in PubMed and Scopus databases. From the 22 articles searched between 2018 and 2022, we studied eight papers with the most relevant topic and extracted their results.

Results : Some studies showed that the FMT method increases the effectiveness of glucocorticoid drugs in treating SLE and helps reduce the side effects of these drugs. FMT is also effective in regulating the balance of intestinal microbial flora and ultimately controlling SLE by increasing the ratio of Firmicutes to Bacteroides and beneficial bacteria such as Ruminococcaceae and Bifidobacterium (from bacteria that produce short-chain fatty acids beneficial for body metabolism). A study found that FMT not only can increase the diversity of the gut microbiome of patients with SLE, like a healthy microbiota but also can change the function of the population of these bacteria from pro-inflammatory to anti-inflammatory.

Conclusion : According to the above findings, we can explain that fecal microbiota transplantation is a safe, effective, and efficient method for treating many metabolic diseases, including systemic lupus erythematosus, and helps to restore the balance of the body's microbial flora and reduce the complications of the disease.

Keywords : systemic lupus erythematosus, fecal microbiota transplantation, FMT, SLE

P261-169: Evaluation of species distribution and virulence factors of oral mycobiome in hospitalized patients with COVID-19: A case–control study

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Background and Aim : COVID-19 has highlighted the importance of paying attention to the mycobiome of the oral cavity and its alterations. The oral mycobiome might favor a severe outcome of COVID-19 infection through different mechanisms, including alteration of the respiratory epithelium, promotion of adhesion of respiratory pathogens, increase of local inflammation, and related virulence factors. The present study aimed to determine the prevalence and species distribution of oral mycobiome in patients with COVID_19 and the virulence factors of isolated fungal agents compared with healthy controls.

Methods : We conducted a case–control study of 144 patients with coronavirus infection and 144 controls. Cases and controls were matched for age, gender, body mass index, and the history of receiving antibiotic and antifungal medications. The study was carried out for 12 months (May 2021–May 2022) at Razi referral hospital, Rasht, Iran. All the samples were subjected to fungal culture and PCR-sequencing. The enzymatic activity index (EAI) was measured for important virulence factors including proteinase, esterase, and hemolysin activity using the relevant protocols.

Results : The results showed that in comparison with the control group, the prevalence of oral mycobiome in patients with COVID_19 was 3-fold higher. The genus of Candida (n=152, 100%) was the single fungal genus isolated from the oral mycobiome of COVID-19 patients and healthy controls and Candida albicans (n= 138, 90.79%) was the most common isolated species. Phospholipase, proteinase, and hemolysin activity of Candida species was significantly higher in patients than in healthy people. The activity of the Candida albicans virulence factors in both groups was greater than that of non-albicans.

Conclusion : How the virulence factors of oral mycobiome are working in COVID-19 patients is essential to develop new antifungal agents and determine the cause of drug resistance and management of patients.

Keywords : Mycobiome, COVID-19, oral cavity, Candida species, Hemolysin factor, Proteinase, Esterase.

P262-170: Study of skin and nail Candida species as a normal flora based on age groups in healthy persons in Tehran-Iran

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Background and Aim : The skin is the body's largest organ that hosts heterogeneous inhabitants. Until now, the diversity of the cutaneous microbiome was mainly investigated for bacteria and there is a little information about the skin fungal flora. Also, among skin fungal flora, Candida is found as a main member whose distribution is affected by sex, age, climate.

Methods : In this study, differences in Candida community structure associated with 9 different skin sites of 238 healthy people during 10 months from July to March 2016, are described. These subjects were divided by age into 4 groups: infants, children, adults and geriatrics. The collected samples were examined by culture on Sabouraud Chloramphenicol Agar and CHROM-agar Candida. For precise identification of species ITS1-5. 8S-ITS2 rDNA regions were sequenced where needed.

Results : The frequency of Candida species was significantly different between age groups. The most Candida isolations were related to the elderly age group and the fewest in the infants. C. parapsilosis virtually, was the predominant isolated species in all age groups.

Conclusion : This study showed no statistically significant effect of the subject's sex on Candida population resident on human skin surface.

Keywords : Skin residents; Cutaneous Candida composition; Different age groups; DNA sequencing; Culture; Microbial epidemiology; Iran

P263-171: Epidemiology, laboratory diagnosis and clinical aspects of fungal pulmonary infections in 384 patients hospitalized in pulmonary units in Guilan province, Iran

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Background and Aim : The respiratory tract is the most common site for developing fungal infections. People who have a weakened immune system are more susceptible to respiratory system involvement with fungi. Fungal infections of the respiratory tract are largely unrecognized and their true burden is elusive. Therefore, the aim of the current study was to evaluate the clinical spectrum, demographic characteristics, risk factors, and etiology of fungal respiratory infections in 384 patients hospitalized in pulmonary units of Razi hospital, Guilan province, Iran.

Methods : A total of 384 lung specimens (192 Bronchoalveolar lavages (BAL) and 192 sputa) were obtained from patients who met the inclusion criteria. All samples were analyzed by direct microscopy and culture. Fungal identification was accomplished by internal transcribed spacer (ITS) and beta-tubulin sequencing. Also, in patients suspected to invasive pulmonary aspergillosis BAL specimens were tested for galactomannan (GM) antigen. According to the host factors (clinical symptoms, radiology findings and predisposing factors which were defined as inclusion criteria), and the positive results in direct examination, culture and serology (GM for aspergillosis) the infection was confirmed.

Results : Fungal respiratory infection was confirmed in 137 cases (35.67%) including 86 (62.77%) males and 51 (37.23%) females and the highest prevalence of infection was found in the age group of 46-72 years (n=75, 54.74%). Cough (n=129, 94.16%), dyspnea (n=111, 81.02%), purulent sputum (n=85, 62.04%) and weight loss (n=77, 56.2%) were the predominant symptoms. Tuberculosis (n=34, 24.81%), taking chemotherapy regimen (n=30, 21.89%) and diabetes mellitus (n=27, 19.70%) were the predominant underlying conditions. Candida albicans (37.22%) and Candida tropicalis (21.89%) represent the two most commonly isolated species in the current study. Furthermore, according to revised EORTC/MSG (2008) definitions for invasive fungal infections, from 5 cases of pulmonary aspergillosis, 2 (40%) cases of probable invasive pulmonary aspergillosis (IPA) and 3 (60%) cases of possible IPA were diagnosed.

Conclusion : Many physicians missed fungal pulmonary infection because it does not show specific clinical manifestations. Given that some of uncommon causal agents of fungal

pulmonary infections are intrinsically resistant to routine antifungal drugs and could cause treatment failure, mycological examinations should be considered for proper treatment.

Keywords : Bronchoalveolar lavage; Sputum; Candidiasis; Fungal respiratory infections; Invasive pulmonary aspergillosis; Galactomannan antigen

P264-172: Study of skin and nail Trichosporon species as a normal flora based on age groups in healthy persons

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Background and Aim : The skin is the body's largest organ that hosts heterogeneous inhabitants. Until now, the diversity of the cutaneous microbiome was mainly investigated for bacteria and there is a little information about the skin fungal flora and Trichosporon is occasionally found as normal flora of skin.

Methods : The skin is the body's largest organ that hosts heterogeneous inhabitants. Until now, the diversity of the cutaneous microbiome was mainly investigated for bacteria and there is a little information about the skin fungal flora and Trichosporon is occasionally found as normal flora of skin.

Results : The frequency of Trichosporon species was not significantly different between age groups. The most Trichosporon isolations were related to the adult age group and the fewest in the infants. T.asahii was the predominant isolated species in all age groups.

Conclusion : This study showed statistically significant effect of the subjects' sex on Trichosporon population resident on human skin surface.

Keywords : skin residents, cutaneous Trichosporon composition, different age groups, DNA-sequencing, culture, Microbial epidemiology, Iran

P265-184: The role of probiotics in inducing apoptosis in oral cancer

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Background and Aim : Oral cancer is the sixth type of cancer in the world, despite many advances, oral cancer is one of the ten major causes of death due to late diagnosis. Oral cancer is associated with the composition of oral and intestinal microbiota. In this context, the administration of probiotics has recently been considered as a good cancer prevention strategy due to their immunological effects. In this field, little research has been done on the effects of probiotics in the development of oral cancer. Some probiotics have anticancer activity by inducing apoptosis. Pattern recognition receptors (PRRs) play an important role in the proper functioning of the innate immune system. Recent studies have shown that PRRs are highly expressed and active in many types of cancer. Physiologically, toll-like receptors identify bacteria and other microorganisms in the oral cavity; However, the role of Toll-like receptors in oral squamous cell carcinoma (OSCC) is unclear.

Methods : The purpose of the present study is to systematically review past studies in examining the positive effects of probiotics on health and their relationship with cancer. Articles related to the subject in Springer Science Direct and Google Scholar databases were searched in English and clinical trials and systematic review articles that investigated the effects of probiotics in the prevention and treatment of oral cancer were included in the study.

Results : Research has shown that in each type of cancer, certain types of TLRs are expressed more, which can be used as markers, and the expression of TLRs, in turn, increases the expression of downstream pathways such as NF-KB and BCL2, which also prevent apoptosis in cells. They become cancerous. By reducing the expression of TLRs, probiotics regulate the downstream pathways, which will cause apoptosis in cancer cells and improve tumor tissue.

Conclusion : Some of the probiotics have anticancer activity by inducing apoptosis, which has made it possible to consider them as an agent for treatment, which is very safe and does not leave any side effects in the host. This idea can be used in the future of probiotics along with other medical treatments to speed up the recovery of the disease.

Keywords : Oral cancer - probiotics - apoptosis

P266-193: Interplay of microbiome and host genetics promote inflammatory bowel disease

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Background and Aim : The precise pathogenesis of inflammatory bowel disease (IBD) remnants uncertain, however it has been distinguished that IBD happens as a consequence of complex connections concerning genetic disposition, environmental features (diet, antimicrobial habit, smoking, etc.), socio-economic progress, and microbial establishment.

Methods : In this review, we discovered the microbiota arrangements linked with healthy and IBD-affected intestines and the consequence of present IBD treatments on the gut microbiota arrangement.

Results : The prevalence of IBD has been growing altogether over latest years, but there is not adequate suggestion to expansively describe its etiology. The most recognized concept of IBD pathogenesis contains connections concerning host genetics, immune systems, and eco-friendly issues that lead to abnormal inflammatory immunological answers. Namely, NOD2 and ATG16L1 genes are assumed to play inadequacies in the role of the epithelial obstacle plus microbial identification and deletions, which involve intestinal microbes as agents of IBD-related inflammation. In IBD sufferers, improvements established on metagenomic sequencing of microbial RNA have initiate a drop in bacterial arrangement and mixture when matched to natural persons.

Conclusion : In conclusion, there is a multifaceted interface concerning the intestinal epithelial cells, the host immune system, and the plenty of gut microbiota. Therefore, many aspects can donate to the commencement of inflammation.

Keywords : inflammatory bowel disease, genetic, gut, microbiota

P267-195: Investigation of the relationship between the gut microbiota and inflammatory bowel disease in a mouse model

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Background and Aim : Aim: Inflammatory bowel disease (IBD) is a group of chronic gastrointestinal disorders affecting millions of people worldwide. Several factors are involved in the development of this disease, but the gut microbiota is known to be one of the most important factors. The aim of this study was to determine the relationship between gut microbiota and IBD using mouse model.

Methods : Methods: In this study, two methods were used: chemical induction with dextran sulfate sodium (DSS) and biological induction with stool from human with IBD (fecal microbiota transplantation) to induce inflammation in the gut of mice. The populations of the gut microbiota in both groups were studied using real-time PCR. In addition, the serum levels of inflammatory cytokines and the colon tissues of the mice were analyzed.

Results : Results: The pathological results showed that the colon tissue in the FMT group had inflammatory changes as in the DSS group. The changes in the intestinal microbiota population in both FMT and DSS groups on the last day of the study also showed a similar pattern, such that the bacteria belonging to Phyla Actinobacteria, Firmicutes and Bacteroidetes decreased, while the population of γ-Proteobacteria increased significantly. An increase in serum levels of IL-1 and IL-6 was observed in both groups.

Conclusion : Conclusion: The results of this study show that there is a mutual relationship between the gut microbiota and inflammatory diseases, and that the gut microbiota is not only the cause of IBD but may also be a consequence of this disease. In fact, by chemically inducing inflammation, the gut microbiota was altered. On the other hand, performing FMT from human stool with IBD altered the gut microbiota of mice and induced inflammation in the mouse model.

Keywords : Inflammatory bowel disease, gut microbiota, fecal microbiota transplantation, dextran sulfate sodium

P268-217: Amplification of Choosing Isolation-Sources with an Approach to Ameliorate Screening for Diverse Yeasts with Probiotic Potential: a Comparative Study

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Background and Aim : Probiotics are known for their health-promoting benefits in the consumer. In the past few years, probiotics of yeast origin have gained more attention regarding their role in different applications due to their exclusive characteristics and longer viability. The criteria of choosing the right practical probiotic species are vital in the industrial processes and isolating a diverse variety of industrial probiotic yeast species with new comprehensive features secures and qualifies the status of upcoming product outputs. A thorough yet precise acquaintance on potential sources of probiotic yeasts leads to an efficient timesaving screening and isolation process with chances of attaining greater yeast biodiversity and subsequently a more convenient yield. This study is designated with reliance on collating scientific progress on the implication of choice of different potential probiotic sources in yeast isolation.

Methods : A total number of 57 research articles with emphasis on yeast isolation from different sources, also opting for probiotic potency of the isolates, were selected and browsed from GoogleScholar and other online scientific databases and journals (from 2011 to July 2022). Precise data about isolation-sources and number of yeast isolates with considerate probiotic potential was assembled, compared and later pinpointed.

Results : Studies eventuated that sources cheese, kefir, olives, alcoholic beverages, fruits, batters and sourdough are the most substantial probiotic sources respectively. The results corollary affirmed that on 4 major source-categories of food, dairy, beverages and environment, 43% of isolated yeasts are from food sources, 31% from dairy products, 16% from beverages and 10% from environment sources. Silva et al. (2011) and Fernandez-Pacheco Rodr?guez et al. (2018) isolated the most number of yeast from food sources (273 and 215 isolates respectively) while Gürkan ?zlü et al. (2022), Alvarez et al. (2022) and Merch?n et al. (2020) successfully declared the most number of probiotic yeast strains (15 each) from dairy products, wine makery and traditional cheese.

Conclusion : With an accretion of probiotic yeast strains application and importance in the industry, it is essential to continuously look for new practical species to fulfil future product

variety lacks and market demand, thus raising awareness about different sources of isolation is considered a great tool.

Keywords : Probiotics, Yeast, Fermented Foods, Dairy Products, Food Microbiology, Food Technology

P269-241: Effects of Escherichia coli strain Nissle 1917 on goldfish (Carassius auratus) tissues histomorphology challenged with arsenic

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Background and Aim : Arsenic contamination in natural water resources has become a great disaster throughout the world which poses serious health problem. The current study was performed to evaluate the protective effects of Escherichia coli strain Nissle 1917 (EcN) against arsenic (As) exposure on the intestine, kidney, liver, gill and skin histomorphology in goldfish.

Methods : Fish were fed with different doses (0, 106, 107, and 108 CFU g-1) EcN for 80 days and then challenged with As for 96 h.

Results : Results showed that supplemented EcN did not have any side effects on various vital organs. It was also observed that the damages to kidney, liver, gill, and skin were pronounced in fish exposed to As. However, the histopathological damages in fish tissues induced by As were less pronounced in the EcN treated groups compared to the fish fed with the basal diet.

Conclusion : These findings indicate that EcN had potential for ameliorating the toxicity induced by As.

Keywords : Escherichia coli, Goldfish, Arsenic, Probiotics, Histopathology

P270-266: New method for Membrane Vesicle (MV) extraction from Gram-positive Bacteria, a nanoparticle useful in biomedicine and nanotechnology

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Background and Aim : Bacterial Membrane vesicles (BMVs) play noticeably roles in various biological processes such as variation in the composition of the microbiota and facilitate host-microbe network, particularly applications in biomedicine and nanotechnology and take part in developing novel vaccines. We aimed to describe the novel, simplest and less expensive MV extraction protocol with available equipment.

Methods : Bacillus subtilis 6051 was cultured in Brain Heart Infusion (BHI) medium for 24h with shaking in ~250×rpm then removed B. subtilis cells and cellular debris by several speeds centrifugation (40000×g) and times at 4 °C. Adding detergent to MV sediment, vortexing at high-speed and striking by hand for 20 to 30 minutes. MVs were pelleted just by one step centrifugation at 52000×g for 2h then washed with a phosphate buffered saline solution (PBS) and filtrated by a 0.45 µm syringe filter.

Results : MVs morphologic produced by Bacillus subtilis 6051 were seen through Scanning Electron Microscopy (SEM) and Transmission Electron Microscopy (TEM), and the spherical shape was confirmed, also, diameters MVs 150 nm was assessed.

Conclusion : The result of this study demonstrated that the novel protocol for extraction the Gram-positive bacteria's MVs is a simple by using common equipment in laboratories and can be performed as an alternative method with low-speed centrifuges available in most research laboratories.

Keywords : MV, gram positive bacteria, novel protocol, detergent

P271-267: Enterococcus parabiotic regulate inflammatory response induced by Poly (I:C) in the lungs of mice

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Background and Aim : The probiotic paradox states both live and dead cells in probiotic products can generate beneficial biological responses and the term parabiotics was selected to indicate the inactivated dead probiotics cells. Enterocooci are lactic acid bacteria (LAB) and because of their tolerance to salts and acids, and the production of antimicrobial bacteriocins were traditionally accept as probiotic and involved in the preparation of fermented foods. However concerns over the safety of Enterococcus spp. as a probiotic have been increasingly raised todays. In the current study we used the Enterococcus sp. parabiotic to manage the lung inflammation in mice following the administration of viral mimic Poly inosinic:polycytidylic acid (poly I:C).

Methods : Enterococcus cells (that was previously obtained from the traditional pickles) were inactivated by heat pre-treatment at 80 ºC for 30 min.Male BALB/c mice, 8-12 weeks-old, were intranasally administered 20 µL of Enterococcus parabiotic (10^8 CFU/mL) for 5 consecutive days under inhalation anesthesia with isoflurane. Mice received three doses of 20 µl poly (I:C) (1 mg/ml) on days 6-8 and were euthanized on day 9 i.e. 24 h after the last intranasal treatment. Control animals received phosphate buffered saline(PBS) instead of parabiotic. The immune-modulatory activity of Enterococcus parabiotic was determined based on the measure of cytokine levels in the BALF (bronchoalveolar tissue lavage fluid), lung histology, and the lung wet-to-dry (W/D) weight ratio

Results : The quantitative analysis of pro-inflammatory cytokines revealed that TNF-?, IL-1? and IL-6 were significantly reduced by 3.1, 4.2, and 4.4 folds in the mice received inactivated Enterococcus ($P<0.05$). The lung tissue samples from the parabiotic treatment group displayed typical histology of normal lungs with thin alveolar walls and absence of intra-alveolar edema. Compared with the control group (6.7?±?0.15), the wet/dry weight ratios of lung tissues in the parabiotic group (5.7?±?0.13) were significantly decreased($P<0.05$).

Conclusion : Our findings indicate that Enterococcus parabiotic modulates the inflammatory response in bronchial epithelial cells and it can be a useful tool to manage the acute respiratory distress syndrome (ARDS).

Keywords : Enterococcus, Parabiotic, Acute respiratory distress syndrome, Inflammation

P272-343: The effect of psychobiotics on consumer health

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Background and Aim : Psychobiotics are probiotic bacteria which was used as a sufficient dose of bacteria to improve intestinal and brain function. Because intestinal microbes can affect the central nervous system using several mechanisms. Probiotics are living microorganisms that supplements. They include Lactobacillus and Bifidobacterium species, which are used in the health of the brain and immune system, reducing inflammation and allergies, and improving the symptoms of intestinal syndrome.

Methods : Eating probiotic foods such as pickles, kimchi, sauerkraut, and dairy products that contain bacteria are logical to increase beneficial intestinal bacteria. Today, new probiotic products are being developed, Lactobacillus(La5), Acidophilus, and Bifidiobacterium(Bb12) Lactin.

Results : There is a potential relation between the brain and the gut. So the information which is related to the the digestive system is transmitted to the brain and causes the perception of events such as nausea and pain.

Conclusion : Psychobiotics affect human excitement and stress, which requires the reduction of pro-inflammatory cytokines and The increase of cytokines is anti-inflammatory. Another effect of psychobiotics is on learning and memory. Recent observation showed that sequencing or spectroscopic, bioinformatics and nutrobiotic technologies are the basis for research on the effects of psychobiotics.

Keywords : Psychobiotics, probiotics ,nutrobiotic ,Brain, stress

P273-357: The effect of Bacteroides thetaiotaomicron extracellular vesicles and it's supernatant on gene expression involved in Epithelial –Mesenchymal Transition in HCT-116 Cell line

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Background and Aim : Objective: Human gastrointestinal tract microbiota plays roles in metabolism and interaction with the host cells through several mechanisms such as outer membrane vesicle (OMVs). This study aims to address the effects of Bacteroides thetaiotaomicron (B. thetaiotaomicron) OMVs and its supernatant on the expression of cdh1,cdh2,snail1,zeb1,and zeb2 genes involved in Epithelial-Mesenchymal Transition in HCT-116 Cell line.

Methods : The supernatant was extracted using centrifugation. OMVs extraction was done using tris-ethylenediaminetetraacetic acid (EDTA)-sodium deoxycholate buffer treatment and centrifugation. protein content and profile of the OMVs were assessed by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS- PAGE) and nanodrop. Human colon cancer (HCT-116) cell line as the model of intestinal cancer cells was used to study the effects of B. thetaiotaomicron's OMVs and supernatant.

Results : B. thetaiotaomicron's OMVs and supernatant increased the expression of snail1 and cdh1 genes while reduced cdh2 and zeb2 expression. It may be able to act as an influential factor in EMT. B.th and its products did not have considerable effect on gene expression of zeb1.

Conclusion : While B. thetaiotaomicron OMVs showed not cytotoxic effects on human intestinal cells, their effects on cdh1,cdh2,snail1,zeb1, and zeb2 genes. Based on the features and benefits that have been shown in various studies, with more scrutiny they could be considered as promising factors and new candidates for treatment. However, more research is needed to examine their effects in more detail.

Keywords : Bacteroides thetaiotaomicron , extracellular vesicles , HCT-116 Cell line

P274-364: Investigating the Presence of tolC Efflux pump Gene in Urinary Isolates of Klebsiella Pneumoniae in Clinical Samples in the city of Zahedan

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Background and Aim : Klebsiella pneumoniae is the cause of many infectious diseases such as blood infection, wound, pneumonia and meningitis. Improper use of antibiotics and new mechanisms used by bacteria to survive have caused antibiotic resistance and made treatment difficult. Studies have shown that one of the most important mechanisms of antibiotic resistance is the expression of efflux pump in bacteria. Efflux pumps are one of the most important mechanisms of antibiotic resistance. The aim of this study was to investigate the presence of tolC efflux pump gene in infectious Klebsiella pneumoniae isolates from clinical samples in the city of Zahedan.

Methods : In this study, DNA extraction was performed by Boiling method from 96 Klebsiella pneumoniae urinary isolates. The presence of tolC efflux pump gene was checked by using PCR method.

Results : The results showed the presence of tolC efflux pump gene in 95.83% of the isolates.

Conclusion : Suppression of tolC efflux pump gene may be useful in the treatment and control of Klebsiella pneumoniae infections.

Keywords : Klebsiella pneumoniae, Efflux pump genes, tolC, Urinary isolates, Zahedan

P275-368: Investigating the Presence of AcrAB Efflux pump Gene in Urinary Isolates of Klebsiella Pneumoniae in Clinical Samples in the city of Zahedan

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Background and Aim : Klebsiella pneumoniae is the cause of many infectious diseases such as blood infection, wound, pneumonia and meningitis. Improper use of antibiotics and new mechanisms used by bacteria to survive have caused antibiotic resistance and made treatment difficult. Studies have shown that one of the most important mechanisms of antibiotic resistance is the expression of efflux pump in bacteria. Efflux pumps are one of the most important mechanisms of antibiotic resistance. The aim of this study was to investigate the presence of AcrAB efflux pump gene in infectious Klebsiella pneumoniae isolates from clinical samples in the city of Zahedan.

Methods : In this study, DNA extraction was performed by Boiling method from 96 Klebsiella pneumoniae urinary isolates. The presence of AcrAB efflux pump gene was checked by using PCR method.

Results : The results showed the presence of AcrAB efflux pump gene in 97.91% of the isolates.

Conclusion : Suppression of AcrAB efflux pump gene may be useful in the treatment and control of Klebsiella pneumoniae infections.

Keywords : Klebsiella pneumoniae, Efflux pump genes, AcrAB, Urinary isolates, Zahedan

P276-423: Co-aggregation of Lactobacillus reuteri isolated from yogurt against pathogenic Helicobacter pylori for reduction load of H. pylori in human

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Background and Aim : Lactobacillus reuteri is a well- known probiotic with beneficial effects to human health. This species can be found in different organs of the body such as skin, breast, gastrointestinal tract, and urinary tract. Due to its antimicrobial effects, the beneficial effect against Helicobacter pylori which is a pathogen in the human gastrointestinal tract can be tested. Therefore, the main aim of this study was to determine the antimicrobial properties of L. reuteri against H. pylori.

Methods : To doing so, different samples of yogurts around Iran were collected, then 1gr of each samples weighted and solved in 10 mL Saline, then 10 mL of this was added to 90 mL of MRS broth, following that were cultured on MRS agar and incubated to reach the colonies, each of colonies were identified and characterized by staining, biochemical and sequencing analysis to determine the species. After culturing the H. pylori, the co-aggregation and antibacterial effects were studied.

Results : The sequencing results revealed that the isolated species was L. reuteri and coaggregated strongly with H. pylori with large numbers of co-aggregation clumps formed at the bottom of the tube and a clear upper suspension. The results of co-aggregation showed that there is 91.8% co-aggregation between L. reuteri and H. Pylori.

Conclusion : In summary, based on these results it can be found that the L. reuteri which is a probiotic can be applied in therapeutic application for treatment of disease related to H. pylori in gastrointestinal tract.

Keywords : probiotic, co-aggregation, L. reuteri, H. pylori

P277-438: Human gut and SARS-CoV-2

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Background and Aim : Respiratory syndrome coronavirus-2 (SARS-CoV-2) mainly affects the respiratory system; nevertheless, the digestive system can be involved. The human gut microbiome and health status have a direct correlation. While it is affected by different diseases and vice versa. The main gastrointestinal (GI) effect of the virus is in the intestine. Diarrhea is a highly manifested symptom. Furthermore, SARS-CoV-2 utilizes ACE-2 receptors (expressed in the intestine) to enter the cells and exerts its virulence. Also, it modifies the gut microbiome community. Herein, the effect of SARS-CoV-2 on the gut microbiome and the gut microbiome involvement in the respiratory system is discussed.

Methods : The current paper is a review article. A literature search was done in PubMed and Web of Science databases. Also, Google Scholar and Science Direct search engines were searched.

Results : The angiotensin-converting enzyme-2 receptor is the receptor for SARS-CoV-2, which is expressed in the lungs, intestine, and kidney, and the expression is directly correlated with age. Gut microbiota has a direct and indirect effect on the health of the respiratory system. Gastrointestinal symptoms manifest in Covid-19 patients, and diarrhea is the most manifest symptom. The alteration of the gut microbiome was observed in Covid-19 patients; Firmicutes was higher compared to healthy individuals, but Bacteroides was vice versa. Besides, in the fungal community of gut microbiota, Candida albicans is the most presented fungi in the mycobiota of the patients. Instability was observed in the gut microbiome of the patients, and it lasted for six months after healing.

Conclusion : Although Covid-19 is a severe respiratory condition, it affects individuals' GI tract. The effects can be varied, firstly, by receptors entering the cells and secondly by gut microbiota. The most manifested GI symptom was diarrhea, which might result from microbiota community alteration. Gut microbiota is a highly diverse communication of microorganisms involving the health of several organs in humans; it also is an essential factor during hospitalization of Covid-19 patients, which modifies on the stages of the condition. Morganella morganii, Collinsella tanakaei, Collinsella aerofacien, and Streptococcus infantis species are presented highly in Covid-19 patients. Additionally, C.albicans predominated the gut microbiota in the patients.

Keywords : Gut microbiota; bactibiota; mycobiota; Covid-19; SARS-CoV-2

P278-450: In vitro and in vivo effects of Pseudomonas plecoglossicida strain IAUK2313 on growth of Helianthus annuus

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Background and Aim : Biofertilizers constructed by obtained from rhizosphere of plants are good alternative for chemical fertilizers. Helianthus annuus is an important strategic oilfield crop. The aim of this research was to isolate beneficial plat growth promoting rhizobacteria and evaluation their effects on vegetative stage of Helianthus annuus in pot experiment.

Methods : Sampling was performed from rhizospheric soils of different fields in Kerman district. Different bacterial strains were isolated from rhizospheric samples. Direct mechanisms We nitrogen fixation, ammonia production as well as evaluation of their resistance to envaromental re carried out as zinc and phosphate solubilization, stress. Molecular characterization using 16R rRNA sequences was used to identify the selected isolate. A pot experiment was also conducted to investigate the effects of selected PGPR isolate on the growth of Helianthus annuus.

Results : Strain numbers of isolates were considered as IAUK2301-2330. All of selected strains were resistant to the different temperatures between 25-42°C as well as having normal growth in salt concentrations between 5-7 and PH=4-8. Maximum phosphate solubilization efficiency was 350 and related strain was selected for further experiments. Molecular characterization using 16R rRNA sequences suggested the identity this isolate Pseudomonas plecoglossicida strain IAUK2313. Pot experiment by this strain revealed meaningful plant growth promoting traits in seedling stage on shoot height, root length and dry weight of Helianthus annuus.

Conclusion : According to the in vitro and in Vivo results, Pseudomonas plecoglossicida IAUK2313 may have a good potential for field experiments before usage as the new biofertilizer.

Keywords : Phosphate solubilization, Pot experiment, Heliantus annuus, Pseudomonas plecoglossicida.

P279-453: Growth performance, mucosal immunity and disease resistance in goldfish (Carassius auratus) orally administered Escherichia coli strain Nissle 1917

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Background and Aim : The current research aimed at shedding light on the efficacy of Escherichia coli strain Nissle 1917 (EcN) on goldfish growth, gut immunity, morphology, bacterial nutritional enzyme activity and resistance to Aeromonas hydrophila infection.

Methods : Goldfish with mean weight of 1.81 g were fed the experimental diets including basal diet (EcN0), 106 CFU g-1 (EcN1), 107 CFU g-1 (EcN2) and 108 CFU g-1 (EcN3) for 80 days. The intestinal tissues (anterior, mid and posterior parts) were obtained from each fish and immune assays, evaluation of immune related genes by q-RT-PCR, enumeration of bacteria related to digestion, and histological examination were performed. In the end, challenge experiment was carried out by injecting A. hydrophila intraperitoneally to the remaining fish and the obtained data was analyzed statistically.

Results : The fish fed with E. coli at 106, 107 and 108 CFU g-1 showed an enhanced growth compared to those fed with basal diet. Also, fish gut innate immunity, in terms of lysozyme activity, immunoglobulin and total protein levels, was improved in the treatment fish better than those with basal diet, with the best result being observed in fish fed E. coli at108 CFU g-1. In addition, an increase was noted in the up-regulation of immune-relevant genes, namely lysozyme, interleukin -1ß, inducible nitric oxide synthase and tumor necrosis factor α of fish intestine treated with E. coli. A marked surge in the number of proteolytic and heterotrophic bacterial was noted in the gut of fish nourished with the probiotic. Histological studies showed an improvement in the intestinal absorption surface area, intraepithelial lymphocyte count and goblet cell density of fish fed with probiotic-supplemental diets.

Conclusion : These data exhibited the beneficial effect of E. coli on goldfish growth, digestive enzymes and fish intestine heterotrophic bacteria, with the administration of E. coli at108 CFU g-1 yielding the most favorable results.

Keywords : Escherichia coli, Goldfish, Gut microbiota, Mucosal immunity, Disease resistance.

P280-486: How Dysbiosis (Microbiota interruption) leads to colorectal Cancer

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Background and Aim : The human intestinal microbiota is a collection of different microorganisms, systematically participates in the nutrition, metabolism, and immune functions of the human body. When the intestinal microbiota is affected by multiple factors such as diet, environment, and host genes, dysbiosis occurs, which alters the microbiota composition and bacterial bioactivity. Therefore, dysbiosis may cause diseases such as inflammatory bowel disease and colorectal cancer (CRC). This study investigates the relationship between dysbiosis and CRC

Methods : This research was conducted using keywords, including colon cancer, Microbiome, dysbiosis, and inflammation, published in reliable databases such as PubMed, Scopus, and Google Scholar during January 2020 to January 2022. According to the inclusion and exclusion criteria of the related articles, their information was extracted and entered into the checklist and finally analyzed.

Results : Based on the various studies, dysbiosis can induce CRC through inflammatory reaction, immune response, damage to DNA, and modulation of cell proliferation. Fusobacterium and Bacteroides fragilis cause the development of CRC due the modulation of the immune response. While, Escherichia coli cause cancer by damaging DNA. Some genera in Enterobacteriaceae, such as Salmonella and Shigella stimulate the transepithelial migration of neutrophils and then reduce the number of bacteria producing SCFAs (Short chain fatty acids). Evidences show that dysbiosis results in alterations of the physiological function, which leads to the pathogenesis of various diseases. Dysbiosis often occurs in CRC tissues and adjacent mucosa. However, due to the different classification criteria and methods used in past studies, new methods are currently being developed to identify more important species related to the development and progression of CRC.

Conclusion : According to the findings of this study, dysbiosis is one of the most important causes of CRC. Therefore, the altered microbiota or metabolites of substituted microorganisms are promising tools for appropriate and timely diagnosis of CRC.

Keywords : Colon cancer - Microbiome - dysbiosis - inflammation - Gut microbiota

P281-736: Association of altered gut microbiota composition with chronic urticaria

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Background and Aim : An altered gut microbiota composition has recently been linked to some types of allergies. To compare the relative amounts of Akkermansia muciniphila, Clostridium leptum, Faecalibacterium prausnitzii, and Enterobacteriaceae as members of gut microbiota among patients with chronic urticaria (CU) and healthy controls.

Methods : A total of 20 patients with CU and 20 healthy individuals matched by age and sex participated in the study. Fresh fecal samples were collected, and DNA extracted from stool samples was analyzed by real time polymerase chain reaction for the qualitative and quantitative assays of the so-called bacteria.

Results : The frequencies of A muciniphila, C leptum, and F prausnitzii in healthy controls' stool samples were significantly more than those of patients with CU ($P < .001$, $P < .01$, and $P < .05$, respectively), whereas the Enterobacteriaceae family was detected in all patients and healthy controls' stool samples. The relative amounts of A muciniphila in healthy control positive samples were significantly higher than those of samples from patients with CU ($P < .001$). Furthermore, there was a corresponding increase of relative amounts of C leptum and F prausnitzii in healthy control positive samples compared with those of patients with CU ($P = .09$ and $P= .08$, respectively). The mean of the relative amounts of Enterobacteriaceae family in the stool samples from patients with CU was more than that of healthy controls; however, the difference was nearly significant ($P = .12$).

Conclusion : The results reveal a change of frequency and relative amounts of A muciniphila, C leptum, and F prausnitzii in patients with CU compared with healthy controls. This is the first study, to our knowledge, to show the change of microbiota composition in patients with CU.

Keywords : gut microbiota, hronic urticaria, Akkermansia muciniphila, Clostridium leptum, Faecalibacterium prausnitzii, and Enterobacteriaceae

P282-17: Glanders Re-emerging in Few Horses in East Azerbaijan, Iran

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Background and Aim : Glanders is a zoonosis caused by Burkholderia mallei (B. mallei). Glanders has been re-emerging in recent years due to war in the Middle East, unauthorized transfer, the lack of formulated action plans, etc.¬ The prevalence of glanders in Iran and the risk of B. mallei transmission and infection is high, therefore requires the quickly identify this disease in animals, particularly in horses. This study investigated glanders re-emerging in horses in East Azerbaijan Province, Iran.

Methods : From 22 September 2020 to 20 March 2021, six-month periodic tests such as the complement fixation test (CFT) were implemented by the Veterinary Administration of East Azerbaijan to detect glanders in horses. In the case of positive CFT results, the mallein test was conducted. According to the test results, blood samples were taken to culture and prepare serum for the ELISA test.

Results : Deep swab samples were collected from nasal mucosa, lymph fluid, and blood. The CFT results indicated 12 horses susceptible to glanders, and three horses were diagnosed with glanders based on the mallein confirmatory test results. B. mallei were not isolated in culturing the samples. Three cases were positive in the ELISA test which was consistent with the CFT and mallein test results. However, the molecular test results were negative.

Conclusion : It is challenging to isolate B. mallei in the early stage of disease, and the negative molecular diagnostic test result may be misleading in glanders diagnosis. In susceptible cases with a positive CF test result, glanders can be diagnosed by skin mallein and ELISA tests.

Keywords : Burkholderia mallei, Glanders, equine, Complement fixation test, Mallein test, ELISA

P283-49: Antifungal activity of eugenol-loaded polyacrylonitrile nanofibers against dermatophytes

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Background and Aim : Dermatophytes are a group of pathogenic zoonotic fungi that are involved in different types of skin disorders in animals and humans. The aim of this study was to investigate the possibility of using eugenol in a drug delivery system made of polyacrylonitrile nanofibers, which can be used at a reasonable cost to provide a practical structure for its topical use in the treatment of dermatophytosis.

Methods : Polyacrylic nitrile was added to the polymer solution using electrospinning synthesis technique and different percentages of eugenol (10-40%). Scanning electron microscope was used to measure the diameter of nanofibers. Drug loading and release rate was measured using a spectrophotometer. Antifungal effects and biocompatibility of drug-releasing nanofibers in vitro using disk diffusion and their toxicity were investigated using MTT assay on macrophage cell line of A.1 J774 mice.

Results : Growth inhibition rate of Trichophyton mentagrophitis, T. rubrum and T. tonsurans in the presence of polyacrylonitrile nanofibers loaded with eugenol 40%, 30%, 20% and 10% were evaluated about 90, 70, 50, and 25%, respectively. Also, polyacrylonitrile nanofibers with concentrations of 10 to 40% eugenol had not shown any effect on cell survival of macrophage cells of J774 A.1 mice using MTT technique for 24 and 48 hours.

Conclusion : Considering the results of antifungal effects of the polyacrylonitrile nanofibers loaded with eugenol and its lack of cytotoxicity, it is possible that eugenol as an antifungal compound can be released directly into the site of infection and show more effective contact between the fungal target and the drug.

Keywords : Dermatophytes, Eugenol, Polyacrylonitrile, Nanofibers, Antifungal activity

P284-86: Seroprevalence Study of Brucellosis and Toxoplasmosis Infections Among Women in Ardabil, Iran

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Background and Aim : Brucellosis or Malta fever is an endemic disease in many countries, including Iran. This bacterial disease is the most common cause of stillbirth in pregnant animals in addition to the severe complications in the affected population. On the other hand, Toxoplasma gondii is one of the most common causes of parasitic infections of human throughout the world. This protozoan is the causative agent of acute, chronic and congenital toxoplasmosis and as the most important infectious factor of stillbirth in the first trimester of pregnancy in humans. The main purpose of this study was to evaluate the serum levels of anti-Toxoplasma gondii IgM, IgG and Brucella antibodies in the serum of blood donor women in Ardabil, Iran.

Methods : Blood samples were obtained from 550 blood donor women in Ardabil by random sampling. Serum levels of anti-Toxoplasma gondii IgM and IgG were determined by ELISA technique and brucellosis infection was assessed using Wright and Wright's agglutination tests, respectively.

Results : Out of 550 samples, 19 cases (3.5%) were positive for anti-Toxoplasma gondii IgM and 197 cases (35.82%) for anti-Toxoplasma gondii IgG, respectively. On the other hand, the results of Wright's test and agglutination test showed that 44 cases (8%) of the studied individuals were infected by brucellosis. Totally, 3.5% of the studied population were infected simultaneously by brucellosis and acute toxoplasmosis (IgM positive) and 2.9% by brucellosis and chronic toxoplasmosis (IgG positive).

Conclusion : According to the results of this study, it is concluded that toxoplasmosis and brucellosis are prevalent among women of Ardabil. Therefore, monitoring of these infections is recommended in women especially during pregnancy.

Keywords : Toxoplasma gondii, Toxoplasmosis, Brucellosis, Women, ELISA, Wright test

P285-87: The Most Effective Medicinal Plants for the Treatment of Toxoplasmosis Infection

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Background and Aim : Toxoplasmosis is a prevalent zoonotic disease that is caused by Toxoplasma gondii. The infection by this protozoan can lead to acute, chronic and congenital toxoplasmosis. Stillbirth and abortion is one of the important outcome of the congenital toxoplasmosis infection especially during the first trimester of pregnancy. The aim of this systematic review study was to introduce the most effective herbs for the treatment of toxoplasmosis.

Methods : In order to collect the scientific information about using of the medicinal plants in the treatment of toxoplasmosis, it was referred to scientific websites including Google Scholar, PubMed, Web of Science, Magiran and Elsevier. The keywords and phrases used in the internet search was: Medicinal plants, Toxoplasmosis, Herbs, Toxoplasms gondii, Medicinal plants in treatment of toxoplasmosis

Results : The findings of this study suggest that there are 19 different species of medicinal plants with therapeutic effects on toxoplasmosis. But among of these herbs, two plants has the highest and strongest therapeutic effect in the treatment of toxoplasmosis: 1. Feijoa sellowian (Myrtaceae family) which contains flavonoids, tannins, terpenes and steroidal saponins. 2. Artemisia absinthium (Asteraceae) that contains gamma-terpinene, phenyl 4-2-pentadiene, beta-myosin and camphor.

Conclusion : Based on the results of the present study, it is concluded that two plants named Feijoa sellowian and Artemisia absinthium are the most effective medicinal plants for the treatment of toxoplasmosis infection.

Keywords : Medicinal plants, Treatment, Toxoplasmosis, Herbs, Feijoa sellowian, Artemisia absinthium

P286-105: Identification and prevalence of Helicobacter pylori virulence genes; babA and cagA in Wolinella spp. of the oral cavity of dogs

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Background and Aim : It has been indicated that dental calculi and the oral cavity discharge of dogs play a major role as the reservoir of Helicobacteraceae infections in the gastrointestinal tract. Regarding close contact between humans and their companion animals, immediate diagnosis and adequate treatment of Helicobacteraceae infections should be considered from the aspect of the zoonotic risk and public health. Wolinella spp. and Helicobacter spp. have been repeatedly reported in the oral cavity of dogs and are associated with periodontal diseases. Compared to Helicobacter spp., Wolinella strains are the predominant organisms in the oral cavity of dogs. The only known species of this genus, Wolinella succinogenes, was considered nonpathogenic until sequence analysis of its genome revealed homologous genes resembling virulence factors in H. pylori. This has led researchers to question the nonpathogenic status of W. succinogenes. CagA and BabA are examples of crucial virulence factors in H. pylori pathogenesis. We aimed to evaluate the prevalence of these genera in addition to assessing the genome of the Wolinella strains in terms of the presence of the mentioned virulence factors.

Methods : For the present study, multiple specific PCR tests were performed on oral secretion samples collected from 62 dogs by sterile cytobrush to evaluate the genera, species, and presence of mentioned virulence genes.

Results : The species-specific 16s rRNA genes of the genus Helicobacter and Wolinella were detected in 58.06% and 83.87% of oral samples of dogs, respectively. Helicobacter pylori were not detected in our specimens. We did not detect cagA and babA genes in the genome of Wolinella spp. as well as non-pylori Helicobacters.

Conclusion : In conclusion, our result confirmed that Wolinella spp. has a predominant population compared to the Helicobacter organisms in the oral cavity of dogs, and apparently the incidence of Helicobacter infections is generally associated with Non-pylori Helicobacters. Despite the hypothesis of great genomic homology between Wolinella

succinogenes and Helicobacter pylori, the cagA and babA virulence genes were not identified in any of the oral samples of dogs.

Keywords : Wolinella succinogenes, Helicobacter pylori, baba, caga

P287-198: Sequence analysis of the flaB2 gene among Leptospira interrogans serovars from Iran

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Background and Aim : Leptospira interrogans is a bacteria belonging to the leptospiraceae family that can cause a common infection in humans and animals by pathogenic Leptospira. Several factors are known as virulence factors of L. interrogans such as flagellins, adhesions, outer membrane proteins. Motility is an essential virulence factor for the pathogenic species that encoding flagellum protein. The aim of this study was to analyse the nucleotide sequence of flaB2 gene L. interrogans from Iran and phylogenetic comparison with isolates from other countries.

Methods : In this study, 12 pathogenic Leptospira serovars and two non-pathogenic Leptospira serovars were used. The pathogenic serovars of Leptospira interrogans were cultured into the selective medium EMJH and the genomic DNA was extracted by standard Phenol-Chlorophorm method. The flaB2 gene were amplified with PCR and specific primers. The nucleotide sequences of flaB2 gene were analysed by MegAlign software with NCBI database.

Results : The PCR product of flaB2 gene was 1050 bp. All pathogenic serovars of L. interrogans contained flaB2 gene. No PCR products were amplified from two non-pathogenic L.biflexa. Sequence analysis by BLAST showed 100% similarity among similar pathogenic serovars compare with published sequences in the GeneBank.

Conclusion : The results of this study showed that the flaB2 gene was highly conserved among pathogenic Leptospira. The results suggested that may useful for diagnostic of leptospirosis or candidate for recombinant vaccine and can also be used in an ELISA kit for the serodiagnosis.

Keywords : L. interrogans, flaB2 gene, virulence factor, sequence analysis

P288-216: Measuring the effect of Ribavirin on Crimean-Congo Hemorrhagic Fever Virus(CCHFV)

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Background and Aim : Aim: The effect of ribavirin treatment on viral populations by deep sequencing analysis of plasma samples obtained from a CCHFV infected patient before, during, and after a 5 day regimen of ribavirin treatment. Background: Crimean Congo hemorrhagic fever virus (CCHFV) is a tick borne virus(Ixodidae family) that causes Crimean Congo hemorrhagic fever. CCHFV is a negative stranded, segmented RNA . In the genus Orthonairovirus ,family Nairoviridae. Treatment options for patients are limited. Ribavirin has also been used for treatment and prophylaxis, although its efficacy remains controversial.

Methods : Five days into the course of infection, the patient received 1000 mg of ribavirin orally every 6 hours for 24 hours and intravenously for the next 24 hours, followed by 500 mg of intravenous ribavirin every 8 hours for 4 days, in addition to supportive care . Plasma samples were collected during the course of treatment and used for deep sequencing and genomic analyses. Viral loads were measured by quantitative RT PCR analysis.

Results : To define the type of mutations occurring in each sample during and after ribavirin treatment, the frequency of indels and transversions was measured over time .Transversions increased between day 2 and day 3 of ribavirin treatment. The nucleotide diversity further increased by day 6 after the cessation of treatment and plateaued in the subsequent days. The indel frequency increased dramatically between days 2 and 3 of ribavirin treatment and remained high until day 8.

Conclusion : The CCHFV load dropped during ribavirin treatment and subclonal diversity (transitions) and indels increased in viral genomes during treatment.These data demonstrate the mutagenic effect of ribavirin on CCHFV in vivo.Studies measuring the mutational effect of ribavirin on viral populations have identified an increase in G to A and C to T transitions. Despite these findings, systematic reviews of studies measuring the effect of ribavirin on CCHFV infected patient outcomes have been incomplete or inconclusive, leading the field to doubt ribavirin’s efficacy for human treatment.

Keywords : Crimean–Congo hemorrhagic fever virus; Ribavirin; Treatment; mutational

P289-218: The Prevalence Rate of Candida albicans in Proventricular of Poultry in Babol City

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Background and Aim : The Prevalence Rate of Candida abidans in Proventricular of Poultry in Babol City Abstract Among human food requirements, animal derived proteins are very important because of their role in body growth, health and evolution. Biosecurity and controlling animal food pollutants are important principles for disease controlling. Most of viral and bacterial infections of poultry industry can be prevented or attenuated by vaccination; however, fungal diseases in poultry industry are only can be controlled by biosecurity. Candida albicans is an agent that can easily enter into poultry houses and can make economic loses by reducing chicken growth. In this study, 100 carcasses from Babol poultry houses are investigated in order to determine prevalence rate of C. albicans. After sampling, samples were cultures in SDA medium containing Chloramphenicol and after microscopically examination, positive ones (have Candida yeasts) were cultured in generative tube containing human serum. After microscopically examination, each tube having clubby form agent was reported as positive and cultured in Corn Meal Agar medium to see big spherical Candida yeast cells. In this study, the prevalence rate of C. albicans in proventriculus of Babol poultry hoses chickens was 4%. Statistical analysis result from K2 test showed that there was a significant correlation between Candida albicans prevalence and litter (sig<0.021) and poultry house (sig=0.002). there was a significant differ between kind of litter and poultry house (sig=0.000). According to the results of the following study, the important role of biosecurity cannot be ignored, in order to prevent pathogen agents and their damages in poultry industry.

Methods : In this study, 100 carcasses from Babol poultry houses are investigated in order to determine prevalence rate of C. albicans.

Results : Statistical analysis result from K2 test showed that there was a significant correlation between Candida albicans prevalence and litter (sig<0.021) and poultry house (sig=0.002). there was a significant differ between kind of litter and poultry house (sig=0.000).

Conclusion : According to the results of the following study, the important role of biosecurity cannot be ignored, in order to prevent pathogen agents and their damages in poultry industry

Keywords : Candida albicans, Candidiasis, poultry, proventriculus.

P290-220: Molecular identification of virulence gene hlyE in different serovars of Salmonella isolated from human and livestock in Iran

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Background and Aim : Salmonella is zoonotic bacteria and one of the most frequently isolated foodborne pathogens. Recently, there is no cost effective vaccine available, so it is a major worldwide public health concern. The hlyE gene can be activated by the salmonella transcription factor (slyA). This gene encodes HlyE protein which is a pore-forming hemolysin that accumulates in the periplasm. The aim of this study was to analysis of the presence of hlyE virulence gene in different serovars of Salmonella isolated from human and livestock in Iran, so that it can be used for diagnosis.

Methods : A total 68 isolate of 25 different Salmonella serovars from the microbial collection of the Razi Vaccine and Serum Research Institute were used. Biochemical tests and serotyping were used to confirm the serovars. DNA extraction was performed by boiling method. Detection hlyE gene (294bp) in different Salmonella serovars was performed by PCR then amplified products were analyzed by agarose gel electrophoresis.

Results : A total 50 out of 68 Salmonella isolates were positive (73.5%) for hlyE gene. The results showed the presence of hlyE gene was the most common in S.typhi (100%),fallowed by S.paratyphiB (85.7%) and S.paratyphiA (84.6%), while low prevalence of this gene was observed in S.typhimurium (42.8%).

Conclusion : The results indicated the presence of the hlyE gene in different Salmonella serovars. The detection of this gene helps to understand the pathogenesis of salmonella. Moreover, presence of hlyE gene in S.typhi shows that they are specific target for molecular identification.

Keywords : Salmonella serovar- hlyE gene- Virulence genes- PCR

P291-228: Molecular detection of lsa21 gene encoding an adhesion protein of pathogenic leptospiral serovars

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Background and Aim : Leptospirosis is an allinclusive broad zoonosis which caused by pathogenic leptosires. To get into molecular pathogenicity of leptospirosis, it is essential to study the genetic characteristics of genes encoding outer membrane proteins. The Lsa21 is one of the leptospiral proteins which has extracellular matrix-binding properties. It is an immunogenic protein which is only present in pathogenic serovars, Therefore it is a suitable candidate to be used in an effective vaccine preparation and diagnostic methods. Hence detection of pathogenic leptospires from non-pathogenic serovars with PCR assay was conducted on lsa21 gene.

Methods : Leptospiral serovars required in this study were obtained from microbial collection of Razi institute, karaj, Iran. The leptospiral genomic DNA was extracted by Phenol-Chloroform extraction method. The gene was amplified by PCR from pathogenic Leptospira serovars and saprophyte serovars genomic DNA. Inorder to confirm the results, the number of PCR products containing the target gene were sequenced. The sequence analysis was performed using blastn and Chromas.

Results : The PCR of lsa21 gene was a 540 bp fragment which was observed in pathogenic serovars and not observed in non-pathogenic serovars. The basic sequence examination was carried out to discover homologous target sequence of nucleotide from the distinctive databases showed high similarity among the leptospiral serovars and reference sequences submitted in GenBank.

Conclusion : The result indicated that lsa21 gene has high conservation between pathogenic leptospiral serovars. Molecular discovery of pathogenic leptospires based on lsa21 gene can be utilized for laboratory diagnosis as a recombinant antigen and planning subunit vaccines of leptospirosis.

Keywords : Leptospirosis, Rice-Field Fever, lsa21 gene, molecular detection, Leptospira Infections

P292-237: Survey of plasma alterations of hepcidine, cholinesterase and total sialic acid in sheep with naturally infected Sarcocystosis

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Background and Aim : Sarcocystis parasitic protozoa are one of the most common parasites of domestic animals and in some intermediate hosts such as cows and sheep it leads to severe infections due to the direct relationship of these animals with humans, infestation in human societies is also an important health problem. The present study was also conducted with the aim of studying the plasma changes of hepcidin, cholinesterase, and total sialic acid in sheep suffering from Sarcocystis. Considering that hepcidin generally plays an active role in the pathological process of many iron disorders in the body, it is expected that the measurement of its concentration in the biological fluids of the body will help in the diagnosis of diseases. Cholinesterase is one of the most important enzymes that is needed for the proper functioning of the nervous system. Sialic acids are present in many mammalian tissues so their concentration increases in inflammatory diseases and other diseases.

Methods : In this study, blood samples were taken from 80 sheep affected with Sarcocystis and were analyzed in two groups, control, and patient.

Results : The statistical results show that the studied parameters in the sick sheep had a significant increase compared to the control group ($P<0.05$).

Conclusion : The results show that there is a significant increase in the level of enzymes studied in the patient's group compared to a healthy group, which can be used to diagnose this disease.

Keywords : Sarcocystosis, Hepcidine, Cholinesterase, Total Sialic Acid, Sheep

P293-239: Evaluation of Animal Bite & Rabies Epidemiological in Kermanshah Province During 2011-2019

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Background and Aim : Background: Rabies is a dangerous disease all over the world. Animal bites have high health and economic importance. The causative agent of rabies is a lyssavirus from the rhabdoviridae family and has a single-stranded RNA genome. The main reservoir of rabies virus is many bat-like and carnivorous mammals, including dogs, cats, foxes, wolves, etc. Aim: This research was conducted with the aim of investigating the epidemiology of animal bite disease in Kermanshah province during 2011-2019.

Methods : Methods: A descriptive-cross-sectional survey was conducted using the information of individuals bitten by animals in the geographical area of Kermanshah province in 2011-2019 from the health centers of the cities and the deputy health department of the University of Medical Sciences of Kermanshah province. All extracted data were entered into SPSS18 software for statistical analysis through Excel 2010 software and were analyzed by means of descriptive statistics (mean, variance and standard deviation) and chi-square statistical tests.

Results : Result: The incidence of animal bite cases has been increasing in the past 9 years, however, no case of death due to rabies has been reported in Kermanshah province. The most aggressive animal was the dog with 85.4%. In terms of anatomical location, the most injuries were in the lower limbs (50.42%). The highest number of bites was related to men with 68.75%.

Conclusion : Conclusion: Considering the absence of disease during the studied years despite the increase in the number of animal bite cases, it is necessary to pay attention to other disease control methods in the form of effective training and vaccination.

Keywords : Keywords: Epidemiological, Rabies, Kermanshah

P294-253: Study of mycobacterium, a zoonosis threat to ornamental fish; review article

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Background and Aim : Piscine mycobacteriosis could be considered one of the most important chronic diseases in the ornamental fish industry . The influence of economic values and importation and also the chance to be presence in zoonotic disease, this micro organism is highly valuable. The influence of economic values, transportation and listed to be presence in zoonotic disease, this microrganism has made this microorganism important from different perspectives.

Methods : The aim of this study was to evaluate Mycobacterium infection based on preliminary review data and to investigate the multi-sectoral nature of fish farms in Tehran, Kerman and Qazvin provinces. A questionnaire was developed based on accurate data of fish and human for processing and analysis. In addition, one case of fish tank granuloma has been reported.

Results : Symptoms in fin fish include excessive weight loss (P: 41.2%), scarring of the body (P: 37.1%), deep or surface ulcers (49.1%) and appearance of white nodules in the internal organs of the body (P: 34.2%). Diseases, especially diseases that have no clinical symptoms, can erode the popularity and prosperity of these fish in the market and reduce their material and commercial value. Asymptomatic diseases (P: 26.1%) can cause almost serious diseases in humans, especially in people with certain underlying diseases. However, some of these symptoms may overlap and add to the difficulty.

Conclusion : The main cause of this disease is disregard for health standards. Some of these cases include pollution of fish farm (18.31%), water source and artificial fish ponds (32.4%) and non-compliance with safe communication rules between colleagues (P: 19.6%, etc. Health standards are suggested, and adhering to principles along with ongoing studies can help as a preventative or controlling factor and reduce its harmful effects.

Keywords : Mycobacteriosis, zoonotic diseases, ornamental fish

P295-269: The effects of aqueous and alcoholic extracts of Nymphaea alba on Candida albicans and determine effective products and comparing the results to clotrimazole

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Background and Aim : The effects of aqueous and alcoholic extracts of Nymphaea alba on Candida albicans and determine effective products and comparing the results to clotrimazole

Methods : In this study, the aqueous, ethanolic and methanolic extracts of Nymphaea alba were studied on Candida albicans with disc, wells, minimum inhibitory concentration (MIC) and minimum fungal concentration (MFC) concentrations. Also, the amount of active component in Nymphaea alba essential oil was measured by gas chromatography (GC). 6,7-Dimethoxy-2-methyl-1 with 20.24% was the most active component in Nymphaea alba

Results : The average of growth inhibitory diameter for the aqueous, ethanol and methanol extracts in the well method was 13.92, 17.75 and 15.75 mm, respectively. Meanwhile, in the wells containing clotrimazole, the absence of growth was 45 mm

Conclusion : The aim of this study was to investigate the effect of Nymphaea alba aqueous and alcoholic extract on Candida albicans. In this study, the aqueous, ethanolic and methanolic extracts of Nymphaea alba were studied on Candida albicans with disc, wells, minimum inhibitory concentration (MIC) and minimum fungal concentration (MFC) concentrations

Keywords : Nymphaea alba, Candida albicans, Antifungal activity, Clotrimazole

P296-287: Antimicrobial effect of Alternaria metabolite isolated from tomato on Staphylococcus aureus

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Background and Aim : Antimicrobial effect of Alternaria metabolite isolated from tomato on Staphylococcus aureus

Methods : To evaluate the antimicrobial effects, the diameter of inhibitory zone was measured using disk diffusion and agar diffusion methods. In addition, the minimum inhibitory concentration (MIC) and Minimum bactericidal concentration (MBC) were determined by macro dilution method.

Results : Disk diffusion results shows that no inhibitory zone for extract against S. aureus in 110, 120 and 150 µl. Agar diffusion results shows no inhibitory zone in 170, 200 and 220 µl for S. aureus. MIC was 500 mg/ml and MBC was 0 mg/ml.

Conclusion : Based on data, Alternaria metabolites had antimicrobial effect against S. aureus but not strong.

Keywords : Antimicrobial effect, S. aureus, Alternaria, Metabolites

P297-307: Molecular detection of Rickettsia and Ehrlichia isolates in ticks collected from domestic livestock of Torbat Heydariyeh-Iran-2020-21

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Background and Aim : Ticks belong to the spider class and Acarina subfamily and are mandatory blood-sucking external parasites affecting birds, mammals, reptiles and amphibians and are an economic and health problem in tropical and subtropical regions of the world. Ticks are very important vectors for the transmission of bacterial pathogens such as Rickettsiae spp. and Ehrlichia spp. The study and diagnosis of these pathogens can play an important role in disease preventing and human health promotion. In this study, the molecular screening of Rickettsiae spp. and Ehrlichia spp. from ticks in domestic livestock was investigated in Torbat Heydariyeh, Iran, 2021.

Methods : 200 isolated ticks were collected from domestic livestock in Torbat Heydariyeh during 2020-2021, stored in 70% ethanol, and transferred to the laboratory and stored at -20. The genus and species of ticks were identified using a stereo-microscope according to morphological parameters. DNA was extracted and Rickettsiae spp. and Ehrlichia spp. were identified using primers aimed to ompA and 16S rRNA by PCR technique.

Results : The genus identification of ticks revealed high diversity, with 2 genera and 9 species were identified. Among these, the distribution of Rhipicephalus Sanguineus and Hyalomma marginatum was 46% and 17%, respectively. On the other hand, the prevalence of Rickettsiae spp. and Ehrlichia spp. in 200 ticks were 58 (29%) and 36 (18%), respectively. Sequencing results showed that the amplified ompA and 16S rRNA genes belonged to R. aeschlimannii and Ehrlichia spp, respectively. Both bacteria were isolated from Rhipicephalus Sanguineus.

Conclusion : Since ticks play an important role in the transmission of pathogens, and also high prevalence of Rickettsiae spp. and Ehrlichia spp. was identified in the collected ticks, the attention of health officials and the development of control programs seem necessary.

Furthermore, it is suggested to expand the current study to recognition of the species and strain of the identified bacteria, as well as other tick-related pathogens in our region.

Keywords : Ticks, Rickettsia, Ehrlichia

P298-331: Serological diagnosis of Brucella spp. in the camel population of southern Kerman province of Iran

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Background and Aim : Brucellosis is a global problem in public health and livestock. The occurrence of disease in humans is mainly due to animal reservoirs. Brucellosis disease in camels can also cause significant economic losses and is very important in terms of public health. The present study was conducted with the aim of determining the status of Brucella infection in the camel population of South Kerman by serological methods.

Methods : One hundred blood samples without anticoagulant were taken from female camels in the south of Kerman province, three months old and older. Then, their serum was separated and their infection with Brucella bacteria was evaluated by measuring the presence of antibodies using the Rose Bengal, Wright and 2-mercaptoethanol techniques.

Results : Out of 100 camel blood serum samples, only one sample was positive in the Rose Bengal test and was used for additional tests including wright and 2ME. The serum titer in the wright and 2ME tests showed a titer of 1:1280. In other words, the prevalence of brucellosis in this study was about one percent.

Conclusion : Considering the prevalence of this disease in camels and the high population of camel herders in the south of Kerman and the large slaughter of this animal species in slaughterhouses as well as the consumption of its milk by citizens and villagers in raw and unpasteurized form, the diagnosis of this disease with other diagnostic methods such as Serology with higher sensitivity and molecular techniques are also needed.

Keywords : Camel, Brucella, serology

P299-341: Anisakis Allergy

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Background and Aim : Anisakis simplex (A. simplex) infection, in humans, causes a series of clinical manifestations affecting the gastrointestinal tract known as Anisakiasis/Anisakidosis. Patients may also present allergic manifestations such as hives and/or angioedema and even anaphylactic shock. The aim of this study was to investigate whether aquacultured fish could be considered A. simplex-free food and constitute a safe, alternative, wild-capture fish food for Gastro-Allergic Anisakiasis (GAA) sensitized subjects. The diagnosis of Anisakiasis is documented by the occasional finding of L3 larvae in the infected gastro-intestinal tract. Currently, about 14 allergens have been described, among which Ani s1 and Ani s4, both highly heat-resistant, appear central in Anisakiasis anaphylaxis and necessary to cause allergic reactions. Food has to be considered Anisakis-free only when heat-resistant Anisakis allergens are not present.

Methods : Protein extracts from A. simplex larvae in the third stage (L3) and from the edible part of heavily infected horse mackerel (Trachurus trachurus) and aquacultured sea bream, have been tested for A. simplex allergens presence by immunological analysis. Western blot analysis using, as a source of specific Anisakis allergens antibodies, serum samples from subjects referring allergic symptoms after raw fish ingestion, was performed. These subjects showed high levels of specific IgE anti A. simplex allergens determined by clinical laboratory tests (ISAC test).

Results : Our data demonstrate the presence of Ani s4 allergen in both infected and aquacultured fish extracts, providing a possible interpretation for the allergic manifestations reported by subjects, already sensitized to A. simplex, who ate frozen or well-cooked or, even, aquacultured fish.

Conclusion : The present data stimulate more accurate prophylaxis suggestions for Anisakis allergy and more specific controls of fishmeal used in aquaculture.

Keywords : gastro-allergic anisakiasis; aquacultured fish; food allergy; clinical microbiology; public health; clinical molecular biology; fishmeal; Anisakis allergy

P300-351: A decision regarding the role of ticks as the proven and suspected vectors of CCHFV (Crimean-Congo hemorrhagic fever virus): A meta-analysis review

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Background and Aim : There are many studies present in literature performed to isolate CCHFV from ticks. However, gaps in knowledge for lack a decision regarding the role of ticks as CCHFV vectors caused to conduct this review.

Methods : From papers identified, 57 papers were selected to become the study meta-analysis.

Results : The decision regarding the role of ticks as CCHFV vectors administrated based on the study and a separately literature search regarding the role of ticks as CCHFV vectors; CCHFV infection rates and records; and trend of CCHFV infection records in 31 tick species. The trend of CCHFV infection records in 31 tick species exhibited a decreasing trend indicating the degree and importance of their roles as CCHFV vectors.

Conclusion : Among 31 CCHFV infected tick species, 15 species have been enrolled as proven vectors and 16 species are suspected as potential vectors.

Keywords : CCHFV infected ticks, decision regarding the role of ticks as CCHFV vectors, potential vectors, proven vectors

P301-401: The use of Gecko cell line in the cultivation and preparation of live attenuated Toxoplasma gondii strain

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Background and Aim : Toxoplasma gondii is an obligate intracellular parasite that causes Toxoplasmosis. Until now, no cost-effective treatment method has been found to deal with Toxoplasma and the best way to deal with the infection is vaccination. Live vaccines compared to other vaccine platforms against pathogenic protozoa have had successful results so far. In this study, the efficacy of a live attenuated experimental vaccine through long-term passages on a cell line of reptilian origin (Z1) has been evaluated in inducing a protective immune response in a Balb/c mouse model.

Methods : Thirty mice divided into three equal groups including; Group one: non-immunized/challenged as a control (injection of culture medium), group two: immunized/challenged (injection of attenuated strain) and group three: immunized/unchallenged (injection of attenuated strain). One month after immunization, the studied mice were challenged with 1_x103 live tachyzoites of RH Toxoplasma acute strain. Serological investigations, including evaluation of antibody, gamma interferon, interleukins 2, 4, 10 and 12 were performed. Also, at the end of the study, a molecular test was performed on brain and liver tissues to check the presence of parasites.

Results : The results obtained from serological tests in the vaccinated group have a significant difference with the control group ($p<0.05$); So that after the challenge in the vaccinated group, the survival rate of mice was 50%. Also, the molecular results showed the absence of parasites in brain and liver tissues.

Conclusion : Therefore, the use of the attenuated strain caused a significant humoral and cellular immune response in the vaccinated groups. Also, in group three, the attenuated strain of Toxoplasma gondii had no pathogenicity and all mice survived until the end of the study. In conclusion, the results of this study showed that this attenuated strain can promise new research in order to achieve a promising vaccine against Toxoplasmosis, which is worth further evaluation in intermediate and definitive hosts.

Keywords : Toxoplasma gondii, attenuated strain, vaccine, immunogenicity, Gecko cell line

P302-403: Evaluation the immunogenicity of Toxoplasma gondii experimental vaccine in pregnant sheep

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Background and Aim : Toxoplasma gondii is a zoonoses protozoan of the Apicomplexa family that causes Toxoplasmosis in the worldwide. It is estimated that approximately 30-50% of the world's population is infected with this parasite. This infection not only reduces meat production by causing abortion in sheep and goats, but it can be both a source for human infections and a reservoir for parasites, therefore; It causes severe economic losses in the sheep industry. The aim of this study was to evaluate the immunogenicity of the live attenuated vaccine with different adjuvants in sheep as an intermediate host.

Methods : 20 two-month-old pregnant Iranian Qashqaeian serum-negative sheep for Toxoplasma gondii were randomly divided into five groups of four. Group one injected with media and served as control. Three experimental groups were immunized subcutaneously with 1 ml of 25 ×106 (25 million) inactivate tachyzoites formulated with Montanide, Aluminium hydroxide, and Chitosan, respectively. Last group was inoculated with live attenuated tachyzoite with the same dose. Immunization was performed once. After 21 days, blood samples were collected for ELISA test to evaluate the humoral immune response and gamma interferon measurement to evaluate the cellular immune response.

Results : The highest antibody titer was obtained in the group immunized with Montanide adjuvant, which was significantly different from other groups ($P < 0.05$). However, the highest cellular immunity according to gamma interferon measurements was related to live attenuated vaccine which was significantly different from other groups, followed by Chitosan or Aluminum hydroxide adjuvant. It should b notice that all immunized groups had a significant difference with the control group ($P < 0.05$).

Conclusion : According to the successful immune response in the live attenuated vaccine, the results of this study showed that this attenuated strain can provide new research in order to achieve a promising vaccine against Toxoplasmosis, which is worth further evaluation in various intermediate and definitive hosts.

Keywords : Toxoplasma gondii, live attenuated vaccine, adjuvant, immune response, sheep

P303-416: Report of a case of dog infection with Hepatozoon canis (Apicomplexa: Adeleorina) parasite in north of Iran

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Background and Aim : Blood parasites of the genus Hepatozoon (Apicomplexa, Hepatozoidae) infect all groups of terrestrial vertebrates. Canine hepatozoonosis is recognised as a clinical disease ranging from relatively asymptomatic in low level cases, to severe in high level cases. Typical characteristics include fever, lethargy, myalgia, lameness and mucopurulent ocular discharge in severe cases. Reasons for the difference in the clinical signs between the two species, apart from infection to novel hosts, may be due to the fact that merogonic development takes place in different target organs. H. canis primarily infects the spleen, bone marrow and lymph nodes. The aim of this study was detection of H.canis in stray dogs from Guilan province, Iran by molecular method.

Methods : To assign distribution of this parasite, a total number of 10 blood samples were collected from different randomly selected dogs from Guilan province. The smears prepared and stained by Gimsa solution (10%) and Light microscop was used to examination of blood smears. The parasite samples were used to molecular analysis.

Results : The microscopic results showed that one of samples was infected by parasites. PCR was runed with18s RNA and its product was sequenced by sanger method. Based on the molecular 18s RNA gene blast, the parasite recognaized as Hepatozoon canis.

Conclusion : This is the first report of molecular detection of H.canis in stray dogs from Guilan province, Iran. Because of few molecular studies on Hepatozoon species, and because of the humidity of this region and suitable conditions for the activity of ticks, more studies are recommended.

Keywords : Hepatozoon canis, Molecular detection, Stray dog, Hepatozoonosis

P304-427: Comparing Diagnostic Accuracy of the fliD Gene and the glmM Gene in Helicobacter Pylori

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7. *Student research committee, Tabriz University of Medical Sciences, Tabriz, Iran.*
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Background and Aim : Helicobacter pylori (H. pylori) is one of the most common human bacterial infections, accounting for the infection of half of the world's population. The polymerase chain reaction (PCR) has high specificity and sensitivity in diagnosing this bacterial infection. The present study aimed to compare the sensitivity and specificity of the fliD gene and the most widely used glmM gene in the PCR technique.

Methods : This cross-sectional study enrolled patients with indications for upper endoscopy from April 2019 to April 2020 at Qom, Iran. Determination of H. pylori was done on endoscopic biopsies using our described gold standard which combined of Rapid Urease Test (RUT) and histopathological techniques, simultaneously. Then, the DNA extraction and PCR assay were conducted for our proposed gene (fliD) and the most widely used glmM gene. At the end, we compared the sensitivity and specificity of these 2 genes in detection of H. pylori.

Results : The participants encompassed ninety-nine participants aged above 18 years. Their median age was 45.92 ± 13.63 years. The most common complaints of the patients were epigastric pain and heartburn. Our described gold standard detected 61.6% and 38.4% as positive and negative, respectively. The sensitivity and specificity were 72.1% and 100.0% for the routine PCR (glmM gene) and 80.3% and 94.7% for the proposed PCR (fliD gene).

Conclusion : Different genes have been used to detect H. pylori in PCR. The glmM gene is easily used to diagnose the H. pylori infection; however, according to the present findings,

the fliD gene has higher sensitivity than the glmM gene. Accordingly, the former can be used as a screening gene for the H. pylori infection in the PCR technique.

Keywords : Helicobacter pylori, Polymerase Chain Reaction, fliD, glmM, Sensitivity, Specificity

P305-460: Updated population genetic understanding of Mycobacterium bovis in the Iranian cattle, a search for major clonal complexes frequently observed in the world

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Background and Aim : Bovine tuberculosis (bTB) is a neglected disease that affects both cattle and humans. Up to now an increasing number of globally important groups, so called clonal complexes, of Mycobacterium bovis have been detected and characterized with their spatial distribution reported ranged from very extensive to limited only to few regions. In 2011 the RDEu1, the first ever known clonal complex of M. bovis, was shown not to be circulating in Iran. Interrogation of the Iranian M bovis population has been continued in search for other clonal complexes including RDEU2, African 1 and African 2. Here we report the most recent findings of this investigation

Methods : Using reported PCR protocols, the amplification of target regions were performed on genomic material from as many as 25 M. bovis isolates prepared through plain heating in boiling waterbath. Amplicons were sized using conventional gel electrophoresis/ imaging and gel images were analyzed against standard DNA ladders. MLVA genotyping using 21 loci was also performed to evaluate level of genetic diversity among the selected panel of M bovis isolates

Results : Viewing the sized PCR products, no evidence to confirm presence of any of the aforementioned clonal complexes was tracked

Conclusion : We assume while there are historical records of the first dairy cattle being systematically imported into Iran in 1920s and 1930s as part of the livestock and dairy development projects, these might have had no or little in introducing exotic M. bovis strains into Iran. The related MLVA typing findings and scenarios explaining the observations have been put forwarded and discussed

Keywords : Mycobacterium bovis, Clonal complex, Iran, cattle

P306-496: Molecular identification of Echinococcus granulosus sensu lato in stray and domestic dogs in Shahrekord, Central Iran

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Background and Aim : Echinococcus granulosus is a tapeworm parasite and causing agent of cystic echinococcosis, a life-threatening disease in humans. Stray and domestic dogs are the most important definitive hosts for this parasite. The aim of this study was to determine the prevalence of Echinococcus granulosus sensu lato among stray and domestic dogs using copro PCR method in the central Iran.

Methods : From April 2015 to February 2018, the intestinal parasites of 204 stray dogs and 204 domestic dogs were determined by stool examination in Shahrekord, central Iran. Genomic DNA was extracted from dog faecal samples and COX1 and SSU-rDNA markers were applied in order to detect taeniid parasites from Echinococcus granulosus sensu lato, respectively.

Results : Totally, taeniid parasites were observed in 29 (7.1%) samples, of which 14 (3.43%) samples in domestic dogs and 15 (3.67%) samples in stray dogs were detected. Moreover, of 29 taeniid positive samples, 17 (4.16%) samples were positive for Echinococcus granulosus sensu lato.

Conclusion : The findings of the current study specified that the overall prevalence of Echinococcus granulosus was low (4.16%) in domestic and stray dogs in the examined area. monitoring of the prevalence of echinococcosis in both the final hosts and the intermediate hosts might assist the policy makers to take sanitary measures to control the disease.

Keywords : Echinococcus granulosus; Dog; Iran

P307-528: Bioactive agent for prevention & control of Mycobacterium avium subspecies paratuberculosis

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Background and Aim : Mycobacterium avium subspecies paratuberculosis (MAP) is the causative agent of paratuberculosis, Johne's disease or (JD) in cattle & Crohn's disease (CD) in human. Currently there are not any successful treatments for MAP so development of an effective method for prevention will be yielded significant results. Pathogen-specific IgY secretory antibodies can be produced and purified with high efficiency from egg yolk by inexpensive and reliable methods and can be used for complementary prevention and treatment of JD or CD disease. The aim of this study was to investigated the effects of IgY on growth of MAP growth in vitro.

Methods : Specific IgY was produced by immunizing hens with formalin-killed MAP strains III & V. The Specific IgY against MAP was purified from the yolks using PEG 6000. IgY was identified by SDS-PAGE and its activity against MAP was measured by ELISA. The protein concentration of the purified IgY was determined using Kjeldahl method. The growth inhibition assays were also conducted to monitor the growth changes.

Results : The ELISA result indicated the specific activity of purified IgY to the MAP. The growth inhibition assay revealed that the lowest concentration of anti-MAP IgY was 2µg/ml. The possible mechanism of bacteriostatic function of IgY is due to adherence of the immunoglobulin to exposed factors on the surface of MAP, resulted in alteration of cellular signaling. IgYs could also cause of MAP agglutination , leading to their immobilization, therefore it interferes with the growth.

Conclusion : Anti-MAP IgYs may play as a promising new preventative bioagent for enteric pathogen infections.

Keywords : inhibition of bacterial growth, chicken egg yolk antibody, IgY, ELISA, Mycobacterium avium subspecies paratuberculosis

P308-592: Serological survey of Toxoplasma gondii infection in dogs with breeding disorders

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Background and Aim : Toxoplasma gondii infections are common in humans and animals worldwide. Toxoplasma gondii is one of the major causes of reproductive disorders in cats and dogs. Dogs rarely suffer from toxoplasmosis as a primary disease, and in most cases, this disease is observed following immunosuppression and lack of vaccination against common infectious diseases like canine distemper virus (CDV) which are prevalent in kennels. Reports of high seroprevalence in the canine population and venereal and congenital transmission of T. gondii in dogs have been presented all around the world. Accordingly, the seroprevalence of T. gondii infection in dogs may reveal the level of parasite contamination in their environment. Therefore, dogs are used as sentinel animals for T. gondii infection because of their close contact with humans.

Methods : In this study, male and female dogs suffering from reproductive disorders were selected in kennels in the southeast of Iran, Kerman, and blood samples were taken from a cephalic vein after complete clinical examinations and under physical restraint. sera were separated and screened by MAT method (Toxo-Screen DA®; BioMerieux SA®, Marcy-l'Etoile, France).

Results : In this study, 46 dogs were selected from breeding kennels with reproductive disorders in Kerman, southeast Iran. Of the46 samples, 17 (37%) were females and 29 (63%) were males. These dogs were categorized into different age groups and past medical history focused on reproductive disorders was documented. Serological surveillance was done and the overall infection rate was (20/46) 43.47% which consisted of 11/17 (64.7% between females and 9/29 (31.3%) males. Raw meat and unpasteurized feeding, rodent pest infestation, and, population density were the major risk factors in the studied kennels.

Conclusion : This survey indicated that T.gondii infection was quite high among kennels with breeding disorder dogs so this pathogen has an important role in the occurrence of reproductive disease in male and female dogs and can cause economical loss for breeders and severe health problems for infected puppies. Primary Screening and definitive diagnosis of toxoplasmosis with molecular methods are highly recommended for thoroughbred dogs before entering the kennels.

Keywords : Toxoplasma, Modified Agglutination Test (MAT), Dog, Serology

P309-599: Serological survey of H9N2 influenza viruse in Domestic Pigeons of Ardabil, Iran

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Background and Aim : Pigeons can be carriers of some human and poultry pathogens and contribute to transmission and spread of drug resistant infectious agents to human and poultry. The aim of this study was to investigate serological prevalence of H9N2 subtype of avian influenza virus in domestic pigeons of Ardabil.

Methods : This cross-sectional study was conducted during first six months of 2022. One hundred and twenty unvaccinated domestic pigeons randomly selected different parts of Ardabil were examined. Blood samples were collected from the wing veins and samples were sent to serological laboratory. All sera samples were was tested by HI for detection of antibodies against H9N2 virus.

Results : The birds with sera titer =>4 (log2) were considered as positive. The sera sample of 18 birds (15%) out of 120 were positive. This is the first report of sero- prevalence of AIV in domestic pigeons of Ardabil.

Conclusion : The Results of this study showed prevalence of avian influenza viruse H9N2 among pigeons. Improving the health and biosecurity, and continuously surveillance of the birds to control the disease is necessary.

Keywords : Avian influenza virus, Pigeons, Seroprevalence, HI

P310-626: Isolation and Antimicrobial Resistance Profiles of Salmonella enteritidis From an Alexandrine Parakeet (Psittacula eupatria): a Potential Zoonotic Source

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Background and Aim : Genus salmonella from the family enterobacteriacea has two species, enterica and bongori. Members of the genus are gram-negative, facultative aerobic-anaerobic, and mostly motile. To date, more than 2500 serotypes are recognized in species enterica lots of them can overcome mucosal immunity and cause disease in a wide number of mammals, birds, and reptiles (1, 2, 3). Different species of birds are susceptible to infection by Salmonella (1). In addition to mortality in birds, the bacteria can transfer to humans (4). This study aimed to detect probable salmonella infection and evaluate antibiotic susceptibility patterns.

Methods : In this case, an alexandrine parrot with severe respiratory signs was presented with gasping, tail bubbing, dyspnea for the last two days, and anorexia and vomiting history for three days. Unfortunately, the bird died. At necropsy, hyperemia at the trachea and lungs and cloudy air sacs were obvious. Swabs from the trachea, lungs and air sacs, bone marrow, liver, and digestive tract were cultured on Blood agar. After 18 hours of incubation at 37°c, at lung and air sacs culture, lactose-negative bacteria with mucoid colonies were evident. Then the unknown bacteria was recultured on Mack-Conkey agar. After incubation, like the previous step, colonies were lactose negative and colorless. By considering possible salmonellosis, the bacteria was transferred to TSI and Urea agar mediums.

Results : The urea was positive, and TSI was basic at the surface and acidic at depth, with H2S production. From the results, it was clear that the bacteria were from the genus Salmonella. At serological tests, antiserums for O and H antigens were mixed with bacterial colonies, and agglutination was evaluated. Based on the O antigen, bacteria were from serogroup D in the Kauffman-white classification. Based on the H antigen, it was phase 1 positive and phase 2 negative.

Conclusion : For precise detection, multiplex PCR was performed with three pairs of primers (Table 1). At last, we performed an antibiogram test with 21 discs of common antibiotics (Table 2). The results showed resistance to most of the antibiotics.

Keywords : Salmonella Enteritidis, Zoonosis, Alexandrine Parakeet, PCR, Serology, Bacteriology

P311-638: Evaluation of the killing effect of chitosan and chitosan-amphotericin B in vitro and in vivo

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Background and Aim : Cutaneous leishmaniasis (CL) is a neglected tropical disease (NTD), caused by a protozoan of the genus Leishmania, which are transmitted through the bite of female sand flies. Considering the resistance outbreaks to drugs conventionally used in CL therapies and differential responses to the current treatments, there is a continuing and urgent need for new therapies against leishmaniasis that are safe and effective in inducing a long-term cure. In recent years, the focus on herbal and natural compound in medicine, especially in the treatment of microbial infections, has increased rapidly.

Methods : In this experimental study, anti-leishmanial effects of chitosan and chitosan-loaded amphotericin B were assessed. The anti-leishmanial activities on promastigotes were assessed using vital staining and infected BALB/c mice were used to assess the in vivo anti-leishmanial effects. Cytotoxic effects of chitosan and chitosan-amphotericin B (different concentration) on the L929 cell line was confirmed by an MTT assay and the in vitro hemolytic activity was performed by spectrophotometric method.

Results : The results of in- vitro study revealed that chitosan-loaded amphotericin had valuable inhibitory effects against Leishmania major in comparison to each of chitosan and amphotericin B alone ($P<0.05$). Also the results of in vivo assay showed that the chitosan-loaded amphotericin- B has a synergistic effect to wound size decrease.

Conclusion : The results of this in vitro and in vivo study showed that chitosan has very acceptable anti-leishmanial effects, which are greatly increased by the addition of amphotericin B.

Keywords : killing effect, Leishmania major, chitosan, amphotericin B

P312-649: Serological survey of Leptospira infection in abortions of small ruminants

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Background and Aim : Leptospirosis is probably one of the most widespread and prevalent zoonotic diseases worldwide. This infectious disease is caused by pathogenic leptospiral serovars (more than 260 serovars). Leptospirosis affecting most of small ruminants (goats, sheep) in which it causes several signs including abortions, stillbirths and mummification. The aim of this study was to determine the prevalence of leptospirosis in small ruminant by MAT testing in IRAN

Methods : Sera were collected from 41 abortions cases with clinically suspected leptospirosis attending the department of Microbiology, Razi Vaccine & serum Research Institute, Karaj during the period of April 2019 and March 2021. Serlogical survey of antibodies against different leptospiral serovars was carried out by Microscopic agglutination test (MAT) at dilutions from 1/50 to 1/1280. The antigens used in MAT were live 20 leptospira serovars. Statistical methods were performed to determine the significant association of various demographic data using the statistical software SPSS.

Results : A total 14 (34.1%) out of 41 serum samples were positive by MAT. Antibody titers include 1/400 for 8 (57.1%), 1/800 for 4 (28.5%) , 1/1600 for 2 (14.2%) samples. The most prevalent leptospira serovars were Grippotyphosa 4 (28.5%) Icterohaemorrhagiae 3 (21.4%), followed by Sejroe hardjo 2 (14.2%) Canicola 2 (14.2%) Autmnalis 1 (7.1%), and Pomona 1(2.4%).

Conclusion : The results showed that certain serovars such as Grippotyphosa and Icterohaemorrhagiae are common in abortions of small ruminants. The results suggested that leptospira may have important role in abortion in small ruminant. Although large scale serological studies can enhance our understanding of leptospirosis in small ruminants in different part of Iran.

Keywords : Leptospirosis, Leptospira, Small ruminants, MAT, Serovars, abortion

P313-666: Seroprevalence of Brucella Antibody Titer (Wright's Test) in Suspected Cases in Kashan, Iran

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Background and Aim : Iran is one of the endemic areas infected with Brucellosis disease. Brucellosis is a zoonotic disease and its traditional diagnosis is based on blood culture and serological methods. This study investigated the prevalence of Brucella infection in patients referred to clinic with brucellosis symptoms in Kashan, Iran.

Methods : The present study was done on patients with brucellosis symptoms referred to laboratory in Kashan, Iran, from March 2021 to June 2022. Serums were taken from all patients. Patients' information, with age, sex was entered. Results of tests were obtained and analyzed via SPSS v. 22. A titer >= 1/80 is considered positive.

Results : This study was performed on 1450 patients with brucellosis symptoms. In this study, 130 patients showed a titer (1:20 to 1:1280). On the basis of the results, the prevalence of wright test positive in the participants' serum was 71 out of 1450 (4.9%). A total of 71 patients were 51 males and 20 females with mean age of 37.5 years. There was a significant statistical relation between gender and Wright's titer ($p<0.05$). There was, but, no significant statistical correlation to age ($p>0.05$).

Conclusion : According to the results of our study, in Kashan, Iran, it is concluded that brucellosis disease is still an important public health problem in Iran.

Keywords : Brucelloses, Brucella, Wright's Test, Kashan, Iran

P314-673: EXPRESSION AND PURIFICATION OF rLOA22 OF LEPTOSPIRA INTERROGANS IN PROKARYOTIC SYSTEM

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Background and Aim : Leptospirosis, an overlooked zoonotic infection disease, is a worldwide public health problem affecting both domestic animals and humans. Outer membrane proteins of leptospire are among the most effective antigens which can stimulate remarkable immune responses during the infection processes The outer membrane protein A-like protein Loa22 from Leptospira interrogans is a 22KDa lipoprotein (195 aa) with an OmpA domain in the C-terminus. Loa22 is also the first genetically described virulence factor in Leptospira that confirmed by a mutagenesis studies. The objective of the present study was expression and purification of recombinant Loa22 antigen from Leptospira interrogans in prokaryotic system.

Methods : PCR product of Loa22 gene was clonned in E. coli strain plysS using pET23a (+) plasmid as a vector and induced with 0.5mM IPTG at 37 °C for 5 hours. The bacterial pellet was obtained by centrifugation (5,000 rpm). The resuspended cells were disrupted by sonication. The cell lysate was solubilized in sample buffer plus 2ME , Proteins were separated on 12% SDS-PAGE and followed by Coomassie Brilliant Blue staining. Expressed protein was purified using Ni-NTA resin and analyzed with sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and Western Blotting.

Results : The protein was successfully expressed in E.coli plysS strain and purified. the production of higher level of soluble rLoa22 in native state was at the highest level when post induction incubation, IPTG concentration, and duration of induction were 37ºC, 0.5mM and 8 h in 2xTY medium respectively. SDS-PAGE results showed that the full-length 38kD protein was induced by IPTG that confirmed with western blot assay.

Conclusion : This study is a practical guide to the expression and purification of recombinant loa22 protein for the design of diagnostic kits or vaccine studies based on the recombinant protein individually or in combination with other leptospira surface antigens.

Keywords : Loa22, expression, Pet32a(+), E. coli strain plysS, soluble protein

P315-689: Analysis of MicroRNA-146a gene polymorphism in patients with brucellosis: A Case-Control Study

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Background and Aim : Single nucleotide polymorphisms (SNPs) represent the most abundant genetic variation in the entire human genome. MicroRNAs (miRNAs) are a type of evolutionary conserved small single-stranded non-coding RNAs which control the target gene expression negatively via mRNA degradation or translational expression at the post-transcriptional level. MiR-146a was first recognized as a regulator of the immune system responding to microbial infections. The aim of the present study was to investigate the association between the risk of brucellosis and genetic variations in miR-146a.

Methods : In this case-control study included 108 Brucellosis patients and 108 healthy controls. We genotyped two SNPs (rs2910164 and rs57095329) of the miR-146a using tetra-primer amplification refractory mutation system-polymerase chain reaction (T-ARMS-PCR) and restriction fragment length polymorphism-polymerase chain reaction (RFLP-PCR) methods.

Results : Co-dominant (P = 0.047) and recessive (P = 0.018) models were significant at position rs57095329 between the two groups of patient and healthy. The rs2910164 SNP was significantly associated with brucellosis in co-dominant [OR = 4.27, 95% CI = (2.35–7.79, P = 0.001] and dominant [OR = 3.52, 95% CI = (1.97–6.30, P = 0.001] models. The A C haplotype (rs2910164 and rs57095329) was associated with brucellosis in the assessed population [OR (95% CI) = 1.98 (1.22–3.20), P = 0.0059].

Conclusion : Our study showed significant differences in genotype and haplotype frequencies of miR-146a variants between brucellosis and controls. Further studies on the larger sample sizes are required to verify the observed associations.

Keywords : Brucellosis, Genetic variations, miR-146a

P316-690: Investigating the prevalence of Listeria monocytogenes and the pathogenic genes inlA, inlB, prfA, and hlyA in abortion

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Background and Aim : Listeria monocytogenes is an important food pathogen and one of the most common cases of abortion. The uterus of infected women is the source of infection for the fetus during pregnancy or birth. If it is not identified, it will lead to repeated abortion and increase antibiotic resistance. This study was conducted to determine the frequency of Listeria monocytons in cases of abortion and check the frequency of pathogenic genes inlA, inlB, prfA, and hlyA.

Methods : This cross-sectional-descriptive study was conducted to determine the frequency of Listeria monocytogenes contamination of the placenta in abortion cases. The bacteria were isolated by enriching the samples at 4 ° C and cultured in specific enriching environments, and the 16srRNA and prs genes of Listeria monocytogenes were confirmed using standard biochemical tests and polymerase chain reaction molecular test. The presence of inlA, inlB, prfA, and hlyA genes was investigated by PCR technique.

Results : Of the 53 samples of aborted placentas suspected of listeriosis, 7 (5.71) samples were found to be infected with Listeria monocytogenes. The presence of pathogenic genes inlB, hlyA, and prfA was detected in all isolates and inlA with frequency (71.43%).

Conclusion : Due to the importance of the pathogenicity of Listeria monocytogenes, prevention, and timely treatment play an important role. Considering the prevalence of 71.5% of Listeria monocytogenes in aborted fetuses, it seems that inlB, prfA, hly, and inlA genes play an essential role in the pathogenicity of this bacterium. This confirms the importance and necessity of continuous monitoring and the development of a detailed program for the identification of this bacterium in timely diagnosis and preventive health guidelines.

Keywords : Listeria monocytogenes, Listeriosis, Placental bits, abortion, virulence genes

P317-709: Isolation of Campylobacter from aborted cases in sheep in Qazvin province

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Background and Aim : Abortion is one of the problems of sheep breeders in the country and it delivers a significant economic benefit to the breeders. Economic damages include abortion in the last months of pregnancy, premature lambs, weak lambs, deaths of aborted ewes, and prevention and treatment costs. The main cause of abortion in sheep and goats is infectious agents. Campylobacter fetus is one of the most common causes of sheep abortion in the world. In Iran, the role of this factor in abortion has been studied more than other factors. The highest percentage of Campylobacter infection among these studies related to Zanjan province was reported as 51.9% Campylobacter infection. The aim of this study was to isolate Campylobacter from cases of abortion in small ruminants in Qazvin province by usual laboratory methods.

Methods : Tissue sampling was done from aborted fetuses (38 cases during the period of April 2019 and March 2021) under sterile conditions. Digestive contents, liver and lung were cultured on the special medium of chocolate agar. 48 hours of incubation at 37°C. Gram staining of colonies suspected of Campylobacter was performed. Purification was performed if the colony and the microscopic shape of the suspicious colony matched.

Results : Of the 38 aborted cases, five Campylobacter agents were isolated (approximately 13%).

Conclusion : The results show the importance of this microbial agent in causing abortion in the region. This result is consistent with a survey in Isfahan. The inconsistency with other results in the country and the world is due to different investigation methods (Isolation, serum and molecular).

Keywords : Campylobacteriosis, Campylobacter, Small ruminants, Qazvin, Abortion

P318-720: Isolation and molecular identification of Brucella species from human and livestock in Hamadan province by PCR method

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Background and Aim : Brucellosis is a widespread zoonotic disease causing considerable economic and public health problems. Despite animal vaccination, brucellosis remains endemic in some areas such as Iran, especially in the Hamadan province. The aim of this study was the isolation and molecular identification of Brucella abortus and Brucella melitenensis species from human and animal samples in Hamadan province.

Methods : In this study, 70 isolates were examined, so that 30 isolates were studied from patients with a clinical diagnosis of brucellosis who referred to the Infectious Diseases Ward of Sina Hospital in Hamadan Province between Nov 2021 and July 2022. Blood samples were collected for the diagnosis of brucellosis using the BACTEC blood culture system . And 40 isolates were isolated from the livestock of Hamadan province (including cows, sheep and goats). In this way, culture and isolation were done from milk samples, abortion products, amniotic fluid and lymph nodes from animals with positive serological tests . The initially identified Brucella isolates were further characterized using phenotypic and molecular approaches. . In molecular studies, the isolates were identified with specific primers for the identification of Brucella genus (B4,B5) , and in the next step, specific primers for the identification of B. abortus and B. melitensis species (IS711 AB , IS711 BM) were used.

Results : A fragment of 223 bp, which is specific to the genus Brucella, was observed in all isolates, and a fragment of 498 bp related to Brucella abortus (beavers 1, 2, and 4) was detected in 25% of the isolates, 15% of which were related to animal isolates and 10% was related to human isolates. And finally, a fragment of 731 bp for Brucella melitensis was identified in 75% of the isolates.

Conclusion : The identified primers revealed high levels of sensitivity and specificity. Therefore, they can be considered along with culture in clinical trials.

Keywords : Brucella . Hamadan province . PCR

P319-723: Anti-leishmaniasis activity of Rhamnus cathatica on amastigote stages of Leishmania major standard strain invitro

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Background and Aim : Leishmaniasis is one of the most important parasitic diseases in arid and semi-arid regions of the world and clinically causes cutaneous, cutaneous-mucosal, visceral and cutaneous leishmaniasis. Cutaneous leishmaniasis is caused by Leishmania major and Leishmania tropica species and is the most common form of the disease in our country. Due to the increasing prevalence of this disease and the increasing reports of glucantime resistance, a common treatment drug, it seems necessary to study and find a safe and natural alternative drug for the treatment of leishmaniasis. Due to this necessity, the use of methanolic extract of Rhamnus catarthica plant as antibacterial, fungal and anti-cancer compounds has been studied. The aim of this study was to evaluate the anti-leishmaniasis effects of methanolic, hydroalcoholic and chloroform extracts of Rhamnus catarthica on Leishmania major parasite in vitro.

Methods : The standard strain of Leishmania major parasite was prepared from Leishmaniasis reference laboratory of Tehran University of Medical Sciences and cultured in RPMI-1640 culture medium. After collection, Rhamnus catarthica was dried in room tempreature away from light and turned into powder by electric shredder. The resulting father was extracted using massage method and solvents of methanol, hydroalcohol (water and methanol) and chloroform and concentrations of 100, 200, 400 and 800 µg / ml were prepared. The effect of different concentrations on Leishmania parasite was evaluated after 12, 24 and 48 hours. The results were obtained using SPSS 22 software analysis of variance, LSD post hoc and Reppeted meager for data analysis.

Results : In this study, methanolic, hydroalcoholic and chloroform extracts of Ramenus cathartica in all concentrations had acceptable antiparasitic effects against Leishmania major parasite and among different extracts, chloroform extract had the best effect. Concentration of 800 µg / ml in all extracts after 24 and 48 hours showed a better effect than glucantime.

Conclusion : Considering the lethality of chloroform extract of Rhamnus catarthica plant on Leishmania major parasite and better effect than positive controls, it can be concluded that the above compounds can be a suitable candidate for the treatment of leishmaniasis, of course, after additional studies.

Keywords : Leishmania major; Rhamnus catarthica; cutaneous leishmaniasis

P320-724: Determining the effect of the hydroalcoholic extract of Terminalia chebula on the tachyzoite of the Toxoplasma parasite in laboratory conditions (in vitro)

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Background and Aim : Toxoplasmosis is a disease caused by Toxoplasma gondii parasite. Considering the increase in the prevalence of this disease and the increasing reports of resistance to the common anti-toxoplasmic drugs and the possible teratogenicity of these drugs, it is necessary to study and investigate the possibility of finding an alternative medicine, even if it is herbal, for the treatment of toxoplasmosis. Due to this necessity, the use of hydroalcoholic extract of Terminalia chebula as anti-bacterial, anti-fungal and anti-cancer compounds is the basis of the present study. The aim of the present study is to investigate the anti-toxoplasmic effects of the hydroalcoholic extract of the Terminalia chebula plant on the Toxoplasma gondii parasite in vitro.

Methods : Rh strain Toxoplasma gondii parasite is obtained from the country's toxoplasmosis research center located in the Faculty of Health, Tehran University of Medical Sciences and is inoculated into the peritoneum of laboratory white mice until the number of parasites reaches 500.000 per milliliter. The hydroalcoholic extract of the Terminalia chebula was prepared in serial concentrations of 100, 200, 400 and 800 µg/ml. The effect of different concentrations at 60, 120 and 180 minutes on the parasite in 24-well plates containing RPMI-1640 was investigated in comparison with the positive control. The results were obtained using SPSS 22 software, analysis of variance, posterior LSD and repeated meager tests for data analysis.

Results : The hydroalcoholic extract of Terminalia chebula in all concentrations had acceptable anti-parasitic effects against Toxoplasma gondii parasite. At a concentration of 800 micrograms/ml of the hydroalcoholic extract of Terminalia chebula after 60 minutes, better effects than the positive control have been reported.

Conclusion : According to the killing power of the hydroalcoholic extract of the Terminalia chebula on the Toxoplasma gondii parasite and its better effect than the positive controls, it can be concluded that the above compounds can be suitable candidates for treatment after further studies.

Keywords : Toxoplasma gondii; anti-toxoplasmosis; hydroalcoholic extract; Terminalia chebula.

P321-727: Prevalence and molecular characterization of Shiga toxin-producing Escherichia coli in Sheep farms of Sanandaj-Iran

Pouya Ghaderi [1] *, Elham Ahmadi[2] , Amir Mohammad farrokhi[3] , Fazel Moshrefi[3] , Abbas Rezaei[3] , Kiarash Siavashi[3] , Qumars Ghavami[3] , Khaled Rahmani[4] , Aram Sharifi[5]

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Background and Aim : Shiga toxin-producing Escherichia coli (STEC) strains have emerged as important foodborne pathogens of global public health concern, causing life-threatening diseases. Animal and their products have been documented as important reservoirs for STECs, especially E. coli O157. The aim of this study was to investigate STECs from healthy and diarrheal sheep in Sanandaj, Iran.

Methods : In the current study, a total of 81 samples taken from sheep feces (22 samples from diarrheal sheep and 59 samples from healthy sheep). E. coli and subsequently STEC strain was detected according to standard protocol (cultural characterization and PCR assays). Finally, the frequency of Shiga-toxin producing gene(s) (stx1, stx2), intimin (eaeA) and enterohemolysin (hlyA) was detected among STEC isolates using duplex PCR.

Results : Totally, 42 E. coli were isolated from 81 fecal samples (51.85% contamination). Of these, 34 isolates (80.9%) were identified as STEC patotypes based on cultured on Sorbitol-MacConkey (SMAC) medium and also the presence of stx1 and/or stx2. Of these, only 3 isolates (7.1%) were identified as serotype O157:H7 based on PCR assay. In addition, the results showed that 22.7% of healthy samples and 49.2% of diarrheal samples had STEC bacteria. Overall, the PCR results showed that 33 (97%), 12 (35.3%) and 8 (23.5%), isolates carried stx1, stx2 and hlyA, respectively. The eaeA gene was not found in any isolates

Conclusion : In conclusion, the present study revealed high prevalence rate of STEC bacteria including serotype O157:H7 and non-O157:H7 among sheep feces which highlight the importance of sheep as a reservoir of STEC pathogen in Sanandaj region. Therefore, the more control and preventive measures must be done to control the contamination by this pathogen.

Keywords : Shiga toxin-producing Escherichia coli, stx1, stx2, eaeA, hlyA

P322-91: Identity Confirmation of IRIBA vaccine by multiplex PCR Assay and phage typing

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Background and Aim : Brucellosis is a zoonotic bacterial infection caused by Brucella spp. in Iran which causes great direct and indirect economic losses to the livestock industry. The effective vaccine against bovine brucellosis is the Brucella abortus strain IRIBA vaccine which was used in cattle in Iran. The aim of this work was to identify and distinguish the IRIBA vaccine by phage typing and multiplex PCR techniques.

Methods : For this purpose, two multiplex PCR through the Bruce-ladder and wboA-based PCR were used to identify the IRIBA vaccine. Evaluation of the IRIBA vaccine also was performed through the classical phage typing according to the OIE protocol.

Results : The IRIBA identification through the molecular methods showed as the sensitive approaches for detection of IRIBA vaccine strain from B. abortus filed vaccine. Bruce-ladder PCR with 16 primers showed that IRIBA and 544 have three common PCR bands, 450, 578, and 794, but the vaccine strain IRIBA has amplified a 2524 band instead of 1682 in the reference 544. The wboA-based PCR with three primers was amplified (400 bp from field B. abortus and 900 and 1,300 bp from IRIBA). Strain IRIBA was biotyped as a typical rough B. abortus biovar 1 and was resistant to rifampin and penicillin. There is no agglutination with A or M antiserum. However, IRIBA is agglutinated with acriflavine.

Conclusion : Distinguishing IRIBA vaccine strains from field Brucella abortus strains that cause infections among vaccinated cattle herds in the field is essential. This study showed the PCR-based assay to identify the IRIBA vaccine.

Keywords : RB51, vaccine, brucellosis, cow, IRIBA

P323-162: Comparison of efficacy between three clinical samples (blood, urine, semen) for molecular detection of Brucella Spp infection in male dogs

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Background and Aim : Dogs are the main hosts of Brucella canis. Infection with B. canis is considered zoonosis disease, although it rarely seen in humans. Other species that cause brucellosis in dogs include B. abortus, B. melitensis and B. suis. The symptoms are mainly genital and abortion is common in 7 to 9 weeks of pregnancy. Embryonic absorption has also been reported 2 to 3 weeks after breeding. The normal morphology of the sperm is altered in infected males. Sometimes inflammation of the epididymis, testes and scrotal edema is occurred. Male dogs often show irreversible infertility despite treatment. Studies have indicated the inability to clear the infection of the prostate gland, so the identification and removal of infected dogs from the kennel have particular importance.

Methods : In this study, 37 male dogs in kennels with reduced reproduction were selected. After complete clinical examinations, blood samples were taken from cephalic vein. Semen and urine samples were taken by digital manipulation and catheterization method. DNA was extracted by GeneAll® ExgeneTM extraction kit by manufactured instruction. Brucella spp. was confirmed by PCR with specific primers IS711 (Ouahrani-Bettache 1996).

Results : From 37 breeding dogs, 14(43.75%) of urine,11(29.27%) of semen and 4(10.8%) samples were positive, which represents very significant infection rate. There was a significant relationship between history of contact with farm animals and positive PCR test results (P = 0.045). In comparison with blood (10.8%) and semen (29.72%), urine is a very good clinical sample for evaluation of brucella infection in male dogs.

Conclusion : Due to the high prevalence of Brucella infection in breeding male dogs in kennels and considering the fact that each male dog mates with at least 20 to 30 female dogs, male dogs monitoring before entering the kennels for brucellosis is highly recommended. The zoonotic aspects and economical loss of disease are both very crucial so definitive diagnosis is very important and the selection of the best clinical samples and diagnostic methods are very essential which is noted in the present investigation. our study provides evidence of the usefulness of the urine and semen samples for the diagnosis of canine brucellosis as much as that of blood samples.

Keywords : Dog, Brucellosis, Semen,urine, blood, PCR, Infertility, Genital disease, Zoonosis

P324-264: New protein and bacteriophage immunoassay techniques for detection Brucella

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Background and Aim : Brucellosis is the most zoonotic diseases caused by the Gram-negative bacterium Brucella genus that are affecting livestock and humans. The diagnosis assessments of human brucellosis are considered for managing disease. The aim of this study was to bring forward diagnosis techniques of brucellosis.

Methods : The novel protein immunoassay and detection based on bacteriophage techniques for diagnosis of brucellosis were explored in databases such as Web of Sciences, Google Scholar, Scopus and PubMed by using index words Brucella, human brucellosis, detection, diagnosis, Serology, protein and bacteriophage between February 2017 and January 2022.

Results : Many reports demonstrate that novel protein immunoassay and bacteriophage-detecting techniques can identify brucellosis in high sensitivity and specificity in comparison with Rose Bengal test (RBT), complement fixation test (CFT). These techniques were based on Brucella species lipopolysaccharide or outer membrane proteins as a diagnostic antigen that was performed on serum samples.

Conclusion : The result of this study indicated that protein and bacteriophage immunoassays are rapid, cost effective, highly specific and sensitive methods used for detecting Brucellosis rapidly and can be potentially used as reliable techniques because of potential usefulness rapid detecting and identifying method and do not require complex equipments.

Keywords : Brucella, brucellosis, diagnosis, bacteriophage, protein

P325-325: Molecular Detection of Brucella spp. in camel population in southern Kerman Province of Iran

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Background and Aim : Brucellosis is a global problem in public health and livestock. The occurrence of disease in humans is mainly due to animal reservoirs. Brucellosis disease in camels can also cause significant economic losses and is very important in terms of public health. The present study was carried out with the aim of determining the status of Brucella infection in the camel population of South Kerman by molecular methods.

Methods : One hundred blood samples with anticoagulant were taken from female camels in the south of Kerman province, three months old and older. Then their DNA was extracted. Their infection with Brucella bacteria was evaluated by PCR technique using IS711 primer.

Results : In the current study, out of the hundred blood samples tested, six samples were infected with Brucella bacteria. In other words, the prevalence of brucellosis in this research was about six percent.

Conclusion : Considering the prevalence of this disease in camels and the high population of camel herders in the south of Kerman and the large slaughter of this type of animal in the slaughterhouse as well as the consumption of its milk by citizens and villagers in raw and unboiled form, planning to apply more effective care and prevention policies It is necessary to produce vaccines, extensive training to prevent disease epidemics, identify and eliminate sick cases, etc.

Keywords : Camel, Brucella, PCR

P326-479: Epidemiology of clinical and paraclinical findings and treatment of patients with brucellosis admitted to Beheshti Hospital in Kashan during 2011 to 2021

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Background and Aim : Brucellosis is the most common infectious disease between humans and animals. Considering that Kashan is one of the endemic areas of brucellosis, the epidemiology clinical presentation their treatment can play an important role in policy to control this disease in the region.this study was done to evaluate epidemiologt ,clinical and paraclinical manifestations of brucellosis during the years 2011 to 2021 in Kashan.

Methods : This is a retrospective descriptive study of existing data on 200 patients with brucellosis who were admitted to Beheshti Hospital in Kashan during the years 2011 to 2021. A questionnaire containing demographic and underlying disease information, clinical and laboratory findings and variables of study was completed by reviewing the medical records of patients. The information was entered into SPSS software 20 and the results were statistically analyzed using Chi-square test.

Results : Most patients were male (57.5%). The mean age of patients was 39.38±20.59 years and they were mostly in the age group of 20-30 years (27.1%). Most of the patients were Iranian. Most of the patients' occupations were agriculture (28%) and housekeeping (23.5%). 23.5% had at least one underlying disease, of which diabetes (59.6%) and hypertension (53.2%) were the most common. 65.5% had a history of consuming local dairy products. Fever (79.5%) and joint pain (70.5%) were the most common symptoms. There was a statistically significant relationship between sex with liver involvement and age with joint involvement. ESR and CRP levels were elevated in most patients. In most patients, Wright test was 1.320 and Combs Wright and 2-Mercaptoethanol tests were 1.80.

Conclusion : Due to the history of local dairy consumption as a most common risk factor, education in the field of pasteurized dairy consumption and boiling local milk seems necessary, and given that fever and joint pain were the most common symptoms of patients in all patients with fever and joint pain, brucellosis should be differentiated. key words: Epidemiology, brucellosis, clinical findings, paraclinical, treatment

Keywords : Epidemiology, brucellosis, clinical findings, paraclinical, treatment

P327-510: New therapeutic and diagnostic methods in cases of Malt fever: New Insight

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Background and Aim : Brucellosis is a systemic bacterial disease of the Brucella family with more than half a million new cases reported annually as a worldwide zoonotic disease It can infect any organ that causes Malt fever in humans and fetal tetanus in animals. Antibiotics ordinary used to treat brucellosis include tetracyclines, aminoglycosides, trimethoprim, and sulfonamides. The current method that is the standard for the diagnosis is blood cultures. right now, various rapid detection methods based on immunological tests, including enzyme-linked immunosorbent assay (ELISA) and fluorescence polarization immunoassay (FPIA) have been successfully used. LAMP technique, is a sensitive detection method, due to the deficiency of accurate diagnosis in this method, a nanoparticle-based lateral flow immunoassay (LFIA) biosensor was developed to confirm LAMP products.

Methods : Amongst the methods accomplished in the subject of two combination LFIA detectors linked to LAMPtechnique (LAMP-LFIA) was developed and used for identification of brucella and treatment by using the dynamic light scattering (DLS) technique The number of solid lipid nanoparticles loaded with doxycycline and hydroxychloroquine was measured

Results : The result showed that drug-loaded NPs significantly reduced acute and chronic brucellosis and no chemical reaction occurred between the components of the NPS. but The effect of free drugs and NPS on bacteria was similar and the Use of synthesis of Nanomaterials in these studies had promising therapeutic results Meanwhile, the detection LAMPtechnique (LAMP-LFIA) was specificity and there was no cross-reactivity for other Brucella members and non-Brucella strains, which can be used as a diagnostic tool and/or screening for B. abortus in the basic and field laboratories

Conclusion : The general results show that the use of nanoparticles is a promising approach and an alternative to other treatments, these technique is highly specific and sensitive to the detection of bacterial species. The use of these new methods is for the treatment and diagnosis of pathogenic infectious diseases worldwide.

Keywords : Diagnostic Method, Brucellosis, LAMP, Lateral Flow Immunoassay

P328-596: Clinical manifestations and paraclinical findings of brucellosis patients admitted to Imam Reza Hospital, Mashhad – a 10-year retrospective study

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Background and Aim : Brucellosis remains a common infectious disease in Iran, with highly variable clinical manifestations leading to its inclusion in the differential diagnosis of many diseases. This study aims to investigate the common patterns of presentation, and the outcome of patients diagnosed with brucellosis in Imam Reza Hospital of Mashhad, Iran.

Methods : In this retrospective cross-sectional study, we reviewed the medical records of all patients admitted to Imam Reza Hospital, Mashhad from March 2008 to 2017, who met clinical and paraclinical criteria required for a diagnosis of brucellosis. Extracted data included demographic information, relevant personal history (occupational or dietary exposure, etc.), clinical manifestations, paraclinical findings, and outcome.

Results : A total of 209 adults (mean age 45.04±19.58), of whom 117 (56%) were male, and 56 children (mean age 6.85±3.72) were included. 131 (62%) lived in rural areas, where 54 (25.8%) adults were occupied with animal husbandry. 47 (22.5%) reported a history of previous affliction with brucellosis. A history of fever was reported in 184 (80.4%), arthralgia in 101 (48.3%), and weight loss in 80 (38.3%) cases. The most common syndromes at presentations were arthritis (84 - 40.2%) and spondylitis (42 – 20.1%). 55 (26.3%) patients had Wright agglutination tests with a titer of 1/320, accounting for the most common measurement. Only 1 patient died in the hospital, due to complication with endocarditis.

Conclusion : The most common syndrome at presentation was arthritis, while fever and arthralgia were the most common manifestations. The only mortality was due to complication with endocarditis.

Keywords : brucellosis, clinical presentations, outcome

P329-116: Investigation and monitoring of microbial pollution (bacteria and Giardia protozoan) in urban water and production water of household water treatment plant in Ardabil, Iran

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Background and Aim : Household water purifiers are widely used in recent years to improve the quality of drinking water by removing odor, taste, turbidity, color, pathogenic organisms, toxic chemicals, organic matter, and carcinogens. The indexes of heterotrophic bacteria, Total Coliform, Thermotolerant Coliform, E.coli, and Giardia lamblia protozoan were investigated in this study from March 2021 to February 2022 in untreated water, municipal water, and water produced by a household water purifier in Ardabil, Iran.

Methods : In this descriptive-analytical study, water samples from Yamchi dam (Ardabil) and 50 samples from water distribution network and inlet and outlet of domestic water purifiers were collected. Coliforms and HPC were tested by the standard methods using MPN method, Spread Plate, IMVIC and TSI diagnostic tests, as well as Giardia lamblia by the membrane filtration method.

Results : The findings of this study revealed that there is a significant difference in the number of colonies in the Total Coliform, Total Coliform, Thermotolerant Coliform ($p < 0.001$) and E.coli ($p < 0.05$) bacterial colonies in water samples collected behind the dam, municipal water distribution network and treatment plant outlets household water (winter season) in different seasons of the year. The bacteria colonies were high in water samples collected behind the dam. There were no reports of Giardia lamblia. There is no significant relationship between temperature ($p = 0.1$) and chlorine ($p = 0.8$) and heterotrophic bacteria in the water produced by household water purifiers. In the purifier, however, there is a significant relationship between water pH and HPC ($p = 0.01$).

Conclusion : The presence of Total Coliform, Thermotolerant Coliform, and E.coli bacteria in the untreated water behind the dam differs significantly from municipal water and the output of household water purifiers. It also slightly increases the growth of Heterotrophic bacteria in home water treatment systems due to pH changes.

Keywords : Coliforms, Municipal Water, Household Water Purifier, Giardia Lamblia, HPC, MPN

P330-179: Investigation of microbial contamination of Mahabad Dam reservoir in different seasons

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Background and Aim : Investigation of microbial contamination of Mahabad Dam reservoir in different seasons

Methods : Mahabad Dam Lake was constructed to supply drinking water, irrigation and electricity generation on Mahabad River that located in west Azerbaijan, Mahabad.

Results : In this research, bacterial pollutions of mahabad reservoir were investigated. In terms of geographical aspect of this reservoir, 3 stations (near the dam, Koter branch and Bitas branch) determined and samples were taken monthly over all the year via Rottner from different depths of the reservoir.

Conclusion : ial pollutions (Total Coliforms, Fecal Coliforms and Fecal Streptococci) were surveyed after transferring the samples to laboratory. Results indicated that values of Total Coliforms, Fecal Coliforms and Fecal Streptococci were varied between 2.33 ± 1.20 and 1166.67 ± 33.33, 0.0 and 30.33 ± 6.74 and 0.0 ± 16.67 ± 6.33 MPN/100 ml respectively during over all the year. These values were in the allowed range according to the drinking water and recreation standards of Iran.

Keywords : Key word: Mahabad dam reservoir, Total Coliforms, Fecal Coliforms, Fecal Streptococci, seasons

P331-181: Identification of bacterial agents causing sugarcane peduncle soft rot in Khuzestan Provine, Iran

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Background and Aim : The flowering of sugarcane varieties is a 10 to 12 years process under controlled conditions in the greenhouse. For crossbreeding between selected parents of sugarcane, seed production, and selection of new cultivars and genotypes, flowering stems play an essential role in this strategic plant. In the flower production greenhouse, due to the high humidity for flowering, symptoms of a disease were observed in sugarcane plant, including irregular soft and water-soaked lesions in the peduncle and top canes. In severe cases, the top cane become soft, peduncle breaks leading to the death of the flowers. Therefore, the current study aims to identify the causal agent of the newly emerged disease on sugarcane in Iran.

Methods : During 2020, suspected sugarcane samples were collected in the research green-house of the Iranian Sugarcane Research and Training Institute (ISCRTI) in Khuzestan province (30°57'04.3"N and 48°32'55.9"E). Samples were placed in plastic bags and transferred to the laboratory for bacterial isolation on YPGA and YDC media. To identify bacterial isolates, morphological, biochemical, and physiological characteristics were investigated. To perform the pathogenicity test, bacterial suspension (106 CFU/ml) was injected into the peduncle under greenhouse conditions. For molecular identification, 16S rRNA and gyrB gene were sequenced in representative strains.

Results : The obtained bacterial strains were grouped in three clusters, and representatives were selected from each group. In the pathogenicity test, symptoms of the disease included small, water-soaked lesions observed on the peduncle seven to ten days post-inoculation. Phylogenetic analysis of the target gene sequences showed that the causal agent belongs to different genera and species. Based on biochemical, molecular, and pathogenicity results, the representative strains were identified as, Serratia sp., Bacillus sp., Pantoea dispersa, and Pantoea agglomerans.

Conclusion : Our results showed that these bacteria are serious threats to the sugarcane seed production greenhouses and it seems important to take suitable actions to control and prevent the spread of pathogens.

Keywords : emerged disease, gyrB gene, seed production, sugarcane

P332-185: Inhibition of histamine accumulation by novel histamine-degrading species of Staphylococcus sp. isolated from goats and sheep milk

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Background and Aim : Histamine is an active amine compound that occurs in various fermented food that may causes adverse effects on the human health. Certain microorganisms are able to degrade histamine by an oxidative deamination reaction.

Methods : Therefore, the present study aimed to quantify histamine forming and/or degrading activity of the isolates derived from milk of goat and sheep herds, in Iran, by Capillary Zone Electrophoresis (CZE) method; and we evaluated the molecular characteristics of staphylococcal isolates.

Results : Among 243 staphylococcal isolates, 29 histamine-degrading bacteria were identified. One of these isolates, identified as Staph. epidermidis, No. 605, exhibited the highest activity compared to others, degrading available histamine to 58.33% within 24 h. By PCR analysis, the isolate, No. 605 that exhibited remarkable histamine-degrading activity lacked the genes encoding coagulase and DNase, nor did it harbor any of the five classical enterotoxin genes.

Conclusion : This is the first report that seven Staphylococcus species including, Staph. chromogenes, Staph. aureus, Staph. haemolyticus, Staph. epidermidis, Staph. pseudintermedius, Staph. agnetis and Staph. hyicus were able to degrade histamine, which were hitherto not known to have this capacity. Therefore, Histamine-degrading activity is a definite criterion to introduce fermenting organisms able to decrease histamine content in different food products.

Keywords : Staphylococcus; histamine degradation; milk; capillary zone electrophoresis; enterotoxin

P333-194: Effect of Hydroalcoholic and Aqueous Extracts of Carum Copticum on Escherichia Coli Strains in comparison with Gentamicin

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Background and Aim : In Persian medicine Ajwain (Carum Copticum (L.)) is recommended for the treatment of some infections. Due to bacterial resistance to antibiotics, a new antibacterial agent is essential. In this research, bactericidal and bacteriostatic effects of hydroalcoholic and aqueous extracts of Ajwain on E. coli was investigated.

Methods : In this in -vitro study a standard sample and 30 clinical isolates of urine culture of children with urinary tract infection from Amirkola Pediatric Hospital in Babol and were used. Antibacterial effects of 2 groups including hydroalcoholic and aqueous extracts of Ajwain by measuring the diameter of the inhibition zone using disc diffusion (concentrations 16, 32, 64, 128, 256 and 512 mg /disc) and Minimum Bactericidal Concentration (MBC) and determination of Minimum Inhibitory Concentrations (MIC) with Microdilution method was compared with Gentamicin (30mg /disc) as a positive control

Results : Results: Regarding to the inhibition zone with Gentamicin at concentrations of 64, 128, 256, and 512 mg/disc in standard and clinical samples, there was no significant difference. Gentamicin was significantly better at concentrations of 16 and 32. The extract of 512 mg /disc (12.93±2.66) of hydroalcoholic extract of Carum Copticum was significantly better than 256 mg /disc (9.53±1) (p=0.002). The MIC and MBC for standard samples were 4 and 8, respectively, and for clinical samples 3.83 ±2.36 and 5.8 mg / ml, respectively. aqueous extracts of Ajwain was not able to inhibit the growth of Escherichia coli .

Conclusion : The Hydroalcoholic extract of Carum Copticum has bacteriostatic and bactericidal effects on standard and clinical isolates of Escherichia coli.

Keywords : Anti -Bacterial Agents, Ajwain, Persian Medicine

P334-236: The General Information About food health and Safety, A Case Study

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Background and Aim : Background: Paying attention to food hygiene and safety is a biological necessity in preventing infectious and allergic diseases and also preserving the environment. Knowledge of the dangerous reactions to foodborne illness is essential to the development of a lifestyle improvement. Students are an important element in the healthy population of the country. Aim: The aim of this study was to evaluate the general knowledge about food health and safety, improve and enhance the self-efficacy of lifestyle of students in educational centers of Kermanshah province as part of the target population of Iran.

Methods : Methods: Using a descriptive-analytical questionnaire of questions in three sections, to assess the level of knowledge, attitude and practice of students in Kermanshah educational centers in two different genders and fields of study (N = 400), about food health and safety as an essential biosafety approach was investigated. Data were analyzed using SPSS software version 19 by one-way ANOVA, Chi-square (X2) and correlation coefficient test.

Results : Results: The level of information of biological science students with 76.7%, 83.9% and 80.3% respectively compared to non- biological science with 58.25%, 74.4% and 76.25% and in women with 71.1%, 82.8% and 80.6% compared to men with 63.85%, 75.5% and 75.95% had a significant difference in knowledge, attitude and practice, respectively (P <0.05).

Conclusion : Conclusion: Knowledge of food health and related diseases is effective in the quality of life of individuals and their families. There was a significant difference between biological science students compared to non- biological science in both sexes. Therefore, holding training workshops and determining courses in this field can be useful.

Keywords : Keywords: Awareness, attitude, practice, hygiene, food safety, health

P335-282: Identification of Salmonella spp from food outbreak in Tehran during 1400-1401

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Background and Aim : one of important problems that can be transmitted by contaminated food to human is food infection, this transmission can sometimes lead to the contamination of many people who have fed from the same source.

Methods : all the samples that were sent to the food microbiology research center during one year were microbiologically examined. After biochemical investigations, Salmonella spp isolates were analyzed by the presence of the invA gene. This gene is considered as one of the important genes in coding the secretory system of Salmonella, whose product is 1010 kilobases. The drug resistance of these isolates investigated through Kirby-bauer disk diffusion method. Imipenem, ceftriaxone and trimethoprim-sulfamethoxazole antibiotic were investigated.

Results : 40 isolates contained the invA gene, which indicate the presence of Salmonella spp in food outbreak samples. In relation to the trimethoprim-sulfamethoxazole, the level of resistance is lower than the other antibiotic, and a number of isolates shown intermediate resistance to this antibiotic.

Conclusion : Despite the development of health protocols and adherence to health guidelines, it is still observed that bacterial diseases can cause food outbreaks as in the past. Considering that coliform bacteria were also present in the majority of the samples, it is a sign of oral-fecal transmission, so it is suggested to reduce food outbreaks by monitoring the preparation of traditional food and also by training the people who prepare the food. In this study, it was determining that the antibiotic trimethoprim-sulfamethoxazole can be the suitable drug for treatment.

Keywords : Salmonella, food borne disease, coliform bacilli, antibiotic resistance.

P336-289: Prophage typing of methicillin-resistant Staphylococcus aureus in the traditional dairy products of Ilam

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Background and Aim : The extensive use of antimicrobial agents in animal husbandry contributes to the selection of drug-resistant strains. The aim of this study was to determine antibiotic resistance pattern and investigate some profagetypes, SGFa, SGFb and SGB in methicillin-resistant Staphylococcus aureus isolates from traditional dairy specimens in Ilam.

Methods : One hundred and sixteen samples were collected from dairy products from 39 traditional dairy stores in Ilam. All the samples were tested by using specific biochemical, microscopic to identify S. aureus. Multiplex PCR for the femA and mecA genes was performed to confirm the identification and methicillin resistance of S. aureus. For prophage typing all S. aureus isolates were screened for SGFa, SGFb and SGB genes by PCR. Susceptibility to ten antibiotics was determined according to CLSI guidelines by using disk diffusion test.

Results : Thirty of the samples were identified S. aureus and according to the presence of mecA gene, 7% were Methicillin Resistance S. aureus (MRSA). The highest resistance to antibiotic were observed for doxycycline (87%). For other antibiotics, 67%, 57%, 43%, 16%, 13%, 10% and 6.5% resistance were observed to tetracycline, cefexime, cefotaxime, penicillin G, vancomycin, amoxicillin and cefazolin, respectively. The least resistance were seen to imipenem antibiotics (3%). One S. aureus was positive for SGFa and one isolates positive for SGFb and two isolates were positive for SGB.

Conclusion : Generally, all isolates were resistant to at least for 3 antibiotics. According to the results for MRSA isolates and the presence of the prophages gene can be concluded the traditional dairy product could be a resource of the S. aureus that carry these genes. This may pose a public health hazard, since it has been shown that S. aureus that carrying prophage genes and MRSA clone have the zoonotic potential.

Keywords : MRSA, Prophage, Bacterial resistance, Virulence factors

P337-329: Native Probiotic LAB Strains Inhibit the Growth of Listeria monocytogenes and S.aureus in Lactic Cheese Samples

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Background and Aim : Several probiotic LAB species are recognized as a targeted intervention for the control of food pathogens mainly in dairy products. The aim of present study was to evaluate the possibility of using indigenous LAB strains for enhancing the safety of lactic cheese so as to extend its nutritious and health values and most importantly target L. monocytogenes and S.aureus.

Methods : Twenty probiotic Lactic Acid Bacteria (LAB) obtained from Razi vaccine and Serum research Institute, were grown in MRS (DeMan Rogosa and Sharpe), at 37C under anaerobic conditions. After confirming the purity of the isolates, all were analyzed for their physiological and technological characteristics, proteolytic activity and antibacterial activity against L.monocytogenes and Staphylococcus aureus, under invitro conditions. The isolates demonstrating significant antibacterial properties were added as an adjunct to prepared lactic cheese samples that were contaminated with the mentioned pathogens. Survival of LAB and the growth of both pathogens in the cheese samples during the ripening period was evaluated. All results were analyzed statistically and the significance of study highlighted.

Results : Three LAB isolates including Lactobacillus plantarum (RTCC1290-1), Lactobacillus acidophilus (RTCC1299) and Lactobacillus casei (RTCC1296-1) showed maximum inhibitory activity towards the tested pathogens and were of significant proteolytic and technological characteristics. Addition of the three LAB isolates (107 cfu/ml) in the prepared lactic cheese led to significant reduction of the pathogen count within a week of incubation. LAB added cheese samples declined the growth of L.monocytogenes to negligible levels (0.2 Log CFU/g) within day 30, compared to S. aureus (1.88 Log CFU/g). Lactobacillus isolates showed significant survival in the Lactic cheese samples during 45 days of storage with only one log decrease when stored at room temperatures.

Conclusion : The indigenous LAB isolates in current study being potential producer of antimicrobial metabolites might be recommended as a novel bio-preservative agent for the control of spoilage bacteria in different food products. Presently, the mentioned LAB isolates are being scrutinized for their probiotic potential in order to introduce them to food industry for production of functional dairy products.

Keywords : Lactic cheese, Lactic acid bacteria, Antibacterial activity, L.monocytogenes, Staphylococcus aureus.

P338-338: The application of different types of packaging in controlling the microbial spoilage of food

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Background and Aim : Microbial contamination, followed by microbial growth, reduces the shelf life of food and increases the risk of foodborne diseases. Heat processing, drying, freezing, cooling, irradiating, adding antimicrobial agents are new methods of preserving food. It is a food that has been a promising method in the packaging of some foods, especially meat and meat products.

Methods : Antimicrobial materials used in packaging can increase the lag phase of microorganisms. Packaging is one of the important issues in the field of food preservation which use of Nano science can improve the quality and efficiency of packaging materials. Types of packaging: nanoparticles and nanostructures, silicate packaging, active and smart packaging using nano sensors and organic and inorganic composite nanoparticles. They are aimed at increasing the shelf life of food. Some nanoparticles that have antimicrobial properties are used in packaging, among which are Nano clay, silver, titanium dioxide, zinc oxide nanoparticles, silicon oxide, silicon oxide nanoparticles and silver oxide.

Results : Edible films are produced as a thin layer before being used in food packaging, and then they are used for packaging like synthetic polymers. Edible films and coatings have unique advantages compared to synthetic polymers. Very good prevention of the exchange of respiratory gases and as a result of controlling the respiration of fruits and vegetables, prevention of the transfer and exchange of aromatic compounds and the taste of medicine, as well as protecting the product against mechanical damage are among the most important advantages of edible films and coatings.

Conclusion : Active and useful food, in addition to delaying environmental factors affecting food, is a logical way to preserve the product. Active packaging containers include materials that solve some problems. By making new containers that designed to extend the shelf life and traceability of food products, there is a possibility of spoilage of materials. Therefore, the

purpose of using antimicrobial substances is to destroy pathogenic microorganisms of spoiled substances, which includes bacteriocins, chitosan, silver ion and hydrous acid.

Keywords : foodborne diseases, packaging, nanoparticles, microbial spoilage of food

P339-396: Investigation of contamination of Fecal Escherichia coli in vegetables collected from Sistan

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Background and Aim : : Fruits and vegetables are important items in the food basket, microbial contamination of fresh products is a global concern despite acceptable hygienic techniques for washing and processing. Therefore, fresh fruits and vegetables can act as carriers of pathogenic bacteria. The population of microorganisms on food, especially vegetables, can be very large and diverse. Faecal Escherichia coli is a member of the Enterobacteriaceae family, which plays a significant role in foodborne outbreaks. Escherichia coli is an important indicator in the detection of contamination of vegetables with human or animal feces. Purpose: The purpose of this research is to investigate the presence of fecal Escherichia coli bacteria in vegetables collected from different parts of Sistan.

Methods : In this descriptive cross-sectional study, 100 samples of vegetables from different places (north, south, east and west) were collected from itinerant sellers and markets of edible vegetables in Sistan. The degree of contamination of the samples with fecal Escherichia coli was investigated by the maximum probable number (MPN) method.

Results : Out of 100 vegetable samples collected, 32 samples (32%) contained heat-resistant coliform. Among the samples containing heat-resistant coliforms (n=32), one sample (3.1%) contained 23MPN/g heat-resistant coliforms and 31 samples (96.9%) contained 100 MPN/g or more heat-resistant coliforms. It was hot.

Conclusion : The results of this research show the poor health quality of the studied area, which is worrying for public health.

Keywords : fecal Escherichia coli, vegetables, Iran, MPN, Sistan

P340-417: Evaluating the Effectiveness of Natural Detergent and Disinfectant on Gram-Positive and Gram-Negative Bacteria

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Background and Aim : Fruits and Vegetables play an important role in health maintenance and human living conditions improvement and their daily consumption can have positive effects on the prevention of diseases outbreak. It is natural that like any other type of food, they may be exposed to the attack of microbes and cause poisoning and illness in humans. The purpose of this study is evaluating the effectiveness of a detergent and disinfectant, all its components are consist of natural materials and it is a product of Zist Faravard Pars company on two bacteria, Escherichia coli and Listeria monocytogenes.

Methods : In this experimental study, fruit and vegetable samples (Parsley, Cucumber, Celery, Grape by E.coli) and (Tomato, Kiwi, Lettuce, Green plum by L.monocytogenes) were infected with a concentration of 0.5 McFarland (1.5 × 10 to the power of eighth cfu/ml) and were investigated in terms of microbial growth, Then natural detergent and disinfectant was sprayed on the desired samples and after washing with sterile distilled water, They were investigated and compared in terms of the growth of bacteria. The minimum inhibitory concentration (MIC) and the minimum Bactericidal concentration (MBC) of the natural detergent and disinfectant were determined using the broth dilution method against the used microorganisms.

Results : The results of this study with comparing cultured plates before and after using natural detergent and disinfectant showed that the growth of E.coli and L.monocytogenes decreased significantly after using the desired detergent and disinfectant. MIC values for E.coli and L. monocytogenes was determined 0/1, 0/5 mg/ml to the power of minus one respectively and MBC values for E.coli and L. monocytogenes was determined 0/01, 0/05 mg/ml to the power of minus one respectively.

Conclusion : The desired natural detergent and disinfectant has significant effectiveness in inhibiting the growth of Gram-positive and Gram-negative bacteria used in this study.

Keywords : Natural detergent and disinfectant, Inhibitory, Escherichia coli, Listeria monocytogenes

P341-553: Investigating on the biological interaction of maize seedling soft rot bacteria

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Background and Aim : In recent decades, bacteriocins have received substantial attention as antimicrobial compounds. Infections caused by antibiotic-resistant bacteria have been declared as a global threat to public health. Bacteriocins represent a potential solution to this worldwide threat due to their broad or narrow-spectrum activity against antibiotic-resistant bacteria. In the present study, the capacity of eight bacterial species causing the soft rot disease of maize to produce bacteriocin were investigated.

Methods : During the years 2020-2021, eight bacterial species causing stem and maize crown soft rot of were isolated and identified from Tehran, Alborz and Khuzestan Provinces. Inoculations were made by swabbing approximately 10 µl of bacterial suspension (1 × 108 CFU/mL) on the surface of yeast extract peptone glucose agar (YPGA) medium in three corners of an imaginary triangle; the cultures were then incubated at 25–27 °C for 72 h. Approximately 200 µl of the resulting suspension of the strains was sprayed the surface of the YPGA plates, containing previously inoculated isolates.The plates were incubated at 25–27 °C for 3 days and the growth inhibition was quantified by measuring inhibition zone radius (IZR).

Results : The capacity of species including Pantoea stewartii subsp. stewartii, P. agglomerans, P. ananatis, Stenotrophomonas maltophilia, Enterobacter cloacae, Kosakonia cowanii, Pseudomonas sp. and sp. Acinetobacter sp. were significantly different. All isolates were able to create an inhibition zone with different radius. Pseudomonas sp. showed the highest sensitivity to bacteriocin production compared to other isolates. The inhibitory zones produced by Pseudomonas sp. were larger than other isolates. Two strains of Acinetobacter sp. and P. ananatis had the lowest level of bacteriocin production compared to other isolates.

Conclusion : The unravelling of the occurrence and roles of bacteriocins from plant pathogens has only just begun. The potential advantages of creating more knowledge are obvious, new narrow-spectrum antimicrobials may emerge that can contribute to covering agriculture's need for more sustainable and effective strategies for plant disease control.

Keywords : Maize, public health, antibiotic-resistant bacteria, bacteriocin.

P342-559: The safety and quality properties of raw beef meat in slaughter plants of Kermanshah province using HACCP

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Background and Aim : The aim of the present study was to evaluate the safety and quality properties of raw beef meat in slaughter plants of Kermanshah province based on the hazard analysis critical control points (HACCP).

Methods : According to the national standard No. 6121 (general guideline for the implementation of the HACCP in production units - full processing of red meat and poultry meat (production, packaging, labelling)-slaughter of animals) of the Iranian National Standard Organization, the microbial evaluation in the following CCPs was carried out in the two cattle slaughterhouses (Kermanshah, Iran): CCP1 (peeling), CCP2 (bowel and visceral emptying), CCP3 (cutting off), CCP4 (final carcass washing), and CCP5 (carcass cooling). Microbial properties of raw beef meat (210 samples), including the total microbial count, Escherichia coli, Salmonella spp., and Listeria monocytogenes were evaluated using standard plate count during winter 2020 and spring 2021.

Results : Based on our findings, the CCPs of carcass cooling (CCP5) and bowel and visceral emptying (CCP2), had the lowest and highest bacterial contamination, respectively. The percentages of Salmonella spp. in CCP1, CCP2, CCP3, CCP4, and CCP5 were 9.5%, 16.5%, 14%, 12%, and 7%, respectively. The following contamination percentage at corresponding CCPs was found for L. monocytogenes; 0%, 12%, 9.5%, 7%, and 7%, respectively. The E. coli contamination percentage in CCP1, CCP2, CCP3, CCP4, and CCP5 were found to be 16.5%, 21.5%, 16.5%, 12%, and 7%, respectively.

Conclusion : The results of the present study showed that the evaluated slaughterhouses were in hygienic and standard conditions, and the low level of microbial contamination in this study also confirms the appropriate microbial condition of the equipment and tools used in the production of raw beef meat.

Keywords : raw beef meat, HACCP, Kermanshah

P343-563: Determining microbial contamination of poultry plants in Kermanshah province

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Background and Aim : The aim of the current study was to determine microbial contamination of poultry plants in Kermanshah province based on the hazard analysis critical control points (HACCP).

Methods : The microbial contamination of 225 poultry meat in five poultry plants, located in the Kermanshah, Iran, including Staphylococcus aureus, Escherichia coli, Salmonella spp. and Listeria monocytogenes were evaluated using Baird parker agar, Eosin methylene blue agar, Salmonella Shigella agar, and PALCAM Listeria selective agar, respectively.

Results : According to the results of this study, the highest level of contamination in terms of S. aureus, E. coli, Salmonella spp. and L. monocytogenes was found in the intestinal and visceral emptying (CCP2) and the completion of intestinal and visceral emptying (CCP3). The counts of L. monocytogenes (2.25 log CFU/g), Salmonella spp. (2.31 log CFU/g), E. coli (2.41 log CFU/g) and S. aureus (2.18 log CFU/g) were decreased significantly after storing the product under refrigerated conditions.

Conclusion : Our findings indicate that, although, the microbial count of poultry carcasses decreases after cooling, due to the cross-contamination with bacterial pathogens, particularly Salmonella spp. and S. aureus, improvement of the poultry plants and effective training of workers regarding hygiene is necessary.

Keywords : Poultry meat; Poultry plants; microbial pathogens

P344-587: Occurrence, Virulence Characteristics, and Serogroups of Shiga Toxin-Producing Escherichia coli Isolated from Sheep and Goats in Razavi Khorasan Province, Iran

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Background and Aim : Shiga toxin-producing Escherichia coli (STEC) is known as a foodborne pathogen associated with human disease characterized by mild or bloody diarrhea hemorrhagic colitis and hemolytic uremic syndrome (HUS). The presence of STEC in livestock has been considered a serious risk to public health. The contribution of sheep and goats to the food production systems made them one of the main livestock species in developing countries. Hence, this study aimed to investigate the characteristics of STEC in sheep and goat isolates originating from Razavi Khorasan Province, Iran.

Methods : Among 70 faecal samples, isolated from April 2022 to June 2022, a total of 30 (42.8%) STEC strains were detected. The isolates were obtained from faecal samples of sheep (n=23) and goats (n=7) animal hosts. All isolates were subjected to Paton's multiplex-PCR assay to detect the major virulence genes (stx1, stx2, ehxA, eae) of the STEC strains. Then, they were tested for the top 13 important O-groups by conventional PCR amplification based on the protocol offered by the EU Reference Laboratory for E. coli and some other important serogroups by different PCRs.

Results : Of 30 STEC isolates, 33.3% harbored stx1 and stx2, 63.3% only stx1, and 3.3% stx2 solely; and 53.3% of the isolates were positive for ehxA and all the studied STEC (100%) were negative for eae gene. The predominant serogroups were O103 (46.6%), O128 (30.0%), O5 (16.6%), and O113 (6.6%) respectively.

Conclusion : The occurrence of STEC strains in sheep and goats reported here (42.8%) is in accordance with prior studies in Iran that have noted a similar distribution range of STEC in these animal sources which is considerable. Furthermore, it could be inferred that the STEC isolates related to sheep and goats are less important for human disease since the genes stx2 and intimin (eae)—which are well known to have a significant role in severe cases of the disease—were only detected in one isolate (3.3% for stx2 solely), and all were negative for intimin gene. Finally, the detection of O103 as the predominant serogroup in sheep and goats (46.6%), posed an unanticipated and interesting finding that future studies are recommended.

Keywords : Shiga toxin-producing Escherichia coli; STEC; serogroups; sheep and goats; Iran

P345-670: Antibacterial activity of disinfectant column with UV lamp on some bacteria polluting surface water

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Background and Aim : In most poultry and aquaculture industries, the drinking water is used without a disinfection process, which sometimes causes animal mortality and much economic damage. On the other hand, Ultraviolet light (UV, 254 nm) has potent antimicrobial activity. However, it has not been user-friendly due to some problems. Therefore we designed a large disinfectant tube with a UV lamp supported by a quartz tube (coated with silica nano clay to prevent the formation of calcium carbonate deposits). Also, a mobile application makes easy use of and maintenance by sensors (temperature, turbidity, flow, and UV light intensity), a display, and monitoring. Then we discussed its antibacterial activity on some important water-contaminating.

Methods : A high concentration of bacteria (107/ml) investigated the column performance over time, including Escherichia coli, Pseudomonas aeruginosa, Enterococcus faecalis, Staphylococcus aureus, and Salmonella typhimurium. The sampling times were 0, 1, 3, 5, 10, 20, 30, and 60 seconds. Samples were cultivated on blood agar and incubated at 37 oC overnight.

Results : 1 second of UV light reduced nearly 10,000 times the number of bacteria. The number of Escherichia coli, Pseudomonas aeruginosa, and Enterococcus faecalis bacteria from the initial values dropped to zero in the third second. These values were 5 and 10 seconds for Staphylococcus aureus and Salmonella typhimurium, respectively.

Conclusion : This equipment can reduce the number of bacteria by 100 times with a flow rate of 2 liters/second and eliminate 100% of the mentioned bacteria with a flow rate of 0.6

liter /second. UV light can serve as an excellent alternative for disinfection surface water bacteria.

Keywords : Antibacterial, UV light, Column, Water, Disinfection

P346-719: Investigation of the most important bacteria contaminating traditional Iranian dairy products

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Background and Aim : Most of the traditional dairy products are fermented products, and have been one of the most important food products for human in during the past centuries. Iran has a long history of producing a wide variety of fermented dairy products that the most important of them are including traditional yogurt, cheese (such as Liqvan, Kurdi cheese and etc.), butter (such as Maske), Dough (such as Chal) and various other products. It has been determined that these products have unique Properties technological, nutritional and Health benefits (such as gastrointestinal health, immunity, anti-cancer properties, anti-fungal, anti-microbial, etc(. Besides the useful benefits of these products, but hospital reports and various researches has shown that them can be a threat to the health of the consumer by causing diseases and food poisoning. Therefore, it is necessary to investigate the most important bacterial contaminating these products.

Methods : In this study, we searched for papers and book in electronic databases (PubMed, Medline, Google scholar, Web of Science, Scopus) using keywords such as: Iranian dairy products, traditional, contamination, Coxiella burnetii, Brucella, Salmonella, Campylobacter and cheese.

Results : The results showed that Coxiella burnetii, Brucella, Salmonella, Campylobacter, Staphylococcus aureus, Escherichia coli, coliforms and Bacillus cereus are the most important foodborne pathogens, especially in various traditional dairy products, therefore them can be cause of diseases such as Q fever, malt fever, salmonellosis, infection and food poisoning and they can be transmitted between humans and animals.

Conclusion : These pathogens are considered one of the main health problems of the country, and they cause the waste of human and financial resources of the country. Most of these pathogens in the traditional production process, may remain in the product due to lack of use of heat or low temperature and cause illness in the consumer. So, in the production of these products, appropriate temperatures (necessary to destroy the indicator pathogens) should be used as well as the conditions of storage and distribution of them should be monitored more.

Keywords : dairy products, contamination, cheese, indicator pathogens

P347-154: Emergence of amoebic dysentery mimicking Covid-19: A human case report from Iran

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Background and Aim : Identical symptoms of coronavirus disease-19 (Covid-19) with infectious and non-infectious disease have become challenging issue for health professions. In the present study, we describe a human case of amoebic dysentery mimicking SARS−CoV-2 infection in Iran with an emphasis on morphological and molecular diagnostic aspects of E. histolytica parasite.

Methods : A 32-year-old woman with a history of abdominal pain, diarrhea, and mild fever of 38°C was diagnosed as Covid-19 with no prescription of real-time RT-PCR as standard confirmatory laboratory tests. The patient's fresh stool sample was transferred to the Department of Medical Parasitology at Tehran University of Medical Sciences for parasitological diagnosis such as direct microscopy and trichrome stain. Also, for molecular diagnosis, total DNA was extracted using a stool DNA extraction kit (Yekta Tajhiz Azma, Iran) and followed by a nested-PCR assay for detection of Entamoeba genus with species-specific primers. Moreover, the PCR product of the 18S rRNA gene related to the current sample was purified and sequenced using the Sanger sequencing method on an ABI PrismTM 3730 Genetic Analyzer by the Macrogen Company (Macrogen® Corp., Seoul, South Korea). The sequence chromatogram was observed using Chromas Version 1.0, and nucleotide sequences were edited using BioEdit, version 7.0.5, and examined using the phylogenetic program MEGA X. To different phylogenetic analysis for the Entamoeba complex (E. histolytica, E. moshkovskii, and E. dispar) we selected the Neighbor-Joining method (NJ) using Kimura 2-parameter models in MEGA X.

Results : Not only were hematophagous trophozoites of E. histolytica observed in the trichrome-stained slides using a light microscope (Zeiss, Germany), but also PCR and subsequent sequencing confirmed the diagnosis. The sequence was submitted to GenBank under the accession number using BankIt - NCBI - NIH (GenBank Acc. No: MW659191).

The current sequence was 99-100% identical to the available GenBank sequences for E. histolytica isolated from Iran and other regions of the world. Also, Treatment was completed with antiparasitic drugs including oral Metronidazole 500 mg, 3 times/day for ten days, and oral Iodoquinol 650 mg 3 times/day for twenty days.

Conclusion : By continuing the Covid-19 pandemic, clinicians must be vigilant in all aspects of diagnosis, treatment, and management of patients to prevent any medical errors and misdiagnosis.

Keywords : Entamoeba histolytica, amebiasis, SARS−CoV-2, Covid-19, Iran

P348-161: Detection of SARS-CoV-2 in household dogs and cats living with COVID-19 infected owners by Real-time PCR during Delta and Omicron variant waves in Iran

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Background and Aim : The animal origin of the novel coronavirus SARS-CoV-2 led to a discussion about the possible transmission of the disease to humans through animals. The emergence of SARS-CoV-2 infection in dogs and cats in different countries worldwide raises concerns that pets are at a higher risk for spreading or transmitting SARS-CoV-2 to humans and other pets and increased the research about the zoonotic aspects and natural routs of infection in companion animals.

Methods : Detection of SARS-CoV-2 in household dogs and cats living with COVID-19 infected owners was done by Real-time PCR from April 2021 to 2022 in the southeast of Iran, Kerman. Deep oropharyngeal and rectal swabs were collected from 20 cats and 10 dogs.

Results : Natural infection was detected in 10% of household cats. This study indicated that close contact with COVID-19 infected owners could create a low risk of SARS-CoV-2 transmission to pet cats so infected owners should eagerly limit close contact with their pets during the infection period.

Conclusion : SARS-CoV-2 could be transmitted from owners to their pets by hand-mouth, eye conjunctiva, or by touching the nose with hands contaminated by saliva or respiratory droplets. Kissing, petting, or hugging pet animals may facilitate the transmission. Pet owners should apply hygienic measures during contact with their pets, and COVID-19 infected owners should limit close contact with pets. Although there is no evidence that dogs or cats can transmit SARS-CoV-2 to humans, the usual precautionary measures should be urgently considered as part of global control and the ‘one health’ approach.

Keywords : SARS-CoV-2 - Pet - Iran - Covid19

P349-186: A review of the ZIKV virus and possible preparedness for the resulting epidemic

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Background and Aim : ZIKV virus is a gram-positive single-stranded RNA virus in the Flaviviridae family. ZIKV is a mosquito-borne flav virus. The virus is spread mainly through the bites of infected Aedes aegypti mosquitoes. Due to the rapid spread of the virus in some countries, we decided to do a review study on the awareness and preparedness against this virus.

Methods : The present study is a systematic review study. Therefore, in order to review the ZIKV virus review and possible preparedness for the resulting epidemic, the keywords ZIKV, epidemic, virus in pubmed database, google scholar, Elsevier search and articles The target was studied.

Results : Since 2015, ZIKV has been expanding at an alarming rate. With a prevalence in 87 countries, it has been reported that a blood meal of infected patients following a mosquito bite can easily cause an outbreak in one country, as happened in the United States. Contaminated urine, mosquito bites, sex, blood transfusions and from mother to fetus ZIKV causes syndromes such as GBS, microcephaly and symptoms such as joint pain, skin rash, headache, fever, and conjunctivitis, with an incubation period of about one In addition, some patients vomit. They have diarrhea, red eyes, weakness and edema.

Conclusion : Considering that there is no known vaccine or drug for this pathogen, so the necessary care should be taken to prevent the occurrence of this disease. This virus is transmitted through different means, so we should try to be aware of this virus and how It increased its contamination among the people, quarantined infected and suspected people if necessary, and used the experience of the COVID19 epidemic in this regard.

Keywords : ZIKV, epidemi, virus

P350-244: Design a multi-epitope vaccine against influenza A virus with a bioinformatics approach

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Background and Aim : Influenza is a virus of the Orthomyxoviridae family whose genome is single-stranded RNA with negative polarity. Members of this virus include influenza type A, B and C. .The purpose of this study is to design a multi-epitope vaccine candidate protein structure based on hemagglutinin protein against influenza A virus

Methods : First, the hemagglutinin protein sequence of influenza A strain (A/reassortant/X-47(Victoria/3/1975 x Puerto Rico/8/1934) (H3N2)) was extracted from the UniProt database. And by using IEDB server, epitope prediction was done based on cellular and humoral immunity,H2-Kd, H2-Ld, H2-Dd, H2-IEd, H2-IAd alleles in mice were considered to predict cellular immunity. For all predicted epitopes, antigenicity, toxicity and conservancy parameters were checked with VaxiJen, ToxinPred and Epitope conservancy analysis tools for epitopes, respectively. Finally, two epitopes with the best characteristics were selected for humoral and cellular immunity. Epitopes were joined together with GPGPG and EAAAK linkers. After checking the allergenicity with the AllerCatPro tool, the final sequences were modeled with the I-TASSER server and Validation of the model was done with PSVS and ProSA-web tools. Physicochemical properties were analyzed with ProtParam tool and post-translational modifications with MusiteDeep tool for the final model. To evaluate the immunogenicity of the vaccine candidate model, TLR7 was docked with HDOCK tool

Results : Multiple screenings of epitopes obtained from predictions led to the identification of two linear humoral epitopes that also exhibit structural features. Also, both epitopes selected based on cellular immunity had a high score. All four epitopes had over 90% conservation. The three-dimensional structure of the vaccine candidate had a good modeling score. The molecular docking study between the vaccine candidate protein and TLR7 showed a high docking score

Conclusion : Influenza virus epidemics and pandemics cause many diseases and deaths around the world. The use of vaccines with multi-epitope platform provides the potential and providing high immunity against all antigenic changes of the virus. In this study, the designed candidate vaccine has shown promising results, and it is suggested that laboratory and animal analyzes be considered for further investigation

Keywords : Influenza A, multi-epitope vaccine, epitope prediction, conservancy

P351-538: Epidemiological use of nested PCR targeting the QpRS plasmid associated with the chronic form of Q fever in horses of West Azarbaijan province

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Background and Aim : Q fever is a worldwide zoonosis caused by the obligate intracellular pathogen Coxiella burnetii, affecting a broad range of animal hosts including horses. Q fever causes highly variable symptoms ranging from acute (often self-limited) infection to fatal chronic infection. The manifestations of chronic Q fever are endocarditis, hepatitis, osteomyelitis, or infected aortic aneurysms. Most of the isolates found, carry plasmids which genetic studies of C. burnetii strains suggest a critical role in C. burnetii survival. Although the correlation between an isolated plasmid type and the chronic or acute nature of the disease has always been controversial, strains with a QpRS plasmid are associated with chronic Q fever. This study was conducted to investigate the prevalence of C. burnetii QpRS plasmid in horses and to assess the potential role of these animals as reservoirs of infection and transmission.

Methods : Nested-PCR assays were performed on 320 blood serum samples drawn from horses in the West Azarbaijan province. In total, 26 (8.1%) Q fever-positive samples, based on containing the IS1111 gene were tested by the Nested- PCR approach to amplify QpRS plasmid segments.

Results : Based on these results all the diagnosed Q fever samples were negative for the QpRS plasmid. And horses of west azarbaijan are free of chronic Q fever. The results indicate that the Nested PCR method could be suitable for routine diagnosis, gathering new information about the shedding of C. burnetii, and improving the knowledge of contamination routes.

Conclusion : Thus, the identification of C. burnetii plasmids may provide important information for the differential diagnosis of Q fever and epidemiological investigations.

Keywords : plasmid, Coxiella burnetii, Nested-PCR, horse blood sera

P352-672: Investigating the process of infection caused by intestinal parasites in Iranian HIV positive patients: a review article

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Background and Aim : AIDS is now recognized as a worldwide crisis. Gastrointestinal parasites are the main cause of infection in HIV positive patients. Protozoa and helminth parasites are the most common opportunistic parasitic infections associated with the gastrointestinal tract in immunocompromised patients. Objective: This study was conducted with the aim of investigating the prevalence of intestinal parasites in Iranian HIV positive patients.

Methods : We searched MEDLINE via PubMed, Scopus, Science Direct, Web of Science (ISI), Google Scholar (as English databases); Magiran, Iran Medex, Iran Doc, and SID (as Persian databases) during 1996 to September 2021using the terms: parasitic intestinal infections , Giardia lamblia , Cryptosporidium, Enterobiusvermicularis (oxyure),Isospora belli , Ascarislumbricoides , Entamoeba histolytica, Human immunodeficiency virus(HIV) , Acquired immunodeficiencysyndrome (AIDS), Iran.

Results : In general, intestinal parasites have a high prevalence in the HIV+ population. In particular, most of the parasites identified in the HIV+ population during studies conducted in Iran include: Giardia lamblia, Blastocystis hominis, Chilomastics mesnili, Entamoeba coli and Cryptosporidium parvum, Endolimax nana, E. histolytica cyst, Dientamoeba fragilis. , are enteromonas. IPI has been reported in different regions of Iran, and the most common parasites causing parasitic infections in the HIV+ population in Iran include G. lamblia, B. hominis, and C. mesnili species.

Conclusion : The present study shows the importance of infection caused by intestinal parasites in HIV positive patients and emphasizes the need to increase the awareness of doctors regarding the occurrence of parasitic infections in these patients. Routine examination of stool samples for parasitic infections can significantly benefit HIV-infected individuals by helping to reduce morbidity, mortality, and improve quality of life.

Keywords : HIV+ Patients, Intestinal parasites, Iran

P353-696: Designing of a multi-epitope protein composed of essential virulence factors of SARS-Cov-2 virus and evaluation of its immunogenicity in animal model

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Background and Aim : The current COVID-19 pandemic resulted in high mortality and morbidity in the world. In the pandemia of SARS-Cov-2 virus, there was no vaccine for treatment or prevention of the virus, and this showed the need for studies to develop an effective vaccine against the virus. Therefore, we designed a multi-epitope of essential virulence factors of the virus including the proteins S, N, nsp3, and nsp8 to inhibit the virus from several pathways and expressed it in a prokaryotic system to evaluate its immunogenicity in the animal model

Methods : In this study, by bioinformatic studies, a multi-epitope composed of proteins S, nsp3, nsp8, and N in SARS-Cov-2 was designed to stimulate both humoral and cellular responses. The final synthesized gene was ligated into pET28a expression vector and transformed into the BL21 (DE3) host by heat shock protocol. After culture of the transformed bacteria on the Luria bertani (LB) medium, the recombinant plasmids were screened using PCR, enzymatic digestion, and sequencing. The expression of the multi-peptide was performed by adding IPTG inducer and was evaluated by SDS-PAGE and Western blot. The recombinant protein was purified by Nickel resin. After inoculation of mice with the recombinant protein, evaluation of humoral response was done by ELISA.

Results : Two B-cell epitopes, 3 HTL epitopes, and 3 CTL epitopes were selected from S, N, and Nsp3 proteins to design the vaccine construct, and about Nsp8 protein, one was selected from each B-cell, HTL, and CTL epitope. After synthesis of the multi-epitope gene, its expression was successfully performed. Evaluation of the expression of the protein by SDS-PAGE and western blot showed its expression with a size of about 45 KD, which was purified by nickel column with high purity. The results of the evaluation of humoral responses showed that the group of mice receiving the purified protein was able to significantly induce IgG and IgA responses compared to the control group (PBS group).

Conclusion : Considering the significant immune responses induced by the multi-epitope protein, it is recommended that a challenge mice model design to evaluate the protective efficacy of induced immune responses against the experimental infection.

Keywords : COVID-19, SARS-Cov-2, bioinformatic studies, multi-epitope, vaccine candidate, humoral responses

P354-743: Emerging of infections caused by multi-drug resistant (MDR) and Extensively-drug resistant (XDR) Acinetobacter baumannii in hospitalized patients in Iran; A systematic review.

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Background and Aim : Acinetobacter baumannii is an opportunistic pathogen that has an important role in causing hospital-acquired infections and increasing the rate of mortality among hospitalized patients. Its resistance against many antibiotics has been significantly reported, that indicates the complexity of treatment and also the prevention strategies of hospital infections caused by A. baumannii. This study aims to investigate the prevalence of multi-drug and extensively-drug resistant strains of A. baumannii in the last 5 years.

Methods : The international and Iranian national databases were explored according to the given keywords by Medical Subject Headings (MeSH). The search results were limited to the last five years, from 2018 to 2022 in Iran. Twenty-four English and Persian original articles were selected for this study. The original papers containing clinical MDR (Multi-drug resistant) and XDR (Extensively-drug resistant) A. baumannii information were regarded as included criteria. Most of the studies have been done in Tehran.

Results : A total of 2106 clinical isolates of drug-resistant A. baumannii were investigated in those articles. The results analysis showed that 1735 (82.38%) isolates and 1153 (54.74%) isolates were considered as MDR and XDR, respectively. The selected studies were performed on various types of clinical specimens, mostly wounds (including burn wounds) and respiratory tract samples (including tracheal aspirates). These specimens were taken from different wards of hospitals, mainly ICUs and burn wards. Antibiotic susceptibility patterns indicated that most of A. baumannii isolates (78.1%) were resistant to ceftazidime and 20.9% of isolates were sensitive to Polymyxin B.

Conclusion : This review shows the high prevalence of drug-resistant A. baumannii circulating in different wards in many Iranian hospitals recently. The necessity of rapid and accurate diagnosis of the infections caused by MDR and XDR strains, also finding novel effective antibiotics must be considered as effective rules to reduce the high mortality among hospitalized patients.

Keywords : Acinetobacter baumannii, Multi-drug resistance, Extensively-drug resistance, Iran

P355-6: evaluating the effect of methanolic extract of Quercus persica on Pseudomonas aeroginosa in combination with specific lytic phage

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Background and Aim : Introduction: Based on the recent reports of World Health Organization, increased antibiotic resistance prevalence among bacteria represents the greatest challenge to human health. antibiotic resistance is rising to dangerously high levels in all parts of the world. New resistance mechanisms are emerging and spreading globally, threatening our ability to treat common infectious diseases. Quercus persica is the most important tree species of the Zagros in Iran. Iranians use its seed in traditional medicine. Due to the rise of multidrug-resistant infections in humans, phage therapy is gaining renewed attention in Western medicine. Despite the increasing number of publications focussed on the isolation, characterization and in vitro performance of different phages, there is still a lack of concise pre-clinical information to guide the application of phage therapy in clinical practice. Phage Therapy is the therapeutic use of lytic bacteriophages to treat pathogenic bacterial infections.

Methods : Method: The present study describes the effect of methanolic extract of Quercus persica Boiss on Pseudomonas aeroginosa alone and in combination with 2 specific lytic phage against these pathogens. Methanol extracts were prepared by maceration method, filtered and concentrated by rotary evaporator apparatus.

Results : Result: MIC value of methanolic extract of Quarcus persica for Pseudomonas aeroginosa was 1.25 mg /ml . MOI value For lytic Phage was 100. The effects were improved by combining the extract with phage. In combination extracts with phage,concentrations lower than MIC (for extracts) and less than optimal MOI (for phages) completely inhibited the growth of Pseudomonas aeruginosa.

Conclusion : Conclusion: Both phages were effective in preventing from formation and eliminating Pseudomonas aeruginosa biofilm. Combination with methanolic extract of Quarcus persica enhanced the effect of phages.

Keywords : Bacteriophage, methanol extract, Quercus persica, Pseudomonas aeruginosa

P356-22: Bacteriophage-derived endolysins as a novel candidate for treatment of P. aeruginosa infection

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Background and Aim : Pseudomonas aeruginosa is a ubiquitous organism which has emerged as a leading cause of hospital-acquired infections. Overuse of antibiotics has significantly expanded the emergence of multi-drug resistant bacterial infections that can't be treated with multiple antibacterial drugs. While whole phage treatment demonstrated tremendous effects against a variety of P. aeruginosa clinical and general laboratory strains, phage-encoded endolysins have also shown promising results in external peptidoglycan degradation without the assistance of phage. Therefore, in this study we aimed to design a product from blending of different endolysins derived from Pseudomonas phages to be used as a treatment for P. aeruginosa infections.

Methods : According to the current literature endolysin Q859G4 demonstrated highest efficacy toward pathogenic P. aeruginosa. The UniProt search was done to find similarity with protein Q859G4 based on its host. The similar proteins were deposited in PDB and Swiss-Model. The 3D structure checked on PyMOL and the PPI was done in HADDOCK2.2.

Results : There are 48000 proteins similar to endolysin Q859G4 (endolysin of P.aer phage gh.1) but only 246 of identified proteins showed endolysin activity, among which 10 have effect on P. aeruginosa. Forty percent (4/10) of these phage endolysins had more than 50% identity to endolysin Q859G4 (endolysin of chf-19, CHF.7 shl2 and MR2 phage).

Conclusion : The Q859G4 endolysin is similar to endolysins from chf-19, CHF.7 shl2 and MR2 phages; therefore blending of these endolysins in the same product could be an appropriate candidate for treatment of P. aeruginosa infections.

Keywords : Multidrug resistance, Bacteriophage therapy, endolysin

P357-31: Bacteriophage isolation against MDR Enterococus strains

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Background and Aim : Enterococci are the normal flora in the human gastrointestinal tract and many mammals. They are also found in the human oral and vaginal cavities, soil, water, and food. In healthy people the presence of Enterococci usually has no negative effect on the host, but under certain conditions can cause infection and diseases such as endocarditis, abdominal abscesses, bacteremia and urinary tract infections and play an important role in the distribution of resistance genes. Enterococci are Facultative anaerobic bacteria, Gram-positive, and catalase-negative that include an important and diverse group of bacteria. Among the species of Enterococci, Enterococcus faecalis and Enterococcus faecium are the main pathogens. With the prevalence of Enterococci and the increasing use of antibiotics, MDR Enterococci are one of the most common nosocomial pathogens worldwide. This has led researchers to look at alternative ways to eliminate and control these bacteria. Phage therapy using bacteriophages to treat infection caused by pathogenic bacteria is considered as one of the alternatives to antibiotics. The aim of this study was to isolate effective bacteriophages against MDR enterococcal strains and to identify them.

Methods : After collecting Enterococcus samples from Isfahan hospitals, disk diffusion method was used and all samples were resistant to the meropenem, moxifloxacin, vancomycin, streptomycin, gentamicin, and ciprofloxacin.

Results : . Microbiological, biochemical, PCR and 16S rRNA gene sequencing methods was performed to know specific bacteriophage and bacteri. Bacteriophages were examined for plaque formation and after enrichment and concentration, plaque was saw ,and it mean bacteriophage and 2 strains of bacteria were found

Conclusion : The aim of this study was to isolate effective bacteriophages against MDR enterococcal strains and to identify them. And after gene sequencing two strain of Enterococcus faecium,E1 andE11were found and then they were registered in NCBI.

Keywords : Enterococci, , Phage therapy, Bacteriophage

P358-60: Evaluation the treatment of diarrhea by phage cocktail product

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Background and Aim : Diarrhea is one of the most common types of gastrointestinal infections. Salmonella enterica, Shigella flexneri cause diarrhea. The inappropriate use of antibiotics in common infections such as diarrhea has contributed to antibiotic resistance throughout the world. Alternative treatments such as bacteriophages are suggested. Bacteriophage solely target and kill bacteria. Unlike antibiotics, they do not affect the normal bacterial flora, eukaryotic cells. Chitosan as drug delivery system is required to protect phages from being destroyed under the acidic conditions in the stomach. This current research intended to study the construction of a chitosan encapsulated bacteriophage cocktail against bacteria causing diarrhea.

Methods : This was investigated using 64 Wistar female rats (8 weeks old, 180 ± 200 g) infected with Salmonella enterica, and Shigella flexneri. 0.5 mL of the phage cocktail was orally gavaged daily. In the placebo group and the positive control group, chitosan and cefixime were orally gavaged daily and the group was not treated. Briefly, the phage cocktail was isolated from sewage. The spot test was performed to determine the lytic activity of the phage cocktail.

Results : The results showed that in the treated group with cefixime, weight loss was significant compared to the chitosan encapsulated bacteriophage cocktail group ($p < 0.05$). The weight loss for rats in the non-treated and placebo groups was significantly higher than the group treated with phage ($p < 0.001$). Positive cultured stools were reduced after 4 days in the treated group with the bacteriophage cocktail.

Conclusion : chitosan encapsulated bacteriophage cocktail treatment of diarrhea was successfully developed.

Keywords : Bacteriophage Cocktail; Diarrhea ; treatment

P359-128: The control of Multi-Drug Resistant Klebsiella pneumoniae wound infection by Bacteriophage in a Rat Model

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Background and Aim : Multi-drug-resistant Klebsiella pneumoniae (MDR-KP) has persistently raised beyond antibiotic control. Wound infection kills many patients yearly due to the entry of multidrug-resistant (MDR) bacterial pathogens into the skin gaps. However, a bacteriophage (phage) is a potential antibiotic alternative for treating bacterial infections. The aims of study to isolate and characterize a specific phage and evaluate its topical activity against MDR-KP isolated from infected wounds.

Methods : A lytic phage KshKPC-M was isolated using a clinical isolate KP(Ksh-1) as a host strain and then characterized. Additionally, the phage was assessed for its in vitro host range, temperature, ultraviolet (UV), and pH sensitivity. The therapeutic efficiency of phage suspension and a phage-impeded gel vehicle were assessed in vivo against a K. pneumoniae infected wound on a rat model.

Results : The phage produced a clear plaque and was classified as Siphoviridae. The phage inhibited KP(Ksh-1) growth in vitro in a dose-dependent pattern, and it was found to resist high temperature (<70 ◦C) and was primarily active at pH 5; moreover, it showed UV stability for 45 min. Phage-treated K. pneumoniae inoculated wounds showed the highest healing efficiency by lowering the infection. The quality of the regenerated skin was evidenced via histological examination compared to the untreated control group.

Conclusion : This research represents the evidence of effective phage therapy against MDR-KP.

Keywords : Gram-negative; Klebsiella pneumoniae; antibiotics; multi-drug resistance (MDR); bacteriophage; phage therapy; wound healing; in vivo; phage isolation; phage haracterization; bioinformatics; wound infec

P360-148: Isolation, characterization, and genome investigation of vB_SenS_TUMS_E4, a polyvalent bacteriophage against Salmonella enteritidis

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Background and Aim : Salmonellosis is a critical and common infectious malady between people and animals caused by Salmonella bacteria. With the advent of antibiotic resistance, it is essential for new methods to be replaced to prevent and treat infections. Bacteriophages are promising choices.

Methods : In this study, phage vB_SenS_TUMS_E4 against Salmonella enteritidis isolate has been separated from poultry wastewater. Determination of phage characteristics, including plaque formation, imaging with transmission electron microscopy, growth curve, structural proteins profile, host range, and pH and temperature parameters. Also, the Phage genome was extracted, sequenced, and annotated, and by utilizing Average Nucleotide Identity and phylogeny was compared with reference Salmonella phages.

Results : The burst size was large, nearly 287 plaque-forming units per cell (PFU/cell) and elevated stability to many temperatures and pH values. Phage vB_SenS_TUMS_E4 was effective on various clinical and environmental strains of Salmonella but did not affect bacteria of other genera. The morphological analysis indicated that phage vB_SenS_TUMS_E4 belongs to the Siphoviridae family. The genome of vB_SenS_TUMS_E4 is a linear dsDNA molecule of 43,018 bp with a G+C content of 49.7%. It includes 60 protein-coding genes, yet it contains no tRNA genes. Among the 60 detected putative protein-coding genes, just 43 gene products were contained in database searches. No genes associated with antibiotic resistance, virulence factor, and lysogenic were realized in the vB_SenS_TUMS_E4 genome.

Conclusion : The findings indicate that the high lytic potency vB_SenS_TUMS_E4 polyvalent phage is an antibacterial agent for controlling Salmonella in food production, prevention, and Salmonella treatment.

Keywords : Bacteriophages, Antibiotic resistance, Salmonella enteritidis, Siphoviridae, Antibacterial agents

P361-316: Isolation, Characterization and Genomic Analysis of vB_PaeS_TUMS_P81, A Lytic Bacteriophage against Pseudomonas aeruginosa

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Background and Aim : Pseudomonas aeruginosa is an opportunistic human pathogen that can lead to nosocomial infections which are in turn life-threatening. The increase in antibiotic resistance, at an alarming rate, has resulted in a pressing need for alternative therapeutic approaches such as phage therapy, which hold promise according to several studies. This study featured the isolation and characterization of vB_PaeS_TUMS_P81, a new lytic Pseudomonas phage.

Methods : Untreated municipal and hospital wastewater samples were collected and screened. The host range determination was performed against standard strains and clinical isolates. The morphological characterization of the phage was made by transmission electronic microscopy (TEM). Then, the phage genomic DNA was extracted, sequenced and and analysed.

Results : Morphologic, genomic and phylogenetic analysis indicated that P81 is a member of the genus Litunavirus, belonging to Schitoviridae family. The whole-genome sequencing indicated that it has a genome of 73,167 bp containing 93 predicted coding sequences and genes involved in virulence or lysogeny pathway was nowhere to be found in the genome.

Conclusion : The current study indicated that P81 is potentially safe when it comes to therapeutic applications and it lays the groundwork for further research on treatment of P. aeruginosa infections.

Keywords : Pseudomonas aeruginosa; Multi-drug resistance; Phage therapy; Genome sequencing

P362-402: ENZYBIOTICS ARE A GOOD ALTERNATIVE TO ANTIBIOTICS

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Background and Aim : Researchers have replaced traditional treatment approaches due to the spread of antibiotic resistance. Use of phages, or bacteria-contaminating particles, are antibacterial agents with a long-standing experience in some countries, currently employed to treat numerous infectious disorders.

Methods : The most recent information was gathered for this research using keywords, including enzybiotics, antibiotics, bacteriophages, phage therapy, biological treatment, bacterial infection, and microbial resistance. The data were collected from databases such as Irandoc, Scopus, PubMed, and Google Scholar for the studies during 2018 and 2022.

Results : Bacteriophages are viruses that can eradicate bacteria with little harm to the host cells. Therefore, They can be used either alone or in combination with antibiotics to treat bacterial infections. Phage lysosomal enzymes can break down bacterial cell walls, which can be used to decelerate the spread of infectious agents. In this regard, the term "biotic enzyme," which refers to a large family of enzymes that can inhibit the growth of germs and functions similarly to some antibiotics, was developed. Moreover, bacteriophage resistance is easy to cure condition compared to antibiotics. The adverse effects of this type of treatment are less severe than those of standard antibiotic therapy because the target cells (bacteria) and the invading agent (virus) have a very specific relationship to receptors that are not present in the host cells. The native flora, on the other hand, is scarcely impacted by this treatment. To effectively eliminate bacteria that create toxins, new viral strains are now being designed that kill bacteria rather than lyse them. Therefore, it is evident that enzybiotics are a viable choice for infection treatment.

Conclusion : The results of the studies show that enzybiotics are effective in the treatment of infection, and the use of phages as new drugs in limiting the growth of infectious bacteria is of high priority and importance and needs to be fully considered.

Keywords : Bacteriophage, Phage Therapy, Microbial Resistance, Antibiotic, Enzybiotics

P363-410: Isolation and Characterization of Lytic Bacteriophages of E. coli from Anzali Lagoon

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Background and Aim : Escherichia coli (E. coli) is a Gram-negative, facultative anaerobic Bacillus, whose pathogenic strains are responsible for some infections of the digestive, urinary, pulmonary, and neurotic systems. They are among the most common causes of septicemia in most hospitals. On the other hand, the rapid spread of antibiotic resistance to bacterial pathogens in the world has led to many research to discover new antimicrobial agents. The use of the antibacterial potential and specific function of bacteriophages is one of the most important ones. In this research, an attempt was made to extract and identify phage(s) from a source with high probability of containing this bacterium (Anzali lagoon) that have an effect on E. coli.

Methods : Several water samples were collected from different places of the lagoon. Each sample was passed through sterile filters of 0.22µm and 0.45µm after centrifugation. The presence of lytic phage (s) were investigated by plaque formation assay on double-layer Luria-Bertani (LB) agar medium containing bacteria E. coli. Then, serial dilutions were prepared from each of the more transparent and distinct plaques that indicated the possibility of the presence of at least one type of phage. For further purification, the steps of filtration and culture on double-layer agar and plaque formation were repeated until obtaining a specific plaque in relatively same shape and size. At the end, the representative samples were imaged by TEM electron microscope after negative staining on Grid-Formvar/Carbon Coated.

Results : 3 types of lytic phages which were effective on E. coli were identified in the images. They probably belong to the Myoviridae family based on the reference size and shape.

Conclusion : 3 types of isolated phages as specific antimicrobial agents of E. coli bacteria can be used individually or as cocktails.

Keywords : Lytic bacteriophages, E. coli, Phage therapy, Antibiotic resistance

P364-95: Effectiveness of inactivated COVID-19 vaccines among Stem Cell Transplant Recipient

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Background and Aim : Considering the dearth of research on the complications of Sinopharm coronavirus disease 2019 (COVID-19) vaccine in the immunocompromised individuals and the lack of available data on COVID-19 vaccination from Iran. This study aimed to investigate the complications and efficacy of Sinopharm COVID-19 vaccine in bone marrow transplant (BMT) recipients.

Methods : This was a retrospective cross-sectional study was conducted on 250 patients with BMT who were referred to Montaserieh Hospital, Mashhad, Iran. Among them 53 case who received at least two doses of Sinopharm COVID-19 vaccine from March to January 2021 were entered in this study. The data were extracted from a student dissertation (Code:4000370).

Results : Sinopharm vaccine side effects were reported only in 7.7% of the patients, and Shingles was the only serious side effect of the Sinopharm vaccine, which was observed only in one case.The results also revealed that Sinopharm COVID-19 vaccine side effects were not related to age or gender. Infection with Delta variant of COVID-19 was reported in 7.5% (n=4) and no mortality was reported among them. Vaccine failure was reported in 39.6% of the cases; however, no mortality was reported among patients infected with the Omicron variant of COVID-19.

Conclusion : In summary, it seems that Sinopharm COVID-19 vaccine adverse effects were not serious among stem cell transplant recipients. However, it may lead to some severe complications in the population. Vaccine failure against the Delta and Omicron variants of COVID-19 has been reported among more than one-third of BMT patients; however, no mortality was observed among BMT patients infected with the new variants of COVID-19.

Keywords : COVID-19, Side Effects, Transplant, Vaccination, Sinopharm, Stem Cell

P365-134: REVERSE TRANSCRIPTION LOOP- MEDIATED ISOTHERMAL AMPLIFICATION (RT-LAMP) FOR THE RAPID DIAGNOSIS OF CORONAVIRUS SARS- COV- 2

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Background and Aim : The novel coronavirus disease 2019 (COVID-19) has emerged, has rapidly extended globally within a short period. Has posed a global threat. Thus, evolve rapid and reliable diagnostic testing. is crucial to control the spread rate of the virus. Reverse transcription loop-mediated isothermal amplification (RT-LAMP) as one of these novel approaches to faster and cheaper testing. The LAMP technique is an alternative to the conventional quantitative RT-PCR methods that do not require expensive instruments and LAMP may achieve higher sensitivity on crude clinical samples than RT-PCR. Using saliva as testing specimen,. LAMP has taken an important place for the diagnosis of SARS-CoV-2.

Methods : : in this study, we aim to validate the clinical performance of the reverse transcription loop-mediated isothermal amplification (RT-LAMP) method for COVID-19 diagnosis, using RNA was extracted from 100 isolated of suspected patients with COVID-19 in selected hospitals in Tehran. and RT-PCR assay was performed. At the same time, the RT-LAMP was tested directly from nasopharyngeal and oropharyngeal. without RNA extraction from samples.

Results : : of 50 positive samples identified by RT-PCR, 45 positive samples nasopharyngeal and oropharyngeal swabs, was detected by Direct RT-LAMP assay. Compared with RT-PCR, overall sensitivity and specificity of RT-LAMP were (90 %) and (95 %) respectively.

Conclusion : RT-LAMP have high diagnostic sensitivity and specificity for field diagnosis of COVID-19.has few pipetting steps and requires minimal equipment. In addition, RT-LAMP can be used as a diagnostic method for COVID-19 as an alternative to RT-qPCR in the acute symptomatic phase of COVID-19. we also that RT-LAMP method paves a way for a large screening at public domain and hospitals.

Keywords : RT-LAMP , SARS-CoV-2 , RT-PCR

P366-141: Scorpion venom: dangerous or potency for COVID-19 treatment

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Background and Aim : Coronaviruses have caused two large-scale epidemics in the past two decades, SARS and Middle East respiratory syndrome (MERS). Later, a novel coronavirus SARS-CoV-2 (also known as COVID-19) is an ongoing global pandemic which caused the severe acute respiratory syndrome. To date, limited available antiviral vaccines and drugs against novel viruses likewise, the current SARS-CoV-2 draw attention to the importance of discovery and developing of new antiviral agents. In that case, venomous animals such as scorpions are considered promising sources for discovering new antiviral drugs.

Methods : This review summarises and classifies available literature about some important scorpion venom peptides with pharmaceutical activities. Several databases, including PubMed, Web of Science, Science Direct, Springer Link, Wiley Online Library, and Google Scholar databases were searched to find, collect and classify all relevant data published from January 2003 to June 2022.

Results : Despite scorpion's public health dangers worldwide, their venom is a valuable source of bioactive compounds and according to previous studies, scorpion peptides might have antimicrobial (AMPs), anti-cancerous, Bradykinin-Potentiating and Immunosuppressive activity potentials. AMPs isolated from scorpions also display a broad spectrum of antiviral activities. Some prospective scorpion antiviral peptides are included, Smp76, Hp1090, Hp1036, Hp1239, and Kn2-7. Recently, it is been reported that Mucroporin-M1 from the Lychas mucronatus venom can successfully inhibit measles, SARS-CoV and influenza H5N1 virus activities. It is been revealed that the interaction of the RBD domain of spike protein S1 domain SARS-CoV-2 with ACE2 receptor could be applied as a potential target for the development of anti-SARS-COV-2 drugs. Through virtual assessment, meucin-18 and its mutation A9T had effective interaction with the RBD domain of spike protein.

Conclusion : The potential in vitro and in vivo antiviral activity of scorpion venom in the treatment of the SARS-COV-2 virus should be further explored.

Keywords : Scorpion venom Peptides, SARS-COV-2, Antiviral peptides, Pharmacological properties.

P367-163: Development of a potent recombinant antibody against the SARS-CoV-2 by in-depth immunoinformatics study

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Background and Aim : As good candidates against the coronavirus infection, antibodies have been attracted high attentions. Accordingly, the current study was designed to harness the power of bioinformatics study for the development of a potent recombinant antibody against the SARS-CoV-2 spike's RBD.

Methods : The prediction of B-cell epitopes (BCEs) in the RBD was done based on the multi-method approaches. Following the primary screening of antibodies according to their binding to BCEs, the comprehensive screening was performed based on the various criteria. Thereafter, using this hierarchal approach, one antibody was selected. A serine-glycine linker was used to link the variable part of light and heavy chain. The construct was engineered by addition of pelB signal sequence to direct this single-chain fragment variable (scFv) antibody to the periplasmic space of E. coli.

Results : Among the various hit antibodies in our library, only one lead antibody met the various criteria and its good in silico reaction was confirmed with the verified/predicted BCEs. Moreover, the results did not show any interaction between paratope-mutable RBD residues.

Conclusion : As one of limited research in the field of immunoinformatics, the current study could be considered as a platform for design the neutralizing antibodies against the SARS-CoV-2 and other infectious agents, too.

Keywords : SARS-CoV-2; Bioinformatics; B-Cell epitope; recombinant scFv antibody; RBD; Virtual screening

P368-164: The successful expression of a potent recombinant scFv antibody against the SARS-CoV-2

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Background and Aim : There are many platforms for expression of recombinant proteins. Among this, Escherichia coli has been successfully used for production of recombinant proteins since 1980s, due to the ease of manipulation, low costs, the rapid growth, etc. In this regard and based on the importance of antibodies against the SARS-CoV-2, the main goal of the current study was study on the expression of a recombinant scFv against the SARS-CoV-2's RBD which recently designed based on the in-depth bioinformatics studies.

Methods : For study on the anti-RBD scFv expression, the expression of pET28a (+)-scFv vector was performed using E. coli BL21. The time-course studies of induction by 0.5mM and 1mM of IPTG was done and periplasmic proteins' extraction was performed. The results were analyzed using SDS-PAGE and recombinant protein expression was verified using western blotting (WB). The protein's purification and study on its efficiency is doing.

Results : Comparing the expression results in various times after induction showed the best induction results in presence of 1mM IPTG and the successful expression in all hours ranging from 2-24hrs after induction. The WB analysis showed the specific single-band of anti-RBD scFv (~30kDa) on the nitrocellulose membrane.

Conclusion : The production of high quality recombinant therapeutical proteins is essential for their usage for humankinds. In this study, we successfully produced a potent recombinant scFv by E. coli BL21 expression system in relatively high amounts and good stability.

Keywords : SARS-CoV-2; recombinant scFv antibody; RBD; Escherichia coli; Expression; Western blotting

P369-222: Molecular mechanisms of galidesivir as a potential antiviral treatment for COVID-19

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Background and Aim : COVID-19 causes respiratory severe problems that can lead to death. The International Committee on Taxonomy of Viruses named this virus as severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2). RdRp is a vital enzyme in the virus life cycle and is responsible for the synthesis of multiple copies of complementary RNA from the viral template RNA. Targeting this enzyme can stop the virus from multiplying and leads to virus death. Galidesivir is a nucleoside RdRp inhibitor drug developed for treating Ebola. It is a broad-spectrum antiviral drug that affects the coronaviruses family and other RNA viruses such as HCV, Ebola, and Yellow fever by preventing the growth of these viruses in cell culture.

Methods : The study purposed to evaluate the therapeutic effect of galidesivir in COVID-19 by reviewing the articles in PubMed, Scopus, Google Scholar, and Embase databases. The eligible articles regarding the effects of galidesivir on COVID-19 were selected. The articles were available online, in English, and without a publication date limitation.

Results : A molecular docking study showed the effect of galidesivir on inhibiting RdRp, by modeling, validating, and targeting with galidesivir and different anti-polymerase drugs currently available in the market approved for use against various RNA viruses. Galidesivir attached to the RdRp by four hydrophobic and six hydrophilic bonds with comparable binding energies to the main nucleotide ligands, which demonstrated that the drug could bind tightly to the catalytic center of SARS-CoV-2 RdRp. Another study showed that among 37 compounds that were considered as candidates for attaching to the virus, galidesivir interacts with more than two protein structures of SARS-CoV-2. These protein structures include SARS-CoV-2 main proteases with co-crystallized structures (PDB ID 5R7Y, 5R7Z, 5R80, 5R81, and 5R82).

Conclusion : As a result, we conclude that galidesivir can attach tightly to the catalytic center of RdRp and some other structural proteins of SARS-CoV-2 and inhibit the replication of the virus so it can be considered as a useful treatment for new coronavirus disease.

Keywords : Coronavirus, COVID-19, Galidesivir, RNA dependent RNA polymerase, SARS-CoV-2

P370-223: Novel immunological aspects of sirolimus as a new targeted therapy for COVID-19

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Background and Aim : COVID-19 involves a severe inflammatory response from neutrophils, lymphocytes, macrophages, and immune system inductors and also increases inflammatory cytokines, which are a cause of death in patients. Accordingly, mTOR plays a key role in the inherent immune system and increases inflammatory cytokines. Therefore, the inflammatory cytokine production through NF-κB activity and release of IL-10 by activated signal transducer and activator of transcription 3 (STAT3) in human monocytes is inhibited via mTOR inhibition. Sirolimus (Rapamycin) is a macrolide molecule produced by Streptomyces Hygoscopius, which weakens the immune system and paradoxically strengthens T cell activity during pathogen invasions. Sirolimus is also known to have antibiotic, antitumor, and antifungal effects.

Methods : A literature search was conducted using scientific databases such as Web of Science, Medline (PubMed), Scopus, Google Scholar, and Embase. The most relevant articles regarding the potential effects of sirolimus against COVID-19 were gathered.

Results : Another mechanism that places sirolimus as an ideal candidate for COVID-19 treatment is its inhibitory effect on the mTORC1 receptor. According to reports, viral protein expression and virion release have been effectively blocked by sirolimus which is an inhibitor of the mammalian target of rapamycin (mTOR). mTOR is a protected Serine/threonine-specific protein kinase that regulates cell growth and cell cycle progression through Phosphatidyl 3-kinase (PI3K) and kinase-B protein. Research on old-aged individuals also showed that the inhibition of mTOR via sirolimus enhanced the individuals' immune systems.

Conclusion : Since COVID-19 engages the human immune system and given the expressed mechanisms, sirolimus can be used as an effective drug in the COVID-19 treatment protocol. Currently, several clinical trials are in the process of evaluating the therapeutic effect of sirolimus in the treatment of COVID-19. However, large-scale clinical trials should confirm routine administration of sirolimus as a component of a standard treatment protocol for COVID-19.

Keywords : Coronavirus, COVID-19, SARS-CoV-2, Sirolimus, Rapamycin, mTOR

P371-229: Spore probiotic modulates lung inflammation triggered by the viral pathogen-associated molecular pattern poly (I:C) in BALB/c mice.

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Background and Aim : Several viral pathogens including SARS CoV 2 are associated with the lung inflammation. The severity of disease is associated with the production of a cytokine storm (CS) by the macrophages inside the host cell post-viral attack. Since the cytokine storm is the life-threatening through the elevated levels of circulating cytokines, factors targeting these pro-inflammatory proteins may be an ideal strategy for the management of various inflammatory disorders like coronavirus disease. In this study, the intranasal administration of spore probiotic was investigated to modulate the lung inflammatory response of Balb/c mice triggered by the viral pathogen-associated molecular pattern polyinosinic acid-polycytidylic acid (poly (I:C)).

Methods : Male BALB/c (approximately 20 g, 8–12 weeks old) were obtained from the Razi Institute (Mashhad, Iran) and housed in a conventional animal house with 12-hours dark/light cycles. Water and pelleted food were provided ad libitum. The animals were anesthetized by isoflurane inhalation and 20 µl of heat-inactivated spore probiotic cells (10^8 CFU/mL) were administered intranasally for 5 consecutive days. On days 5-7 mice received three doses of 20 µl poly (I:C) (1 mg/ml). Mice were euthanized on day 10 i.e. 24 h after the last intranasal treatment. Control animals received PBS instead of bacterial suspensions. Inflammatory modulatory activity of spore probiotic was determined based on bronchoalveolar tissue lavage (BALF) cytokines, lung histology, and the lung wet-to-dry (W/D) weight ratio.

Results : Pro-inflammatory cytokines including TNF-?, IL-1? and IL-6 were reduced 2.5, 1.8, and 14.5 folds while the anti-inflammatory cytokines i.e. TGF-? and IL-10 were increased 1.06 and 2.2 folds in the mice received spore probiotic, respectively. Compared with the control group (6.7?±?0.15), the wet/dry weight ratios of lung tissues in the probiotic group (5.75?±?0.12) were significantly decreased($p<0.05$).The effect of probiotic treatment on lung pathology was revealed that lung injury and the number of mononuclear cells were significantly reduced in animals treated with probiotic($p<0.05$).

Conclusion : Spore probiotics are probably promising agents to modulate life-threating inflammation associated with viral infections like SARS CoV 2.

Keywords : Probiotic,Inflammation,Lung,SARS-Cov2,Bacillus

P372-309: The effect of opium contained in the herbal medicine Alerguard (Stopcivir syrup) on reducing the respiratory symptoms of patients with COVID-19

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Background and Aim : The studies of researchers from the past have shown the positive effects of opium alkaloids, especially morphine, in the treatment of lung inflammation.Alerguard herbal medicine, which was designed and produced by prominent researchers of Mazandaran University of Medical Sciences and contains liquid extracts of Zataria multiflora, Boiss ،Alium Sativum ،Heracleum persicum ،Satureja hortensis ،Dianthus ، Foeniculum vulgare , and opium tincture (morphine), was attacked and unaccepted by the treatment staff, despite the 99% effectiveness in treatment, due to the rumor that addicts do not suffer from Corona)

Methods : The toxicology department of the reference laboratory for the detection of narcotics and psychotropic substances of the anti-narcotics police, as an authority to handle cases related to narcotics, measured the amount of morphine in this herbal medicine by entering this article.

Results : According to the toxicological studies and measurements, the amount of morphine in this drug is about 27 MME. which is according to the MME (morphine milligram equivalent) standard, and in the Iranian Pharmacopoeia is allowed between 40 and 50, in the treatment period of 3 to 5 days (depending on the severity disease).

Conclusion : This amount of narcotic in medicine is allowed, non-addictive and effective in reducing the inflammatory effects of corona disease.

Keywords : Stopcivir syrup,opium,morphine milligram equivalent,non-addictive

P373-348: Analysis of laboratory parameters used for diagnosis of COVID-19 in suspected patients in Iran

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Background and Aim : The recent outbreak of SARS-CoV-2 has spread all over the world. Evaluation of laboratory parameters in suspected patients is a vital issue for rapid and accurate diagnosis of COVID-19, which improves the survival of the patients.

Methods : This study was performed on 4987 participants suspected of SARS-CoV-2 referred to a medical diagnostic laboratory in Tehran, Iran, from March 2020 to September 2020. Real-time PCR was performed for the detection of the N and Orf1ab genes. Blood test evaluation was performed by examining white blood cell count (WBC), lymphocyte count (Lymph), C-reactive protein (CRP), and IgM and IgG antibodies. Data analysis was done using the receiver operating characteristic curve analysis method to evaluate the accuracy of the test.

Results : The RT-PCR was positive in 12.65% of cases. The CRP level and WBC count were significantly different between the positive and negative groups (P-value <0.001). The leukopenia was observed in 44% of infected patients in the group with cycle time (CT) 15-31. The accuracy of the CRP test was in the low range, whereas the accuracy of other laboratory serological parameters and antibody tests was poor (P-value <0.001).

Conclusion : According to obtained results, RT-PCR is the standard gold method for SARS-CoV-2 diagnosis. IgM-IgG antibodies levels and other clinical laboratory tests such as WBC, lymphocyte, and CRP can provide an overall picture of the patient's health status and prediction of the infection stage. No blood test by itself is reliable for determining the status of SARS-CoV-2.

Keywords : SARS-CoV-2, C-reactive protein, COVID-19, Leukopenia.

P374-407: Optical nanobiosensors used for HCoVs detection

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Background and Aim : The worldwide pandemic of coronavirus disease 2019 (COVID-19) has offered us with an extreme public health crisis. To fight the virus, and detect and slow down its spread, sensitive and cost-effective strategies have currently been developed. Although rRT-PCR-based techniques are presently common strategies for the detection of novel human coronaviruses (HCoVs), nanobiosensors as nanoanalytical tools have substantially contributed to this disease. This review examines the latest virus detection technology based on optical nanobiosensors.

Methods : The keywords of optical nanobiosensors in the detection of HCoVs, activity of optical nanobiosensors have been searched in PubMed and Google Scholar databases between 2020 and 2022.

Results : Optical nanobiosensors are photonic devices designed based on colorimetry, light scattering, fluorescence, etc. Optical biosensors measure modifications in the optical properties of the emitted light (i.e., absorption, polarization, intensity, wavelength, scattering, or refractive index) and might operate in a label-free configuration. (Do not need for fluorescent, colorimetric, enzymatic labels) Because they rely on tracking modifications on the surface of a biosensor chip, they may be adapted to any type of purpose. (e.g., detection of viruses, bacteria, nucleic acid sequences, or antibodies). Localized surface plasmon resonance (LSPR) biosensor systems consist of optical biosensors that are suitable for different classes of analytes. Molecular binding and refractive index alternate LSPR sensor systems show excessive sensitivity to local changes because of the enriched plasmonic field at the site of a nanostructure. Therefore, LSPR is an ideal candidate for label-free and real-time detection of micro and nanoscale analytes. For the detection of SARS-CoV-2, a Surface plasmon resonance (SPR) sensor coated with a peptide monolayer and functionalized with the nucleocapsid protein of SARS-CoV-2 was developed, which detects viral antibodies in human serum in the nanomolar range inside 15 minutes of sample contact.

Conclusion : Over the years, many investigations had been carried out to identify infections; that nanobiosensing systems have provided tremendous improvements in contamination detection in terms of selectivity, effectiveness, sensitivity, specificity and reaction time. This

review shows that viral respiratory infections may be rapidly detected using optical nanobiosensors activated with nanomaterials.

Keywords : COVID-19, SARS-CoV-2, Optical nanobiosensors, Surface plasmon resonance

P375-421: Evaluation of Association between TLR7 Single Nucleotide Polymorphism (rs179008 and rs179009) with Susceptibility to Acute SARS-CoV-2 Infection in confirmed patients in Tehran from April to May 2020

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Background and Aim : Following the COVID-19 pandemic, numerous studies to clarify the main reason for the discrepancy in susceptibility to COVID-19 among populations are undergoing. Host genetic changes like single nucleotide polymorphisms (SNP) is one of the main factors that influence the patients susceptibility to viral infectious diseases. This study aimed to investigate the association between host genetic polymorphisms of Toll-like receptor7 (TLR7) gene that Involved in the immune system and susceptibility to COVID-19 disease in a sample of the Iranian population.

Methods : This study is a retrospective case-control study which in 244 and 215 patients with COVID-19 disease (positive confirmed with molecular test) as case group and 156 and 122 suspected patients to COVID-19 disease (negative confirmed with molecular test) as control group were genotyped for TLR7 polymorphism TLR7: rs179008 A/T and rs179009 T/C respectively. Studied population selected from Ghods clinic affiliated to Tehran Medical Sciences, Islamic Azad University, Tehran. Genomic DNA was extracted from nasopharyngeal and oropharyngeal specimens and genotyping of gene polymorphisms were performed using Polymerase Chain Reaction Restriction Fragment Length Polymorphism (PCR-RFLP) method.

Results : In the male gender AA, AT and TT genotypes distribution in TLR7 rs179008 were 53.6%, 36.6% and 9.8% in case group and 76.3%, 15.8% and 7.9% in control group respectively and there was a significant association between TLR7 rs179008 SNP (P= 0.001, OR = 3.303, 95%CI: 1.580-6.906) and the susceptibility of COVID-19 disease. Also, in TLR7 rs179009 TT, TC and CC genotypes distribution were 45.1%, 41% and 13.9% in case group and 76.9%, 10.3% and 12.8% in control respectively and significant association between TLR7 rs179009 SNP (P< 0.0001, OR = 6.818, 95%CI: 3.107-14.961) and the susceptibility of COVID-19 disease was found between case and control groups.

Conclusion : Our results shows that single nucleotide polymorphisms in TLR7 (rs179009) For both females and males and TLR7 (rs179008) for male gender are considered as a host genetic factor that could be influenced individual susceptibility to COVID-19 disease.

Keywords : COVID-19, susceptibility, SNPs, TLR7

P376-426: Evaluation of the association between rs3775296 and rs3775291 single nucleotide polymorphisms of TLR3 gene with susceptibility to acute SARS-CoV-2 infection in confirmed patients in Tehran

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Background and Aim : The increasing prevalence of the COVID-19 disease has led scientists around the world to look for differences in susceptibility to COVID-19 in different populations. Research has shown that genetic differences in individuals are a factor influencing the functioning of the host immune system when dealing with various infectious agents, including viruses. Since the presence of SNPs in genes involved in innate human immune system is influential, we investigated the association between host genetic polymorphism in TLR3 gene and its association with COVID-19 disease in a sample of Iranians.

Methods : In this study, 235 and 218 patients with COVID-19 Which had a positive molecular test result considered as case group for genotyping TLR3 rs3775291 and TLR3 rs3775296 respectively. also 106 and 98 suspected patients to COVID-19 disease Which had a negative molecular test result considered as control group for genotyping TLR3 rs3775291 and TLR3 rs3775296 respectively.Studied population selected from Ghods clinic affiliated to Tehran Medical Sciences, Islamic Azad University, Tehran. Genomic DNA was extracted from nasopharyngeal and oropharyngeal specimens and genotyping of gene polymorphisms were performed using Polymerase Chain Reaction Restriction Fragment Length Polymorphism (PCR-RFLP) method.

Results : In TLR3 rs3775296, frequency of CC, CA and AA genotypes was 73.4%, 24.8% and 1.8% in patints group and 83.7%, 14.3% and 2% in controls group, respectively.In TLR3 rs3775291,frequency of CC, CT and TT genotypes was 55.4%, 37.4% and 7.2% in patints group, respectively. Also in controls group were 64.2%, 30.2% and 5.6%. The frequency distributions of CC, CT, TT TLR3 rs3775291 and AA, CC TLR3 rs3775296 genotypes were not significantly different between those with COVID-19 and suspected PCR-negative individuals. Only TLR3 rs3775296 CA genotype frequency (P = 0.021, OR = 2.703, 95% CI:

1.161-6.297), especially in males between case and control groups, had a significant relationship with susceptibility to COVID-19.

Conclusion : According to the results of this study, polymorphism in TLR 3 rs3775296 can be considered in males as one of the factors that increase the susceptibility to COVID-19 and may also affect the progression of the disease.

Keywords : COVID-19, susceptibility, SNPs, TLR3

P377-430: Assessment of Variations in RBD domain within spike protein of SARS-COV2 during different waves in South Khorasan, East of Iran

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Background and Aim : Genomic analysis of SARS-COV2 have shown a lot of variation in all around the viral genome. So, according to lack of these data from Iran as well as the region of study we aimed to investigate the polymorphic variation of S gene in COVID-19 samples of South Khorasan province.

Methods : The sampling was performed from January 2021 to March 2022. Cases with confirmed positive PCR result were selected based on severity and symptoms; next, divided to mild, moderated and sever groups. Demographic, clinical and virological examinations data were recorded. Nasopharyngeal samples were given and RNA extracted and forwarded for synthesis of cDNA. Using an in-house PCR assay Partial amplification of S gene was performed for sequencing of RBD region. The sequenced were analyzed in the biological software including Bioedit, Mega7, CLC and online tools such as NCBI and Nextclade databanks. Statistical analysis was performed in the SPSS version 22.

Results : In overall there were 272 RNA samples with a confirmed positive PCR test. The PCR product of 142 samples were sequenced to determine RBD region. Among which 71 samples (50%) were male, and the rest were female. The mean age of participants were 45.7 ± 20.9 years. Mutations were mostly accumulated in the RBD and especially RBM motif. The mean numbers of mutations per sample was 5.1 ± 3.4. Result of analysis in nextclade showed that 39.9% samples are belonged to the clade Rec, and then followed by clades alpha, 20A, 19A and omicron. 19A was distributed in all times and months. Clades delta, 20A and Rec were significantly associated with the ICU admission and death rate. Viral load was significantly lower in death group rather than comparison group. The well-known D614G mutation is now completely established among the current circulating variants.

Conclusion : The result of this study demonstrated a lot of mutations accumulated in the RBD region and RBM motif in the spike protein of SARS-COV2. So, these huge numbers of established variants require next studies for continuous sequencing and following of SARS-COV2 genome in specific S gene.

Keywords : corona virus, COVID, COVID-19, SARS-COV2, spike, mutation, genotype, variant, clade, South Khorasan, Birjand

P378-437: Investigating single nucleotide polymorphism (SNP) of different SARS-CoV-2 variants and evaluating their effects

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Background and Aim : Since the Covid-19 pandemic, the SARS-CoV-2 virus has been constantly deleting, replacing, and inserting in some parts of the genome in its host and has evolved into the strains that have been identified and reported so far. The omicron variant (BA.1) and other substrains such as BA.1.1, BA.2, BA.3, BA.4, and BA.5 have the highest number of changes among other SARS-CoV-2 variants and the reason for specific mutations that increase transmission, the severity of pathogenicity and escape from vaccines and treatment methods, have again caused concern at the global level.

Methods : Genome sequencing of different variants with the help of selection in laboratory conditions, investigation and analysis of spike libraries, yeast display, epidemiological and structural studies, especially for the spike region of newer cases, studying the pattern and type of mutations by examining the SNP related to structural and non-structural proteins common between viral samples helps to locate, identify the nature and diversity of the lineages currently circulating.

Results : S:H69-/V70- in omicron variants (except BA.2), alpha, beta, and other variants will cause S or SGTF gene target failure phenomenon and negative TaqPath PCR test results. Ba.2 test results will not be detectable, especially with delta variant in PCR. S:L452R and S:F486V mutations play a role in contagion and immune response evasion in BA.4 and BA.5, respectively. S:D614G is associated with viral loads in the upper respiratory tract and patients' age. S:K417N, S:E484K, and S:N501Y in the RBD region increase the binding affinity of spike protein to ACE2 receptor in humans. S:N679K, S:P681H, and S:H655Y near the furin cleavage site increase transmissibility by facilitating spike cleavage into S1 and S2 domains. S:K417N/T and S:E484A are associated with immune system evasion.

Conclusion : The pattern of mutation and its frequency varies in different hosts, countries, and times. Based on the analysis of the genomic sequences of different variants, there is a direct relationship between the mutations occurring in the viral genome and changes in pathogenicity. Also, important spike mutations that can escape from monoclonal antibodies and convalescent serums can play a role in the development and updating of epitopes in vaccine production.

Keywords : mutation, single nucleotide polymorphism (SNP), sequencing, spike protein

P379-459: Exopolysaccharide (Postbiotic) Therapy: Possible Treatment for Covid-19

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Background and Aim : Postbiotics are molecules of functional bioactive or metabolites secreted from live probiotics that are produced during the fermentation process of them. Therefore, postbiotics don't have probiotics adverse clinical effects. Extracellular polysaccharides (EPS) from lactic acid bacteria are an example of postbiotic compounds. Bacterial exopolysaccharides show significant antiviral activity by destroying viral particles, reducing virus titers, preventing the replication of viral DNA and the releasing of virus particles. The SARS-CoV-2 pandemic threatens global health and postbiotics can be potential promising strategy for this disease. The aim of this study was to review the available clinical evidence on the effects of exopolysaccharide from probiotic bacteria as a post-biotic in the treatment of covid-19.

Methods : Articles related to the subject were searched in PubMed and Sciencedirect databases and articles that evaluated the effects of postbiotics, especially exopolysaccharides, in the prevention and treatment of covid-19 disease were included in the study.

Results : According to the available evidence, biological polysaccharide with long molecular chain (EPS) can be a potential inhibitor of viral infection, especially in the systemic and respiratory system. In some studies have been investigated EPS effects of probiotic bacteria as an antiviral agent against some known viral diseases. Exopolysaccharides of Leuconostoc, Pediococcus and Streptococcus have shown a strong therapeutic effect against several types of viruses, including adenovirus type 5, rotavirus, gastroenteritis corona virus and influenza virus. However, the antiviral mechanism of EPS has not been sufficiently studied and requires further studies in this field.

Conclusion : According to postbiotics special characteristics (non-toxic, high stability, resistant to digestive system enzymes), postbiotics have different functional properties, including antimicrobial, antioxidant and immune system modulating properties. And they can be used in the form of different types of delivery systems (pharmaceutical, food) to achieve the goals of improving the health status of the host. However, there is limited evidence to recommend the use of postbiotics for treating and preventing SARS-CoV-2, but according to

researches related to antiviral impacts of postbiotics, they are suggested as candidates for prevention and treatment of SARS-COV-2.

Keywords : Postbiotic ،Exopolysaccharide ،Treatment ،Covid-19

P380-473: COVID-19 and parasitic diseases: A systematic review

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Background and Aim : Co-infection of COVID-19 with other diseases increases the challenges related to its treatment management. Despite other microbes, COVID-19 co-infection with parasites is rarely studied and most studies in this regard are case reports or case series. Here, we aimed to systematically review the cases of parasitic disease co-infection with COVID-19.

Methods : Using reputable databases, all relevant articles on COVID-19 co-infected with parasites (protozoa, helminths, and ectoparasites), were recovered and screened through defined inclusion/exclusion criteria.

Results : Of 1878 initial records, 24 studies remained for final data extraction. The majority of studies were about COVID-19 co-infected with malaria, followed by strongyloidiasis, amoebiasis, chagas, filariasis, giardiasis, myiasis, and other various parasitic diseases. The most co-infected cases were adult men who resident of or travel to parasite-endemic countries. No or low manifestation differences were reported between the co-infected cases and naïve COVID-19 or naïve parasitic disease.

Conclusion : There was a relatively low number of reports on parasitic diseases-COVID-19 co-infection, COVID-19 and some parasitic diseases have overlapping symptoms and also COVID-19 conditions and treatment regimens may cause some parasites re-emergence, relapse, or re-activation. Therefore, more attention should be paid to the true and on-time diagnosis of COVID-19 and the co-infected parasites.

Keywords : Co-infection, COVID-19, Parasitic disease, Systematic review

P381-489: COVID-19-associated fungal infections in Iran: a systematic review

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Background and Aim : Following the COVID-19 spread in Iran, cases of CAFIs have been reported from different parts of the country [14-16]. To date, there is no comprehensive study of fungal infections in patients with COVID-19 in Iran. In this systematic review, we aim to summarize the studies that have reported COVID-19-associated fungal infections (CAFIs) in Iran.

Methods : PubMed, Web of Science, Scopus, Cochrane Library, SID, Magiran, IranDoc, and Google Scholar were searched for Persian and English articles published from January 1, 2020, to November 5, 2021, using a systematic search strategy. Studies on Iranian patients suffering from CAFIs were included in the review.

Results : Twenty-two studies comprising 169 patients were retrieved. Reported CAFIs included candidiasis (85, 50.30%), mucormycosis (35, 20.71%), aspergillosis (29, 17.16%), fusariosis (6, 3.55%), three cases caused by rare pathogens (Rhodotorula mucilaginosa, Diaporthe foeniculina, and Sarocladium kiliense) and 11 (6.51%) uncharacterized mold infections. The most common underlying diseases were diabetes (67/168, 39.88%), cardiovascular diseases (55/168, 32.74%), and hypertension (43/168, 25.59%). The use of antibiotics (111/124, 89.52%), corticosteroids (93/132, 70.44%), and mechanical ventilation (66, 51.16%) were the most common predisposing factors. Totally, 72 (50.35%) of 143 patients with CAFIs died (data were not available for 26 patients).

Conclusion : Fungal infections are evident to be a complication of COVID-19 in Iran; thus, clinicians should consider them as a differential diagnosis, especially in patients with comorbidities and previous antibiotic or corticosteroid use.

Keywords : COVID-19, mycoses, candidiasis, mucormycosis, aspergillosis, fusariosis, Iran

P382-495: Evaluation of mortality risk factors in patients who died due to covid-19 at Boushehr shohadaye khalije fars Hospital, 2020-2021

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Background and Aim : we are examining the clinical and laboratory findings of people who died with Covid-19 in the shohadaye khalije fars Hospital to identify the risk factors associated with covid-19 death.

Methods : the files of patients with covid-19 who were admitted to the Hospital,were reviewed. For this purpose, All information related to the patient were extracted from the records and entered in the checklist. Patient information was divided into two groups of living patients and dead patients and compared with each other.Raw data were entered into SPSS software and statistically analyzed.

Results : The univariate study did not show a significant relationship between gender, nationality, marital status ,alcohol and cigarette addiction, gastrointestinal disease,chemotherapy,transplantation and mortality. The association of mortality with heart disease, hypertension, positive troponin, respiratory diseases (other than asthma) is significant.

Conclusion : this study has shown, underlying heart disease, underlying respiratory disease (excluding asthma), hypertension,positive troponin, underlying diseases (hypothyroidism and hypothyroidism, HLP, rheumatoid arthritis and mental disorders), longer hospital admission, ICU hospitalization, non-invasive respiration, and intubation increase mortality in patients with Covid-19.

Keywords : covid 19, mortality, pneumonia

P383-509: Pediatric Multisystem Inflammatory Syndrome Temporally associated with SARS-CoV-2 symptoms in Iran and literature review

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Background and Aim : In this case series, we report two cases of pediatric patients diagnosed and treated for Pediatric Multisystem Inflammatory Syndrome which is temporally associated with SARS-CoV-2 symptoms.

Methods : Patients & Methods: In the current study, two previously healthy 3 and 4-year-old boys were referred to hospital with 5 days of 39 0C fever, and the symptoms such as erythema multiform in the lower extremities, irritability, refusal to eat, restlessness, lymphadenopathy, conjunctivitis, and abnormal echocardiography. Their blood parameters, including CRP, ESR, D-Dimer were 2-3+, 65-115, and > 100000.0 ng/dl, respectively.

Results : Results: They were diagnosed to have Pediatric Multisystem Inflammatory Syndrome temporally associated with SARS-CoV-2 (PIMS-TS) symptoms and then, they were treated with Remdesivir, vitamin C, IVIG, Methylprednisolone, and Ceftriaxone. Patients After 8 days of hospitalization, were showed decreased of D-dimer and CRP level and improvement of rash and conjunctivitis and other normal vital signs, these issues led to their discharge from the hospital.

Conclusion : Conclusion: The present case series it raised several issues for physicians includes how to get SARS-CoV-2, its complications, diagnosis and treatment. Based on our results and literature, it's recommended that in the COVID-19 epidemic, pediatrics with PIMS-TS first screened for SARS-CoV-2, then treated with mixed of anti-viral, anti-inflammatory, antibiotics and IVIG. More study are needed to understanding the clinical features and outcomes of COVID-19 and their complication in children

Keywords : COVID-19, PIMS-TS, IVIG, SARS-CoV-2

P384-539: In silico study of natural chalcone derivatives against RNA dependent RNA polymerase (NSP12) of SARS-CoV-2 using molecular docking tools

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Background and Aim : COVID-19 is a disease caused by SARS-CoV2 as a novel coronavirus that has been causing a pandemic. Nsp12 protein, also known as RNA dependent RNA polymerase (RdRp), catalyzes the synthesis of viral RNA and hence plays an important role in the replication process of SARS-CoV-2 virus proliferation. The inhibitory effects of natural chalcone derivatives investigated against nsp12 of the SARS-CoV-2.

Methods : The molecular docking process was performed using AutoDock software to predict the mode of interaction between the best possible conformations of compounds in the active site of nsp12 enzyme. The 2D structures of chalcone derivatives including phloretin, phlioridzin and chalconaringenin were prepared by Chem Draw ultra 8.0 software and converted into 3D format by Hyper Chem7 using AM1 semiempirical method. The derivatives were docked into the active site of nsp12 (PDB ID: 6M71) by AutoDock software.

Results : The docking results showed a high potency of chalcone derivatives as nsp12 inhibitors with binding energies of -12.60 to -14.50 kcal/mol and chalcone derivatives bind strongly with some of the amino acid residues in the active site of nsp12 and these active derivatives could form hydrophobic interactions with Pro620 and Leu758 and hydrogen bonds with Asp623, Tyr619, Asp760, Asn691, Glu81 and Asp761.

Conclusion : These results showed that chalcone derivatives could be considered as promising compounds for the development of COVID-19 potential inhibitors after further studies.

Keywords : SARS-CoV-2, Molecular docking, Chalcone

P385-602: Systematic Reviews of Different Types of Drug Delivery in the Treatment and Prevention of Oral and Dental and Cardiorespiratory Diseases in Patients and Animals Involved in the Disease

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Background and Aim : This study has systematically investigated the types of drug delivery in the treatment and prevention of oral and dental and cardiorespiratory diseases in patients and animals involved in the disease. Early recognition of risk factors and primary prevention significantly reduces complications and mortality in chronic heart diseases. Lifestyle modification with diet, exercise and smoking cessation is very important to reduce cardiovascular risk factors.

Methods : In the first days of the disease, when the patient has mild symptoms and has not yet developed respiratory symptoms, you can start treatment with painkillers for headache, sore throat and body pain, along with taking antitussive medicine and vitamin D and C, although scientifically the effect of vitamin C It is not proven, but considering that we still do not have extensive studies on this disease, it seems that taking vitamins may help the patient. Sometimes, some patients themselves start treatment with azithromycin, while this antibiotic has an effect on antibacterial infections and has no effect on the disease of Covid-19.

Results : Favipiravir treatment should be started in high-risk outpatients with corona. Of course, along with treatment with favipiravir and similar antiviral effects, it can be effective in the treatment of corona. Famotidine and melatonin, which help improve sleep and are said to have antiviral effects. Of course, melatonin medicine should be taken at around 11 to 12 at night. Because it affects the sleep and wake cycle. Montelukast, along with fexofenadine, can have antiviral effects for covid-19 patients.

Conclusion : Since the beginning of the Corona pandemic, the world has emphasized on the monthly consumption of vitamin D, but if you do not have a monthly intake, use 1000 milligrams daily or up to 50 thousand units every week and after some time continue to

consume vitamin D on a monthly basis. It is also recommended to take vitamin C and magnesium, and it is better for patients to eat foods rich in protein, potassium, and dairy products.

Keywords : Drug Delivery, Oral and Dental Disease, Cardiorespiratory Disease, Vitamin, Corona

P386-609: Protection and Efficacy of the commonplace Vaccines against COVID-19

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Background and Aim : The global pandemic of coronavirus disease 2019 (COVID-19) has imposed a challenge On human health international, and vaccination represents a vital method to govern the pandemic.Up to now, more than one COVID-19 vaccines had been granted emergency use authorization, along with Inactivated vaccines, adenovirus-vectored vaccines, and nucleic acid vaccines. These vaccines have One-of-a-kind technical standards, if you want to necessarily cause variations in protection and efficacy. Consequently, we intention to put into effect a scientific evaluation through synthesizing medical experimental records blended With mass vaccination statistics and undertaking a synthesis to evaluate the protection and efficacy of COVID-19 Vaccines.

Methods : this study become accomplished utilising the keywords within the on-line databases, which includes Scopus, web of science, PubMed. We included each human and non-human studies because of the vaccine novelty, restricting our potential to encompass sufficient human studies.

Results : In comparison with different vaccines, detrimental reactions after vaccination with inactivated vaccines Are fantastically low. The efficacy of inactivated vaccines is about 60%, adenovirus-vectored Vaccines are 65%, and mRNA vaccines are ninety%, which might be continually green in opposition to asymptomatic Intense acute respiratory syndrome coronavirus 2 (SARS-CoV-2) contamination, symptomatic COVID-19, COVID-19 hospitalization, excessive or critical hospitalization, and dying.

Conclusion : RNA-based totally vaccines have some of blessings and are one of the maximum promising vaccines diagnosed thus far and are particularly critical throughout a virulent disease. However, further upgrades are required. In time, all of the antibody levels weaken regularly, so a booster dose is wanted to keep immunity. As compared with homologous high-increase immunization, heterologous top-boost immunization prompts extra sturdy humoral and mobile immune responses.

Keywords : COVID-19; SARS-CoV-2; safety; efficacy;COVID-19 vaccines; prime-boost strategies

P387-648: Stem cell therapy for COVID19: The impact of coronavirus infection on recipients of hematopoietic stem cell transplantation

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Background and Aim : coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus has become a global pandemic. COVID-19 can lead to a cytokine storm and patients usually have early respiratory signs and further secondary infections, which can be fatal. COVID-19 has entered an emergency phase, but there are still no specific effective drugs for this disease. In the past, many researchers have conducted various studies on the immunomodulatory properties of stem cells. This property of stem cells led them to modulate the immune system of autoimmune diseases like diabetes, multiple sclerosis, and Parkinson's. Because of their immunomodulatory properties, stem cell-based therapy employing mesenchymal or hematopoietic stem cells may be a viable alternative treatment option in some patients. By priming the immune system and providing cytokines, chemokines, and growth factors, stem cells can be employed to build a long-term regenerative and protective response. This review addresses the latest trends and rapid progress in stem cell treatment for Acute Respiratory Distress Syndrome (ARDS) following COVID-19.

Methods : A literature search was performed on PubMed, Medline, Google Scholar, Scopus and Clinical trials. for studies reporting the efficacy/effectiveness of stem cells in patients with COVID-19.

Results : Mesenchymal stem cells may help to restore the lung microenvironment, preserve alveolar epithelial cells, prevent lung fibrosis, and treat pulmonary dysfunction that is caused by COVID-19 associated pneumonia. Mesenchymal Mstem cells therapy may suppress aggressive inflammatory reactions and increase endogenous restoration by improving the pulmonary microenvironment. Furthermore, clinical evidence suggests that intravenous injection of mesenchymal stem cells may radically reduce lung tissue damage in COVID-19 patients. With the advancement of research involving mesenchymal stem cells for the treatment of COVID-19, mesenchymal stem cells therapy may be the main strategy for reducing the recent pandemic. The analysis showed that stem cell therapy could significantly reduce the mortality rate and morbidity in patients with COVID-19.

Conclusion : The present study suggests that stem cell therapy has a remarkable effect on reducing mortality and morbidity of patients with COVID-19. Further large-scale studies are needed to approve these results. Defining a protocol for stem cell therapy in patients with COVID-19 can lead to achieving the best clinical outcomes.

Keywords : COVID-19, Mesenchymal stem cells, Pandemic, Stem cell therapy

P388-660: Investigation of Anti-SARS-CoV-2 IgG and IgM Antibodies among the Shahid Hashminejad hospital staff with three different exposure levels with COVID- 19 patient, Mashhad

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Background and Aim : At present, PCR-based SARS-CoV-2 RNA detection from respiratory samples, as the gold standard, and serological antibody tests, as the supplemental methods, provide direct and indirect evidence of COVID-19 infection. The aim of study is to investigate the level of the serum level of COVID Ig M-Ig G in three different exposure levels: first groups (working in departments with direct contact with COVID- 19 patients) – second groups (emergency department with the possibility of unpredictable contact with COVID- 19 patients) third group (department Wards without contact with the patient) in educational and therapeutic center of Shahid Hashminejad Hospital. The relationship between disease symptoms and the serum level of covid antibodies was studied using SPSS software.

Methods : A total of 170 serum samples obtained from Shahid Hashminejad Hospital staff between march 2020and march 2021. Determination of the serum level of COVID antibodies (Ig M-Ig G) was done by ELISA method (Pashgaman kit). The direction of the interpretation of antibodies was that the serum level less than 0.9 was considered negative, the serum level 1.1-0.9 was considered suspicious and more than 1.1 was considered positive. And finally, the data was evaluated with SPSS26 software.

Results : Among the 170 investigated samples, 53 staff were in the predictable contact group, 51 staff were in the unpredictable contact group, and 66 staff were in the low risk group. 22 people had positive IgG, 13 people had IgG in the borderline range and 135 people had negative IgG. Also, 9 people had positive IgM, 1 people had borderline IgM and 160 people had negative IgM.

Conclusion : The results obtained from this study showed that activity in the wards related to covid-19 patients and direct contact with these patients has no significant relationship with the increase in IgG and IgM levels, but being in the wards with more contact with covid-19 patients causes more fever symptoms. Cough, sore throat, chills, shortness of breath, olfactory disorder and digestive symptoms occur in them.

Keywords : COVID-19, ELISA, Antibody,hospital staff

P389-677: A review of Nerium oleander effects as herbal therapy: a possible candidate in the treatment of COVID-19

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Background and Aim : Coronavirus disease (COVID-19) is an infectious disease, caused by the acute respiratory syndrome virus (SARS-COV-2), which occurred in late November 2019 in Wuhan, China, has become a major health crisis. Although there is no completely efficient antiviral drug with low toxicity and side effects against COVID-19, the use of medicinal herbs with less side effects can be of great help in the treatment of patients with COVID-19. Thus, the aim of this study is to review the therapeutic effects of Nerium oleander as a possible candidate in the treatment of patients with COVID-19.

Methods : The present study is a review study by searching in reliable scientific databases including Pubmed, Google Scholar and Scopus from 2000 to 2022, using the keywords SARS-COV-2, Covid19, Nerium oleander, Treatment, Anti-inflammatory, Antiviral, Antibacterial, Antifungal.

Results : In this study, 125 articles were reviewed. Therefore, with active and effective compounds such as Cardenolides, Glycosides, Triterpenoids and Oleandrin, the plant can have anti-viral, anti-inflammatory, anti-bacterial, anti-fungal and antioxidant activities and the results of in vitro and in vivo studies confirm the therapeutic effects of Nerium oleander as well.

Conclusion : Considering the pandemic nature of COVID-19, severe involvement of lung and other complications including secondary bacterial and fungal infections, shock, cytokine storm and pulmonary fibrosis, there is a need for effective drug on the aforementioned factors and according to the review study of Nerium oleander, due to its effects, a therapy can be evaluated as a drug candidate in the treatment of COVID-19 patients in a clinical trial.

Keywords : Nerium oleander, COVID-19, therapy, treatment.

P390-678: A review of the Anti-inflammatory effects of Artemisia spp as a possible candidate in the treatment of patients with COVID-19

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Background and Aim : Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spread worldwide rapidly. Due to the lack of suitable medicine for the treatment of COVID-19 disease, many studies have shown that plant extracts can have a wide range of biological effects like immunomodulatory properties. This study aimed to review the anti-inflammatory effects of Artemisia spp as a possible candidate in the therapy of patients with COVID-19.

Methods : The present study is a review study by searching reputable scientific databases such as Pubmed, Google scholar and Scopus from 2010 to 2022 using the keywords: SARS-CoV-2, COVID-19, Cytokine storm, Artemisia spp, Treatment, Anti-inflammatory.

Results : In this study, 45 articles were found and reviewed. Therefore, Artemisia spp is a collection of herbaceous and perennial plants with immunomodulatory and anti-inflammatory properties. Different extracts of this plant group suppress the induction of IL-1β, TNF-α and PGE2 cytokines. Lycorine, which is the active ingredient of this plant, inhibits pro-inflammatory mediators while increasing anti-inflammatory mediators. Extracts of this plant can significantly reduce the production of NO in isolated mouse peritoneal macrophages and reduce COX-2 and iNOS as well. Therefore, the mechanism of reducing inflammatory cytokines is by blocking the NF-κB signaling pathway and inhibiting the phosphorylation of IκB and p65, as well as inhibiting the nuclear translocation of NF-κB and P65. As a result, Lycorine reduces the induction of inflammatory cytokines and increases anti-inflammatory cytokines.

Conclusion : Due to cytokine-induced complications such as respiratory distress, shock, lung injury, mortality, and abundance of Lycorine and other biological compounds in the extract Artemisia spp, which modulates the immune system, this plant species is recommended for clinical trials in patients with Covid-19 and other viral diseases.

Keywords : COVID-19, SARS-CoV-2, Artemisia spp, Cytokine, Lycorine

P391-679: A review of the antifungal effects of Zataria multiflora as a possible candidate in the treatment of secondary fungal infections in patients with COVID-19

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Background and Aim : Secondary fungal infections are one of the most important causes of death in patients with COVID-19, and among these fungi, we can mention Candida, Aspergillus, and Mucorales strains, which respectively cause candidemia, pulmonary invasive Aspergillus, and mucormycosis in these patients. Therefore, increasing the acquired resistance of these fungi to antifungal compounds has made the use of alternative compounds necessary, especially medicinal plants. Thus, the aim of this study is to review the antifungal effects of Zataria Multiflora as a possible candidate in the treatment of secondary fungal infections in patients with COVID-19.

Methods : The present study is a review study by searching in reliable scientific databases including Pubmed, Google Scholar, Scopus and Web of Science from 2000 to 2022 using the keywords: SARS-CoV-2, COCID-19, Treatment, Zataria multiflora and Aspergillus spp, Mucormycosis , Antifungal, Candida spp. Latest information obtained.

Results : In this study, 80 articles were reviewed. The plant Zataria multiflora belongs to the genus Zataria and has effective antifungal compounds including thymol, carvacrol and parsimol. These compounds showed effective antifungal effects with high inhibitory effects and lethality against Candida albicans, Candida glabrata and Candida tropicalis, Aspergillus fumigatus, flavus, niger and mucoral strains, and the results of these studies confirmed the antifungal effects of this plant by in vivo, invitro and clinical trials plant.

Conclusion : Considering the prevalence of COVID-19 disease, one of the important complications of this disease is the secondary bacterial and fungal infections seen in ICU patients and immunosuppressive patients, which can cause biofilm, shock and sepsis, respiratory distress, eye, nose, and brain infections and high mortality in patients with COVID-19. Considering the effective antifungal substances of thymol, carvacrol in the mentioned plant, and the resistance of fungi to antifungal compounds, this plant can be used to be evaluated in COVID-19patients with secondary fungal infections with Candida, Aspergillus, and Mucorales. and other fungal infections.

Keywords : Zataria multiflora, Antifungal, COVID-19, Treatment

P392-682: bioinformatic analysis of Nucleocapsid (N) gene in human coronaviruses Comparing with other animal Coronaviruses

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Background and Aim : Due to the recent coronavirus epidemic and the widespread spread of COVID-19, the importance of studying coronaviruses, especially in the field of their molecular characteristics, became more clear Based on pervious archives, the first disease related to the coronavirus recorded so far was probably related to animals. However, the most evolutionary studies focused on S1 gene, Survey on other gens of coronaviruses such an N gene, that is important in immune responses against virus, could be very helpful.

Methods : Human, porcine, rodent, avian, bovine, feline, Canine, and bat coronavirus N genes were collected from the gene bank (NCBI database). After the alignment of N gene of all used coronavirus sequences, using Mega X software (version 11), the similarity rate between the N gene sequences of human and animal coronaviruses was determined. Then, phylogenetic tree was drawn based on N gene sequences.

Results : According to the results, the rate of nucleotide similarity was shown about 92-95%. The highest similarity was between SARS-CoV is WGS-36 and bat coronavirus BM48-31 and the lowest similarity was related to bat coronavirus BM48-31 and another used isolate SARS-Cov. Based on the evolutionary tree, human SARS coronaviruses grouped together with a bat coronaviruses and rodent coronavirus and also three bovine coronaviruses while some other bat coronaviruses were clustered in other group distinct from SARA-Cov.

Conclusion : Evolutionary studies of different genes of various coronaviruses specially which has notable role in immunity against the viruses could be significant to control the disease and design effective vaccines. Also, different similarity rates between SARS- Cov isolates and bat coronavirus BM48-31 could be explain the possibility of mutations in the N gene of coronaviruses.

Keywords : coronavirus, bioinformatics, N gene

P393-722: Covid- 19 patients neutrophil against Staphylococcus aureus and Pseudomonas aeruginosa

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Background and Aim : COVID-19 was first described in December 2019. It spreads through the respiratory tract with lymphopenia and cytokine storms and caused severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). It mainly happened in severe disease and showed the existence of immunological dysregulation in severe disease.Neutrophils have significant role in the host defence against micro-organisms and are the important effector cells to combat and killing of pathogens by oxidative burst andphagocytosis. The peripheral blood of COVID-19 patients have increased numbers of neutrophils which are important in controlling the bacterial infections observed in COVID-19. Since bacterial co-infection is observed in COVID-19 patients, we hypothesized that neutrophils from these patients may have functional defects with respect to bacterial killing of Staphylococcus aureus and Pseudomonas aeruginosa. Thus, we aimed to compare the ability of peripheral blood PMN obtained from healthy control subjects and COVID-19 patients to evoke bacterial killing ex vivo over time.

Methods : 34 COVID-19 patients and 9 healthy control subjects were enrolled at the Masih Daneshvari Hospital. PMN cells were isolated from whole blood. The Methicillin Resistance Staphylococcus Aureus (SA) and Pseudomonas Aeruginosa (PA) were used. Isolated PMN were co-cultured with PA and SA, The plate was placed in the FLUOstar and GFP fluorescence was measured and then stained with Annexin V-FITC and PI (Invitrogen™ 88-8005-72) (UK) based on the manufacturer's instructions. the result data were calculated based on FL1 and FL2 (FlowJo™ software).

Results : PMN from COVID-19 patients were significantly less efficient reducing the lag time of GFP-SA (22 ± 0.9 versus 9.2 ± 0.5 hours, $P < .01$ and GFP-PA (12.4 ± 0.6 versus 4.5 ± 0.22 hours, $P < .01$ than cells from healthy control subjects.

Conclusion : This pilot study demonstrated a decreased bacterial killing capacity of neutrophils isolated from the systemic circulation of COVID-19 patients in comparison with control healthy subjects against both Gram-positive and Gram-negative bacteria.

Keywords : COVID-19, Neutrophil, Staphylococcus aureus, Pseudomonas aeruginosa

P394-726: Evaluation of Bacterial Coinfection in COVID-19 Patients Referred to Educational hospitals of Isfahan

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Background and Aim : In people with viral respiratory infections, complications of bacterial infections are associated with poor clinical outcomes. The purpose of this study was to determine the Prevalence of bacterial infections and antibiotic resistance in patients Coronavirus disease (COVID-19).

Methods : In this cross-sectional study, reverse transcription real-time polymerase chain reaction was performed to detect COVID-19. sputum and tracheal aspirate samples were also collected and cultured on different media to support the growth of the bacteria. After incubation, formed colonies on the media were identified using Gram staining and other biochemical tests.

Results : Of these 150 patients with COVID-19, a total of 50 (30%) had secondary bacterial infections. The most common bacterial / fungal co-infections isolated by sputum and trachea included Klebsiella pneumoniae , Staphylococcus epidermidis, Acinetobacter baumannii, Pseudomonas aeruginosa and Candida spp.

Conclusion : Bacterial coinfection is relatively rare in hospitalized COVID-19 patients. Based on the results, one of the causes of death in these patients may be a secondary infection.

Keywords : COVID-19, SARS-CoV-2, Coinfections

P395-252: Meta-analysis of latent tuberculosis in healthcare workers in Iran: a retrospective review

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1. *andishesazan olom paye mazandaran*

Background and Aim : Here we review the status of latent tuberculosis (LTB) in Iranian healthcare workers (HCWs).Mycobacteria are microorganisms that cause various human diseases. These microorganisms are divided into two groups: tuberculosis (TB) and non-TB mycobacteria.1,2 One-third of the world's population is infected with Mycobacterium tuberculosis as a latent TB (LTB) infection. In approximately 10–15% of individuals with LTB, the infection may progress to active TB.3 Currently TB is an important global public health concern. In addition to the policies announced by the World Health Organization (WHO) to eradicate TB, it is also vital to develop highsensitivity diagnostic methods for both LTB and active TB.4,5

Methods : A literature search was conducted using keywords according to the Preferred Reporting Items for Systematic Review and Meta Analyses instructions. Cross-sectional studies published from 1 January 2000 through 1 January 2019 were retrieved. Meta-analysis was performed using Comprehensive Meta-Analysis software using the random effects model, Cochran's Q and I2 tests. Publication bias was estimated by funnel plot and Egger's linear regression test.

Results : Among 774 articles retrieved in the primary literature search, 21 studies met the eligibility criteria. No publication bias was observed among the included studies ($p=0.07$). The prevalence of LTB ranged from 7% to 63% in Iranian HCWs from different geographical areas. The overall combined prevalence of LTB among Iranian HCWs was 30.9% (95% confidence interval 24.2 to 38.5). Also, 52.4% of the included studies showed a significant correlation between occupation and LTB incidence ($p<0.05$).

Conclusion : The prevalence of LTB was high among Iranian HCWs. This requires developing comprehensive information databases and surveillance systems for detecting LTB among HCWs. It is also essential to periodically screen for LTB in HCWs to provide a timely diagnosis of the infection. It is recommended to perform a tuberculin skin test, a useful tool for screening and treatment of LTB, on an annual basis in HCWs.

Keywords : healthcare workers, latent tuberculosis, Mycobacterium tuberculosis

P396-254: A case report of feline tuberculosis: diagnosis and its dangers to humans

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Background and Aim : The possibility of feline tuberculosis is increasingly recognized as a zoonotic disease. The treatment is challenging, and the prognosis varies greatly from case to case. Tehran Oxygen Veterinary Hospital received a Cat with two years of age with symptoms of anorexia, weight loss, shortness of breath, and coughing. As a result of physical examination, the patient showed tachypnea (respiratory rate 40 bpm) and increased inspiratory and expiratory effort, as well as mild lymphadenomegaly of the mandible and harsh lung sounds. Eventually, the cat died from bloody diarrhea after two days.

Methods : To determine the cause of death, an autopsy was performed. For smear preparation, culture, and molecular testing, samples were taken from granulomatous lesions. A Ziehl-Neelsen staining was Conducted. In addition, Lowenstein-Jensen (LJ) Medium (contains sodium pyruvate) was used for culture. A 37°C incubator was used for 8 consecutive weeks of incubation. Based on standard protocols, a number of biochemical tests were performed, including catalase production, niacin production, and nitrate reduction. Van Soolingen method was used to extract DNA. PCR was performed using JB21-JB22 specific primers. As a positive control, a standard strain of Mycobacterium bovis (ATCC/19210) was used.

Results : Miliary tuberculosis was observed on autopsy, especially in the lungs. Multifocal granulomatous pneumonia were clear and palpable, the intestines were hyperemic, and the kidneys contained Multifocal granulomatous nephritis. In smear samples taken from tuberculosis, acid-fast tuberculosis bacilli were present. Biochemical tests confirmed M. bovis. based on culture results, tuberculosis was confirmed and the PCR test detected M. bovis species.

Conclusion : As a member of the Mycobacterium tuberculosis complex (MTBC), M. bovis causes tuberculosis in humans, cattle, deer, dogs, and cats. It affects a wide range of hosts and is one of the most important zoonotic hazards. In cats, it is usually caused by ingestion of infected meat, unpasteurized milk, wild rodents or contact with contaminated material. this report and the observation of this pathogen illustrate the critical role meat inspection plays in

ensuring food safety, and they raise the need for additional research into infection mechanisms and immune responses of cats to M. bovis.

Keywords : tuberculosis, Mycobacterium bovis, Autopsy, Case report, Miliary tuberculosis, Bacteriology

P397-293: A systematic review study on Role of long non-coding RNAs (lncRNAs) in tuberculosis

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Background and Aim : Mycobacterium tuberculosis is the bacterial agent that causes tuberculosis. In this bacterium long non-coding RNAs (lncRNA) can positively and negatively alter the expression of various genes through various mechanisms such as activating transcription factors or binding to DNA targets of the chromatin complex. The purpose of current study was a review of the lncRNAs in M.tuberculosis

Methods : We searched with the keywords lncRNAs, lncRNA, Long ncRNA, LincRNAs, Long ncRNA, Long noncoding RNA, Tuberclosis ,TB, Pulmonary Tuberculosis ،Pulmonary TB, Mycobacterium tuberculosis in PubMed, Web of Science Direct, Scopus, Scientific Information Databases, and Google scholar

Results : A total of 124 articles were found in Pub Med, Web of Science Direct, Scopus, Scientific Information Databases, and Google scholar, of which 20 articles were shared between the databases. In the revision of title and abstract, 84 articles were excluded from our study. Finally, 19 articles were included in our study, which included 4444 patients with tuberculosis. All studies were performed in China using the qRT-PCR method. We also studied the relationship between LNCRNAs in terms of biomarkers, therapeutic goals, drug side effects, and clinical features of tuberculosis.

Conclusion : The results of present study showed there is an acceptable association between lncRNA and SNP with tuberculosis and M.tuberculosis. Also, these regulatory factors play an important role as diagnostic biomarkers and the development of new therapies

Keywords : Mycobacterium tuberculosis; long non-coding RNAs (lncRNA); systematic review;biomarker ;TB

P398-310: Detection of resistance to rifampicin and isoniazid in Mycobacterium Tuberculosis isolates by High Resolution Melting (HRM) Real-Time PCR to set-up this method in Tuberculosis Reference Laboratory

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Background and Aim : Drug resistance to isoniazid (INH) and rifampin (RIF) as two main drugs of the first line of tuberculosis (TB) treatment in Mycobacterium tuberculosis (Mtb) isolates is increasing due to the excessive use of these drugs. Isoniazid resistance is mainly caused by mutations in the catalase-peroxidase (katG) gene and the mabA-inhA gene regulatory regions, and mutations in the rpoB gene are responsible for RIF resistance. Detection of Mtb drug-resistant isolates by conventional methods is time-consuming. Thus, developing rapid molecular techniques seems vital for detecting drug resistance and preventing the spread of drug-resistant bacteria. Therefore, this study was carried out to evaluate antibiotic susceptibility to RIF and INH in Mtb isolates using High-Resolution Melting Analysis (HRMA).

Methods : Twenty rifampin and isoniazid-resistant Mtb isolates were evaluated by standard proportional method from 431 tuberculosis patients who were referred to the Northeast Tuberculosis Reference Laboratory in Mashhad from 2016 to 2018. All drug-resistant Mtb clinical isolates were screened for genetic mutations in rpoB, katG, and promoter region of the inhA gene using PCR and real-time PCR amplification. Then, the presence of mutations in these genes was investigated by the HRMA method.

Results : Proportional resistance analysis showed that 11 out of the 20 studied isolates (2.55%) were resistant to both isoniazid and rifampin, 7 (1.62%) of which were only isoniazid-resistant and 2 (0.46%) were only rifampin resistant. HRMA assay identified katG gene mutations and the mabA-inhA promoter region in 15 of 18 isoniazid-resistant samples, and rpoB gene mutations were successfully evaluated in 11 out of 13 RIF-resistant samples. The sensitivity and specificity of the HRMA method were 83.3% and 91% for isoniazid and 84.6% and 85.1% for rifampin, respectively. In this study, 100% of rifampin-resistant samples had mutations in the rifampin resistance determining region (RRDR). Also, 88.8% of

isoniazid-resistant samples had mutations in the katG gene and the mabA-inhA promoter region.

Conclusion : The results of this study showed that HRM assay is a rapid, accurate, and cost-effective method possessing high sensitivity and specificity for determining antibiotic resistance among Mtb clinical isolates, screening of their associated mutations, and preventing the emergence of possible MDR strains.

Keywords : Mycobacterium tuberculosis, Drug resistance, HRMA, Isoniazid, Rifampin

P399-363: Detection of rifampicin resistance strains of Mycobacterium tuberculosis using multiplex allele-specific polymerase chain reaction (MAS-PCR) in Ardabil, Iran

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Background and Aim : Mycobacterium tuberculosis (MTB) is the main causative agent of a highly infectious disease called tuberculosis (TB). Currently, TB remains a major public health concern worldwide and is one of the most common life-threatening infections due to the high rates of multidrug-resistant tuberculosis (MDR-TB) and drug-resistant tuberculosis (DR-TB) cases in many parts of the world. Multidrug-resistant tuberculosis (MDR-TB) is defined as strains that are resistant to the first line of anti-tuberculosis agents, including Rifampin (RIF) and Isoniazid (INH), two most potent anti-TB drugs. Resistance to Rifampin alone is an identification marker of MDR strain. Therefore, this study was conducted to determine the rate of rifampicin-resistant M. tuberculosis (RR-MTB) among presumptive TB patients attending the Health Center, Ardabil, Iran.

Methods : This cross-sectional study was conducted in the Health Center of Ardabil province from 2016 to 2020. After checking the completeness of the necessary information on tuberculosis-presumptive cases, a lot of 111 sputum and bronchoalveolar lavage (BAL) samples were collected from Registration booklets of the health center of Ardabil province.

Results : Among 111 rifampicin-susceptible isolates, 36 (32.43%) rifampicin-resistance tuberculosis isolates were identified. The frequency of mutations was in codon 526 (26%), codon 516 (11.71%), and codon 531 (7.20%) in the rpoB gene, respectively. In our study, the most common mutation was reported in codon 526.

Conclusion : This study showed that in the samples isolated from Ardabil city, the high rate of mutation associated with rifampin-resistant tuberculosis strains was located in the rpoB526 gene. This result confirms that the screening of this gene region is suitable for determining resistance to rifampin in clinical samples of M. tuberculosis in Ardabil city. Molecular methods are appropriate and rapid to identify the MDR strain M. tuberculosis.

Keywords : Mycobacterium tuberculosis, Drug resistance, rpoB gene, tuberculosis (TB), rifampicin (RMP), multidrug drug-resistant tuberculosis (MDR).

P400-454: Isolation and identification of Mycobacterium from poultry and personnel of Bird's Garden of Alborz province

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Background and Aim : Mycobacterium genus causes many important diseases in humans, livestock and poultry. Non tuberculosis mycobacteria (NTM) are considered as atypical mycobacteria, some of which cause important diseases. Mycobacterium avium complex (MAC) a kind of NTM, causing casualties in immunosuppressed patients with Acquired immunodeficiency syndrome (AIDS). According to the report of the World Health Organization, the second infectious cause of death after Covid-19 virus disease is tuberculosis, and the second cause of death in AIDS patients is mycobacteria, especially the Mycobacterium avium complex (MAC) group. Therefore, investigating the presence of these mycobacteria in the population of birds and personnel and determining their exact identity helps public health, especially in AIDS patients.

Methods : Near 100 samples from personnel's sputum and poultry feces of Alborz bird's garden were collected, decontaminated by HPC and NaOH method, then cultured on mycobacterial medium like Lowenstein-Jensen. The Mycobacterial genomic DNA was extracted by Phenol-Chloroform extraction method. By using 16srRNA PCR method, Mycobacterium genius detected and three kinds of its species identified by their specific primers like IS900-901,IS6110 and IS90-91.

Results : In 45 bird's samples, 15 samples were detected as Mycobacteria. Among those 15 samples, TB complex and NTMs such as Mycobacterium avium complex were identified.

Conclusion : The result in this study indicated that different kinds of important mycobacteria were isolated from specimens. Hygiene measurements should be taken to prevent these bacterial transmission to people, especially people with immune deficiencies.

Keywords : Bird's garden, Non tuberculosis Mycobacteria, Mycobacterium avium complex.

P401-458: Molecular identification of Mycobacteria isolated from Alborz zoos

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Background and Aim : background and aims: Due to the importance of tuberculosis in human societies and its role in transmission to humans and the lack of examination of the presence of mycobacterial contamination in the wildlife of Alborz province, the aim of this pioneering research is to isolate and determine the molecular identity of mycobacterium from zoos in Alborz province.

Methods : Materials and methods: This study was carried out on animal feces samples from zoos in Alborz province, and they were separated by NAOH and HPLC methods. The research and analysis was carried out using culture and preparation of Nelson staining slides, PCR and PCR-RFLP.

Results : Findings: In this study, pcr16srRNA was extracted from DNA samples to confirm the genus of Mycobacterium and Multiple rounds of 6110 PCR PCR IS900 and PCR IS901 tests showed paratuberculosis and other non-tuberculosis species.

Conclusion : Conclusion: Considering the importance of increasing diseases caused by non-tuberculous mycobacteria all over the world, a study was conducted to evaluate the frequency of these diseases in Iran in order to identify and investigate the prevalence of non-tuberculous mycobacteria in Iran from different clinical samples, during a An 8-year period was conducted in Masih Daneshvari Hospital. In this descriptive study, patients with pulmonary tuberculosis symptoms were conducted during 1983-2019 and are isolated from environmental samples, considering the role of some mycobacterial species as a reservoir and their role in transmission to humans and the lack of examination of the existence of mycobacterial contamination in the wildlife of Alborz province, the necessity of investigation in this field seems necessary. Although many researches have been done on wildlife animals in the world, but not many studies have been done in Iran

Keywords : Mycobacterium,pcr RFLP,Molecular identification,isolated

P402-485: Development of drug resistant mycobacterium tuberculosis strains

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Background and Aim : It is estimated that 75 million people will die from drug-resistant tuberculosis in the next 35 years. Resistance to drugs used in the treatment of tuberculosis is a danger to the strategies that are deployed to control and eliminate multidrug-resistant tuberculosis (MDR-TB) and extensively drug-resistant tuberculosis(XDR-TB). Drug-resistant Mycobacterium tuberculosis strains have emerged as a threat to public health, highlighting the need to develop new tuberculosis prevention and treatment strategies. There is a critical need to understand the mechanisms of resistance development and access to the genetic diversity of Drug-resistant Mycobacterium tuberculosis.

Methods : An organized review was completed on original research extracted from PubMed, Elsevier, and Google scholar. The search term "Tuberculosis AND drug resistance AND infectiousness AND reproductive fitness" were used to identify relevant articles reporting the evolution of drug-resistant tuberculosis.

Results : Drug-resistant strains often suffer an initial reduction in fitness, they continue to grow by acquiring one or more secondary-site mutations that can improve or even restore the f fitness of these strains over time; this process is known as compensatory evolution. Importantly, this process happens even in the absence of drug pressure. Strain diversity can influence the outcome of infection and disease in humans. Extensively drug-resistant tuberculosis has the lowest treatment success rate among other forms of tuberculosis.

Conclusion : The evolution of drug-resistant Mycobacterium tuberculosis depends on factors, such as bacterial fitness, the strain’s genetic background, and its capacity to adapt to the surrounding environment, and host-specific and environmental factors.

Keywords : Extensively Drug-Resistant Tuberculosis- Biological Evolution- Genetic Variation

P403-490: Bio-incidence of Mycobacterium avium subspecies paratuberculosis infection in goat milk samples using IS900-PCR

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Background and Aim : John's disease (JD) is a chronic granulomatous enteric disease of domestic live stocks caused by Mycobacterium avium subspecies paratuberculosis (MAP). It has the potential to be a great pathogen. JD has a global distribution and causes severe economic losses to the meat, wool, and milk industry. Better diagnostic tests would be needed in these programs. IS900 PCR has shown high sensitivity and has been frequently used as a detection test. The present study aimed to estimate the bio-incidence of MAP in the raw goat milk samples using IS900-PCR.

Methods : A total of 42 raw milk samples were collected from individual goats from farmers' herds in different parts of northern India. Raw milk samples were screened to estimate the bio-incidence of MAP using whole milk as a test sample by IS900 PCR. Whole milk DNA was isolated using the phenol-chloroform extraction method.

Results : Of the 42 raw milk samples collected from individual animals, 9 (21.4%) were positive for the presence of MAP using IS900 PCR.

Conclusion : Consumption of raw milk continues to be considered one of the main potential routes of human exposure to MAP and a high biological charge of MAP in raw milk could lead to contaminated dairy products. Consequently, the use of multiple diagnostic tests was recommended to estimate the prevalence of MAP in animals for JD control programs.

Keywords : John's disease, Mycobacterium avium subspecies paratuberculosis, IS900 PCR, Raw Milk.

P404-551: A Novel Mutation in the Efflux Pump Rv1258c (Tap) Gene in Mycobacterium tuberculosis Clinical Isolates Resistant to First-Line Drugs in Iran

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Background and Aim : Tuberculosis (TB) remains a serious health problem worldwide, causing millions of deaths annually. It is estimated that one-third of the world population is infected with latent TB. Drug-resistant TB is considered a major and growing global threat. Despite the great variety of mutations in the resistance genes of Mycobacterium (M.) tuberculosis, the drug resistance mechanisms are still controversial. Recently, the presence of efflux pump genes in drug resistance was reported, adding to this complexity. Also, the increased expression of some efflux pump genes, such as Rv1258c, has been observed in the presence of antibiotics.

Methods : We performed a molecular analysis Rv1258c gene in drug-resistant and sensitive (n = 53) clinical isolates by Polymerase chain reaction (PCR)-sequencing. All custom DNA amplicons were sequenced, using both forward and reverse primers.

Results : A novel Rv1258 gene mutation was found at Ala148Thr in rifampicin monoresistant isolate 1/33 (3%), as compared to the H37Rv reference strain. Also, a cytosine nucleotide insertion was found between positions 580 and 581 in 2/20 (10%) drug-sensitive strains at identical gene positions.

Conclusion : These results indicated the possibility of mutation in the efflux pump genes and suggested the important role of Tap efflux pump genes in drug-resistant M. tuberculosis isolates. However, further research is required to determine the direct association of these mutations with resistant M. tuberculosis.

Keywords : Mycobacterium tuberculosis, Molecular analysis, Drug resistance, efflux pump, Rv1258c (Tap) gene

P405-568: Liposomal delivery system/adjuvant for subunit vaccine against tuberculosis

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Background and Aim : As reported by the World Health Organization, in 2020, about 10 million individuals were infected with tuberculosis (TB) worldwide. Moreover, approximately 1.5 million people died of TB, of which 214,000 were infected with HIV simultaneously. Due to the high rate of infection, the need for effective TB vaccination is highly felt. Until now, various methodologies have been proposed for the development of a protein subunit vaccine for TB. These vaccines have shown higher protection than others, particularly the Bacillus culture vaccine. The delivery system and safety regulator are common characteristics of effective adjuvants in TB vaccines and the clinical trial stage. The present study investigates the current state of TB adjuvant research focusing on the liposomal adjuvant system. Based on our findings, the liposomal system is an excellent adjuvant for vaccinations against TB, other intracellular infections, and malignancies. Clinical studies can provide valuable feedback for developing novel TB adjuvants, which ultimately enhance the impact of adjuvants on next-generation TB vaccines.

Methods : -

Results : -

Conclusion : Currently, TB vaccines are being tested with four adjuvants. While our knowledge about the mechanisms of action of these adjuvants is improving, they were established during a time when IFN- was the dominant screening method. New technical progress in vaccine research, e.g., single B/T cell whole transcriptome analysis and systems immunology, results in significant discoveries. Therefore, it is essential to examine the intersections between innate and adaptive immunity (21). One of the variables that will be critical in the development of an effective vaccine is the participation of B-cells and antibodies (97). The discovery of downregulated invariant natural killer T cells in the blood of TB patients exhibits that antibodies could be employed to target latent infection. Moreover, the activation of these cells through galactosylceramide could destroy latently infected cells. In some species, vaccination with liposomal vaccines may provide prolonged protection against M. TB infection. Considering these data, it appears that a liposomal adjuvant system is excellent for vaccination against TB and other intracellular diseases, as well as tumors. Systematic analyses of clinical trials can contribute to achieving important

information on developing new TB adjuvants and enhancing adjuvants' effect in next-generation TB vaccines.

Keywords : Liposomal adjuvant- vaccine- tuberculosis

P406-580: Linezolid resistance among multidrug-resistant Mycobacterium tuberculosis clinical isolates in Iran

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Background and Aim : The management of multidrug-resistant (MDR) and extensively drug-resistant tuberculosis (XDR-TB) presents a main challenge and the drug options for treating these infections are very limited. Linezolid (LNZ) has recently been approved for the treatment of MDR and XDR-TB. But, there are narrow data on genotypic and phenotypic LNZ resistance in clinical isolates. So, we aimed to determine the prevalence of LNZ resistance and to identify the mutations associated with LNZ resistance among clinical MDR-TB isolates.

Methods : Twenty-two MDR-TB clinical isolates were collected from Ahvaz Regional TB Laboratory, Southwest of Iran in 2020. The minimum inhibitory concentration (MIC) values of LNZ against MDR-TB isolates in a range of concentrations, from 0.125 to 16 mg/L were determined by the broth microdilution method. All MDR-TB isolates were sequenced in the rrl and rplC genes conferring LNZ resistance. Obtained sequences were aligned together using ClustalW (https://www. genome.jp/tools-bin/clustalw) software to determine the consensus sequences. Consensus sequences were subjected to nBLAST analysis (http://blast.ncbi.nlm.nih.gov) and compared with Mycobacterium tuberculosis strain H37Rv.

Results : Based on the critical concentration (>0.5 mg/L) used for LNZ 3 isolates (13.6%) of the tested isolates were resistant that MIC concentrations were 8 mg/L and >16 mg/L for two and one isolates, respectively. Eighteen isolates (87.4%) had MICs ranging from 0.125 to 0.5 mg/L and were susceptible to LNZ. The MIC for the H37Rv strain was 0.25 mg/L. The genetic analysis illustrated just 1 of the 3 LNZ resistant MDR-isolates sequenced carried substitution mutations at nucleotide 421 (A/G) and 449 (T/A) compared to the reference strain and susceptible isolates, resulting in amino acid exchange from valine to isoleucine at codon 141 and isoleucine to asparagine at codon 150, respectively. However, no resistance-related mutations were indicated in isolates with MICs below or at the critical concentration. None of the isolates harbored mutation in rrl gene. Furthermore, there was no mutation in rplC and rrl genes among LNZ susceptible isolates. The obtained nucleotide sequences have been deposited in the GeneBank database under the MT429771, MT429770, MT429772 (rplC), MT431515, MT431516, and MT431517 (rrl) accession numbers.

Conclusion : The results reveal that the prevalence of LNZ-resistant isolates is 13.6% among MDR-TB isolates and drug susceptibility testing (DST) against LNZ is useful in the management of complicated and drug-resistant cases. However, further studies could identify other possible genetic mechanisms of resistance in TB.

Keywords : Mycobacterium tuberculosis, multidrug-resistance, linezolid, mutation, minimum inhibitory concentration

P407-9: Isolation and Identification of grapevine endophytic bacteria in west Azerbaijan province

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Background and Aim : Grapevine is one of the most important agricultural products in Iran. West Azerbaijan province is considered as one of the biggest production centers of grape in Iran, due to its suitable climatic conditions. The aim of this study was to identify grape endophytic bacteria in West Azarbaijan.

Methods : In this study, 67 endophytic bacteria were isolated from the stems and roots of grapevines. Then, biochemical properties such as hypersensitive reaction, fluorescent and potato soft rot test and the ability to produce proteases, amylase and gelatinase enzymes were tested. Eleven bacterial isolates were selected for molecular identification and it was found that the Bacillus and Pseudomonas are the most abundant genera.Also, the antifungal effect of endophytic bacteria on three fungal species: Chaetomium globosum, Cytospora chrysosperma and Fusarium sp. was done by dual culture method.

Results : According our knowledge, three species of Stenotrophomonas sp., Bosea lathyri and Frigoribacterium faeni are reported for the first time in Iran as grapevine endophytic bacteria. Three isolates of GI6 (Priestia sp.), GI43 (Pseudomonas kilonensis) and GI45 (Bacillus sp.) showed the most growth inhibitory properties against fungi.

Conclusion : Due to the importance of endophytic bacteria, their isolation and identification from different parts of the country seems necessary, as the result, these bacteria can be used in biological control of plant diseases and can be replaced by chemical control.

Keywords : Endophyte, bacteria, grape, biochemical properties, antifungal effect, biological control

P408-12: Exploitation of two selected immunogenic proteins, BauA and OmpA, for protection against Acinetobacter baumannii infection

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Background and Aim : Acinetobacter baumannii is a hospital opportunistic pathogen, a gram-negative and non-flagellated bacillus, which is considered a common nosocomial infection with high mortality mostly causes sepsis and meningitis. And infection of the urinary tract. Reproduction and persistence of A. baumannii in eukaryotes based on iron uptake functions including siderophore biosynthesis. Iron transfer into the cytosol is mediated by specific membrane receptors that detect iron-siderophore complexes. The expression of this Acinetobactin-mediated iron uptake system is critical for the intracellular growth of A. baumannii. OmpA is the most abundant membrane protein gram-negative bacteria and is also the major protein of bacterial pathogenesis. The production of new monoclonal antibodies against outer membrane protein A (OmpA) could be considered a potential tool to improve the treatment of A. baumannii infections. A. baumannii is usually resistant to beta-lactams, aminoglycosides, rifampin, and fluoroquinolones. This bacterium has led to the use of new therapies such as vaccines. No vaccine is known for this bacterium, but it is still worth considering. In this study, we used two separately selected and recombinant proteins, OmpA and BauA, as vaccine candidates to evaluate immunogenicity against A. baumannii in a mouse model.

Methods : Based on a pre-designed primer from Shahed University Bank, BauA and OmpA gene fragments were extracted from the bacterial genome PCR and the clones simulated in pet28 were expressed in Escherichia coli BL21(DE3). The product was analyzed by the SDS-PAGE method and purified by the Ni_NTA affinity chromatography method. These proteins were injected into BALB/c mice separately and in combination. The titer of IgG-specific antibody produced against each group was determined after the experiment using the indirect ELISA method. Bacterial proteins were then identified by IgG immunoblotting.

Results : OmpA and BauA were already reported to raise antibodies against these proteins. The same results were obtained. The combination of the two antigens led to significant protection against A. baumannii in comparison to the single antigens.

Conclusion : Administration of the combined antigens triggers better protection than single antigens.

Keywords : Acinetobacter baumannii, Antigen, Antibody, Vaccine, OmpA, BauA.

P409-19: Designing shRNA Targeting West Nile virus NS3 Gene as a Potential Gene Therapy Tool Using Computational Pattern

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1. *shekofe rezaei*

Background and Aim : Introduction: West Nile virus (WNV) infection is a mosquito-borne zoonosis. The disease affects countries in southern, eastern and western Europe. The virus is transmitted among birds via the bite of infected mosquitoes and incidentally humans and other mammals may become infected. About 80% of WNV infections in humans are asymptomatic. West Nile fever (WNF) is the most common clinical presentation. The elderly and immunocompromised persons are at higher risk of developing West Nile neuroinvasive disease (WNND). No specific prophylaxis or treatment exists against the disease in humans. The NS3 protein has vital roles in the cleavage of polyprotein and viral pathogenesis.

Methods : Material and Methods: ShRNA sequences were designed against NS3 gene of WN using the www.invivogen.com/sirna-wizard website and the most effective molecules were selected using background information. For this purpose, standard search method selected and siRNA motifs with the desired size and thermodynamic properties were designed. Then, in order to design hairpin, the proposed vector and loop sequences (TCAAGAG) submitted, so the most effective shRNAs with desired restriction enzyme sites were designed.

Results : Results: Two potentially effective shRNA molecules were designed. Their sequences and start target positions included WNV shRNA1:GAAATGAGATCGTTGATGTCATCAAGAGTGACATCAACGATCTCATTTC and WNV shRNA2: GCAGCCAGAGGATACATAGCATCAAGAGTGCTATGTATCCTCTGGCTGC with respectively start positions of 60 and 185 of WNV NS3 gene.

Conclusion : Conclusion: The results showed that there are potentially effective shRNA molecules against WNV NS3 gene that can suppress its translation and can be considered as approach against the disease in humans and animals.

Keywords : shRNA, WN, NS3, gene therapy.

P410-20: In silico Design of shRNAs against Crimean-Congo hemorrhagic fever virus RdRPs gene

Shekofe Rezaei[1] *, azam mokhtari[1] , azam mokhtari[1]

1. *shekofe rezaei*

Background and Aim : troduction: Crimean-Congo haemorrhagic fever (CCHF) is a widespread disease caused by a tickborne virus (Nairovirus) of the Bunyaviridae family. The CCHF virus causes severe viral haemorrhagic fever outbreaks, with a case fatality rate of 10–40%. Scince the RdRPs protein has a key role in the viral reolication, we selected it as a target of RNAi.

Methods : Material and Methods: ShRNA sequences were designed against RdRps gene of CCHFV using the www.invivogen.com/sirna-wizard website and the most effective molecules were selected using background information. For this purpose, standard search method selected and siRNA motifs with the desired size and thermodynamic properties were designed. Then, in order to design hairpin, the proposed vector and loop sequences (TCAAGAG) submitted, so the most effective shRNAs with desired restriction enzyme sites were designed.

Results : Results: Three potentially effective shRNA molecules were designed. Their sequences and start target positions included CCHFV shRNA1:GAAGCAAGGTCGTTTATGAGATCAAGAGTCTCATAAACGACCTTGCTTC , CCHFV shRNA2: GATGGTAAAGCTAGTAGGTGATCAAGAGTCACCTACTAGCTTTACCAC and CCHFV shRNA3: GAGACAGGCATGGCAATACTACATCAAGAGTGTAGTATTGCCATGCCTGTCTC with respectively start positions of 60 and 185 of CCHFV RdRPs gene gene.

Conclusion : Conclusion: The results showed that there are potentially effective shRNA molecules against CCHFV RdRPs gene that can suppress its translation and can be considered as an antiviral approach based on RNAi.

Keywords : shRNA, CCHFV, RdRPs, gene therapy.

P411-21: Lentiviral gene vector transformation in Escherichia coli derived DH5α, JM109 and Stbl4 cells

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Background and Aim : Bacterial cell transformation is essential for gene cloning. Although plasmid gene transfer recombinant lentivectors are highly effective, they do not transform readily in most cells. E coli derived Stbl2 and Stbl3 strains maintain structure of lentiviral plasmid pRRL.SIN.cPPT.PGK/Oligo2-IRES-DsRedWPRE and boost colony growth. However, Stbl4 appears to be even more efficient to justify further study. We thus investigated plasmid transformation in DH5α, JM109 and Stbl4 cells derived from Escherichia coli.

Methods : Transformation efficiency was calculated based on the method of Tu et al. (14). by the following two equations: Number of transformed colonies (cfu) = number of bacterial colonies × dilution index× volume of transformed mixture ÷ volume taken to the plate. Transforming efficiency = number of transformed colonies ÷ plasmid concentration in micrograms.

Results : After electrophoresis of recombinant plasmids in different dilutions, plasmid concentration was determined and concentration was adjusted to 1000 ng / ml. The results of plasmid electrophoresis can be seen in Figure 1.

Conclusion : Overall, the efficiency of the transformation in the present study for DH5α, JM109 and Stbl4 averaged 0.26 * 106 , 0.89 * 106 and 1.57 * 106 cfu /µg, respectively which indicated that Stbl4 was a more suitable competent cell for recombinant pCDH vectors.

Keywords : Transformation, competent cell, DH5α, JM109, Stbl4,

P412-24: Isolation and identification of Gallant Super (Haloxyfop-R-methyl) degrading bacteria in canola fields

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Background and Aim : Herbicides are one of the most important and necessary inputs in the cropping systems of developed countries and its residues causes the environmental pollution. Biodegradation by microorganisms is considered as the novel method to reduce these risks. The aim of this study was to isolate and identify bacteria degrading Haloxyfop-R-methyl in soils contaminated with this herbicide, based on biochemical, morphological and molecular characteristics and to investigate the rate of degradation of Haloxyfop-R-methyl by selected strains.

Methods : Topsoil containing organic matter was removed from canola fields in Selseleh city using sterile gloves, and then soil was sampled from a depth of 0 to 30 cm. For the initial isolation of soil bacteria, the nutrient agar medium containing a concentration of 10% the herbicide was used.

Results : In carbon source substitution test using Standard Succinate Medium containing 5% of the herbicide, only 17 bacteria appeared. The isolates were placed in five groups based on the biochemical tests including gram reaction, Xanthomonadin and fluorescent pigmentation production, oxidase, catalase, H2s from cysteine, Levan production, Tween 20 Hydrolysis Test, and oxidative/fermentative tests. For molecular diagnosis, five representative isolates were selected and subjected to amplify 16S rDNA gene using 16s F and 16sR primers and sequenced. Sequences were aligned and compared to the NCBI reference sequences.

Conclusion : Based on biochemical and molecular tests, the isolates were identified as Acidovorax sp, Acinetobacter calcoaceticus, Achromobacter sp., Stenotrophomonas rhizophila and Variovorax paradoxus. The lowest Minimum Inhibitory Concentration(MIC) and Minimum Bactericidal Concentration (MBC) were attributed to V. paradoxus, while the highest MIC and MBC belonging to A. calcoaceticus.

Keywords : Herbicide, MBC, MIC ,

P413-25: Isolation and identification of Trifluralin Degrading bacteria in bean fields

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Background and Aim : Herbicides are one of the most important and necessary inputs in the cropping systems of developed countries and play a significant role in the yield of crops in these countries. Trifluralin is one of the herbicides applied in the soil, and its residues may be problematic for post-bean crops. Therefore, it is necessary to study its biodegradation to reduce these risks. The aim of this study was to isolate and identify bacteria degrading Trifluralin in soils contaminated with this herbicide, based on biochemical, morphological and molecular characteristics and to investigate the rate of degradation of Trifluralin by selected strains.

Methods : Topsoil containing organic matter was removed from bean fields in Selseleh city using sterile gloves, and then soil was sampled from a depth of 0 to 30 cm. For the initial isolation of soil bacteria, the nutrient agar medium containing a concentration of 10% the herbicide was used.

Results : . In carbon source substitution test using Standard Succinate Medium containing 5% of the herbicide, only 17 bacteria appeared. The isolates were placed in five groups based on the biochemical tests including gram reaction, Xanthomonadin and fluorescent pigmentation production, oxidase, catalase, H2s from cysteine, Levan production, Tween 20 Hydrolysis Test, and oxidative/fermentative tests. For molecular diagnosis, five representative isolates were selected and subjected to amplify 16S rDNA gene using 16s F and 16sR primers and sequenced. Sequences were aligned and compared to the NCBI reference sequences.

Conclusion : Based on biochemical and molecular tests, the isolates were identified as Pseudomonas koreensis, Pseudomonas sp. LuM, Pseudomonas sp. LuM3, Rhizobium sp. LuM and Variovorax sp. The lowest Minimum Inhibitory Concentration(MIC) and Minimum Bactericidal Concentration (MBC) were attributed to Rhizobium sp and Variovorax sp, while the highest MIC and MBC belonging to Pseudomonas sp.

Keywords : Herbicide, MBC, MIC ,

P414-26: Bacterial Vaccine

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Background and Aim : Today, we need bacterial vaccines due to the increase in antibiotic resistance genes and bacterial infections. There are several types of bacterial vaccines, such as toxoids, subunit vaccines, killed whole-cell vaccines, OMV, and live attenuated vaccines. The dry form of live or attenuated bacteria can be used to produce live and attenuated bacterial vaccines, which increases the thermal stability of the bacterial vaccines. Bacteria such as Clostridium and Bifidobacterium that are severely anaerobic can be used as vaccines to treat solid tumors. Some bacteria, such as E. coli, Helicobacter pylori, Pseudomonas aeruginosa, Borrelia burgdorferi, Shigella, Salmonella typhi, Neisseria meningitis, and Acinetobacter baumannii can produce outer membrane vesicles (OMV). The outer membrane of germ-negative bacteria is enclosed and is often associated with cellular components such as toxins, DNA, outer membrane components, etc. That produces OMV and acts as the bacterial vaccine. glycoconjugate vaccine is a vaccine that contains a bacterial O-antigen. To produce the glycoconjugate vaccine, the bacterial lipopolysaccharide (LPS) must be isolated and purified, then remove the toxic lipid A and pure O-antigen are produced. The O-antigen was bound to the carrier proteins by chemical or recombinant methods. To produce a bacterial vector vaccine, the antigen gene is inserted into the bacterial plasmid and chromosome, then the bacteria express the antigen. To produce a vector viral vaccine, the Mycobacterium tuberculosis antigen gene (for example Rv034133-4) was inserted into the HAdV-35 and HAdV-5 virus genome, and a viral vaccine was produced. This antigen is expressed on the surface of the virus and as a vaccine stimulates the immune system. The recombinant bacterial antigen is produced and conjugated to an antibody. Antibody against the receptor of dendritic cells (CLR), thus vaccine is better presented to the immune system. Omics science (such as genomics, proteomics, and transcriptomics) can improve vaccine design.

Methods : Review

Results : The rise of antibiotic-resistant genes has threatened public health, and it has become one of the most important health problems for communities. Bacterial vaccines can prevent infectious diseases and reduce antibiotic-resistant infections.

Conclusion : Due to the increasing diversity of antibiotic resistance genes, some bacterial vaccines can't prevent resistance genes. It is difficult to design and produce bacterial vaccines that can stimulate the immune system.

Keywords : Bacterial Vaccines, live bacteria, OMVs.

P415-39: Effect of bacterial starter culture under various temperatures on Kermanshahi roghan fatty acid profiles during the long time storage

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Background and Aim : The study aimed to evaluate the effect of bacterial starter culture under various temperatures on Kermanshahi roghan fatty acid profiles during the long time storage.

Methods : In this investigation, 10 roghan samples were collected from different villages of Gilan-e Gharb County, Kermanshah Province. The roghan bacteria were isolated. Then each roghan was divided into 4 portions and incubated at -4, 4, 25, and 37 °C for 6 months.

Results : Our results indicated that Lactobacillus spp. and Streptococcus thermophilus were isolated. Our data also revealed that roghan short-chain fatty acid levels didn't have significantly different after storage compared with control samples. Although the amount of saturated fatty acids in roghan decreased during the storage, there was a significant difference ($p<0.05$) only at 37 °C. In addition, unsaturated fatty acids in all samples increased compared with roghan samples before incubations which the only significant increase ($p<0.001$) being related to 37 °C. Our findings illustrated that the highest portions of roghan fatty acids were related to C4 and C18:1c n-9, while the lowest portions of fatty acids were associated with C12, C14, and C16 (especially at 37 °C).

Conclusion : Collectively, our findings presented a significant difference between fatty acid levels of roghan only at 37 °C. Moreover, the high temperature (at 37 °C) is more suitable than the low temperatures (-4, 4, and 25 °C) for roghan storage. It can be suggested that bacterial activity occurs at optimum or near-growth temperatures which may cause these changes.

Keywords : Kermanshahi roghan, Fatty acid profiles, Storage

P416-43: Immunogenicity of the Recombinant Cryptococcus neoformans HSP70, a potential Candidate for Developing an ELISA kit

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Background and Aim : Cryptococcus neoformans is an encapsulated fungal pathogen that causes life-threatening meningoencephalitis in immunocompromised patients. This yeast secretes several potent immunogenic proteins by secretory vesicular mechanisms, such as HSP70 chaperone.

Methods : The PCR-amplified HSP70 gene was cloned into a PET-28a(+) expression vector. The purified recombinant HSP70 (rHSP70) was evaluated by western blotting using an anti-His Tag-HRP antibody and then used for immunization of a rabbit. The serum of the immunized rabbit was tested against the whole lysate of C. neoformans in ELISA

Results : The antibodies in the rabbit's serum recognized lysate of C. neoformans yeast. The highest antibody levels were achieved after the third booster injection.

Conclusion : The rHSP70 showed to be a reliable candidate for the designing and development of an ELISA kit for early detection of cryptococcosis, and to screen a large number of specimens

Keywords : Cryptococcus neoformans, Enzyme-Linked Immunosorbent Assay, Heat Shock Protein 70KD

P417-44: The prevalence of ESBLs and biofilm formation in Escherichia coli isolated from urinary tract infection in Isfahan, Iran

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Background and Aim : Background: Uropathogenic Escherichia coli are gram-negative bacilli that most common causes of UTI. This organism has the ability to produce biofilm as an important virulence factor that contributes to the stability and recurrence of the disease.There is a need to do this due to the lack of sufficient information about these resistances in this geographical area and to help increase our knowledge about these genes and their role in creating resistance, as well as the role of biofilm in increasing resistance.

Methods : Methods: 139 E. coli were isolated from urine samples. Antibiotic susceptibility of isolates was determined by disk diffusion method and production of ESBLs confirmed using Double disk synergy test method. Molecular detection of the ESBL genes was performed using PCR. Biofilm formation assay was performed by microtiter plate method.

Results : Results: the most effective antibiotics against this bacterium are Nitrofurantoin. Multidrug resistance was observed in 119 (85.6%) isolates. There was phenotypic resistance to ESBLs in 93 (66.9%) isolates. The results of PCR showed that the prevalence of bla-CTX, bla-VEB and bla-TEM were 45(32.4%), 87(62.6%) and 10(7.2%), respectively. The results of biofilm formation revealed that 65 (46.8%), 58(41.7%), 10(7.2%), and 6(4.3%) of the isolates had non-biofilm, weak, moderate, and strong activities, respectively.

Conclusion : Conclusions: The high prevalence of ESBLs gene is considered as a risk factor for isolates in this region because it is capable of transmitting to other susceptible bacteria and causing resistance in them. The results of this study showed that biofilm production can increase antibiotic resistance.

Keywords : Keywords: Escherichia coli, ESBLs, Biofilm formation, Antibiotic resistant

P418-45: The therapeutic effect of the pexiganan peptide on antibiotic resistance nosocomial pathogens models

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Background and Aim : The appearance of bacterial strains with antibiotic resistance and the need for novel effective therapeutic agents has stimulated interest to develop antimicrobial peptides (AMPs) as a replaced approach. The present study aimed to investigate the therapeutic effect of the pexiganan peptide on antibiotic resistance nosocomial pathogens in vitro and in vivo.

Methods : The inhibitory effect of the pexiganan peptide was assessed on the human primary fibroblast cell line (C654), we also evaluated the hemolytic activity of the peptide on human red blood cells (RBCs). The median lethal dose (LD50) and sub-lethal dose of pexiganan peptide for intraperitoneal (i.p.) administration have been performed by using BALB/c mice. The extensively drug-resistant (XDR) Acinetobacter baumannii, methicillin-resistant Staphylococcus aureus (MRSA), and KPC-producing Klebsiella pneumonia (KPC-KP) strains were used for assessing the antibacterial efficacy of pexiganan peptide, in vitro and in vivo.

Results : In vitro results indicated that MIC (8-71.21µg/ml) and MBC (16-128µg/ml) value of pexiganan had no cytotoxicity effect on human primary fibroblast cell line (IC50=6.03µg/ml). In vivo results showed that sub-lethal doses of pexiganan (3.3mg/kg/i.p.) had no obvious changes in liver and kidney structure which also had no significant difference in biochemical and hematological markers. However, it couldn't significantly reduce the peritoneal loads of bacteria or increase the survival rate of infected mice models.

Conclusion : All these findings demonstrated the great in vitro antibacterial activity of pexiganan, while it couldn't result in a complete therapy in the mice models that were infected with antibiotic resistance nosocomial pathogens.

Keywords : Antimicrobial peptides; Pexiganan; Antibiotic resistance

P419-46: Investigated the therapeutic effect of Tilapia Piscidin 4 (TP4) peptide on antibiotic resistance nosocomial pathogens in vitro and in vivo

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Background and Aim : Antimicrobial peptides (AMPs) are considered potential agents to replace conventional antibiotics. Tilapia piscidin 4 (TP4) is a peptide with antimicrobial activity. This study investigated the potential cytotoxicity and hemolytic activity of TP4 as well as its therapeutic efficacy in vitro and in vivo on nosocomial pathogens resistant to conventional antibiotics.

Methods : Cytotoxicity and hemolytic activity of TP4 were assessed in the human primary fibroblast cell line (C654) and human red blood cells (RBCs), respectively. BALB/c mice were used to determine the median lethal dose (LD50) and a sub-lethal dose of TP4 administered intraperitoneally (i.p.). The antibacterial activity of TP4 was assessed against extensively drug-resistant (XDR) Acinetobacter baumannii, methicillin-resistant Staphylococcus aureus (MRSA), and KPC-producing Klebsiella pneumonia (KPC-KP) in vitro and in vivo.

Results : TP4 exhibited no cytotoxicity against the human primary fibroblast cell line (IC50=1.91 g/ml) at MIC and MBC values ranging from 4 to 25.6 g/ml. Moreover, in vivo data indicated that sub-lethal doses of TP4 (0.8 mg/kg, i.p.) had minimal cytotoxicity for the liver or kidney and were unable to completely alleviate the peritoneal load of antibiotic-resistant bacteria in experimental models.

Conclusion : Despite the promising in vitro results, this study's in vivo findings indicate that a sub-lethal dose of TP4 was unable to induce a perfect cure in mice infected with antibiotic-resistant nosocomial pathogens.

Keywords : Antimicrobial peptides; Tilapia piscidin 4; TP4; Antibiotic resistance

P420-59: Ca19Zn2(PO4)14 Nanoparticles: Synthesis, characterization and its effect on the colonization of Streptococcus mutans on tooth surface

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Background and Aim : The main cause of tooth decay is the biofilm formation of Streptococcus mutans. This study aimed to investigate the effect of the zinc oxide nanoparticles (ZnO NPs), hydroxyapatite nanoparticles (Ca10(PO4)6(OH)2) (HAP NPs), zinc oxide/hydroxyapatite nanocomposites (ZnO/HAP NCs), and Zn-substituted hydroxyapatite nanoparticles (Ca19Zn2(PO4)14 NPs) on the growth and biofilm formation, bacterial adherence, and the expression of ftf and gtf genes in Streptococcus mutans.

Methods : The nanostructures were prepared via simple and fast co-precipitation route. Twelve isolates of Streptococcus mutans collected from children with dental caries referred to the dental clinic of Kashan University of Medical Sciences.

Results : All S. mutans isolates were susceptible to Ampicillin. The mean MIC for ZnO NPs, HAP NPs, Ca19Zn2(PO4)14, and ZnO/HAP NCs were 118, 260, 70.6, and 994 µg/mL, respectively. All prepared nanostructures significantly reduced biofilm formation at MIC and sub-MIC concentrations ($p < 0.01$). In biofilm and cell culture treated with nanoparticles, the expression of ftf and gtfC genes decreased. Results were shown that IC50 for the Ca19Zn2(PO4)14 was 8.5, and for non-toxic concentration, was 0.065 µg/mL. The attachment rate to the denture surface and HGF1 cell line treated with the Ca19Zn2(PO4)14 NPs has decreased

Conclusion : The results showed that the Ca19Zn2(PO4)14 NPs has a better effect than the ZnO/HAP NCs. It can therefore be used as a coating on dental surfaces. Investigation of Ca19Zn2(PO4)14 NPs form for covering dental teeth surface recommended in future study.

Keywords : Hydroxyapatite Nanocomposites Biofilm MIC Dental

P421-64: In vitro assessment of native probiotic bacteria isolated from Lorestan Nomads Dairies

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Background and Aim : Background and aim: A global surge in the application of probiotics as functional ingredients in food, animal feed, and pharmaceutical products has been increased in last decades. The largest sector in food industry is belonged to dairy products where probiotics are employed in sour/fermented milk, yogurt, cheese, butter/cream, ice cream, and infant formula. Many functional characteristics are devoted to dairies using probiotics like improved aroma, taste, textural characteristics and health-promoting properties. One of the most important trends for incorporation of probiotics in dairies is fermentation of dairy products with probiotics isolated from traditional foods or dairies. In this research we isolate, characterize and survey probiotic activity of strains from traditional dairies collected from Lorestan nomads of Iran.

Methods : Eleven different samples of yogurt, cheese, milk, butter, kashk and Dough are collected from nomads migrated to hills near Khoramabad city, Lorestan province. The dairies were then directly transferred to the lab and isolation process were carried on MRS agar, M17 agar, TSA and YPG agar. In vitro probiotic assessment of isolated strains were done according to Guidelines for the Evaluation of Probiotics in Food (FAO/WHO, 2002) and Iranian National Standard No. 19459. Finally, the native probiotic candidates were identified by rDNA sequencing and phenotypic characterization.

Results : From total 124 strains which have been isolated from samples at first step, only five isolates passed all criteria and showed probiotic features. Three of these strains have been isolated from yogurt (Y.L III (25), Y.L III (7), Y.L IV (4)); one of them from Kashk (K.L 2(10)) and the last one from Doogh (D.L II (1)). The rDNA sequencing results demonstrate that strains Y.L III (25) and D.L II (1) belonged to family Saccharomycetaceae and showed the highest similarity with kluyveromyces marxianus and Pichia fermentans, respectively. The other strains include Y.L III (7), Y.L IV (4) and K.L 2(10) belonged to family Lactobacillaceae and showed the highest similarity with Pediococcus acidilactici, Levilactobacillus brevis and Lentilactobacillus buchneri, respectively.

Conclusion : Native probiotics are advantageous for utilization at industrial scales. Some isolates from this research are ideal probiotic candidates which can be applied in the field for the improvement of taste and health of dairies.

Keywords : Lactic acid bacteria, probiotics, Lorestan dairies, native bacteria

P422-65: Bacillus cereus with an ability of oil bioremediation in harsh environmental conditions

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Background and Aim : One of the major environmental problems is the pollution of soil and water with oil. Bioremediation is one of the economical and environmentally friendly methods for removing oil pollutants. This study aims to isolate microorganisms with the ability to bioremediate crude oil in harsh environmental conditions.

Methods : Sampling was done from oil-contaminated soils and was enriched in Mineral Salt Medium with crude oil as a sole carbon source. The grown bacterial colonies in the mentioned solid medium were selected. Then the selected bacteria were cultured in 2% v/v crude oil for 14 days, with a range pH of 5 to 9.5, NaCl concentration of 1 to 8%, and 250 mg of cyanide incubated at 20 to 40°C. These bacteria were molecularly characterized using gene sequencing of 16S rRNA.

Results : A total of 315 isolates were isolated. Among them, one isolate consumed crude oil completely in the culture medium. According to the 16S rRNA genes sequencing, this bacterium with 97% similarity was Bacillus cereus, which could grow at a wide range of pH, temperature, salt concentrations, and presence of cyanide.

Conclusion : Because of spore formation, Bacillus cereus can be a good candidate for oil remediation in harsh conditions. Using this strain for bioremediation of multiple contaminants should be performed extra tests.

Keywords : Bioremediation, Bacillus cereus, petroleum, Molecular identification, 16S rRNA

P423-81: Prevotella As Next Generation Probiotic

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Background and Aim : It is well-known that the human gut harbors millions of bacteria and their metabolic potential is immense. Dietary fiber in the human diet is the main source of accessible carbohydrate substrates for the gut microbiota, hence, using dietary manipulation of gut microbiota to increase the relative number of probiotic bacteria could contribute to the well-being of the host. The Dipeptidyl peptidase-4 (DPP-4) activity influences metabolic, behavioral and intestinal disorders through the cleavage of key hormones and peptides. Some studies describe the existence of human DPP-4 homologs in commensal bacteria, for instance in Prevotella or Lactobacillus.

Methods : Probiotic bacteria protect humans from pathogens through a process known as colonization resistance.Colonization resistance refers to the mechanism used by microbiota that is already present in the gut to maintain their presence, thereby avoiding colonization of the same intestinal sites by pathogens. In the absence of antibiotics, or under healthy conditions, the microbiota can effectively inhibit colonization and overgrowth of invading microbes associated with inflammation via specific interactions between the mucosal immune system and the microbiota. As DPP-4 plays a substantial role in the immune system, particularly in T cell function, DPP-4 has been investigated as a possible target for treating autoimmune diseases including inflammatory bowel disease.

Results : Different studies have shown that Prevotella is a common microbial genus in individuals with a plant-based diet (high in fiber, and low in fats and protein), while an increase in Bacteroides is common in individuals with a Western diet (low in fiber, and high in fats and protein).Growth of Prevotella spp. has also been found to be promoted by barley supplementation in healthy individuals and co-occurred with improved glucose metabolism. A recent human intervention study investigating barley as a prebiotic has also shown that a higher Prevotella/Bacteroides ratio may be beneficial to cardiometabolic regulation and The functions of the DPP-4-like homolog expressed in the gut microbiota could influence dietary protein digestion and thereby contribute to the change in the host response toward these peptides.

Conclusion : This finding indicates that the genus Prevotella plays a role in the dietary-induced improvement in glucose metabolism in observed individuals ،and it can be a potential probiotic, addressing glucose management

Keywords : Prevotella; Probiotics; Dipeptidyl peptidase-4; intestinal disorders

P424-83: The genital hygiene habits and sexual behaviors associated with urinary tract infection in pregnant women

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Background and Aim : Urinary tract infection (UTI) is a bacterial infection commonly occurring during pregnancy. The purpose of this study was to determine the association of UTI with genital hygiene habits and sexual behaviors in pregnant women attending prenatal clinics in Babol

Methods : This case–control study was performed on 100 women with positive urine culture (cases) and 150 healthy pregnant women (controls), matched for age, gestational age, parity, occupation and socioeconomic and education status. The women were selected consecutively from those attending 5 Comprehensive health centers at Babol University of Medical Sciences for prenatal care. The exclusion criteria were a history of > 2 episodes of UTI per year, urinary stones or urinary tract anomaly, chronic disease, consumption of any antibiotic or immune system inhibitory drugs in the previous 3 months, or the presence of any abnormal vaginal discharge. The clean-catch midstream urine specimen were sent to Babol Razi laboratory and the fresh urine was tested immediately. Urinalyses and urine cultures were used for the detection of UTI. A UTI was defined as the presence of significant bacteriuria > 100 000 colony-forming units per mL of urine. A risk profile for UTI was expressed in the form of odd ratios (OR) with 95% confidence intervals (CI) for the 250 women.

Results : Escherichia coli was the infecting organism in 83% of cases. Other causative organisms were S. saprophyticus (10%), Enterococci spp. (4%) and P. mirabilis (3%). Factors associated with UTI included sexual intercourse ≥ 3 times per week (OR = 5.62), recent UTI (OR = 3.27), not washing genitals pre-coitus (OR = 2.16), not washing genitals post-coitus (OR = 2.89), not voiding urine post- coitus (OR = 8.62) and washing genitals from back to front (OR = 2.96).

Conclusion : Due to the fact that the most common cause of UTI in our female sample was caused by fecal bacteria (E. coli), so hygiene habits and sexual behaviors may play an important role in the occurrence of UTI in pregnant women.

Keywords : urinary tract infection; genital hygiene habits; sexual behaviors; pregnancy

P425-89: Investigation of IL-2 and IFN-γ to EBV peptides in stimulated whole blood among multiple sclerosis patients and healthy individuals

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Background and Aim : Epstein-Barr virus (EBV) is a double-stranded DNA virus and has two phases of lytic and latent infection in host cells. After infecting B lymphocytes, EBV becomes persistent in these cells. In healthy individuals T lymphocyte has a major role in killing EBV infected B cells. Statistical studies have shown that the risk of MS, is increased in individuals with symptomatic EBV infection. In the present study in order to measure immune response, especially T lymphocytes, against different components of EBV, the mRNA level of IL-2 and IFN-γ, that impress autoimmune diseases and indicate T cell function, has investigated in treated whole blood (WB) culture with EBNA1 and BRLF1 peptides from 10 healthy individuals and 10 MS patients.

Methods : First of all, the viability percent of cells after treating with viral peptides in different period of time was measured by MTT assay. Then optimal annealing temperature for primers function was determined by PCR. Finally, the mRNA level of IL-2 and IFN-γ in treated and untreated WB culture was evaluated by using real time RT-PCR.

Results : The analysis of the results achieved by real time RT-PCR, demonstrated a significant increased level of IL-2 in MS patients than healthy subjects after exposure to both peptides. Also, the mRNA level of IFN-γ increased in MS patients in EBNA1 treated WB culture.

Conclusion : According to obtained results, EBV peptides can reactivate immune cells, especially T lymphocytes, and may indirectly induce inflammation and develop MS; however, it seems that long time exposure to these peptides has reduced effect on T cell function and face the control of B lymphocytes with difficulty.

Keywords : Epstein-Barr virus, Multiple sclerosis, T lymphocyte, B lymphocyte, interferon-gamma, interleukin-2.

P426-96: Inhibitors of fungal growth from natural origins

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Background and Aim : In recent years, the incidence of fungal infection is raised significantly as one of the most important threats to human health. Due to the high toxicity and drug resistance of current drugs, there is an urgent need to use solutions to detect new antifungal drugs from molecules of natural origin, especially those obtained from plants and microorganisms.There are currently three antifungal drug groups used in clinic including polyenes, azoles and echinocandins. Many anti-fungal drugs have natural origin as phenolic acids, flavonoids, tannins, stilbenescurcuminoids, coumarins, lignans, and quinines. They are produced by the plants during secondary metabolism or when a plant is injured. Microorganisms also have the ability to synthesize various groups of natural antifungal compounds.

Methods : One of the best natural resources for recognizing antifungal compounds of plants is to search for essential oils and extracts obtained from different parts of them.Two methods are suggested for identifying and classifying natural antifungal substances: Cultivation by improving the culture, antifungal substances and compounds can be identified and metagenomics which is based on DNA isolation from plant samples and molecular studies. As a result of these two methods, new antifungal compounds can be identified and further developed from natural sources.

Results : Phenolic compounds, phenylpropanoids, echinocandins, alkaloids and antimicrobial peptides are in the first line of investigation as natural inhibitors of pathogenic fungi growth by targeting the fungal cell wall and cell membrane at cellular and molecular levels.

Conclusion : Fungal infections are still one of the most common problems in the lives of people around the world. At present, the growth trend of novel antifungal drugs is very slow compared to the rise in fungal infections. This study further indicates that broad spectrum bioactive molecules by natural origin which target specific sites in the ergosterol biosynthesis pathway such as α-bisabolol are potential candidates for drug development against a wide array of fungi with least toxicity for the mammalian host.

Keywords : Antifungal natural compounds, Cultivation, Metagenomics, Antifungal activity, Medicinal plants, Green approach

P427-104: Anti-bacterial and Anti-Quorum Sensing Properties of Dionysia Revolute Boiss against Secondary Bacterial Infections of COVID-19 Patients; An in-vitro Study

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Background and Aim : Abstract Background and Aim: Today, the use of traditional plant compounds to kill or interfere with their quorum sensing (QS) mechanisms is considered as an alternative approach to control secondary bacterial infections during or after a viral infection. In this study, anti-bacterial and anti-quorum sensing effect of Dionysia revolute Boiss against five secondary bacterial infections of COVID-19 patients were evaluated.

Methods : Materials and Methods: Extraction of the plant compounds was carried out using n-hexane, methanol, and 96% ethanol mixed solvent. Bacterial samples were collected from respiratory tract fluids among COVID-19 patients and recognized with API kits. Antibacterial activity of the herbal extract was assessed by disc diffusion method as proposed by the Clinical Laboratory Standards Institute (CLSL, 2015). Hence, anti-QS activities of this herbal extract at the sub-minimum inhibitory concentration (MIC) were assessed by violacein quantification assay in Chromobacterium violaceum CV026 biosensor strains in vitro.

Results : Results: As it has been indicated in the Results section, a plant extract from 50 to 0.39 mg/ml exposed their antibacterial impacts via hindering the bacterial growth in comparison with controls and exhibited anti-QS activities via decreasing the violacein formation in C. violaceum CV026 biosensor strain at sub-MIC concentrations (3.1 to 0.39 mg/ml) in vitro.

Conclusion : Conclusion : Our study showed that the antimicrobial activities of Dionysia revolute Boiss could be due to their anti-QS properties. Therefore, this medicinal plant either as a stand-alone treatment or in combination with antibiotics could be used as an efficient choice for curing secondary bacterial infections.

Keywords : Dionysia revolute, Anti-bacterial, Anti-quorum sensing, Secondary bacterial infections, SARS COVID-19

P428-121: An Evaluation of Antibacterial Effects of Human Amniotic Fluid on Pathogenic and Probiotic Bacteria in Vitro

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Background and Aim : Introduction: It is proposed that some compounds in amniotic fluid cause the fetus to remain free from microbial contaminations. This study aimed to evaluate the antibacterial effects of amniotic fluid and to compare its effects on pathogenic and probiotic bacteria.

Methods : Method: This experimental study was conducted on amniotic fluid obtained from 43 healthy mothers who gave birth by selective cesarean section. The samples transferred into the laboratory under sterile condition to investigate the antibacterial effects of amniotic fluids on 5 standard bacterial strains, including Bacillus cereus, Staphylococcus aureus, Pseudomonas aeruginosa, Streptococcus pyogenes and Lactobacillus plantarum by agar well-diffusion method. The inhibition zone diameter of each cultured bacteria around the wells filled with amniotic fluid sample was measured after an overnight incubation at 37º C. Data analysis was performed by SPSS software, version 22 at a significance level of 0.05 by Kruskal-Wallis and Mann-Whitney tests.

Results : Findings: Amniotic fluid revealed an inhibitory effect on the growth of bacterial strains to a different extent. Staphylococcus aureus and Streptococcus pyogenes strains showed growth inhibition in 39% and 17% of samples, respectively. In other bacterial strains, there was growth inhibition in less than 5% of the samples. Also, the zone of growth inhibition for Staphylococcus aureus was significantly higher than the other strains (p-value <0.001) and the zone of growth inhibition for Streptococcus pyogenes was also significantly higher than Lactobacillus plantarum (p-value = 0.004), Bacillus cereus (p-value = 0.004) and Pseudomonas aeruginosa (p-value = 0.001) strains.

Conclusion : Conclusion: The results of this study demonstrate antibacterial activity of amniotic fluid on pathogenic bacteria but to a different extent. Our findings also suggest that

antibacterial effect of amniotic fluid on pathogenic bacteria is significantly higher than the probiotic one.

Keywords : Keywords: Amniotic fluid, Antibacterial, Pathogenic bacteria, Probiotic bacteria

P429-123: Synthesis silver nanoparticles using Peucedanum officinale extract (PO@AgNPs) and investigation antibacterial and antioxidant activities

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Background and Aim : Introduction and aims: Nowadays, the biosynthesis of metallic nanoparticles is on a sharp rise because of its potential in eliminating antibiotic-resistant bacteria. So that, this study reports an eco-friendly and cost-effective methodology for synthesizing biogenic silver nanoparticles (AgNPs) using alcoholic extract of Peucedanum officinale (PO@AgNP).

Methods : Material & Methods: In this research, we used Peucedanum officinale for the green synthesis of silver nanoparticles. In this study, various parameters such as concentration, time and temperature were investigated to achieve optimal conditions to synthesis PO@AgNP. All stages of reaction were monitored by UV-Vis spectroscopy. The PO@AgNPs were characterized in terms of structural properties and morphology with X-ray diffraction (XRD) and Fourier transform infrared spectroscopy (FT-IR) and transmission electron microscopy (TEM) techniques. The broth microdilution method was performed to determine the antibacterial activity of PO@AgNPs. The antioxidant activities of PO@AgNPs were examined as a percentage of DPPH inhibition.

Results : Results: Examination of the XRD data confirmed the synthesis of crystalline particles. The FT-IR spectra showed that phenolic compounds in Peucedanum officinale extract act as a reducing agent of silver ions and formation PO@AgNPs. TEM images showed that PO@AgNPs had a spherical morphology with a size of about 30-40 nm. PO@AgNPs shown strong antibacterial activity against Klebsiella pneumoniae ,Enterococcus faecalis and Streptococcus mitis with minimum inhibitory concentrations (MIC) values were 31.2, 62.5 and 62.5 µg/ml, respectively. DPPH test have shown that with increasing the concentration of PO@AgNPs (62.5 to 500 µg/ml), the percentage of radical inhibition of DPPH increased (25% to 55%).

Conclusion : Conclusion: All investigations showed that PO@AgNPs have high antibacterial activity against gram-positive and negative bacteria and have strong antioxidant properties and introduces it as a very efficient, eco-friendly and cost-effective nanoparticle.

Keywords : Keywords: Silver nanoparticles, Green synthesis, Peucedanum officinale, Antibacterial, Antioxidants.

P430-127: The anti-trichomonial effects of Methanolic extract of Rhamnus cathartica and nanoamodine on Trichomonas Vaginalis

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Background and Aim : Trichomoniasis is a disease caused by the parasite Trichomonas vaginalis and is the most common sexually transmitted disease after viral infections. Due to the increasing prevalence of this disease and increasing reports of metronidazole resistance, it is a common drug for treatment and teratogenicity. The possibility of studying this alternative drug for the treatment of trichomoniasis seems necessary. Emodin has been proposed as the antibacterial, fungal and anti-cancer compounds underlying this study. The aim of this study was to evaluate the anti-trichomonial effects of methanolic extract of Rhamnus cathartica and nanoemodin on T. vaginalis in vitro.

Methods : T. vaginalis should be isolated from the secretions of women referred to medical centers without a history of metronidazole use. 50, 100, 200, 400 and 800 µg / ml were prepared. The effect of different concentrations at 3, 6, 12, 24 and 48 hours on the parasite in 24-well plates containing TYM in comparison with positive control of metronidazole. Results were analyzed by SPSS-22 software and analysis of variance tests.

Results : Methanolic extract of Rhamnus cathartica and nanoemodine at all concentrations had acceptable antiparasitic effects against T. vaginalis. At concentrations of 400 and 800 µg/ml nanoamodine and 800 µg/ml of methanolic extract of Rhamnus cathartica, better effects than positive control have been reported. IC50 levels of methanolic extract of Rhamnus cathartica and nano-emodin were reported to be 7.88 and 7.85 µg/ml, respectively.

Conclusion : Considering the lethal power of methanolic extract of Rhamnus cathartica and nanoemodin on T. vaginalis and the better effect than positive controls, it can be concluded that the above compounds can be a suitable candidate for treatment after further studies.

Keywords : T. vaginalis, Anti-Trichomonas, Rhamnus cathartica, Nano Emodin

P431-136: Survey of Metalo beta Lactamase genes, bla IMP1, INT 1 in Acinetobacter baumanii isolated from burn patients Zare Hospital of Sari

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Background and Aim : Acinetobacter baumanii is one of the most important pathogenic bacteria causing infectious diseases. The aim of this study was to evaluate the antibiotic resistance and determine the frequency of β-lactamase and class I integron genes in clinical strains of Acinetobacter baumanii isolated from burn patients in Zare and BooAli Hospital of sari.

Methods : A. baumanii specimens were collected from 2019 to 2021. After culture in a standard medium, the presence of A. baumanii was confirmed by biochemical tests. Antibacterial sensitivity test against ciprofloxacin, imipenem, meropenem, Cefepime, ceftazidime, gentamicin, amikacin and colistin was performed using disc diffusion method on the Muller-Hinton agar medium. Finally, polymerase chain reaction was performed to determine the resistance genes.

Results : A total of 100 A. baumanii were isolated. The results of the pattern of resistance of A. baumanii to the antibiotics tested were as follows: ceftazidime (90%), cefepime (84%), meropenem (81%), imipenem (78%),ciprofloxacin (70%), amikacin (68%), gentamicin (58%), colistin (10%). The study showed that 34% of the isolates produced the metallo-β-lactamases (MBLs) enzyme. Finally, by PCR method, blaIMP, blaVIM and class I integron were identified in, 55%, 45% and 60% of these isolates, respectively.

Conclusion : This study revealed an increased frequency of MBL-encoding genes (VIM, IMP) and class I integrin in A. baumannii isolates. Also, the results of this study showed that the rate of resistant to antibiotic among A.baumanii is high. In the present study, the only antibiotic that was suitable for the treatment of these patients was colistin.

Keywords : Acinetobacter baumanii, Antibacterial genes , Sari

P432-138: The Effects of Medicinal Plant Extracts of Salvia Xanthochelia on Hepatitis C Virus Replication in Cell Culture

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Background and Aim : Several studies indicated that almost 200 million people infected with hepatitis C virus (HCV) across the worldwide. Interferon-alpha (INF- α) and ribavirin could use as alone treatment has some limitations such as expensive and a lot of side effects, on the other hand less than 50% of patients with HCV genotype 1a have good response to these therapies and clear virus in their body. Salvia Xanthochelia aqueous extract can be used as a suitable treatment in various diseases such as cancer and liver disease. The aim of this study, evaluated the anti-viral efficacy of Salvia Xanthochelia aqueous extractand and INF-α2 pegylated against HCV strain JFH-1 in the HCVcc/Huh7.5 cell culture system.

Methods : e cytotoxicity effect of Salvia Xanthochelia aqueous extract and INF- α2 pegylated were evaluated by MTT assay and also IC50 by prims version5 measured. First the virus was inoculated to cell culture and this combination was added and the virus titer was evaluated by real-time PCR method. Then this combination and virus were added and incubated for 2 hours, after that the virus load was measured by real-time PCR method.

Results : MTT assay results showed that IC50 for Salvia Xanthochelia aqueous extract and INF- ?2 pegylated are 4.936 mg/ml and 87.71 mg/ml. moreover, Real time data revealed that viral load for Salvia Xanthochelia extract and INF- ?2 pegylated are 3510842 and 1621304.

Conclusion : Our findings indicated Salvia Xanthochelia aqueous extract and INF- α2 pegylated show anti-viral effects against HCV strain JFH-1 in the HCVcc/Huh7.5 cell culture system. In addition, these data indicated that these components likely enable to decrease viral load and expression of gene associated with viral load in HCV strain JFH-1

Keywords : HCV, Salvia Xanthochelia extract, Huh7.5

P433-144: Identification of urease positive bacteria other than Helicobacter pylori in endoscopy (stomach biopsy samples) of patients with gastritis and investigation of antibiotic resistance of isolated bacteria

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Background and Aim : Helicobacter pylori is a gram-negative, spiral-shaped, urease-positive microorganism. Today, it is known that urease positive bacteria other than Helicobacter pylori can exist in the oral cavity, stomach, intestine, urinary tract and skin. The purpose of this study is to investigate the pattern of antibiotic resistance and the prevalence of gram-positive and urease-negative bacteria other than Helicobacter pylori present in the stomach of patients with gastritis.

Methods : 165 biopsy samples from the stomach antrum of patients with gastric ulcers referred to Sari hospitals were collected by a gastroenterologist. The samples were transferred to the microbiology laboratory of the Faculty of Medicine after the Rapid Urease Test (RUT) and its positive result in the transfer culture medium. The samples were cultured on Brain Heart Infusion (BHI agar), blood agar MacConkey agar. Non-Helicobacter pylori bacteria present in the stomach were identified by standard bacteriological methods such as cultivation in specific environments, gram staining and performing various tests.

Results : : 100 samples were positive using the urease test kit, 77 samples were infected with Helicobacter pylori and 23 samples were infected with non-Helicobacter pylori bacteria. The highest frequency belonged to Staphylococcus epidermis strain. There is a significant relationship between gastritis severity and pathology test ($p=0.002$), food reflux (p value=0.002), anorexia (p value=0.012), nausea ($p<0.05$) and burning ($p<0.05$). Also, there was no significant relationship between the non-Helicobacter test and the severity of gastritis ($p>0.05$). No significant relationship was observed between other studied variables and severity of gastritis ($p>0.05$).

Conclusion : In the present study, no significant relationship was observed between the antibiotic resistance pattern and the type of non-H. pylori strains detected. According to the present results, the simultaneous use of different antibiotics can be beneficial and rational in preventing the development of bacterial resistance. It was also proved that the presence of

non-Helicobacter pylori bacteria alone cannot play a significant role in the severity of gastritis.

Keywords : Stomach, non-Helicobacter pylori, urease, gastritis, antibiotic resistance, gastric ulcer

P434-146: Improving ethanol tolerance in a commercial yeast strain by a combination of mutation and evolutionary engineering

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Background and Aim : There are crucial factors in the bioethanol production process that affect production efficiency. Accumulation of ethanol during the fermentation process and the inhibitory effect on growth are inevitable. Saccharomyces cerevisiae is widely used for industrial production of ethanol. The tolerance to high ethanol concentrations, high-temperature is essential for process performance. Any increase in ethanol tolerance in the commercial strains led to faster and more complete fermentation, and may also allow the production of more alcohol. .

Methods : In the present study, to improve ethanol production the in the commercial "Razi170" strain, the parent strain was mutated physically and chemically. The mutants were screened using 1-butanol containing medium. The primary parent and the mutants were evolved within 144 days with evolutionary engineering strategy, while ethanol tolerance phenotype of selected strains was investigated.

Results : According to the increase in the maximum growth rate, 8 strains were selected including parental strain and mutants, and the amounts of ethanol production of these strains were evaluated after evolutionary adaptation tests. Ethanol production of R111 and R113 which were mutated with EMS and UV before the adaptive evolution test and then evolved at 9 and 11% v/v ethanol, respectively, was improved from 0.033 h-1 to 0.112 h-1 and 0.098 h-1, respectively

Conclusion : Evolutionary engineering, is a narrow-experimental evolution that mimics this natural phenomenon in laboratory towards the desired phenotype that has been used excessively since two decades ago, and it has an extensive capabilities in creating capable strains in order to increase ethanol tolerance in industrial strains. To increase the genetic diversity of the primary population, before starting the adaptive evolution experiments,

mutation with ethyl methane sulfonate was used, which was more efficient than ultraviolet radiation in accelerating the evolution process to achieve the desired phenotype.

Keywords : Evolutionary engineering, Ethanol production, Mutation, Saccharomyces cerevisiae

P435-147: Increasing ethanol resistance in Saccharomyces cerevisiae using Adaptive laboratory evolution

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Background and Aim : Adaptive laboratory evolution (ALE) is one of the most powerful methods for improving industrial strains. Its main applications are the activation of latent metabolic pathways, the ability to use unusual raw materials, the production of unusual products, and the increase of yield and productivity of the production process. Ethanol is the most widely used product in the world produced by biotechnological processes. It is also an important alternative energy source to fossil fuels. Ethanol is used as an industrial solvent in the pharmaceutical and perfume industries. Members of the Saccharomyces genus have been used for industrial ethanol production. Increasing the tolerance of ethanol-producing strains is one of the most important characteristics of industrial strains. The strains of S. cerevisiae used in alcohol-producing factories in Iran differ significantly in their ethanol tolerance from industrial strains in the world. The aim of this study was to find the most resistant yeast strains in Iran and increase their ethanol tolerance by ALE.

Methods : For this purpose, 11 different strains of alcohol producing yeasts were prepared from different domestic and foreign sources. These strains were screened to find the strain with the highest ethanol resistance. The selected strain was cultured in a medium containing edible sugar as the main carbon source, yeast extract as the main nitrogen source, and 6.5% ethanol. Colonies tolerating 6.5% ethanol were selected and cultured in the same medium with a higher ethanol concentration (0.1%). By repeating the above steps, a strain tolerant to 8% ethanol was obtained. The kinetics of the ethanol production process in the adapted and the initial strains were determined by measuring the yeast growth rate, ethanol production rate, and substrate consumption rate.

Results : The results showed that the biomass production of the adapted strain increased by ~6.8% compared to the parent strain. However, the alcohol production rate of the adapted strain was 2.9 times that of the parent strain, and the specific growth rate of the parent strain was 0.0024, while it increased to 0.030 in the adapted strain.

Conclusion : The result of this study shows the efficiency of ALE method to produce alcohol producing industrial strains.

Keywords : Ethanol; Adaptive laboratory evolution; Saccharomyces cerevisiae; ethanol resistance.

P436-150: Inverse correlation between serum of anti-pneumococcal and ferritin levels after pneumococcal vaccination in splenectomised beta thalassemia major

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Background and Aim : Splenectomy is necessary in beta thalassemia major patients when the spleen becomes hyperactive, leading to extreme destruction of erythrocytes. This study assessed the ferritin effect on serum pneumococcal antibody response following pneumococcal vaccination, in patients with beta thalassemia major after splenectomy.

Methods : In this case series study, convenience sampling was used to recruit 347 splenectomised beta thalassemia patients under the auspices of Jahrom University of Medical Sciences. Demographic data such as age, sex, and time after splenectomy were recorded by a questionnaire. All participants have been splenectomised and received a dose of Pneumovax® 23 vaccine 14 days before surgery. The IgG antibody responses to pneumococcal vaccine and levels of serum specific ferritin were determined by commercial enzyme immunoassay kits. For the analysis, SPSS software version 16 was used. A p-value less than 0.05 was considered statistically significant.

Results : More participants (63.4%) were hypo-responders to pneumococcal vaccine. Also, serum anti-pneumococcal IgG antibody was related to post splenectomy duration and serum ferritin ($p< 0.001$), but not to gender ($p> 0.05$). An important result was a relation of serum anti-pneumococcal IgG antibody to serum ferritin according to post splenectomy duration groups. Therefore, in three groups of post splenectomy duration, the serum ferritin was higher in hypo-responder than in good responder subjects.

Conclusion : Our results indicate that serum anti-pneumococcal IgG antibody decreased with increment of serum ferritin and post splenectomy duration. Thus, there is a need to re-address the approach towards revaccination in this immune-compromised group of patients by administering a booster pneumococcal vaccination in an attempt to recover immunity and reduce morbidity.

Keywords : pneumococcal vaccines; ferritins; splenectomy; beta thalassemia; Iran

P437-151: Seroloprevalence of Hepatits G Virus (HGV) in beta-Thalassemia Patients Jahrom-Iran, 1399

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Background and Aim : People who have multiple transfusions, such as Beta-thalassemia patients, are at risk for the hepatitis G virus (HGV) infection. The aim of the study was the determination of serological prevalence of HGV and its associated factors in beta-thalassemia major patients in Jahrom-Iran.

Methods : This cross-sectional study, was done on 91 beta-thalassemia patients referring to the thalassemia center, Jahrom-Iran, 2021. Blood samples were collected from the patients and anti-HGV antibodies were evaluated by ELISA methods. Serum levels of ALT, AST, ALP and demographic data were extracted from patients' medical records. Descriptive analysis, X2, and T-test were used for statistical analyses by SPSS-16.

Results : The prevalence anti-HGV IgG and IgM were 17% and 5%, respectively. There were significant relationships between the frequencies of anti-HGV antibodies and serum level of ALT, ASL, ALP and also with the history time of transfusion ($P<0.05$). But, there were no significant relationships between the frequencies of anti-HGV antibodies with patients' sex and the mean of age ($P>0.05$).

Conclusion : HGV is one of the etiologic factors of hepatitis in thalassemia patients in Jahrom. Further comprehensive and molecular-based studies are recommended to explore the prevalence of HGV and its role in hepatitis thalassemia patients.

Keywords : Seroprevalence, Hepatitis G virus (HGV), Sero-prevalence, thalassemia, Iran

P438-159: Molecular discrimination of cryptic Candida albicans species complex isolated from patients in southeastern Iran

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Background and Aim : Candida albicans species complex is well known as the main cause of candidiasis, particularly among susceptible individuals. We aimed to report the genetic diversity of the cryptic C. albicans complex isolates from various clinical samples in Kerman, Iran.

Methods : A total of 112 yeast isolates were obtained from different clinical samples and were characterized to the species level by conventional and molecular methods. The isolates were subjected to polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) using enzymes Msp I. The discrimination of the C. albicans species complex was conducted by the partial amplification of the HWP1 gene.

Results : The majority of clinical isolates were C. albicans complex (n=48) followed by C. glabrata complex (n=34), C. parapsilosis complex (n=21), and C. krusei (n=9). Among C. albicans complex, 45 isolates were C. albicans (94%), 2 isolates were C. dubliniensis (4%), and one isolate was C. africana (2%). C. albicans isolates (n=45), were either homozygous with a single band at ~941 bp (27 strains) or heterozygous with two bands at 800 and 941 bp (18 strains).

Conclusion : Regarding the high incidence of Candida infections particularly in susceptible populations and the emergence of an infrequent yeast species, which is indistinguishable using conventional methods, developing accurate molecular methods for laboratory diagnosis should be considered in the clinical setting.

Keywords : Candida albicans, Candidiasis, Polymerase Chain Reaction, Iran.

P439-167: Electrospinning as a novel strategy for Encapsulation of Bifidobacterium animalis subsp. Lactis BB12 in Chitosan and Inulin nanofibers

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Background and Aim : Probiotics are living microorganisms that, when administered at adequate levels, confer health benefits to the host. However, probiotic microorganisms are generally very sensitive to the surrounding harsh environment, such as acidic, high-temperature, and high oxygen conditions. The encapsulation of probiotics aims to create a safe microenvironment for the delivery of these microorganisms into the gut where they regulate bodily functions and human health.

Methods : In the present study, optimization of encapsulation of Bifidobacterium animalis subsp. Lactis BB12 using inulin (2-4% w/v) and chitosan (2.5-3.5% w/v) were investigated. In all experiments electrospinning, the distance from the tip of the needle to the encapsulating agents was 15 cm and the voltage was 18 kV. In the next step, the characteristics of produced microcapsules including pH and the morphology and size of microcapsules were evaluated. Furthermore, the survival of free and encapsulated probiotic bacteria under the simulated gastrointestinal conditions (Pepsin 3 g/L and Oxgall 0.3 g/L) at 37 °C for 48-72 h was studied. The survival of encapsulated probiotics was monitored after 0, 10 and 18 days.

Results : The optimized formula for encapsulation of Bifidobacterium animalis subsp. Lactis BB12 was 3% (w/v) chitosan, 4% (w/v) inulin and 14% (w/v) gelatin in the ratio 0.5:1:6. Scanning electron microscopy analysis revealed the smooth and uniform surface morphology. The diameter of nanofibers was in the range of 0.99 to 1.11nm and the pH of encapsulated nanofibers was 4.93. The viable count in the case of encapsulated cells (1.9×106 CFU/mL) exhibited better survival compared to free cells (1.6×103 CFU/mL). The viable cell count of probiotic bacteria from 6.3×107 at day zero decreased to 5.3×104 after 10 days and 2×101 after 18 days.

Conclusion : The results of this research suggested that the encapsulation of probiotic bacteria could consider as an effective method that improves bacterial survival in gastrointestinal condition and as a result, it can be used during in vivo applications including biopharmacy and the food industry.

Keywords : Chitosan, Encapsulation, Inulin, Probiotics, Nanofibers

P440-174: Epidemiology, risk factors, species distribution, and antifungal susceptibility of candidemia among hospitalized patients with COVID-19

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Background and Aim : The pandemic of COVID-19 has caused a worldwide health crisis. Candidemia is a potentially lethal condition that has not yet been enough discussed in patients with COVID- 19. The current study aimed to investigate the prevalence of candidemia among Iranian COVID- 19 patients and characterize its causative agents and the antifungal susceptibility pattern.

Methods : The present cross-sectional survey was carried out from March 2020 to March 2021 at Imam Khomeini Hospital, Tehran, Iran. Blood specimens were obtained from patients with confirmed coronavirus infection who also had criteria for candidemia and were examined for any Candida species by conventional and molecular techniques. Susceptibility of isolates to amphotericin B, voriconazole, itraconazole, fluconazole, caspofungin, and 5-flucytosine was tested using the CLSI broth dilution technique.

Results : In total, 153 patients with COVID-19 were included and candidemia was confirmed in 12 (7.8 %) of them. The majority of patients were ≥ 50 years of age (n=9) and female (n=8). Moreover, 6 out of the 12 patients were diabetic. The presence of central venous catheters, broad-spectrum antibiotic therapy, ICU admission, and mechanical ventilation was observed in all patients. The C. albicans (n=7, 58.3 %) and C. dubliniensis (n=2, 16.7%) were the most common isolated species. Amphotericin B and 5-flucytosine were the most active drugs. Despite antifungal treatment, 4 out of 12 patients (33.3 %) died.

Conclusion : Due to the high mortality, the early diagnosis and proper treatment of candidemia are essential requirements for optimal clinical outcomes in COVID-19 patients.

Keywords : Candidemia, C. albicans, C. dubliniensis, COVID-19, Iran

P441-176: Fabrication of Nano Ester Fibrs by pure PHB from wild type Azospirillum brasilense

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Background and Aim : Concern about environmental pollution by synthetic plastics, which constitutes a major part of environmental pollution in industrialized and developing countries, new research has emerged to synthesis bioplastics with high biodegradability and with a formula that is friendly to the environment. Biodegradable biopolymers such as PHA and its homopolymer PHB have the ability to replace plastics and be included in the biological cycle. PHAs are bacterial polymers that are formed as naturally occurring storage polyesters by a wide range of microorganisms usually under unbalanced growth conditions. Azospirillum brasilense is a rhizosphere microorganism with potential use as an inoculant for promot-ing crop plant growth

Methods : In this study Azospirillum brasilense was isolated from para-nodule of wild weed and identified by 16s rRNA sequencing. The production of high yield polymer performed in two stages by Taguchi experimental design. The feeding time to high yield biomass were obtained and followed by addition of glucose, K2HPO4 in ammonium depletion media. The pure PHB extracted from biomass and analyzed first by UV spectrophotometer and finally it was characterized by FTIR, NMR and HPLC. In addition, extracted PHB and polyacrilonitryle were mixed together, Then the electrospun PHB/polyacrilonitryle nanocomposite scaffold were fabricated. The nanocomposite were characterized and confirmed by AFM and FTIR

Results : Azospirillum brasilense was isolated from para- nodule of wild weed, showed a good capacity for high growth and production of PHB. For this isolate PHB synthesis was favored under oxygen limitation and high C/N ratio or ammonium starvation for PHB synthetase enzyme inducer. At the end of exponential growth the production of PHB enhanced up to 76% of the cell dry weight. As a result of electrospinning, fibers with a diameter of 2-10 micrometers were obtained.

Conclusion : The feeding time make the industrial production of this polymer valuable. Therefore, the proposed PHB scaffolds prepared in this study can be considered as good candidates in surgery as sutures to repair wounds and blood vessels and bone tissue engineering applications. Also, the biodegradability of PHAS and their compatibility with vital systems have caused them to be used in the controlled release of drugs, tissue engineering, and veterinary medicine.

Keywords : PHB, Bioplastic, Biopolymer, Azospirillum, HPLC, NMR

P442-177: Effect of harmel aqueous extract on LPS- induced NO production in human mononuclear cells in vitro

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Background and Aim : Harmel is a medicinal herb has been used for treatment of several diseases such as some infections. Nitric oxide (NO) has an essential role in inflammation and has been associated with pathogenesis and expansion of various inflammatory- based diseases comprising some malignancies. Anti-inflammatory properties of harmel extracts through suppressing myeloperoxidase, NO and other mediators have been revealed in vivo. In present study, effect of harmel seeds aqueous extract on NO production in human peripheral blood mononuclear cells (PBMCs) has been assessed in vitro.

Methods : Human PBMCs were cultured in RPMI with 10% FBS. Next cells at logarithmic growing stage were treated with optimum dose of lipopolysaccharide (LPS) and then incubated with different concentrations of harmel seeds aqueous extract (0.1 – 1 mg/ml) for 24 hours. Subsequently NO production in culture medium was measured by the Griess method. Data was analyzed by analysis of variance (ANOVA).

Results : Harmel seeds aqueous extract did not display any substantial effect on LPS-induced NO production in human PBMCs after 24 hours incubation time in comparison with untreated control cells.

Conclusion : According to findings of our study, aqueous extract of harmel seeds has no effect on nitric oxide production in human PBMCs. These results propose the anti-inflammatory effects of harmel may be done via NO- independent mechanism(s). Nevertheless more studies to define the harmel aqueous extract influence on nitric oxide expression in other normal and tumorous cells are necessary.

Keywords : Harmel, nitric oxide, PBMCs

P443-188: Evaluation of Shigella flexneri invasion by plaque formation assay

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Background and Aim : Shigella SPP. is an invasive Gram-negative, facultative anaerobe bacilli of the family Enterobacteriaceae which infects millions of people annually and is characterized by watery or bloody diarrhea, cramping, fever, and dehydration. Globally, Shigella infection causes significant mortality and morbidity, nearly 167 million Shigella episodes annually are estimated and most of these cases are related to low income countries. Shigellosis is more common in children under five years old. One of the most invasive shigella spp. with the high distribution among low income countries is Shigella flexneri. Investigating the invasion of Shigella species can be effective in better understanding of this bacterium and improving the treatment process of the disease caused by it. One of the methods of investigating the pathogenicity of organisms is the use of cell culture. Therefore, we decided to evaluate the invasion of Shigella flexneri in Hela cells using the plaque formation assay.

Methods : In this study, 7 virulence genes including ipaH, ipaB, ipaC, ipaD, virA, ipgD and sen were investigated in five Shigella strains using PCR. Invasion of Shigella species was evaluated using the plaque formation assay technique in Hela cells. The diameter and number of formed plaques were analyzed using ImageJ software.

Results : Strain number 2 was recognized as the most invasive strain by having all 7 virulence genes and forming 360 plaques. Strain number 5 contains 4 virulence genes and showed the least invasion by forming 23 plaques. The virulence profile and the number of plaques are as follows: SF1: ipaH,ipaB,ipaC,ipaD,virA/134 SF2: ipaH, ipaB, ipaC, ipaD, ipgD, sen, virA / 360 SF3: ipaH, ipaB, ipaC, ipaD, ipgD, sen, virA / 138 SF4: ipaH, ipaB, ipaC, ipaD, ipgD, sen, virA / 65 SF5: ipaH, ipaB, ipaC, virA / 23

Conclusion : Most species of Shigella flexneri have a high invasion power and can destroy the intestinal epithelium. The reason for the invasiveness of this bacterial species is the diversity of its virulence factors.

Keywords : Shigella flexneri, virulence factors, plaque formation assay, Hela cell

P444-196: Detection of porphyromonas gingivalis DNA in the synovial fluid of rheumatoid arthritis patients bt real-time PCR

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Background and Aim : microbial infections are believed to play an important role in the initiation and prepetuation of rheumatoid arthritis.This study aimed to investigate the relationship between the presence of Porphyromonas gingivalis DNA in the synovial fluid and rheumatoid arthritis.

Methods : the synovial fluid sample wew collected from 22 patient whith rheumatoid arthrities and 20 patient whith no suffering from rheumatism , overall 42 patient were investigated. The presence of P. gingivalis DNA was evaluated by the real-time PCR method.

Results : There was a significant relationship between rheumatoid arthritis and non-rheumatoid arthritis whith the DNA number (Pv<0.05). P. gingivalis DNA were detected in 3 of 20 (13.6%) rheumatoid arthritis patients, but there was no significantrelationship between P. gingivali DNA and rheumatoid arthritis (Pv>0.05).

Conclusion : DNA of peridontal pathogens can be found in the synovial fluid of rheumatoid arthritis patients.It shows oral bacteria may play a role in the pathogenesis of rheumatoid arthritis.

Keywords : Porphyromonas gingivalis , Synovial fluid , Rheumatoid arthritis , Real-time.

P445-199: Spa Typing of Methicillin-Resistant Staphylococcus aureus isolated from broilers in Ilam

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Background and Aim : Staphylococcus aureus has long been recognized as a pathogen of worldwide clinical significance. Over the last two decades, methicillin resistant S. aureus (MRSA) strains have become endemic in hospitals worldwide. Protein A is an antiphagocytic protein encoded by spa gene. spa types can be determined via amplification and sequencing of the X region of the spa gene, which contains polymorphic direct repeats. Diversity of X region causes variation in different protein A Staphylococcus aureus. Strain typing of Staphylococcus aureus is a good tool for epidemiological studies. In this research, the diversity of spa gene in staphylococcus aureus isolated from apparently healthy broiler in Ilam, Iran was established and diversity of MRSA and MSSA isolates were compared.

Methods : In this study, 200 bacterial strains were isolated from broilers in Ilam, of which 107 (53.51%) identified to the species level by standard methods such as Gram staining, blood and mannitol salt agars, catalase and oxidase testing. Isolates were confirmed as MRSA by oxacillin and cefoxitin susceptibility testing according to the CLSI guidelines. All isolates were also reevaluated for the presence of the femA and mecA genes by PCR. All nine strains of confirmed MRSA as well as one isolate of non- MRSA were then subjected to spa typing using the primers SpaF (AGACGATCCTTCGGTGA) and SpaR (CAGCAGTAGTGCCGTTTG). The amplified spa gene fragments were purified and sequenced. spa types were assigned by using StaphType software.

Results : spa typing of the 10 isolates revealed five different spa types. Repeats among the spa types varied from 4 (t4150) to 17 (t4184). Repeats among the spa types varied from five (t567 and t1184) to 10 (t002). Four isolates belonged to t011 (40%); the next majority with each two isolates was belonged to t002 (20%) and t567. Interestingly, three spa types including t304, t567 and t1184, previously not reported from Iran, were identified in this research.

Conclusion : As has been shown by other researchers, spa typing has a good discriminatory power as the current gold standard method, pulsed-field gel electrophoresis (PFGE).

Keywords : Staphylococcus aureus, MRSA, MSSA, femA, mecA, PCR, Spa typing

P446-200: Isolation, Identification and Bioproprospecting the Antibacterial Activity of Actinobacteria Associated with Chamomile sp.

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Background and Aim : Antibiotic resistance is rising dramatically worldwide. Thus, the production of new antibiotics is indispensable. Recent scientific efforts have been aimed at the bioprospecting of microorganisms' secondary metabolites, with special emphasis on the search for antimicrobial natural products derived from endophytes. Endophytes are microorganisms that inhabit the internal tissues of plants without causing apparent harm to their host. Currently, it is strongly believed that all types of plant species do anchorage endophytic bacteria (EB). The natural therapeutic compounds produced by EB do have several potential applications in medicine, agriculture and pharmaceutical industry. To investigate antibacterial properties, in this study, Actinobacteria were isolated from Chamomile sp., identified and bioprospected by morphological and molecular methods.

Methods : Samples were collected from Ilam and then divided into roots, leaves, stems and flowers. After disinfection, they were cut into 2 mm pieces and cultured on casein agar culture medium and incubated at 28 ºC for up to four weeks. Using PCR method targeting 16S rRNA gene, identification of Actinobacteria was carried out. To evaluate the antibacterial properties of the isolated Actinobacteria, the agar diffusion method was used. In parallel, frequencies for the presence of biosynthetic gene clusters, polyketide synthase-(PKS-) I, PKS-II, and nonribosomal peptide synthetase (NRPS) among isolated Actinobacteria were determined.

Results : Ninety bacteria were isolated from different parts of chamomile flowers. It was determined that 47 bacteria (52.22%) of these bacteria belong to the phylum Actinobacteria. and out of 47 bacteria, 15 isolates (31.91%) had antibacterial properties. Of these, 12 isolates (80%) exhibited antibacterial effects against Staphylococcus aureus, 2 isolates (13.33%) against Pseudomonas aeruginosa, 3 isolates (20%) against Escherichia coli and 2 isolates (13.33%) against Salmonella typhi. The results of molecular analysis of NRPS, PKS-I and PKS-II genes showed that out of 47 isolated Actinobacteria strains, 20 isolates (42.55%) had NRPS gene, 6 isolates (12.76%) had PKS-I gene and 23 isolates (48.93%) had PKS-II gene.

Conclusion : This study indicates that Chamomile sp. has a number of active Actinobacteria that produce secondary metabolites with antibacterial properties. Hence, this medicinal plant

can be a valuable source for the isolation of Actinobacteria with the potential of producing new antibiotics.

Keywords : Bioprospecting, Identification, Actinobacteria, Chamomile sp.

P447-204: Investigation of biofilm formation among clinical isolates of Klebsiella pneumoniae in Bushehr province, Iran.

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1. *auther*

Background and Aim : Klebsiella pneumoniae is a Gram-negative bacte¬rium belonging to the family Enterobacteriaceae. K. pneumoniae causes a wide range of infections, including pneumonia, urinary tract infections, bacteremia, and liver abscesses. Biofilm formation on these devices is important in the pathogenesis of these bacteria. It is a com¬plex process characterized into stages involving early attachment, microcolony formation, mature biofilm development and release of planktonic bacteria from the biofilm. This study aimed to investigate biofilm formation among clinical isolates of K. pneumoniae in Bushehr province.

Methods : : In this study, 113 isolates of K. pneumoniae were obtained from various samples referred to seven hospitals in Bushehr province in 2018. Biofilm was assessed phenotypically using microtitre plate assay. Briefly, 200µl of overnight broth culture was transferred onto microtiter plates. Following 24 hours incubation, 25 µl of 1% crystal violet was added to each well and incubated for 15 minutes. Wells were washed three times with phosphate-buffered saline, and then ethanol was added to dissolve the strain. OD values were taken at 540 nm and interpretations were made.

Results : The results revealed that 76.9% of K. pneumoniae isolates were biofilm producers, with 4 (3.5%), 33 (29.2%), and 50 (44.2%) isolates as strong, moderate and weak biofilm producers, respectively.

Conclusion : In the present study most of the K. pneumoniae isolates were biofilm producers. Biofilms have great significance for public health, because biofilm formation is one of the important features, particularly in chronic and recurrent nosocomial infections. In addition, biofilm-associated microorganisms exhibit dramatically decreased susceptibility to antimicrobial agents.

Keywords : klebsiella pneumoniae-virulance factor-biofilm

P448-211: Up-Regulation of VEGF in THP1 leukemic cells by lipopolysaccharide in vitro

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Background and Aim : Vascular endothelial growth factor (VEGF), as a cytokine, has an important role in inflammation and angiogenesis. Angiogenesis, the new vessels generation, plays an essential role in tumor invasion and expansion. Lipopolysaccharid (LPS) is an endotoxin and main constituent of surface membrane of gram negative bacteria. Besides LPS has an important role in inflammation as well as angiogenesis. In this study the effect of LPS on VEGF production in THP1 leukemic cells has been studied in vitro.

Methods : Human leukemic monocytic THP1cells were cultured in RPMI complete medium having 10% FBS. Then cells at the logarithmic growth phase were incubated with different doses of LPS for 24 hours. Afterwards the levels of VEGF in cell culture supernatants were assessed with enzyme-linked immunosorbent assay (ELISA) assay.

Results : LPS significantly augmented the VEGF production in the human leukemic THP1 monocytes in a dose-dependent manner in vitro.

Conclusion : The results of current study display that the LPS up- regulates VEGF production in leukemic monocytic THP1cells. Thus it appears that LPS might be an effective inducer / enhancer of VEGF in leukemic cells. Accordingly LPS effect on angiogenesis may be in part due to its inducting effects on VEGF. Furthermore effect of LPS on leukemogenesis may be partly due to its boosting effects on VEGF.

Keywords : THP1 cells, LPS, VEGF

P449-212: recombinant PepX peptidase from Lactobacillus fermentum hydrolyzes gliadin protein in vitro

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Background and Aim : Wheat, which is one of the leading human food staples, contains proteins called glutens which are resistant to digestion. 1-2% of the world population is allergic to gluten due to an autoimmune disorder called celiac disease and suffers irreversible intestinal tissue damage. One way to control the celiac disease is to use microbial enzymes to digest gluten peptides. Probiotics are microorganisms safe for human consumption; some have x-prolyl dipeptidyl peptidase (PepX), which can degrade these peptides.

Methods : The qualitative proteolytic activity of given microorganisms was studied in a casein-containing medium. The sequences encoding PepX of Lactobacillus fermentum isolated from dairy products was cloned in pET28a and transformed in Escherichia coli BL21 as host. The expression of PepX was induced using IPTG. The PepX activity against z-gly-pro-pNA as substrate was measured by spectrophotometry at 410nm. The wheat flour was treated with recombinant E. coli BL21 and other lactic acid bacteria (LABs) strains, and the extracted fractions of gliadins and glutenins were analyzed using SDS-PAGE with a 10-15% acrylamide gradient.

Results : The qualitative proteolytic activity of L. fermentum isolate was significantly higher than the other LABs in a casein-containing medium. The activity of the recombinant PepX showed an increase than other LABs, and its Km=0.3 µM was found the lowest value reported ever. The SDS-PAGE analysis demonstrated a remarkable reduction in gliadin fraction after treatment with the recombinant PepX because of an increase in PepX expression.

Conclusion : It seems that PepX, as a probiotic metabolite, can be an option to control gluten sensitivity by enzyme therapy since it has a high tendency to the substrate due to its low Km and high Vmax.

Keywords : gluten, celiac disease, Lactobacillus fermentum, x-prolyl dipeptidyl aminopeptidase, gliadin, probiotic

P450-219: Antibacterial activity of kefir drinks prepared under different fermentation conditions

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Background and Aim : Kefir, a complex probiotic, is a microbial symbiotic complex that is obtained from milk fermentation by kefir grains and its consumption is effective in promoting health. The biological roles of this fermented beverage and the reproductive capacity of kefir grains are significantly related to fermentation conditions such as fermentation time, temperature, stirring proportion and type of milk. The aim of the present study was to investigate the effect of different fermentation conditions on the antibacterial activity of milk fermented by kefir grains.

Methods : Activated kefir grains were added to full-fat and non-fat milk and fermentation was performed under stirred and non- stirred conditions at 25 and 37°C. After 24, 48, 72 and 120 h of fermentation, the grains were separated from kefir extract and the antibacterial activity of kefir extract against four gastrointestinal pathogenic bacteria was evaluated based on agar diffusion and using by well method. The effect of type of milk, fermentation time, temperature and stirring conditions on the antibacterial activity of kefir samples were analyzed.

Results : Analysis of variance of mean of inhibition zone diameter of the tested bacteria showed that, with the exception of the effect of temperature on the mean diameter of the inhibition zone of S. dysenteriae, all fermentation conditions tested including temperature, stirring conditions, type of milk and time had a significant effect on the antibacterial activity of kefir samples against four bacteria.

Conclusion : Considering all factors and their interactions, fermented samples at full-fat milk at 37°C, under stirred conditions for 48 h for E. coli, for 48 and 120 h for S. dysenteriae and B. cereus, and for 72 h for S. aureus showed the highest antibacterial activity.

Keywords : Antibacterial Activity; Kefir drinks; Fermentation time; Fermentation temperature; Milk type; Stirring conditions

P451-221: Antibacterial activity of several kombucha beverages prepared with different herbal teas and under different fermentation conditions

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Background and Aim : Kombucha is a sweet and sour beverage, which is obtained by the fermentation of the sugared tea with a symbiosis of yeast and bacteria, especially the acetic acid bacteria. The metabolic concentration and composition of this beverage depends on several factors, including tea type, sugar concentration and fermentation time. This study aimed at the use of response surface methodology to investigate the effect of several fermentation conditions on the antibacterial activity of several Kombucha beverages, which were prepared using four tea infusion at various fermentation times and with different sugar concentrations.

Methods : Four types of tea, including black tea, green tea, lemon verbena and peppermint with three concentrations of sugar (2, 5 and 8%), were prepared and inoculated with actively growing Kombucha culture. After 7, 14 and 21 days, the antibacterial activity of the supernatant of drinks was evaluated against four gastrointestinal pathogens including E. coli, S. dysenteriae, S. aureus and B. cereus based on agar well diffusion method. In this study, the Central Composite Design (CCD) was used in Response Surface Methodology (RSM).

Results : Results showed that increasing sugar concentration and fermentation time had a significant effect on antibacterial activity of Kombucha beverages against all tested bacteria ($P<0.001$). Also, the interaction effect of sugar concentration with tea type in increasing the zone of inhibition of all bacteria was observed. However, the interaction effect of sugar concentration with fermentation time has a significant effect on the antibacterial activity of fermented beverages against S. aureus and S. dysenteriae.

Conclusion : To achieve the most antibacterial activity of kombucha beverage against B. cereus, preparation of beverage with black tea at sugar concentration of 8% and fermentation time of 21 days was recommended. The most antibacterial activity against S. aureus was obtained by the preparation of kombucha beverages with green tea and peppermint with fermentation time of 21 days, at the levels of 2% and 8% of sugar concentrations respectively. Also, the preparation of kombucha beverages with peppermint and lemon

verbena tea with 8% sugar concentration and 21 days fermentation time was recommended to achieve the highest antibacterial activity against E. coli and S. dysenteriae respectively.

Keywords : Kombucha; Antibacterial activity; Sugar concentration; Fermentation time; Fermented beverage

P452-225: Bacteria-induced antimicrobial peptides secretion in Tenebrio molitor hemolymph

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Background and Aim : Antibiotic resistance has become a severe public health problem therefore search for new drugs has become a necessity. Today, antimicrobial peptides have been introduced as an excellent drug candidate for this purpose. Insects are one of the sources of antimicrobial peptides. This study aimed to induct the antimicrobial peptide production in Tenbrio molitor larvae hemolymph and evaluate their activity against Escherichia coli.

Methods : 106 inactive Escherichia coli bacteria were injected into the larvae hemolymph and were incubated for 48 hours then hemolymph was extracted. The larval hemolymph was injected into HPLC then fractions of antimicrobial peptides were isolated. SDS-PAGE method has been used to determine the molecular weight of extracted fractions. Anti-bacterial activities of fractions were determined against reference Escherichia coli strain by MIC/MBC protocol then toxicity and stability of fractions were evaluated by MTT assay and in the conditions of salt, temperature, pH, and pure human plasma respectively.

Results : Eight stimulated fractions were isolated from larvae hemolymph (F1 to F8). These fractions had a molecular weight range between 10-63 KD. The MIC amount of fractions (F2 to F8) was between 128-16 ?g/ml against Escherichia coli ATCC 25922. The MBC amount of fractions (F2 to F8) was between 256-16 ?g/ml against Escherichia coli ATCC 25922. All extracted fractions showed the toxicity of approximately below 25% against human Red Blood Cells and HEK293 kidney cells up to 512 ?g/ml. It found that the activity of fractions, decreased in the presence of different concentrations of salt and temperature of 45° C. Fraction F3 with a dilution of 512 ?g/ml at pH 8.5 was able to inhibit and kill Escherichia coli. Fraction F6 in 512 ?g/ml and pH 5 inhibited and killed Escherichia coli. Fraction F3 in 10% plasma had MIC equal to 64 ?g/ml, and fractions F7 and F8 had MIC equal to 512 ?g/ml in 10% plasma.

Conclusion : according to the MIC and MBC, toxicity and stability-induced antimicrobial peptides showed potent antibacterial activity against Escherichia coli. These peptides also

showed low toxicity against red blood cells and the HEK293 cell line. Extracted antimicrobial peptides are good candidates for more research against Escherichia coli and its infections in vivo and clinical trial models.

Keywords : Antibacterial activities, toxicity, stability, Tenebrio molitor larvae, Escherichia coli

P453-226: Isolation and Recognition of the Hyaline and Dematiaceae Fungi from Broiler Poultry feed in Amol City, Mazandaran

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Background and Aim : One of the important principles in controlling poultry diseases, hygiene and control of poultry feed contamination. This is because most of the inputs to poultry farms are direct and can cause disease directly in the animal and even some of them can cause poisoning by producing toxins. The aim of this study was to isolate and recognition Hyaline and Dematiaceae fungi broiler poultry diets of the city of Amol.

Methods : For this study within 3 months of July, August and September from 5 in poultry broiler rations consumed in the city of Amol, each 5 samples were tested and evaluated and the result was 8 species and the total number of fungi isolated and identified by the number 87. and in vitro in Saburodextrose agar medium containing Chloramphenicol. Were given and incubated at 28 ° C for one week.

Results : Fungi were diagnosed based on microscopic morphological characteristics. These fungi, including Aspergillus niger (10/3%), Aspergillus flavus (19/5%), Aspergillus fumigatus (19/5%), Chatmyom (2/2%) and Alternaria (10/3%), Mucor (26/4%), Penicillium (3/4%) and Acremonium (8/04% respectively).

Conclusion : Of these, only Alternaria belongs to the group Dematiaceae and Mucor belongs to the group of low fungi. Due to the fact that some of these fungi produce toxins, it is necessary to maintain standard and controlled conditions for poultry feed.

Keywords : Broiler, Dematiaceae, Hyaline, Poultry feed

P454-227: Evaluation of the frequency of different species of Aspergillus from the lungs of extinct chickens in Aviculture in Babol county

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Background and Aim : Fungal diseases make heavy damages to poultry industry perennially. High risk of aspergillosis occurrence in modern hatchery units can only be prevented by strict biosecurity rules.

Methods : In this study, by sampling the lungs of 100 extinct chickens from 20 Aviculture in Babol county are investigated in order to determine prevalence rate of Aspergillus spp. After sampling, samples were cultures in SDA medium containing chloramphenicol and after microscopically examination fungus are identified at the species level. Also, the relationship effect of bed type (roll, straw and roll+straw) and type of poultry breeding system (mechanized and non-mechanized) on isolated species was determined

Results : . Among the samples, the prevalence rate of aspergillosis was 8% that A. fumigatus and A. niger were allocated 7% and 1% of the positive samples to themselves respectively. The straw bed and the non-mechanized breeding system were the most contaminated. Statistical analysis result from K2 test showed that there was a significant correlation between Aspergillus prevalence and bed type (sig=0.050) and breeding system (sig=0.002). There was a significant differ between kind of bed type and breeding system (sig=0.000).

Conclusion : According to the results of the following study and reviewed literature, prevalence rate of fungal agents is depended to the biosecurity of poultry houses, therefore, providing solutions such as disinfection of poultry.

Keywords : Aspergillus, chikens, lung, aviculture

P455-233: Multipathogen Detection in Patients with Respiratory Tract Infections; Identification of Non-Respiratory Viruses Using Multiplex Real Time Polymerase Reaction (PCR)

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Background and Aim : Respiratory tract infections (RTIs) impose a burden on healthcare systems. Because of the overlapping clinical characteristics of RTIs and the unavailability of appropriate diagnostic techniques, the diagnosis of RTIs is controversial. Besides, prospective studies have identified more than one pathogen in 4-3% of adults and 23-33% of children suffering from community-acquired Pneumonia (CAP) by using sensitive diagnostic assays. Differentiating a viral origin from bacterial or mixed viral-bacterial infection could substantially decrease antibiotic use, avoid the associated risk of adverse reactions, reduce antibiotic resistance development, decrease hospital-acquired infections, and improve clinical outcomes. The study aimed to prompt the diagnosis of RTIs using commercial multiplex real-time PCR.

Methods : The survey undertook for two years (2019 - 2020) on 144 flu-negative immunocompetent outpatients with moderate to severe respiratory symptoms. Respiratory specimens were collected from patients, including the sputum, anterior nasal swabs, and throat swabs. Commercial multiplex PCR assays were performed on these samples.

Results : Study population consisted of females (n = 77, 53.5%) and males (n = 67, 46.5%). The mean age was 42.8 ± 23.7 years. Thirty-one (21.5%) patients were infected with only one viral or bacterial infection. Eighty-two (57%) were infected with more than one pathogen. Ninety-five (37%) and 161 (62%) tests were positive for bacterial and viral pathogens, respectively. Community-acquired Pneumonia (CAP) and atypical CAP pathogens included 17% and 10% of respiratory specimens, respectively. The predominant pathogens consisted of Human Herpes Virus 7 (HHV-7) (n = 38, 15.5%), Epstein-Barr Virus (EBV) (n = 34, 13.8%), Mycoplasma pneumonia (n = 24, 9.8%), and Human Herpes Virus 6

(HHV-6) (n = 21, 8.5%). There were associations between pathogen findings and special age categories. Fever, cough, dyspnea, and hemoptysis were associated with certain pathogens. There was no substantial difference between viral and bacterial Ct concerning gender, age group, and comorbidities.

Conclusion : The multiplex diagnostic assay provides the early detection of the pathogen spectrum and benefits patients in the clinical decision-making process. In this study, a significant proportion of non-respiratory viruses such as herpesviruses were detected in respiratory samples from immunocompetent symptomatic patients. However, the role of herpesviruses in disease worsening and complications deserves further investigation.

Keywords : Respiratory Tract Infections, herpesviruses, Co-infection

P456-234: Human adenovirus 6 identification in tonsillar tissue of children with tonsillar hypertrophy

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Background and Aim : Tonsillar hypertrophy is a common condition in children that its pathogenesis has not been fully understood. The possible role of respiratory viral infection in tonsillar hypertrophy is still under investigation. Human Adenovirus (HAdV) is one of the probable candidates, which might be involved in inducing cell growth and apoptosis inhibition, leading to a tonsillar hypertrophy induction. This study aimed to estimate the rate of HAdV genome detection, species, and types identification in tonsils of children aged 15 years and younger with tonsillar hypertrophy.

Methods : Nested PCR was performed on 50 tonsil tissues from children undergoing tonsillectomies. Subsequently, Sanger sequencing was performed and phylogenetic tree was drawn.

Results : HAdV genome was detected in 16 (32%) tissue samples in which HAdV-C6 (31.3%, 5/16) was identified as the predominant type, followed by HAdV-C1 (25%, 4/16), HAdV-C5 (18.7%, 3/16), HAdV-C2 (12.5%, 2/16) and HAdV-B7 (12.5%, 2/16).

Conclusion : This study was consistent with other studies that reported HAdV-C (87.5%) as predominant species in tonsil tissues. Interestingly, in this study HAdV-C6 was the most common identified type with the potency of latency in children diagnosed with tonsillar hypertrophy. This type of adenovirus mostly causes asymptomatic infection which results in missing this type by screening symptomatic patients. In order to achieve a better understanding of HAdVs role in tonsillar hypertrophy pathogenesis more studies should be done.

Keywords : Human Adenovirus, palatine tonsil, hypertrophy, Pediatrics

P457-245: Isolation and identification of probiotic bacteria from dairy sewage

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Background and Aim : Probiotics, live cells with different beneficiary characteristics, have been extensivelly studied and explored commercially in many different products in the world. Their benefits to human and animal health have been proven in many researchs. Consumer demands for foods promoting health while preventing diseases have led to development of functional foods that contain probiotic bacteria. Lactic acid bacteria (LAB) members, Lactobacilli as normal flora of gastrointestinal tract have beneficial effects on human health. The aim of this study is to Isolate and identify probiotic bacteria of lactobacillus strains from dairy sewage.

Methods : waste water samples were collected from a Tehran Dairy Co in accordance with standard procedures and enriched in Man-Rogosa-Sharpe (MRS) broth and isolated by growing on MRS agar medium. Small white grown colonies with a semi mucoid consistency were isolated on MRS medium. Gram-positive, catalase-negative, and oxidase-negative bacilli and coccobacilli were selected and subcultured on the new MRS agar culture medium. On new subculture, biochemical tests of sugar fermentation , CO2 gas production , acidic conditions (pH: 2,3,4) and bile salts (0.3), was assessed to investigate probiotic characteristics.

Results : Our findings demonstrated that the identified Lactobacillus spp has a suitable resistance in pH=4 (7×106 CFU/mL). In addition, The highest tolerance against to bile salts is (5×105 CFU/mL after 1h).

Conclusion : According to the results of the present study, dairy sewage is a highly potential and a cheap source for isolating Lactobacillus spps and It also give us a wider perspective to make new probiotic products.

Keywords : Lactobacillus, dairy sewage, Probiotics

P458-249: Antibiotic resistance in farmed carp in Guilan province

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Background and Aim : Aquatic diseases are considered as an obstacle to increasing production and economic development in many countries. Improper use of drugs, including antibiotics and chemicals in farms, in addition to creating resistance to microorganisms, causes the penetration of these toxic and dangerous substances into water and soil and has severely polluted the environment adjacent to farms.

Methods : This study was performed on 98 samples of sick fish with symptoms of disease, from 2015 to 2020 in farmed carp. The fish were transferred to the bacteriological laboratory of the Aquaculture Research Institute in health conditions Parts of the liver, kidneys, and spleen of the fish were sampled and incubated for 24 hours in Blood agar in a 37 °C incubator. chemical tests were performed. Antibiotic susceptibility to disc diffusion method was performed on Mueller Hinton Agar and antibiotic disks including: Chlortetracycline, Clindamycin, Kanamycin, Methicillin, Rifampin, Erythromycin, Nalidixic acid, Oxytetracycline, Gentamicin, Florfenicol, Ciprofloxacin, Enrofloxacin, Amoxicillin,Ampicillin were used.

Results : The highest level of antibiotic resistance in pathogen bacteria were against amoxicillin, ampicillin and erythromycin antibiotics (92.1%) and had the lowest resistance to fluorophenicol)5.3%).

Conclusion : To prevent bacterial diseases and hygienic management of breeding ponds, it is necessary to pay attention to the use and use of antibiotics before treatment.

Keywords : Carp, Antibiotic resistance, bacteria, Guilan province

P459-251: The effects of Galega Officinalis as ingredients of functional food on the treatments of type 2 diabetes patients

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Background and Aim : Diabetes is one of the most common endocrine diseases in the world and is responsible for the death of about 4 million people per year. Diabetes is not known as just one disease, but includes a series of metabolic diseases that are caused by disturbances in insulin secretion or insulin action, or both, and are characterized by high blood sugar. The prevalence of type 1 and type 2 diabetes is increasing worldwide, but the rate of increase of type 2 diabetes is higher than that of type 1 diabetes. The factors of this increase can be due to lifestyle changes, prevalence of obesity and decrease in physical activity. Medicinal plant, Galega officinalis led to the discovery and synthesis of metformin. Galega has long been used in traditional medicine to treat diabetes. This plant is cultivated in Iran and is considered a native plant. Galega officinalis extract shows inhibitory effects on genetically programmed cell death, which shows the normalization of the number of white blood cells containing proteins that regulate apoptosis (P53 and Bcl-2) and poly-(ADP) proteins. -ribosylated in leukocytes of laboratory mice

Methods : Administering Galega as a main ingredient of Functional cake under the 60 days control clinical trials conditions on 36 patients with type 2 diabetes has been done with filling a primary health information questioner from volunteer candidate. All blood diabetic indicator parameters have been measured properly. The data analyzed by ANOVA and the differences between groups has been done by Duncan method of SPSS software. The study was approved by the research council and ethics committee by approve No. of IR.IAU.PS.REC.1398.120 in Islamic Azad Tehran Medical Science University (pharmacy and pharmaceutical science faculty).

Results : The results of this study showed that G. officinalis with amount of 200mg comparing other three groups (including control) have proper effects on all parameters specially Fasten Blood Sugar (FBS) which can be beneficial for the treatment of diabetes.

Conclusion : Even 4th group not only reduction in FBS but also showed significant reduction of body mass Index (BMI) but further experiments with more data and longer period are required for application of the results.

Keywords : diabetes, Galega Officinalis , functional food , Medicinal plant

P460-256: Optimization of Gold Nanoparticle Production by Exopolymer of Chlamydomonas Spp

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Background and Aim : In recent years, due to the wide applications of nanoparticles in various industries, there has been a high tendency for their synthesis. Among the various methods, green synthesis is more popular because is eco-friendly and affordable. One of the most widely used nanoparticles in various industries is gold nanoparticles. Green synthesis with microorganisms can be done both intracellularly and extracellularly. One of the compounds used in the extracellular production of nanoparticles is the exopolymer of microorganisms such as Chlamydomonas .spp that is a suitable candidate for the synthesis of gold nanoparticles due to its high amount of sugars and proteins.

Methods : in this research, Chlamydomonas .spp was cultivated in two mediums, M and BBM, to produce exopolymers. In the second step the gold nanoparticles were synthesized with these exopolymers. Then according to t-test result, the best medium based on the most concentration of the nanoparticles was selected. Also, the exopolymers of two mediums, were characterized with biochemichal tests for total protein, sugar contents.

Results : According to the results, there was no significant difference between the maximum amount of the nanoparticle production with exopolymer of the Chlamydomonas .spp grew in M and BBM mediums.

Conclusion : M medium is affordable. So this medium was selected for the gold nanoparticle production. Biochemical results showed 6.56 and 5.82 mg/lit sugar and 0.983 and 0.291 mg/lit protein for exopolymers of BBM and M medium, respectively. The t-test results showed significant and no significant differences between sugar and protein contents of two exopolymers, respectively. So it is possible some contents of sugar in exopolymer of M medium, were not reduced sugar. According to these results, it is provided to produce green gold nanoparticles with a simple and inexpensive medium for Chlamydomonas .spp,

Keywords : Green Synthesis, BBM, M medium, extracellular,

P461-257: Bioremediation of Heavy Metals by Indigenous Probiotic LAB strains in Invitro Condition

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Background and Aim : The expansion of human industrial activities in the present age has led to a significant increase in the amount of heavy metals in air, water, and soil. One of the major ways of entry of heavy metals into the human body is through food chain, fruits and vegetables contamination. Probiotic Lactic acid bacteria are shown to possess the ability to aggregate heavy metals and thus represent a promising approach to decontaminating heavy metals in food and water, and possibly the gastrointestinal tract. The aim of this investigation is to select probiotics strain to reduce the contamination of heavy metals especially for in fruits and vegetables.

Methods : Effectiveness of several LAB isolates procured from Razi vaccine and Serum Research Institute, were evaluated for their ability to bind cadmium (Cd), Lead (Pb) and nickel (Ni) in in-vitro conditions. The parameters were studied under the conditions of constant pH, temperature, and contact time. All results were analyzed statistically.

Results : Seven LAB strains with probiotic properties (L. casei, L. rhamnosus, L. plantarum, L. fermentum, Ent. faecium, L. helveticus and L. acidofilous) showed different level of binding ability to the tested heavy metals. Among the isolates, L. plantarum, L. fermentum, Ent. faecium showed the highest bioabsorption efficiency and were able to adsorp Pb and Cd (99%) during 15 minutes of initial contact. However, in the case of Ni, highest biosorption rate (91.15±0.01%) was seen within 30 minutes of contact time. Overall, E.faecium showed highest adsorption of the tested heavy metals which were equivalent to 79.75±0.11, 75.28±0.05 and 83.99±0.10% for Pb, Cd and Ni, respectively.

Conclusion : probiotic strains (L. plantarum, L. fermentum and E.faecium) might be a potent natural bio-sorbent for the removal of Cd, Pb and Ni removal from fruits and vegetables.

However, further insitu studies are required to confirm their efficacy and applications for future use.

Keywords : Biosorption, Heavy metals, Lactic Acid Bacteria, Fruits and Vegetable.

P462-258: probiotics Modulate allergic asthma

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Background and Aim : Probiotics are favorable bacteria can modify composition of microbial flore in the intestine and regulate macrophages/ regulatory T lymphocytes lead to reduction of inflammation in the intestine through modulation of inflammatory cytokines. Asthma is a highly prevalent chronic disease needs continuing drug treatment and hospitalization which extremely affects quality of life. Allergic asthma initiates from immune deregulation in early childhood. Moreover role of gut microbiota on asthma initiation and development has been revealed. Besides adverse effects of early infancy infections on the immune system and asthma exacerbation have been shown. In this study impact of probiotics on allergic asthma has been reviewed.

Methods : Papers from years 1960 up to now were studied precisely in Medline. The key words "asthma and probiotics" were used. The related articles were studied and summarized.

Results : Intestinal microbiota is a reservoir of environmental ingredients. Numerous factors in the gut like early infancy infections, dietetic factors, prenatal and initial life contact to environmental contaminants like toxicants and air poisons which have adverse effects on the immune system could exacerbate the asthma. At the otherhand, gut favorable microbiota suppresses expression of certain genes in the fetal lung linked to asthma. Moreover probiotics can induce production of metabolites such as short-chain fatty acids which regulate the methylation of gene promoters in macrophages/ regulatory T cells lead to reduces lipopolysaccharide-induced inflammation in the intestiene through modulation of nitric oxide production and inflammatory cytokines expression.

Conclusion : Role of gut microbiome in immunopathogenesis of allergic asthma have been revealed by various studies. Gut microbiota products (including lipopolysaccharides), dietary interferences and immune modulation, are possible therapeutic approaches in these patients. Diet acting on gut microbiota, profoundly alters airway responses and may represent an approach to prevent asthma. Treatment with probiotics in vivo, could be ideal conditions to understand the precise mechanisms of probiotic actions and their metabolites help to development of more efficient therapeutic strategies for prevention or treatment of chronic inflammatory diseases such as asthma.

Keywords : Asthma, probiotics

P463-259: Vaccino-informatics study of Bordetella pertussis toxin subunit 1 (PTXa), Corynebacteriumdiphtheria toxin (Tox) and Clostridium tetani Tetanus toxin (TetX) to develop a tri-valent DTP synthetic protein as candidate vaccine

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Background and Aim : Vaccino-informatics study of Bordetella pertussis toxin subunit 1 (PTXa), Corynebacteriumdiphtheria toxin (Tox) and Clostridium tetani Tetanus toxin (TetX) to develop a tri-valent DTP synthetic fusion integrated protein as candidate vaccine.In this study Sequence retrieval, modelling and energy minimization of targets Modeling, Energy minimization and validations of models were done. AA47-76: TetX tetanus selected epitopes: AA226-249(cryptic epitope): PTXA Bordetella AA34-64: In this study, a fusion protein (PDT) composed of the immunoprotective S1 fragment of pertussis toxin, the full-length nontoxic diphtheria toxin, and fragment C of tetanus toxin was constructed via genetic means. first, data classification and preparation, sequencing and repair, and selection of the best analysis methods have been done using Bioedit 6.6.2 and MEGA X software, and then the identification of the ep Linear, spatial, and non-continuous balls, domains, and immunodominant regions of crystallized proteins of toxins and fimbriae are studied in all three bacteria.

Methods : Immunobioinformatic

Results : Type of prediction Server name Signal peptide & Transmembrane Topology prediction Position PTXA of epitope (immunogenic region) Linear epitope Prediction (Machine learning approach) ABCpred (Threshold setting (Default value is 0.80)) S1sububite Signal peptide:1-35 Binding site: AA60 Active site: AA69,163 Disulfide bond: 75 ↔ 235 88-112, 127-141, 170-184, 31-45, 3-17, 177-191, 163-177, 143-157 Linear epitope (Prediction by IEDB server) Kolaskar and Tongaonkar Antigenicity Prediction 39-44,72-78, 82-88, 94-99, 118-125,134-144, 152-169, 198-204, 2015-237 Emini surface accessibility Prediction 42-49, 88-94,125-130, 189-197, 201-215, 238-243 Conformational epitope Predicting discontinuous epitopes CBTope (Sequence based method, SVM threashold -0.1) 65-76, 149-164, 206-2018 DiscoTope 2.0 38-53, 96, 147-153 ELLIPRO -EPITOPE 1) 36-39, 47-58, 103-117, 126-130, 140-153, 169-224, 249-251, 260-269 -EPITOPE 2 WITH LOWER RANK): 253-257 Table 1. Predicted linear and conformational (discontinuous) B-cell epitopes of PTXA toxin by physico-chemical properties (Prediction by IEDB server) and Machine learning approaches. corresponding boxes base on their scores.

Conclusion : Type of prediction Server name Signal peptide/Transmembrane Topology prediction Position of epitope Linear epitope Prediction (Machine learning approach) ABCpred (Threshold setting (Default value is 0.86)) Tox Signal peptide: 1 – 25 Chain: 26 – 538 Domain: 26 – 212, 225 – 404 and 406 – 538 14-28, 414-428, 380-394, 350-364, 50-64, 56-70 Linear epitope (Prediction by physico-chemical properties approache) Kolaskar and Tongaonkar AntigenicityPrediction 5-18, 27-36, 50-56, 103-111, 113-121, 157-166, 182-189, 221-232, 305-316, 328-336, 353-381, 383-398, 412-420, 452-463, 493-507, 509-517 Predicting conformational /discontinuous epitopes CBTope (Sequence based method, SVM threashold -0.3) 60-103, 154-169, 2011-222, 270-271, 315-325, 407-441, 469-502, 530-537 DiscoTope 2.0 (-2.0 Threashold, Structural based method) 48-73, 92-103, 191-196, 426-438, 517-527 ELLIPRO 433-440, 450-538

Keywords : Recombinant protein, Corynebacterium diphtheria toxoid, Clostridium tetani toxoid, Bordetella pertussis fimbriae

P464-262: A qualitative investigation of the antimicrobial potential of two lactic acid bacteria supernatant against prevalent skin pathogenic bacteria

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Background and Aim : Skin is the human body's largest organ. It plays a vital role as the primary protective barrier of the body against pathogens [1]. An open wound becomes a suitable place for a wide range of microorganisms [2]. Probiotics are bacteria or yeast that confer a health benefit on the host and may have a role in preventing and treating nonhealing wounds by modulating host-microbe interactions. The most commonly used probiotics are species of lactic acid bacteria (LAB) [3,4]. In this work, we examined the ability of the supernatant of two strains of potentially probiotic lactic acid bacteria (Lactobacillus casei PTCC1608 and Lactobacillus acidophilus PTCC1643) against four of the most common primary skin pathogens including Staphylococcus aureus ATCC25923(Sa), methicillin-resistant Staphylococcus aureus (MRSA), Pseudomonas aeruginosa ATCC27853(Pa), and Pseudomonas aeruginosa PAO1.

Methods : The above Lactobacillus strains were activated for 24 h in MRS broth (Ibresco, Iran) at 37◦C in anaerobic conditions. The pH of the supernatants was measured (Table1). After filtration(0.22 mm pore size; Millipore), three concentrations of lyophilized supernatant (25mg/ml, 50 mg/ml and 75 mg/ml) were prepared using sterile distilled water as a solvent. The antimicrobial activity of supernatants was measured using agar-well diffusion [5]. The above test was also performed using neutralized supernatants of Lactobacillus strains with 8 M sodium hydroxide.

Results : According to the presented data, the diameter of the growth inhibition zone of pathogens was enlarged by increasing the concentration of the supernatants. The highest diameter of the inhibition zone (14.6±0.5 mm) against Pseudomonas aeruginosa was recorded with Lactobacillus casei PTCC1608 supernatant. No inhibition zone was observed in presence of neutralized supernatants of Lactobacillus strains.

Conclusion : A comparison of the inhibition zone produced by Lactobacillus strains supernatant suggests that Lactobacillus casei has more effective antimicrobial activity than Lactobacillus acidophilus. Besides, it was shown neutralization of supernatant of both Lactobacillus strains eliminates the antibacterial property. It seems that the antimicrobial effect of the supernatants is related to the acidic content, which needs more detailed investigations.

Keywords : Agar-well diffusion, bacterial pathogens, skin, supernatant, wound.

P465-271: Simian Virus 40 DNA in Immunocompetent Children with Respiratory Disease

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Background and Aim : Evidence of Simian virus 40 (SV40) DNA sequences or gene products has been reported in a variety of organ systems. However, the route of transmission and the significance of SV40 polyomavirus infection in human are not known. The aim of study was to characterize the frequency of SV40 infection in immunocompetent and immunocompromised patients with respiratory diseases.

Methods : Respiratory specimens (n=280) were screened for SV40 polyomavirus using real-time PCR; co-infection with other viruses was examined. Positive results were confirmed with sequencing.

Results : Of the 280 samples analyzed, 2 (0.71%) were positive for SV40. SV40 was identified in nasopharyngeal aspirate samples from children aged 8 months and 14 months who were immunocompetent. Both patients had upper or lower respiratory tract infection. Co-infections with other viruses were found in 50% of the SV40 positive samples.

Conclusion : The data suggest that SV40 can infect respiratory tract, that respiratory tract may represent a route of transmission or a site for virus persistence, and that with the high rate of co-infection, SV40 may not involved in respiratory diseases.

Keywords : Simian Virus 40; Polyomavirus; Respiratory infection; Co-infection; Immunocompetent.

P466-275: Design of shRNAs against Yaba monkey tumor virus by insulin metalloprotease-like protein gene

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Background and Aim : Yaba monkey tumor virus (YMTV) is a member of the Yata pox virus family. This virus is one of the few smallpox viruses that cause tumors during infection. The virus gets its name from the suburb of Yaba, Lagos because the first case of the virus was obtained from there. In YMTV-infected rhesus monkeys, tumors are thought to derive from histiocytes that have migrated to the site of infection. When the histiocytes are infected, they start multiplying rapidly and become multinucleated and eventually form a polyclonal tumor. Although, the host reservoir of YMTV has not been precisely defined, All pox virus infections have a zoonotic potential. it is assumed that the virus can at least partially cope the mammalian/human immune system by expressing immunomodulatory proteins.

Methods : ShRNA sequences were designed against insulin metalloprotease-like protein gene of Yaba monkey tumor virus using the www.invivogen.com/sirna-wizard website and the most effective molecules were selected using background information. For this purpose, standard search method selected and siRNA motifs with the desired size and thermodynamic properties were designed. Then, in order to design hairpin, the proposed vector and loop sequences (TCAAGAG) submitted, so the most effective shRNAs with desired restriction enzyme sites were designed

Results : One potentially effective shRNA molecule was designed. Its sequence and start target position included YabaV shRNA1: CTCATATAACTTCTAGCCGTTGAT TCAAGAGATCAACGGCTAGAAGTTATATGAG with start position of 18 of Yaba monkey tumor virus insulin metalloprotease-like protein gene gene.

Conclusion : The results showed that there are potentially effective shRNA molecules against Yaba monkey tumor virus insulin metalloprotease-like protein gene that can suppress its translation and can be considered as an antiviral approach based on RNA1

Keywords : shRNA, Yaba monkey tumor virus, insulin metalloprotease-like protein, gene therapy.

P467-276: Antifungal Resistance in Clinical Isolates of Candida albicans species complex in Southeastern Iran

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Background and Aim : C. albicans species complex, including C. albicans, C. africana, and C. dubliniensis, represent an epidemiological concern worldwide since antifungal susceptibility patterns often vary among them. We here aim to investigate the antifungal susceptibility pattern of C. albicans species complex, obtained from different clinical samples in Kerman, southeast Iran.

Methods : A total of 73 Candida albicans species complex including C. albicans (n=66), C. africana (n=4), and C. dubliniensis (n=3), were studied. All Candida isolates were tested for in vitro susceptibility to the amphotericin B, fluconazole, itraconazole, voriconazole, posaconazole, and caspofungin according to the CLSI broth dilution method.

Results : All 73 Candida isolates were susceptible to amphotericin B and posaconazole (100%). Overall, 72.6% and 13.7% of C. albicans isolates were resistant and susceptible-dose dependent to fluconazole, respectively. Besides, 32 isolates (48.4%), and 8 isolates (12.2 %) of C. albicans strains were susceptible and resistant to itraconazole, respectively. In addition, 14.2% of C. albicans isolates were resistant to caspofungin. All the C. africana and C. dubliniensis isolates were susceptible to all the tested antifungals. Cross-resistance to both fluconazole and itraconazole was observed in two C. albicans isolates.

Conclusion : This study demonstrated that for effective management of candidiasis, antifungal susceptibility monitoring of Candida species should be regularly performed since some species show a varying rate of resistance to antifungal drugs.

Keywords : Candida albicans, Candidiasis, Antifungal agents, Iran.

P468-279: Investigating the dominant microbial population and predicting anaerobic naphthalene degrading genes in the Nayband Gulf

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Background and Aim : Naphthalene is one of the polycyclic aromatic hydrocarbons found in petroleum, coal and other petrochemical products and can be a very important indicator of the petroleum originated pollution in the environment. In this study, the microbial diversity and the genes involved in the naphthalene degradation under anaerobic conditions were investigated, in the waters of the national protected area of Nayband Gulf.

Methods : The DNA was extracted from the Nayband Gulf water sample. The extracted DNA sample was sequenced using Illumina HiSeq 2500 platform (Novogene, Hong Kong), by the next-generation sequencing (NGS) technique. QIIME 2 (version 2022.2) was used to analyse 16S rRNA gene amplicon sequencing. To predict the functional genes involved in naphthalene degradation under anaerobic conditions from 16S rRNA gene sequences, we used Phylogenetic Investigation of Communities by Reconstruction of Unobserved States (PICRUSt) (version 1.1.4).

Results : Our findings indicate that the most abundant genera in the Nayband Gulf water were mainly affiliated to Spongiibacter (22%) and Alcanivorax (18.86%). It is predicted that these bacteria have the most prominent metabolic genes coding for naphthalene degradation under anaerobic conditions in their genomes, according to PICRUSt.

Conclusion : The results of this study showed that the presence of petrochemical and oil industries in the Asalouye region has affected the waters of Nayband Gulf and caused oil pollution in this region. Oil-contaminated marine environments have been shown to have increased abundance of bacteria that degrade oil pollutants. Naturally occurring Spongiibacter and Alcanivorax have a high ability to break down naphthalene and can be exploited in designing bioremediation strategies for treatment of naphthalene contaminated sites.

Keywords : Naphthalene, NGS, PICRUSt, QIIME 2, Nayband Gulf

P469-280: Molecular docking simulation of Anti parasitic properties of the main active ingredient of Nigella sativa in the inhibition of N-myristoyltransferase

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Background and Aim : N-myristoyltransferase (NMT: EC 2.3.1.97) is a key cellular enzyme which carries out lipid modification by facilitating the attachment of myristate to the N-terminal glycine of several protein molecules and is a promising drug target in eukaryotic parasites. In this study, The main active ingredient of Nigella sativa, thymoquinone, was evaluated as N-myristoyltransferase inhibitor (NMTI).

Methods : To investigate the mode of interaction of the thymoquinone with N-myristoyltransferase active site, the chemical structure of this compound was designed and optimized using HyperChem Release 8.0.10 software. the protein X-ray 3D structure of N-myristoyltransferase was received from the protein data bank. A docking study was performed by AutoDock 4.2 (AD4) software and Possible H-bonding interactions were assessed using the accelrys program.

Results : The binding energies of best docked compound was −4.78 kcal/mol and Binding model of the best docked pose of compound showed 3 hydrogen bonds by Leu160, Thr203 and TYR80

Conclusion : Considering that Molecular docking studies can be performed before wet-lab experiments to predict the mode of binding of an inhibitor with an enzyme, these in silico results can thus serve as a template for further studies.

Keywords : Anti parasitic, inhibition, molecular Docking, N-myristoyltransferase

P470-281: Risk factors and histopathological profile for unresponsive cases with anthroponotic cutaneous leishmaniasis: A case-control study on treatment outcome

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Background and Aim : Negligible data are present related to anthroponotic cutaneous leishmaniasis (ACL) treatment outcome and resultant unresponsiveness risk determinants. Over the last years, there has been a remarkable increase in the number of unresponsive patients with ACL reported worldwide. The primary objective of this study was to explore the role of demographic, clinical and environmental risk related-factors in the development of treatment failure, relapse and chronic cases compared to responsive patients with ACL. Moreover, molecular, histopathological and immunohistochemical (IHC) findings between these forms were explored.

Methods : This work was undertaken as a prospective and case-control study in southeastern Iran. Culture media and nested PCR were used to identify the causative agent. Univariate multinomial and multiple multinomial logistic regression models and the backward elimination stepwise method were applied to analyze the data. A $P<0.05$ was defined as significant. Also, for different groups, skin punch biopsies were used to study the histopathological and immunohistochemical (IHC) profile.

Results : All samples showed that L. tropica was the only etiological agent in all unresponsive and responsive patients with ACL. Data analysis represented that 8 major risk factors including nationality, age groups, occupation, marital status, history of chronic diseases, duration of the lesion, the lesion on face and presence of domestic animals in the house were significantly associated with the induction of unresponsive forms. The histopathological and immunohistochemical findings were different from one form to another.

Conclusion : Poor treatment adherence has a strong negative impact on treatment outcomes. Regular monitoring of unresponsiveness to drugs and recognition of leading factors linked with chronic, treatment failure and relapse forms of ACL is crucial for proper prophylactic and therapeutic strategic plans. The present findings clearly showed a positive association between ACL and distinct demographic, clinical and environmental risk determinants. Also, the histopathological and immunohistochemical findings will be helpful to improve our knowlege about the several clinical forms of ACL and its diverse histophatogical changes.

Therefore, to overcome this serious public health problem, clinical practitioners and health surveillance staff should be aware of and monitor such perplexing factors to be able to achieve a comprehensive control program and treatment strategy.

Keywords : Risk factors, Unresponsive, Treatment, Leishmaniasis, Case-control study

P471-286: Optimization of the bio-hydrogen production by a phototrophic bacterium

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Background and Aim : Nowadays one of the biggest concerns around the world is providing of sufficient amounts of energy, needed by countries, continuously. Despite the limitation of fossil resources, the information shows the doubling of global energy demand in the recent last decade. So looking for new sources of energy that are renewable and affordable is one of the important approach of researchers. Bio-hydrogen is the best green foul for this purpose.

Methods : In this research, three of the most important factors affecting the amount of biological hydrogen gas produced by Rhodobacter spheroeides, include the type of precursor (including sugarcane molasses, non-alcoholic beverage industry waste, and dairy industry waste), light intensity (2300, 3300, and 5300 lux) and initial pH (7, 8, and 9) were examined. The ANOVA analysis was done to select the best level of each factor. In order to examine the precursors more precisely, the physicochemical characteristics of the precursors (sugar, lipid, and protein content) were analyzed.

Results : According to the results, sugarcane molasses precursor with biological hydrogen production of 571.38 ml/l (in 4 days) medium had the highest amount of hydrogen among the studied precursors. It can be related to the type of nutrients in this substrate. Based on the characterization results of three substrates, beverage waste had the highest protein and carbohydrate content and molass had the highest fat content. Also, the light intensity of 5300 lux with a value of 727.99 ml/l medium (in 4 days) had the best result for biofuel production. It is due to increased stimulation of phototrophic systems. About the initial pH of the culture medium, it was shown that the initial pH of 9 with the production of 895.84 ml/l medium (in 4 days) was the optimum pH.

Conclusion : It can be attributed to increased tolerance to the accumulation of toxic cellular metabolites such as volatile fatty acids. Finally, this rate of biohydrogen production with an inexpensive substrate in such a short time is very important achievement in the energy field.

Keywords : Rhodobacter spheroeides, molasses, beverage, dairy, energy.

P472-288: Molecula detection of probiotic bacteria isolated from Mauremys caspica stool

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Background and Aim : In this study, 56 samples of turtles were collected completely randomly in the cities of Mazandaran province. Due to the role of probiotic bacteria in the intestine and increasing life expectancy, samples were taken from turtle feces. Probiotic bacteria were analyzed by PCR with global primer.

Methods : (Exclusive) was identified. Add one gram of sample prepared with MRS broth in a microtube with a volume of 2 ml and 1 ml of glycerol to the liquid medium and keep at room temperature until stable, then 50 Landa samples are taken from the liquid medium and cultured on MRS AGAR linear medium. Data and put it with gas pack C in the JAR and the colonies after 48 hoursAnaerobic incubation was calculated.Hot staining colonies were prepared which were used for morphological diagnosis, research and probiotic confirmation.

Results : A microbial bank was prepared from a sample of isolated bacteria. Probiotic probiotic bacteria were observed in Amol, Amirkola, Joybar, Behshahr and Gulogah counties using molecular PCR method and Lactobacillus bacteria were observed in Neka, Bahnemir, Sari, Mahmoudabad and Behshahr counties. In samples 18, 21, 25, 38, 39, 54 were Lactobacillus and in samples 10, 36, 44, 52, 56 were pediococcus.

Conclusion : According to the results obtained in this study, probiotic bacteria may have been effective in increasing the lifespan of Caspian turtles.

Keywords : MRS broth, MRS agar, gas pack C, jar, probiotic

P473-292: Co-infection of sexually transmitted pathogens with human papilloma virus in cervical sample: A multicenter study in Iran

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Background and Aim : Sexually transmitted infections (STIs) represent a main cause of morbidity in women. Human Papillomavirus (HPV) infections are among the most prevalent STIs and can cause cervical dysplasia and invasive cervical cancer. The association of other STIs with HPV cervical infection has however not yet been fully elucidated. The aim of this study was to estimate the prevalence of Gardnerella vaginalis, Chlamydia trachomatis, Trichomonas vaginalis associated with HPV-positivity patients who underwent annual routine gynecological exams from different geographical regions in Iran.

Methods : Five hundred thirty-three cervical swab samples were collected from14 different city in Iran, nucleic acid was extracted (Add bio, Korea) and G. vaginalis, C. trachomatis, T. vaginalis were detected by multiplex PCR and HPV genotyping by hybridization method (Operon, Spain). The data were recorded using Microsoft Excel 2007 (Microsoft Corp, Redmond, WA, USA) and analyzed with the SPSS software (version 16; SPSS Inc., Chicago, IL, USA). P value < 0.05 was considered statistically significant.

Results : The mean age of the participants was 34.94 years (age range: 18-63years). A total of 202 (mean range of 33.6 years) patients were found positive for HPV with 36.63% (n=74) and 33.66% (n=68) infected with high-risk type and low-risk type, respectively and 29.70% (n=60) infected with multiple types. Among the 533 women, there were 14.25% (n=76) G. vaginalis infection, 3.0% (n=16) C. trachomatis infection, 0.75% (n=4) T. vaginalis infection. Among 202 women with HPV infection 18.81% (n=38) suffered from G. vaginalis, 4.45% (n=9) C. trachomatis and 1.48% (n=3) T. vaginalis.

Conclusion : HPV infection is associated with a number of factors, including age, pregnancy, and impaired immune function. Studies showed that G. vaginalis infection and HPV infection

may have consistency or synergies. Most of the women who present HPV with G. vaginalis infection were younger than 41 years old. In HPV high-risk type, HPV31 showed the highest prevalence and in HPV low risk-type, HPV6 showed the highest prevalence. STI maybe a cofactor and a risk factor of HPV cause cervical cancer and neoplasia, however this relationship is unclear and a large number of epidemiological and molecular studies are needed.

Keywords : Molecular characterization, co-infection, Human papillomaviruses, Gardnerella vaginalis, Trichomonas vaginalis, Chlamydia trachomatis

P474-294: Dolutegravir versus efavirenz; A comparison of the effectiveness of two antiretroviral regimens in the treatment of HIV patients

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Background and Aim : HIV infection is still a public health threat, infecting over 37 million individuals worldwide. Prior to 2018, WHO guidelines regarding the recommended first-line antiretroviral therapy (ART) for HIV treatment comprised two nucleoside reverse-transcriptase inhibitors (NRTIs) in combination with a nonnucleoside reverse-transcriptase inhibitor (NNRTI) called efavirenz. Then, based on novel studies, dolutegravir, which seemed to have a more desirable profile than efavirenz, replaced this medication in the recommended first-line ART. Given that constant evaluation of the effectiveness of the first-line ART regimen is vital in achieving virological and immunological success in the treatment of HIV, we aimed to evaluate the effectiveness of two regimens; one consisting of tenofovir, emtricitabine, and efavirenz, and the other consisting of tenofovir, emtricitabine, and dolutegravir in providing the optimal virological suppression and immunological recovery.

Methods : This retrospective study evaluated HIV-positive patients who had been referred to the consultation centers for behavioral and infectious diseases in Mashhad, Iran, from March 2017 until March 2021. 43 patients who had been infected via drug injection and 87 who had been infected through sexual contact were selected, and CD4 count and viral load were assessed periodically.

Results : Among the 43 patients who had been infected with HIV via drug injection, 7 patients (15%) had immunological failure, and 3 patients (6.9%) had virological failure, according to Iran's national guidelines for HIV/AIDS care and treatment. Among the 87 subjects who had been infected with HIV via sexual contact, 3 patients (3.4%) were in the category of immunological failure, and 5 patients (5.7%) were in the category of virological failure.

Conclusion : Most cases of virological and immunological failure, as well as cases of non-adherence to treatment, were observed in patients that received the regimen containing efavirenz. In contrast, the rate of CD4 growth was higher in patients receiving the regimen

that included dolutegravir, and fewer side effects and treatment failures were seen in this group. Furthermore, the latter regimen seems to have more economic viability for the healthcare system of the country. Therefore, the use of a combination of tenofovir, emtricitabine, and dolutegravir is recommended as the first line of ART for HIV patients.

Keywords : HIV, Antiretroviral Therapy, ART Regimens, Dolutegravir, Efavirenz

P475-296: Comparison the antibacterial effect of green-synthetized nano-silver with calcium hydroxide in infected canals with Enterococcus Faecali

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Background and Aim : Endodontic treatment is a predictable process which its success rate is between 68% and 86%. The most important cause of failure of root canal treatment involves the presence of bacteria. Enterococcus faecalis is one of the most common bacteria that cause root canal treatment failed. By placing medicine inside the canal, you can prevent the growth of bacteria in the area of the canal. Calcium hydroxide, which is used as the most common medicine inside canals, cannot completely destroy Enterococcus faecalis. The use of new materials, such as nanoparticles can be promising.

Methods : In this study, silver nanoparticles were made by the green method in combination with tannic acid. Then MIC and MBC of nanosilver particles, tannic acid and calcium hydroxide were detected. Then, the MBC for each material was measured. Then the obtained concentration of the material was placed in 48 teeth that were randomly had divided into three groups (nanosilver, tannic acid, calcium hydroxide). After 24 hours, samples were taken from all the teeth and the average number of enterococcus faecalis colonies in both groups was checked together.

Results : By examining the number of Enterococcus faecalis colonies after 48 hours, it was showed that cleaning the channels by silver nanoparticles does not have significant difference by calcium hydroxide (P value > 0.5). But tannic acid showed significantly less effect than these two substances (P<0.1).

Conclusion : It seems that the use of silver nanoparticles in endodontic treatments can be as effective as calcium hydroxide and is a considerable antibacterial material for this purpose and can be a good substitute for calcium hydroxide.

Keywords : Antimicrobial effect, nanoparticle, Enterococcus Faecalis, Nanosilver

P476-306: Investigating the effect of MSI-99 antimicrobial peptide on MexAB-OprM efflux pump of Pseudomonas aeruginosa using molecular docking

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Background and Aim : MSI-99 is a Magainin antimicrobial peptide analogue derived from the African clawed frog (Xenopus laevis) skin secretions. This peptide contains 23 amino acids and has antibiotic-like activity against microorganisms using ionophore properties. The purpose of this study is investigation the function of MSI-99 peptide on MexAB-OprM efflux pump of Pseudomonas aeruginosa.

Methods : Three-dimensional structure of MSI-99 as ligand was modeled by I-TASSER server and target protein (MexAB-OprM efflux pump) of Pseudomonas p.aeruginosa was collected from Protein Data Bank according to 6IOK (PDB ID). Finally, using Patchdock (ver. 1.3) the molecular docking was studied. The clustering RMSD value was set to 4Å.

Results : Analysis of molecular docking indicates that MSI-99 peptide has inhibitory potential to the MexAB-OprM efflux pump and its binding energy is -23.76 kcal.mol-1.

Conclusion : According to our results, MSI-99 peptide has inhibitory potential to efflux pump of P.aeruginosa. Thus, it can be considered as an alternative inhibitor for the efflux pump in P.aeruginosa that is antbiotic resistance.

Keywords : MSI-99 peptide, Pseudomonas aeruginosa, Efflux pump, Molecular docking

P477-344: Synthesis of metal nanoparticles using different microorganisms

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Background and Aim : Today, nanoparticles are very important in the science of nanobiotechnology Nanoscience has grown and developed in various fields of medicine and therapy, including cancer treatment. Microorganisms do not need high pressure, temperature and toxic substances in the synthesis process. Natural microorganisms are bacteria, fungi, yeasts, algae, radionuclides and viruses.

Methods : Copper oxide nanoparticles with a diameter of less than 20 nm in doses of 30 and 60 µg/ml have relatively good antimicrobial properties and can inhibit the growth of almost all existing bacteria, especially Escherichia coli bacteria in the sample. The toxicity of silver nanoparticles, which were given orally in doses of 0.05, 0.1 and 0.2 ml (50, 100 and 200 microliters) to mice, was studied. Acinetobacter sp. SW30 An 18-h culture grown at 2.7 x 109 cfu/mL could synthesize amorphous nanospheres with a size of 78 nm at 1.5 mM and crystalline nanorods at 2.0 mM Na2SeO3 and beyond.

Results : Actinobacteria isolated from different ecosystems are known as potential synthesizers of gold and silver nanoparticles. S. atrovirens is able to produce silver nanoparticles by extracellular reduction. So far, few studies have reported the use of brown seaweed (seaweed) for the production of Pd-NPs. By synthesizing and covering Pd-NPs by PB extract, it causes the bioreduction of Pd2+. Acinetobacter sp. SW30 was found to synthesize intracellular SeNPs, which were characterized by various physicochemical techniques such as UV-Vis spectroscopy, XRD, SEM, energy dispersive X-ray spectroscopy, and TEM. Sathish et al investigated the antibacterial effects of silver nanoparticles synthesized by biological method. Also, investigated the antioxidant, antibacterial and anticancer effects of silver nanoparticles produced using Piper longum plant extract.

Conclusion : In this article, an attempt has been made to investigate the effects of nanoparticle synthesis using different microorganisms. Many microorganisms cause better results of treatment, synthesis and production. Check the effects Different microorganisms have been used in the treatment of breast and lung cancers. For example, copper oxide nanoparticles with a size (less than 20 nm) were used to investigate its effect on the genome

of Escherichia coli as a model for gram-negative bacteria. The anti-tumor effects of zinc oxide nanoparticles were shown in increasing the expression of glutathione peroxidase and glutathione reductase genes in MCF-7 breast cancer cell line.

Keywords : Nanoparticles, Antimicrobial, anti-tumor, breast, lung, cancer

P478-345: The use of actinomycetes in the production of secondary metabolites, including antibiotics, in dealing with MRSA strains

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Background and Aim : Staphylococcus aureus is one of the earliest bacteria detected in infants, children and adults with cystic fibrosis (CF). The rise of methicillin resistant S. aureus (MRSA) in the last ten years has caused a lot of attention to this organism. The most important feature of microbial bioactive compounds are that they have specific microbial producers, their diverse bioactivities and their unique chemical structure. This review trys to check anti methicillin resistant of S. aureus activity of actinomycetes isolated from soil and fresh water, because MRSA is a major health concern, as it causes numerous infections in both health care facilities and communities.

Methods : According to published papers, scientists working on actinomycetes have used a nearly identical method, first collecting samples from different sources, mostly soil, at different depths and distances, and mixing them with different compounds to make Use different jobs.

Results : That most actinomycetes are Mesophile with an optimum growth temperature of 30°C. The factors that affect the activity of actinomycetes in the production of secondary metabolites are temperature, pH, concentration of sodium chloride salt (NaCl), carbon source, nitrogen source and the best media for the growth of actinomycetes.

Conclusion : During research, it has been shown that actinomycetes found in water and sea have better antimicrobial activity against pathogenic bacteria, including MRSA strains, Also, marine actinomycetes in lower concentrations inhibit the activity and growth of pathogenic bacteria.

Keywords : Actinomycetes, Staphylococcus aureus, MRSA, CF, secondary metabolites

P479-347: Investigating the antibacterial and healing effect of medicinal plant extracts along with silver sulfadiazine in the treatment of burn infection

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Background and Aim : In the present study, extracts were first prepared from yarrow, marigold, Arnebia euchroma L and castor oil plants. Then, to determine the MIC (minimum inhibitory concentration) and MBC (minimum lethal concentration) dilution method in broth or microdilution was used. Then, to check the synergistic effects of the extracts, dilution in broth was done for each extract separately. Then, the prepared ointment was tested on an animal model that was infected with Staphylococcus aureus and Pseudomonas aeruginosa bacteria.

Methods : In the present study, extracts were first prepared from yarrow, marigold, Arnebia euchroma L and castor oil plants. Then, to determine the MIC (minimum inhibitory concentration) and MBC (minimum lethal concentration) dilution method in broth or microdilution was used. Then, to check the synergistic effects of the extracts, dilution in broth was done for each extract separately. Then, the prepared ointment was tested on an animal model that was infected with Staphylococcus aureus and Pseudomonas aeruginosa bacteria.

Results : The results of the study indicate that: aqueous and ethanolic plant extracts extracted from Arnebia euchroma L, marigold, castor oil and yarrow caused better and faster healing in burn wounds than the antibiotic silver sulfadiazine in rats

Conclusion : According to the findings of this study, it can be concluded that the extracts of these four plants together with the antibiotic silversulfadiazidin on an animal model have an antimicrobial effect against Staphylococcus aureus and Pseudomonas aerogenza bacteria and have a healing effect on wound infection caused by burns. They can be considered as an antibacterial substance or ointment

Keywords : Staphylococcus Aureus, Pseudomonas aeruginosa, Arnebia euchroma L, marigold, castor oil, yarrow, burns

P480-353: Study on correlation between Demodex mites density and blepharitis.

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Background and Aim : Demodex mites are the most common microscopic ectoparasite found in the human skin. In the eyelids, D. folliculorum can be found in the lash follicle, whereas D. brevis burrows deep into sebaceous glands and meibomian glands looking for sebum which is thought to be their main food source.

Methods : after studing many articles with key words: Demodex mites, blepharitis and tea tree oil; from databases such as Pubmed, Researchgate, google scholar and etc, data have collected

Results : blepharitis can be divided anatomically into anterior and posterior blepharitis. The former refers to infestation of eyelashes and follicles by D. folliculorum, clustering to the root of the lashes, whereas the latter involves infestation of the meibomian gland preferentially by D. brevis. The following action mechanisms have been proposed to explain the pathogenic role of Demodex in blepharitis : Direct damage, Vector for bacteria and Hypersensitivity reaction. Unlike Baby shampoo, lid scrub with TTO not only cleanses cylindrical dandruff from the lash root but also stimulates embedded mites to migrate out to the skin. As a result, daily lid scrub with 50% TTO and lid massage with 5% TTO ointment are effective in eradicating ocular Demodex infestation in vivo, as evidenced by bringing the Demodex count down to zero in 4 weeks in a majority of patients. The two treatments were equally effective in eradicating mites although we presume they may act differently. The 50% TTO has direct killing effect on the mites, whereas the 5% may interrupt their life cycle by preventing mating. Apart from Demodex eradication, TTO treatments resulted in dramatic alleviation of symptoms and marked resolution of inflammation in the lid margin, conjunctiva, and cornea.

Conclusion : Demodex mite plays an important role in the occurrence of a series of ocular surface diseases such as Demodex blepharitis, meibomian gland dysfunction, conjunctival inflammation, and corneal lesions. Ocular infestation has a close relationship with the systemic infestation. Further studies are needed for developing easy and sensitive diagnostic methods and more effective and specific treating regimens.

Keywords : Demodex mites, Blepharitis, tea tree oil

P481-355: Assessing the prevalence of certain bacterial infections in infertile and pregnant women

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Background and Aim : Infertility is one of the major health problems of patients suffering from bacterial infections. Given the high percentage of infertility, the aim of this study was to investigate the prevalence of Chlamydia trachomatis, Mycoplasma genitalium, Neisseria gonorrhoeae and Ureaplasma urealyticum in fertile and infertile women.

Methods : In the prospective study, 65 infertile patients and 54 pregnant women referred to Mahdieh Hospital in Tehran were included. After transferring of vaginal swabs to the laboratory, DNA extraction and Polymerase Chain Reaction (PCR) were performed using specific primers.

Results : Of the 65 vaginal swab specimens, the prevalence of U. urealyticum, M. genitalium, C. trachomatis and N. gonorrhoeae were as 15 (23.1%), 11 (16.9%), 9 (13.8%) and 4 (6.2%), respectively; However, these rate in fertile group was as 6 (11.1%), 3 (5.5%), 5 (9.2%) and 1 (1.8%), respectively.

Conclusion : Bacterial infections were higher in infertile group; therefore, these bacterial agents may be associated with female infertility. Timely control and treatment of infections caused by these organisms, together with other factors, can be important in prevention and treatment of the women's infertility and thereby community health.

Keywords : Bacterial infections, Infertility, C. trachomatis, M. genitalium, N. gonorrhoeae ,U. urealyticum

P482-359: Research on the relationship between Demodex mites density and redness and inflammatory dermatoses

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Background and Aim : Demodex are highly specialized mites that are normal inhabitants of hair follicles and sebaceous glands of the skin. While Demodex mites are part of the normal skin microfauna, overpopulation in man can be associated with significant disease. Finding large quantities of Demodex may play an important role in the pathogenesis of undefined and even defined inflammatory dermatoses and redness of the skin. Then, we aimed to evaluate demodex density in patients with redness and inflammatory skin condition.

Methods : Direct microscopic examination was done noninvasively from 1 cm2 of facial skin and sebum of the skin after collected was analysed for presence of demodex mites density. The patient group consisted of 100 individuals who were admitted Dermatology Clinic and were diagnosed with skin problems. The age range was 16–55 years. The control group consisted of 100 age-, sex-, and skin phenotype-matched healthy volunteers.

Results : A density of more than 5 mites/cm2 specimen has been considered to be pathogenic. Demodex mite sampling was positive in patients (73%) compared with controls (12%). The average of Demodex mite density in patinets with redness and inflammated skin was 42.66 count/cm2 and 2.73 count/cm2 in facial and scalp area, respectively. Demodex mite test was positive in 12 men (17%) and 61 women (83%) in case groups. Research has shown Demodex mite density is higher in patients with the inflammated and redness skin condition, and treatment with acaricidal agents is effective in resolving symptoms.

Conclusion : The host's immune system seems to tolerate Demodex without inflammation as a commensal when their numbers are low. However, it appears they participate in inflammation when their number increases. These inflammatory conditions may be caused primarily by infestation with Demodex mites or may be a byproduct of an eruption of colonization due to an immunocompromised state. increased number of mites is considered to cause an increase in the antigenic load, which in turn bypasses the follicles and induces an inflammatory response in neutrophils. Thus, It is important to consider Demodex mites in the etiology of unexplained or severe cases of skin diseases.

Keywords : Demodex mites, Inflammation, Redness, Dermatoses

P483-360: Methicillin-resistant Staphylococcus aureus in healthy horses in Marvdasht city

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Background and Aim : Nose is one of the most important sites of Staphylococcus aureus colonization. Methicillin-resistant Staphylococcus aureus (MRSA) populations are divided into three groups: hospital-associated, community-associated, and livestock-associated (LA). LA-MRSA is widely present among different livestock and mostly as an asymptomatic colonizer of the nose. In Iran, there is a few research on the colonization rate of S. aureus and MRSA in horses. The aim of the present study was to determine the prevalence of S. aureus colonization and MRSA in healthy horses in Marvdasht city.

Methods : Nasal swab samples of 80 healthy horses, belonging to 23 farms, were collected over a period of 7 months from Marvdasht city. By performing phenotypic methods (catalase, oxidase, mannitol sugar fermentation and coagulase tests) and PCR, S. aureus isolates were identified. Next, PCR was performed to check the presence of the mecA gene and determine methicillin-resistant strains.

Results : 20 horses were carriers of S. aureus, although none of the S. aureus isolates were resistant to methicillin.

Conclusion : It seems that the low density of the number of horses in the farms and the lack of attendance and hospitalization in veterinary clinics and hospitals could be a reason for the absence of methicillin-resistant strains.

Keywords : Staphylococcus aureus, MRSA, Horse, Nasal colonization, Iran

P484-361: Study on correlation between demodex folliculorum density and itchig

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Background and Aim : Demodex folliculorum and Demodex brevis are two species of tiny parasitic mites that live in the hair follicles and sebaceous glands of human skin, respectively. Both species are found primarily on the eyelashes and eyebrows or near the nose. Demodex infestation is relatively common, and is only rarely associated with disease. Occasionally, mite populations can expand, resulting in a condition called demodicosis, which causes itching and inflammation.

Methods : This study included 100 patients (26 male, 74 female; mean age 61_20 years) who were admitted to the Dermatology Clinic and were treated with immunosuppressive therapies for itching. The control group consisted of 100 healthy subjects (34 male, 66 female; mean age 71_ 15 years). 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 mite sampling was positive in patients (80%) and controls (12%). The average of Demodex mite density in patinets with psoriasis was 23.66 Demodex test was positive in 28 men (35%) and 52 women (65%) in itching.

Conclusion : Demodex mites live inside almost every human's hair follicles. The mites usually don't cause any problems, but if they multiply too much, they can cause demodicosis. If you have itchy, bumpy or red skin on your face, you may be infested by high density of Demodex mites

Keywords : Demodex mite, itching, density

P485-366: Assessing the prevalence of certain bacterial infections in infertile and pregnant women

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Background and Aim : Infertility is one of the major health problems of patients suffering from bacterial infections. Given the high percentage of infertility, the aim of this study was to investigate the prevalence of Chlamydia trachomatis, Mycoplasma genitalium, Neisseria gonorrhoeae and Ureaplasma urealyticum in fertile and infertile women.

Methods : In the prospective study, 65 infertile patients and 54 pregnant women referred to Mahdieh Hospital in Tehran were included. After transferring of vaginal swabs to the laboratory, DNA extraction and Polymerase Chain Reaction (PCR) were performed using specific primers.

Results : Of the 65 vaginal swab specimens, the prevalence of U. urealyticum, M. genitalium, C. trachomatis and N. gonorrhoeae were as 15 (23.1%), 11 (16.9%), 9 (13.8%) and 4 (6.2%), respectively; However, these rate in fertile group was as 6 (11.1%), 3 (5.5%), 5 (9.2%) and 1 (1.8%), respectively.

Conclusion : Bacterial infections were higher in infertile group; therefore, these bacterial agents may be associated with female infertility. Timely control and treatment of infections caused by these organisms, together with other factors, can be important in prevention and treatment of the women's infertility and thereby community health.

Keywords : Bacterial infections, Infertility, C. trachomatis, M. genitalium, N. gonorrhoeae ,U. urealyticum

P486-376: Effects of Esculin as an antimicrobial compound on pectate lyase enzyme of Pectobacterium carotovorum by molecular dynamics simulation

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Background and Aim : Esculin, a coumarin glucoside ingredient, has a wide range of roles. It has also shown anti-inflammatory, anti-oxidant. Pectobacterium carotovorum and pectate lyase (PL) as its major pathogenic factor cause a great amount of harm to products such as potatoes and onions annually. This enzyme has also proven to be the cause of methanol production in stored fruits.

Methods : Esculin as ligand and PL as receptor were downloaded from Pubchem and rcsb server, respectively. Molecular docking was done using Autodock 4.2. And also, molecular dynamics simulation was performed by Gromacs software (ver. 2021.1).

Results : The docking results determined their ?G to be -5.54 kcal.mol-1 and also demonstrated amino acids that bonded. Besides, the result of molecular dynamic simulation determined the average and standard deviations of the radius of gyration, area per residue, Root Mean-Square Deviation, Root mean square fluctuation, H-bond, and secondary structure. Pectate lyase-water interaction was considered as the control group.

Conclusion : Based on the results of current study, the effect of esculin on inhibiting the pectate lyase enzyme was concluded. And as a result, its potential to be used in industries against PL enzyme and Pectobacterium carotovorum.

Keywords : Pectobacterium carotovorum, pectate lyase, Esculin, Simulation

P487-379: Study on the routes of Demodex mites transmission

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Background and Aim : The mites Demodex folliculorum and Demodex brevis are ubiquitous and obligatory ectoparasites typically found on man, they asymptomatically inhabit the pilo-sebaceous units of adults. The two species mainly involve the face and the head, but Demodex brevis has a wider distribution on body, these mites are affecting most commonly the perioral, periorbital areas of the face, the lids and lashes. Demodex infestation is relatively common, and is only rarely associated with disease. Occasionally, mite populations can expand, resulting in a condition called demodicosis, which causes itching, inflammation, redness, acne, rosacea, hairloss etc.

Methods : after studing many articles with key words: Demodex mites, demodex transmission and demodicosis; from databases such as Pubmed, Researchgate, google scholar and etc, data have collected.

Results : Demodex mites can be found in any age groups except the new-borns who are presumably infested soon after birth by direct; it is more commonly encountered in young adult when the sebum secretion rate is at its highest. Infection can be transmitted indirectly through household items, as it was shown that the mites can long enough to remain viable outside the host, Demodex can be transferred by contaminated towels, combs, blankets, bath sponge and night clothes. In addition, practitioners often advise patients to start washing their bed sheets and pillowcases regularly in hopes of preventing re-inoculation. In severe cases, patients may even need to consider replacing their pillows altogether.

Conclusion : Demodex are permanent ectoparasite of dermatological importance and it has been shown that these mites are playing an important role in the occurrence of a series of skin diseases. Because Demodex are nocturnal, it is important to limit their ability to reproduce and migrate when they are most active. On the other hand, Transmission of demodex has proved. Demodex infection can be transmitted directly by close contact with the infected people. The mites are transferred between hosts through contact of hair, eyebrows and sebaceous glands. In addition, Makeup cosmetics used by different individuals at short intervals (from several hours to several days) can be a source of transmission of Demodex sp.

mites. These Demodex transmission ways are common but overlooked. We strongly recommend if you have density of demodex remember health tips, preferentially; in hopes of preventing re-inoculation.

Keywords : Demodex mites, Demodex transmission, Demodicosis.

P488-384: Influenza A virus and related secondary bacterial infections

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Background and Aim : Influenza infection is considered to be a serious respiratory disease in humans. Annually, epidemics or even pandemics give rise to the frequent antigenetic variations of virus surface receptors, throughout the world. Bacterial infections followed by influenza are the biggest medical concerns associated with elevated mortality rates. These high morbidity and mortality rates have become a priority in terms of health. Likewise, the economic aspects of the issue have special importance also.

Methods : In the present study, several articles have been investigated with regard to main keywords including influenza A, secondary bacterial infections and pandemics. Then, attempts have been made to summarize the information.

Results : Until this date, a number of influenza pandemics have taken place with varying morbidity and mortality rates because of secondary bacterial infections followed by influenza. However, the 1918 pandemic had the highest death rate recorded. According to investigative studies, Streptococcus pneumoniae and Staphylococcus aureus are the most common isolated bacteria in patients with secondary infections. Other bacteria, such as Haemophilus influenza, Streptococcus pyogenes, and to a lesser degree Legionella spp., are involved in these infections as well.

Conclusion : Currently, it is known that various protease enzymes intensify the influenza virus infectivity. Another important aspect of influenza occurs in the Hajj pilgrimage season and many vaccines have been made to deal with its consequences. These vaccines decrement the mortality rate, however, some have minor side effects.

Keywords : Influenza Virus, Secondary bacterial infection, Pandemics

P489-386: Infantile Botulism: One of the Multiple Etiologies of Acute Hypotonia in Infancy

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Background and Aim : Infant botulism is an uncommon disease with a challenging diagnosis which is often confused with other diseases. This is a report of a case of infant botulism with no history of honey ingestion and responds well to equine immunoglobulin due to the low prevalence and importance of the mentioned disease.

Methods : Our patient was a 1-year-old infant. The patient underwent a thorough evaluation and physical examination after being transferred to our center. Further, the infant was conscious while he had an expressionless face and bilateral ptosis. Furthermore, his crying was weak, and the inability of controlling the neck was noted when he was in his mother's arms. In addition, his pharynx was examined and also stool samples were sent for botulinum toxin detection.

Results : Laboratory tests were normal, including complete blood count differential, erythrocyte sedimentation rate, and C-reactive protein. Additionally, the analysis of cerebrospinal fluid (CSF) was normal, and CSF, along with blood and urine cultures was negative. The patient's chest radiograph was also normal. Moreover, he had no gag reflex by examining the pharynx and, in general, he suffered from hypotonia. Botulinum toxin detection was positive for C. botulinum toxin type B. Treatment was began with equine antitoxin due to the lack of Baby-BIG in our country. The initial complaints were gradually resolved after receiving two doses of equine antitoxin. Further, the patient was transferred to the pediatric ward after reducing hypotonia and improving ptosis relatively and returning gag reflex and improving nutritional status. Finally, he was relieved in a good general condition after about three and a half weeks of hospitalization.

Conclusion : In general, a strong clinical suspicion is required for the diagnosis of infancy botulism, which should be taken into consideration in any infant who presents with constipation, poor feeding, muscle weakness, and ptosis, and then specific tests should be used to confirm the diagnosis. Eventually, specific botulinum immunoglobulin should be applied for treatment prior to laboratory confirmation.

Keywords : Infantile botulism, Clostridium botulinum, Honey ingestion

P490-389: Mycoplasma pneumoniae infection among children: a systematic review and meta-analysis

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Background and Aim : Mycoplasma pneumoniae (M. pneumoniae) is a common cause of community-acquired pneumonia in children and adolescents, which can be fatal in certain cases. Identifying the incidence and severity of this infection in individuals under the age of 18 can assist to improve the treatment and prevention process. In the present study, we aimed to evaluate the frequency of M. pneumoniae infection in young patients.

Methods : Three major databases, including Medline (via PubMed), EMBASE, and the Web of Science, were carefully searched and reviewed for original research articles available in databases and published between 2000 to 2020. STATA (version14) software was used to interpret the data.

Results : Of the 4515 records selected from the databases, 77 studies fulfilled the eligibility criteria to evaluate the prevalence of M. pneumoniae infection among children. The analyses revealed that the prevalence of this infection in young patients was 22.5%. Our analysis based on published data showed that 10 to 18 years age group had the highest prevalence of the M. pneumoniae equal to 23.1% [(95% CI) 6.7-39.4], followed by 5 to 10 years age group with 21.6% [(95% CI) 17.9-25.3], and under 5 years age group with 20.9% [(95% CI) 16.7-25.1].

Conclusion : It is reasonable to conclude, based on the findings of this study that the rate of M. pneumoniae infection has been increasing since 2001. Finally, more extensive studies on the prevalence of M. pneumoniae infections in children throughout the world are needed to assess its exact prevalence and antibiotic resistance trend.

Keywords : Mycoplasma pneumoniae, Children, Infection, Meta-analysis

P491-394: Separation of alkaliphilic indigene reducing agent bacteria from Iron mine wastewaters and using them to eliminate cyanide from solution

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Background and Aim : Mining effluents such as tailings, wastewaters, acidic mine drainage, etc., harm the environment and fauna. Biological treatment is a proven process for such pollution: Cost-effectiveness and eco-friendliness, sustainable, non-toxic, and inexpensive advantages of using bacteria. Several Bacteria species in appropriate conditions could effectively reduce the toxicity of cyanide into less toxic products like Bacillus and pseudomonas sp.

Methods : In this study, bacterial strains W1b, W2, and S1 were isolated from Choghart Bafgh Yazd wastewaters based on the method of serial dilution. Three strains W1b, W2, and S1 were used in a cyanide solution. The density of cyanide solution was tested.

Results : Laboratory results indicated strain S1 could have a better result with a 68% removal rate in 24 hours in 50 ppm density.

Conclusion : Biological treatment can be less expensive but as effective as chemical methods. Under laboratory condition cyanide could be destructed by bacteria.

Keywords : Water pollution, Heavy metals, Cyanide, Bacterial strain, Bio absorption

P492-395: Bacterial synthesis of spinally multi metallic Nanoparticle by indigene Iron mine bacteria

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Background and Aim : Synthesis of metal nanoparticles has become extinct owing to costly and hazardous material by physicochemical methods. Biological nanoparticle synthesis is relatively simple, cheap, and environmentally friendly. The biological synthesis of nanoparticles was performed using microorganism, such as algae, yeast, fungi, and bacteria. In this article, the biosynthesis of metallic nanoparticles by bacteria is highlighted.

Methods : Bacterial strains W1b, S1, and W2 were isolated from the Choghart iron mine in Yazd. Three strains and a consortium W1b, S1, W2 were used to synthesize spinally multi-metallic nanoparticles.

Results : Strain S1 and consortium of all three strains showed better nanoparticle synthesis results.

Conclusion : Microorganisms such as bacteria may be a suitable candidate for the biosynthesis of nanoparticles cause of having a high growth rate, eco-friendly, non-toxic, and low-cost synthesis.

Keywords : Microorganism, Green synthesis, Nanoparticles, Choghart iron mine

P493-399: Probiotic and its relationship with diseases

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Background and Aim : Probiotics are a group of useful bacteria that enter the body orally and can play a role in the prevention and treatment of some diseases. The therapeutic effects of probiotics were first discovered in the 19th century, when a reduction in the population of bifidobacteria was observed in children who had diarrhea, and it was found that oral consumption of bifidobacteria could improve gut health. According to the World Health Organization (WHO) in 2001, probiotics are living microorganisms that, if administered in sufficient amounts, provide health benefits to humans. Usually, most species that have probiotic properties are Bifidobacterium and Lactobacillus species.

Methods : : In order to get information about probiotics and its relationship with various diseases, we searched in indexes such as Pubmed, SID, Silivika, and 12 articles related to this topic were examined, this search was done using the keywords of probiotics. , human intestinal microbiota, digestive diseases have occurred.

Results : Probiotics are used in the treatment of various diseases, including systemic and infectious diseases such as acute diarrhea and Crohn's, cardiovascular disease, genital tract infection, oral and pharyngeal infection, some cancers, food allergies, lactose intolerance, cystic fibrosis, It is used to reduce antibiotic-related side effects, oral and dental disorders, prevent tooth decay, periodontal disease, and treat bad breath. Probiotics are also effective for improving intestinal homeostasis, intestinal growth and protection against pathogenic bacteria, so that in homeostasis, harmful bacteria are reduced in an acidic environment, and beneficial bacteria grow well in an acidic state and cause them to multiply. become Probiotics can be prescribed to control and prevent intestinal diseases such as diarrhea, inflammation or cancer.

Conclusion : Probiotics must be alive during preparation and must be alive in the intestinal tract in order to exert their effect. Probiotics are safe. There have been many studies on the effect of probiotics in the treatment and prevention of diseases, but these studies are in the beginning and the need to determine the efficiency, effective dose, duration of action and the mechanism of action of different types and strains of probiotics needs more study, has it.

Keywords : probiotics, human intestinal microbiota, gastrointestinal diseases

P494-405: The Role of Viruses in Preventing Anoikis and Tumor Spread

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Background and Aim : A specific type of programmed cell death called anoikis occurs when cells are severed from the extracellular matrix. Most cancer cells obstruct anoikis from spreading by metastasis. One factor contributing to the resistance of cancer cells to anoikis is viral infections. This article focuses on how cancer-causing viruses help cancer cells prevent anoikis.

Methods : Web of Science, PubMed, Scopus, and Science Direct databases were evaluated screening literature published online for factors in the resistance of viruses in anoikis. Articles from the start to March 2021 were searched, and the search was only conducted in English. The literature was searched by using following key words: oncogenes, anoikis, programmed cell death, metastasis, and cancer.

Results : Oncovirus resistance to anoikis is a powerful method by which virus-infected cancer cells can colonize new places, disseminate to other organs, and endure. Consequently, viruses can quickly spread throughout the body, and healthy, normal cells can also catch an infection in this way.

Conclusion : For appropriate cell proliferation and tissue homeostasis, proper cell-ECM interactions are required. When these relationships are disrupted, a process called anoikis, a type of cell death, occurs, which allows cancer-causing viruses to live, migrate to other organs, and infiltrate infected cancer cells. New areas are where the virus is active. Consequently, viruses can quickly spread throughout the body, and healthy, normal cells can also catch an infection in this way. Identifying effective therapeutic platforms for treating virus-related malignancies may be aided by future research to acquire an excellent knowledge of how cancer-causing viruses alter anoikis inhibition.

Keywords : Carcinogenic viruses, Anvikiz, Planned cell death, Metastasis, Cancer

P495-409: The use of microalgae in the production of functional foods

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Background and Aim : Microalage are microorganisms with a singular biochemical composition including several biologically active compounds with proven pharmacological activities such as anticancer-antioxidant and anti-inflammatory activities among others. These properties make microalgae an interesting natural resource to be used as a functional ingredient, as well as in the prevention and treatment of diseases, or cosmetic formulations.

Methods : Utilisation of microalgae in multiple scopes has been growing in various industries ranging from harnessing renewable energy to exploitation of high value products. Moreover this work discuss the advantage-potential new beneficial strains-applications-limitations-research gaps and future prospect of microalgae in industry.

Results : The interest in microalgae for industrial applications has been growing in the last decade due to the vast collection of high value biologically active compounds produced by this group. These bioactives are associated with several pharmacological properties, which have been demonstrated to promote beneficial effects for human health.

Conclusion : In conclusion, it is vital that more efforts should be taken in developing multifunctional range of products, that are affordable and is inter-related with nutritional science that could cater for even more health benefits comparatively to the ones in current market. These findings would bring much more insights into the vast potentials of microalgae-derived metabolites that remain to be explored and assessed. Further roadmap towards enhancing phycoeconomy is recommended by uplifting the current biological and technology process by taking into account on sustainability and environmental benefits.

Keywords : microalgae; bioactive compounds; functional food; cosmeceuticals

P496-412: Relationship between Bacterial Genital Infections in Pregnancy Outcomes: A Systematic Review and Meta-Analysis

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Background and Aim : Bacterial infections represent one of the most serious infections in the world, which may bring about consequences such as miscarriage, premature birth, stillbirth, and ectopic pregnancy in pregnant women. The aim of this study was to investigate the relationship between bacterial infections and pregnancy outcomes through a meta-analysis.

Methods : Searching international databases PubMed (Medline), Scopus, Web of Sciences, and Embase (Elsevier) from January 2000 to December 2018 was performed in this meta-analysis using appropriate keywords terms to identify related articles. After retrieving articles in these databases, screening was performed based on the title, abstract and full text of the articles, and the final related studies were selected and evaluated using the Newcastle Ottawa scale checklist.

Results : : The results showed that the risk ratio of preterm delivery in the pregnant women with vaginal infections was 1.57 (95% CI; 1.46-1.67), while the risk ratio of abortion was 2.02 (95% CI; 1.72-2.38).

Conclusion : Bacterial infections increase the risk outcomes of pregnancy such as miscarriage, premature birth, ectopic pregnancy and stillbirth, giving rise to unimaginable and irreparable complications in the fetus with enormous economic costs.

Keywords : Bacterial infection, Premature delivery, Abortion, Ectopic pregnancy, Stillbirth

P497-420: Using the Plackett-Burman design in optimization of cultural parameters of probiotic Lacticaseibacillus casei isolated from dairy products

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Background and Aim : Probiotics are live bacteria with valuable properties on human health. These bacteria or their by-products are used as preservatives in many products. The Lacticaseibacillus casei is one of the well-known bacteria in the probiotic industry. One of the most important and primary steps in probiotic manufacturing is optimizing biomass production. The mathematical and statistical models, such as the Plackett-Burman and the central composite experimental design, are suitable methods for recognizing the importance of various factors in industrial design and optimization.

Methods : Twenty-five samples of local dairy products from rural areas in Tehran province were collected. One of the best strains in terms of biomass production was L. casei, which identified by biochemical tests and selected due to its probiotic properties such as acid resistance, bile resistance, lethal effect on pathogens, etc. The strain was confirmed by 16S rRNA molecular exam. The influence of various parameters, such as mineral elements, nitrogen and carbon sources, and initial pH of culture media was experimented by Plackett-Burman model and optimization process carried out via the central composite experimental design.

Results : The first-order mathematical model based on Plackett-Burman design indicated that dextrose, primary pH, meat extract, sodium pyruvate, and ammonium citrate significantly influenced on biomass production of the examined L.casei. The modified quadratic polynomial regression confirmed that maximum biomass production could be achieved by using of dextrose (13.25 g/l), primary pH (5.6), meat extract (3.86 g/l), sodium pyruvate (2.94 g/l), and ammonium citrate (1.55 g/l).

Conclusion : This optimization process can be useful for the industrial production of the local strain of L.casei in the industry of probiotic supplements.

Keywords : Lacticaseibacillus casei, Probiotic, Dairy products

P498-424: Antibacterial and antibiofilm activities of nanoemulsion containing Nigella sativa essential oil on multi-drug resistant strains of Staphylococcus aureus and Pseudomonas aeruginosa.

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Background and Aim : Multidrug-resistant (MDR) bacteria are an increasing threat to public health, leading to the constant use of higher doses of antibiotics. Nigella sativa essential oil (NS) has antibacterial properties attributed to its thymoquinone. On the other hand, nanoemulsions (NE) can increase the penetration of the active ingredients. Therefore, this study aimed to investigate the antibacterial and antibiofilm activities of NE containing NS (NE-NS) on MDR strains of Staphylococcus aureus (Staph.A) and Pseudomonas aeruginosa (Pseudo.A) isolated from hospital patients.

Methods : After analysis of compounds of NS using GC-MS, the most stable NE-NS was prepared using 5% NS, 30% (v/v) surfactant (17.64% Tween-20 and 12.36% Tween-80), and 65% (v/v) of the aqueous phase and was characterized by the dynamic light scattering (DLS) method. Then antibacterial and antibiofilm activities were determined by minimum inhibitory concentration (MIC) and minimum biofilm inhibitory concentration (MBIC), respectively, using broth microdilution

Results : GC-MS analysis showed 8 hydrocarbon monoterpene components which thymoquinone being the most primary with 92.96%. DLS showed a mean droplet diameter of 58.7 nm with a polydispersity index of 1.016. There is a significant decrease of MIC on the Staph.A. for NS compared to NE-NS from 1.56 to 0.19 µl/ml (4 fold) and a significant decrease of MBIC from 12.5 to 6.25 µl/ml (2 fold). However, these activities were not significant to Pseudo.A.

Conclusion : Thymoquinone is an active ingredient that had more antibacterial and antibiofilm activities on Staph.A. than Pseudo.A., which these activities improved by NE

only about Staph.A. This can be due to the lipopolysaccharide cell wall in Gram-negative Pseudo.A, which prevents active compounds from entering the cytoplasmic membrane.

Keywords : Nigella sativa essential oil, Nanoemulsion, Antimicrobial, antibiofilm, multidrug-resistant

P499-429: Evaluation of Antibacterial Combination Activities of Honey and Alcoholic Extract of Crocus sativus Plant on Staphylococcus aureus: An in vitro Study

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Background and Aim : Bacterial resistance to antibiotics is one of the world most urgent public health and development threat in this century. Accordingly, search for new drugs continues. Today, medicinal plants are known as a source of antimicrobial agents. The purpose of this study is to evaluate the antibacterial combination activities of honey and alcoholic extract Crocus sativus on Staphylococcus aureus by in vitro experiments.

Methods : We prepared the alcoholic extract of Crocus sativus plant and lyophilized the plant extract and honey. Then, the antibacterial activities of these two compounds were examined separately and the combination of honey with alcoholic extract of Crocus sativus plant, respectively with proportions of (50%, 50%), (75%, 25%), (25%, 75%) was determined by the minimum inhibitory concentration (MIC) and minimal bactericidal concentration (MBC) against reference bacterial strain in accordance with the Clinical and Laboratory Standards Institute (CLSI) guideline.

Results : Crocus sativus exhibited more potent antibacterial activities against Staphylococcus aureus rather than compounds that we determined. Geometric means of MIC for Crocus sativus were recorded at 1 mg/µL (Staphylococcus aureus).

Conclusion : Due to the equality of MIC and MBC results of Crocus sativus alcoholic plant extracts and also because of the presence of active antibacterial substances in this plant, alcoholic extract of Crocus sativus plant can be a good substitute for the treatment of infections caused by Staphylococcus aureus.

Keywords : Antibacterial activities, Crocus sativus, Staphylococcus aureus, in vitro

P500-434: Investigation of allergenicity of antimicrobial peptides Magainin and MSI-99 using in silico method

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Background and Aim : Due to the increasing use of antibiotics and the increasing resistance of microorganisms to them, it will be important to study to find alternative compounds for antibiotics. Antimicrobial peptides can be used as an alternative to antibiotics. Magainin peptide and its analog MSI-99 contain 23 amino acids and have a cationic and hydrophobic structure. These peptides cause damage to the cell membrane by creating alpha-helical ion channels. The purpose of this study is to investigate the allergenicity of these peptides using the In silico method.

Methods : In this study, the MSI-99 and Magainin protein sequences were received from the gene bank. The complete sequences of these peptides were then searched in the Allergen database at "http://www.Allergenonline.com" and the Allermach database at "http://www.allermatch.org". In this way, the complete sequences and the sequences of six to eight amino acids were compared with the allergen sequences in the database, respectively. Then, the sequences of these peptides were enzymatically digested with pepsin and trypsin enzymes in silico, and the resulting fragments were examined in terms of allergenicity.

Results : The results of MSI-99 antimicrobial peptide homology study with different methods did not reveal any allergenicity. The fragments obtained from the enzymatic digestion of MSI-99 also had no match with the allergen peptides in the database.

Conclusion : According to the rules of WHO and FAO regarding complete sequences and short peptide sequences, a similarity of more than 55% and 95% with allergen sequences can be significant. Our results proved that Magainin and MSI-99 peptides are not allergenic. Therefore, this research can solve the concerns related to the use of these peptides as a suitable alternative for antibiotics.

Keywords : Allergenicity, Antimicrobial peptide, Magainin, MSI-99

P501-440: Determination of Antimicrobial Susceptibility Testing of Acinetobacter Baumannii and Escherichia coli Isolates from The Heart Blood of Aborted Fetuses in Shiraz, Iran

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Background and Aim : Fetal abortion is one of the critical and controversial issues in most societies' scientific, social, and academic communities due to known and unknown reasons. Furthermore, updating our knowledge about isolated bacteria, their antibiotic resistance pattern, and related factors might be essential for designing and implementing appropriate interventions. The current study was conducted to determine the prevalence of Acinetobacter baumannii (A. baumannii) and Escherichia coli (E. coli) among aborted fetus cases and demonstrate the antimicrobial susceptibility of isolates.

Methods : For this, 153 blood samples were collected percutaneously from the heart blood of aborted fetuses 1-15 hours after birth from 2016 to 2017 at the medical laboratory of Hazrat Zeinab, a major referral hospital for obstetrics and gynecology teaching, Shiraz, southwest Iran. Subsequently, the identification of A. baumannii and E. coli and evaluation of antimicrobial susceptibility testing were performed.

Results : Generally, 51 out of 153 test cultures were positive: including 34 A. baumannii and 17 E. coli isolates. The highest antibiotic resistance was determined against gentamycin and amikacin, while polymyxin B has revealed the highest activity against A. baumannii and E. coli.

Conclusion : The present study suggests that since most of the isolated bacteria were environmental isolates with high antibiotic resistance, such bacteria might be considered the causative agents of abortion in our region. Therefore, it seems that following the general hygiene of pregnant mothers is essential. However, further evidence of a clinical correlation between the isolated bacteria from aborted fetuses and their mothers is required.

Keywords : A. baumannii, , Aborted fetuses, Antimicrobial susceptibility testing, E. coli

P502-441: Prevalence of Mycobacterium avium subsp. paratuberculosis in subclinically infected dairy cattle in Mashhad by Ziehl-Neelsen staining, culture, and PCR

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Background and Aim : Mycobacterium avium subsp. paratuberculosis (MAP) is the cause of Johne's disease in domestic and wild ruminants. Clinically, infected cattle show signs of emaciation, diarrhea, and finally death, but subclinically infected that do not have clinical symptoms can alternately shed MAP through feces and milk and infect other herd animals and increase the risk of infection. The main goal of this study was to identify the prevalence of this disease in the dairy herd by performing Ziehl-Neelsen staining, the culture of feces samples, and molecular testing.

Methods : For this purpose, 348 samples were collected from 15 dairy farms randomly and subjected to these tests. ZN staining of feces samples and PCR nucleotide sequence related to specific gene fragments (IS900, F57) MAP was performed. Also, after decontamination with a solution (0.75% HPC), all the samples were cultured on Herrold's egg yolk agar special culture medium.

Results : PCR test of feces samples, 116 samples (prevalence 33.3%), ZN staining 23 samples (6.6% prevalence), and culture of feces samples only 15 samples (prevalence 4.3%) were infected with MAP. Results were analyzed to determine associations and levels of agreement between pairs of tests. The comparison of the results of the tests shows a poor agreement (kappa statistic: 0.12) between the results of PCR and ZN staining and the highest kappa coefficients (kappa statistic: 0.89) between the PCR tests and feces culture.

Conclusion : This study highlights the advantages of PCR for the detection of MAP in subclinically infected cattle, in comparison with ZN staining and fecal culture. Identification of these shedding animals is extremely important for the prevention of the spread of MAP infection in an animal herd. Due to the relatively high sensitivity and specificity oPCR, it can be applied to test for MAP at the herd or individual level, regardless of animal age or production stage. PCR will allow early detection and control of MAP in any population at risk.

Keywords : Johne's disease, Mycobacterium avium subsp. paratuberculosis, Ziehl-Neelsen, Iran

P503-442: EPIYA Motif Genetic Characterization from Helicobacter pylori Isolates in Distinct Geographical Regions of Iran

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Background and Aim : This study aimed to determine the current EPIYA motifs of the cagA gene in Helicobacter pylori isolates from patients with gastric disorders, and evaluate the association between these patterns and the clinical outcome of H. pylori infection in different geographical regions of Iran.

Methods : We examined 150 patients with gastrointestinal disorders from the central and eastern regions of Iran. The detection of H. pylori and screening of cagA was performed by polymerase chain reaction (PCR). The pattern of the motifs was determined by PCR followed by sequencing.

Results : The overall prevalence of H. pylori was 66.3% in eastern (Mashad) and 50.6% in the central (Isfahan) part of Iran. The frequency of cagA-positive strains in Mashad and Isfahan were 63.4% and 56.7%, respectively. The pattern of EPIYA motif was as follows: 43 (79.6%) ABC, 7 (12.9%) AB, 4 (7.4%) ABCC, and one (1.9%) ABCCC. We also identified a novel EPIYA C sequence motif which showed association with gastric cancer (GC). The relationship between the frequency of specific EPIYA motifs and GC was statistically significant ($P < 0.05$).

Conclusion : This is the first report for the determination of the cagA EPIYA motif of H. pylori in the Northeast and center of Iran. The prevalence of cagA positive H. pylori between the two regions was significant ($P \leq 0.05$). All isolates of the H. pylori cagA were western type (ABC). The increase in the number of EPIYA-C repeats was associated with GC ($P \leq 0.01$).

Keywords : CagA , gastric cancer, gastrointestinal diseases, Helicobacter pylori, Iran

P504-446: A new pathovar of Pseudomonas amygdali as causal agent of bacterial leaf spot and die-back of hazelnut

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Background and Aim : Hazelnut (Corylus avellanae), a plant native to the temperate northern hemisphere, is cultivated in Iran mainly in the northern parts of the country. Irregular reddish-brown necrotic spots on hazelnut leaves and fruit bracts were observed during 2018 and 2019 in hazelnut orchards of the Guilan province. The objective of the present study was identification of the causative agent of hazelnut leaf and bract spot.

Methods : Samples of hazelnut leaves and fruits showing necrotic lesions were collected from orchards in several locations of Guilan province, northern Iran, in the growing seasons of 2018 and 2019. Pathogenicity assays were performed on two years old hazelnut trees cv. Alamut. All strains were subjected to phenotypic assays including LOPAT and GATTa tests. The housekeeping genes gyrB, rpoB, rpoD, gapA, and gltA of four pathogenic strains were partially amplified, sequenced and Phylogenetic trees were constructed.

Results : Symptoms observed on the affected hazelnut trees consisted of water-soaked, small angular lesions, which subsequently turned into reddish-brown necrotic areas. When the lesions expanded, they coalesced and necrotic blotches were formed leading to wilting of leaves and defoliation. Dieback of the defoliated branches followed. Isolation from symptomatic tissues yielded bacterial colonies, which were selected for characterization. Thirty-five strains proved to be pathogenic on hazelnut. All strains were Gram negative, produced a fluorescent pigment on King's medium B and a hypersensitive reaction on tobacco. Thirty-five strains belong to LOPAT group Ia (+—— +) and positive for gelatin liquefaction and aesculin hydrolysis but negative for tyrosinase activity and tartrate utilization (G+A+T-Ta-). Phylogenetic analyses based on partial sequences of the five protein-encoding housekeeping genes indicated that the representative strains were identical to each other and formed a branch in the phylogram among other pathovars of Pseudomonas amygdali.

Conclusion : Based on phenotypic and pathogenicity characteristics and phylogenetic affiliation, the bacterium inciting a not earlier described hazelnut disease, appears to be a novel pathovar of P. amygdali, for which here provisionally is named P. amygdali pv. corylicola.

Keywords : Corylus avellanae, Bract Spot, Multilocus Sequence Analysis, Iran

P505-463: A review of the antimicrobial and anti-biofilm effects of Quercetin as a possible candidate for treating infected patients with pseudomonas aeruginosa

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Background and Aim : Pseudomonas aeruginosa is a ubiquitous Gram-negative bacterium that causes nosocomial infections furthermore death in patients with compromised immune systems. This bacterium is highly notorious for being resistant to antibiotics in the clinical site due to the ability of this bacteria to produce biofilm. Many studies have shown that plant flavonoids such as Quercetin possess various biological activities such as antimicrobial and anti-biofilm. this study aimed to review the antimicrobial and anti-biofilm effects of Quercetin as a possible candidate for treating infected patients with pseudomonas aeruginosa.

Methods : The present study is a review study by searching reputable scientific databases such as Pubmed Google scholar, Scopus from 2011 to 2022 using the keywords Quercetin, Pseudomonas aeruginosa, Anti-microbial, Anti-biofilm, Treatment Latest information obtained.

Results : In this study, 35 articles were found and reviewed. Quercetin (QUE) is a natural flavonoid found in many foods such as apples, onions, and tea. A study showed that the minimum inhibitory concentration (MIC) for Quercetin against Pseudomonas aeruginosa is 80 µg/mL. Another research showed that Quercetin can inhibit 100% of bacteria at a concentration of 500 µg/mL. The antibacterial activity of Quercetin is carried out by inhibiting the nucleic acid synthesis, and the toxic activity of Quercetin on Pseudomonas aeruginosa is known to be due to its effect on proton pump activity and quorum sensing modulation. las and rhl systems are quorum-sensing pathways in Pseudomonas aeruginosa, and Quercetin by knockout of these genes, in addition to inhibiting QS, suppresses biofilm-associated genes and significantly reduces initial bacterial adherence and swarming motility. Studies show that Quercetin can inhibit Pseudomonas aeruginosa PAO1 biofilm formation at a concentration of 8-64 µg/m. In addition, this plant flavonoid has a great protective effect on HEK 293T cells infected with Pseudomonas aeruginosa. Quercetin at concentrations above 10,000 µg/mL had negligible cytotoxicity (3.8-4.8%) on cells.

Conclusion : Due to its antibacterial and anti-biofilm activity against multi-drug resistant isolates, as well as its cytoprotective activity during infection and negligible cytotoxicity at

very high concentrations, Quercetin as a QS-based antibacterial/anti-biofilm drug can be a unique candidate to replace common antibiotics against Pseudomonas aeruginosa. The results require additional confirmation in animal models.

Keywords : Quercetin, Pseudomonas aeruginosa, Anti-microbial, Anti-biofilm, Treatment

P506-465: Occurrence of Klebsiella oxytoca as causal agent of palm date offshoot rot

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Background and Aim : Date Palm (Phoenix dactylifera) as a subtropical product abundantly is cultivated in Khuzestan province. Palm offshoot rot disease was observed in some major palm groves in Khuzestan province during 2019-2021. The objective of this study was identification of the causal agent of date palm offshoots rot based on confirmation of strains pathogenicity and polyphasic taxonomy approach.

Methods : Ten samples were collected from affected palm groves of Ahvaz, Abadan, Khorramshahr, Hamidiyeh, Shadegan, and Karun. Samples were surface disinfected and were grinded with a sterile mortar and pestle. Five µl of resulted suspension was spread on nutrient agar medium. Pathogenicity of strains was confirmed by inoculating petioles and rachises of young two- or three-years date palms cv. Estameran. Common phenotypic assays were performed. Two housekeeping genes, gyrB and infB, of three representative strains were partially amplified; sequenced and Phylogenetic trees were constructed. ,

Results : The disease was characterized with yellowing and dryness of leaves, softening of central bud with brown color. A total of 25 strains with milky colonies were isolated appeared after 48 h incubation at 28ºC. Fifteen strains caused soft rot at the inoculation site on petioles and rachises after 10 days. Strains were negative in Gram reaction, oxidase starch hydrolysis and arginine dihydrolase. However, strains were positive in catalase, gelatin liquefaction, and growth on 4% NaCl medium. All strains were able to rot potato. The MLSA phylogenic tree based on the concatenated partial sequences of two housekeeping genes, gyrB and infB revealed that three representative strains, PA87, PA124 and PA154 strains clustered with Klebsiella oxytoca DSM5175T with 100% bootstrap.

Conclusion : The results indicated that the sequences of the two housekeeping genes, gyrB and infB were verified to be of high differentiation ability in the taxonomy of Klebsiella at the species level. K. oxytoca is an opportunistic human pathogen. Moreover, it has been

identified as agent of soft rot in potato of South Indian. To the best of our knowledge, this is the first report of K. oxytoca causing palm offshoot rot.

Keywords : Common pathogens, Emerging pathogens, MLSA, Phoenix dactylifera, Iran.

P507-480: Isolation and identification of nanocellulose producing bacteria from vinegar

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Background and Aim : Bacterial cellulose is a biopolymer with unique properties that has many applications in all fields from industry to medicine. It has a good potential as wound dressing because it provides a moist environment for wound healing and can significantly control wound exudate. Due to its many applications, the production and optimization of nanocellulose from native strains has received much attention in recent years.

Methods : Native bacterial cellulose producing strains were isolated from ten local vinegar samples. Bacterial cellulose was produced statically in Hestrin Schramm (HS) medium at 28° C for 7 days. The wet and dry weight of the purified nanolayer were recorded and the water holding capacity was determined. The best isolate was selected and identified by different phenotypic methods and 16S rRNA gene sequencing.

Results : Two isolates, namely S2 and C, were isolated from vinegar samples. Both strains were Gram negative non-motile short rods. The production of BC by the strain S2 cultivated in HS broth for 7 days were 16.6 g/L while the strain C demonstrated BC production of 10 g/L. The strains S2 and C shared 98.65% an 100% similarity to Komagataeibacter oboediens and Komagataeibacter sucrofermentans, respectively.

Conclusion : Locally isolated strains have showed significant bacterial cellulose production potential. Further Studies on the BC production, optimization of conditions and structure modifications are highly recommended to improve its potential as wound dressing.

Keywords : bacterial nanocellulose, Gluconacetobacter, Isolation, Wound dressing

P508-481: Occurrence of palm rots disease caused by Citrobacter koseri, a new plant pathogen

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Background and Aim : Date palm (Phoenix dactylifera) is one of the most important garden products in the country. Khuzestan province considers as a main producing province of date fruit. Date palm offshoot rot symptoms include yellowing and finally drying of leaves, rotting and browning of lower parts of the diseased offshoots. The objective of the present study was identification of the causal agent of date palm offshoot rot in Khuzestan province.

Methods : Ten symptomatic samples were collected from affected palm groves of Ahvaz, Abadan, Khorramshahr, Hamidiyeh, Shadegan, and Karun during 2019-2021. After superficial sterilization, the pieces were rinsed three times with sterile water and squashed using a sterile mortar and pestle, and then cultured on EMB medium. Common phenotypic tests were performed and Multilocus Sequence Analysis (MLSA) was conducted.

Results : A total of 20 strains with metallic green colonies were isolated appeared after 48h incubation at 28ºC. Pathogenicity of 12 strains was approved by inoculating petioles and rachises of young two- or three-years date palms cv. Estameran. Pathogenic strains caused soft rot and browning of inoculated site while negative control remained symptomless. The obtained strains were Gram and oxidase negative while they were catalase positive. Strains were negative in starch hydrolysis. All strains rot potato liquefy gelatin and arginine dihydrolase were positive. Strains were able to growth on 4% NaCl. The MLSA phylogenic tree based on the concatenated partial sequences of three housekeeping genes including gyrB, fusA and pyrG revealed that two representative strains, PA65 and PA174 strains clustered with Citrobacter koseri LMG5519T with 100% bootstrap.

Conclusion : Partial sequencing of the three housekeeping genes, gyrB, fusA, and pyrG genes was used as a phylogenetic marker for determination of the phylogenetic relationships of the species of Citrobacter and the results revealed these genes could clearly demonstrate the taxonomy of Citrobacter. C. koseri considered as an opportunistic pathogen in human. To the best of our knowledge, this if first report of C. koseri as a plant pathogen.

Keywords : Common human and plant pathogen, Emerging pathogens, MLSA, Phoenix dactylifera, Iran.

P509-487: The world of the fetal microbiome

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Background and Aim : The study of the human microbiome has evolved significantly, showing that the microbiome plays a variety of significant roles in our bodies. In light of this information, it is crucial to determine the commencement of microbiome colonization. The microbiota of the mother, the placenta, and the fetus all affect fetal growth and undoubtedly play a significant role in the healthy development of the newborn child.We show evidence that, contrary to popular belief, the fetus is not sterile and contains a microbial ecosystem. This article also discusses the link between hormones, immunity, and microbiome alterations.

Methods : We conducted an organized examination of the literature in PubMed, Medline, and Google Scholar using specific search criteria. Because of the novelty of this method, few types of studies have been conducted in this field. We restricted the time period to 2019–2022, and we only allowed English. The search returned 68 relevant items; five articles were reviewed after duplicates were eliminated.

Results : It is still debatable where microbial colonization starts. This concept has been discussed when microbial elements have been discovered in many samples of fetuses even after straightforward pregnancies with healthy term-born neonates. For example, Stinson et al. reported the first comprehensive 16S rRNA gene study of meconium and amniotic fluid. They employed PacBio SMRT cell technology. Their findings imply that bacterial metabolites and DNA are detectable inside the fetus. There is proof that our microbiota, immune system, and pregnancy hormones interact differently. A low-grade pro-inflammatory state can be triggered by alterations in the host immune system of the intestinal mucosa as well as metabolic hormone levels. Progesterone lowers bacterial richness but enhances the growth of Faecalibacterium, Bacteroides, and Bifidobacterium, among other bacteria. The scientists discovered that estrogen administration caused mucosal growth of regulatory B-cells and M2 macrophages, exhibiting a limited protective impact. Also, the microbiota may regulate the number of sex hormones produced, providing another degree of intricacy.

Conclusion : In conclusion, evidence shows that, in contrast to earlier assumptions, scientists now have some data suggesting that the uterus is not sterile. Pregnancy-related

immunological and microbiological changes make distinguishing between cause and effect challenging.

Keywords : Microbiome, Fetus, Pregnancy

P510-493: Isolation of probiotic bacteria of traditional milk in Qom province and investigation of their adhesion to Caco2 cell line

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Background and Aim : Probiotics are living microorganisms that has beneficial effects on the host. Probiotics are naturally present in some foods such as dairy products and can be added to other foods. Dairy products naturally carry strains with potential probiotic properties that can be used as a valuable microbial source in the food industry and produce products with more favorable characteristics. Consumption of probiotics improves the health of the digestive system and helps in regulating the microbiome, treating and reducing the symptoms of its diseases. Probiotics, especially lactobacilli, play an important role in balancing the microbiome of the digestive system. The purpose of this research was to isolate probiotic bacteria with a high ability to be used in the food industry.

Methods : In the winter of 2020, 100 samples of traditional milk were prepared in the city of Qom (Iran). Samples were cultured in MRS medium after dilution, then the probiotic properties of the isolates including tolerance to bile salt and pH were investigated, and the selected isolates were identified morphologically, biochemical, and molecular 16s rRNA gene. The amount of adhesion of the isolates to the Caco-2 cell line as a model of epithelial cells of the digestive tract was investigated, co and autoaggregation and, hydrophobicity was also evaluated for these isolates. finally, the expression of 3 genes effective in adhesion, including mub, mapA, and ef-Tu genes, was investigated. on

Results : Among the grown isolates, 14 Bacillus bacteria, all of them were gram-positive and non-hemolytic, catalase, oxidase, indole, and H2S negative, were molecularly identified, and 5 isolates were Lacticaseibacillus casei, Lacticaseibacillus Paracasei, Lacticaseibacillus rhamnosus, Limosilactobacillus fermentum, and Lactobacillushelveticus were identified with a similarity percentage of 98%. These 5 isolates showed the ability to adhesion to the Caco-2 cell line and contained all three genes simultaneously. Finally, all isolates were registered on the NCBI website.

Conclusion : The results of the present research showed that traditional milk is a very rich source of various probiotic bacteria, the consumption of which is beneficial for health, as well as the possibility of further research and industrial use of isolated bacteria with the ability to adhesion to there, are epithelium cells.

Keywords : probiotic, lactobacillus, Milk, bacteria, Caco-2 cell line

P511-494: Prevalence and Expression of Genes of Type II Antitoxin Toxin Systems in Clinical Isolates of Methicillin-Resistant Staphylococcus aureu

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Background and Aim : Antibiotic resistance of bacteria has been increasing in recent years and reports indicate that some bacterial strains are even resistant to the last treatment line. The survey of MazEF antitoxin-toxin genes in 84 strain of MRSA and and the antimicrobial effect of supernatants on the logarithmic growth stage of the bacteria

Methods : In this study, 84 strains of MRSA were collected. The patients included 48 males and 36 females with a mean age of 39 years. The primers for Staphylococcus aureus type II antitoxin genes were designed. In the first step, using the mecA primer and PCR, the strains were genetically examined to confirm methicillin-resistant Staphylococcus aureus. In the next step, the frequency of MazEF antitoxin-toxin genes was examined.

Results : All strains of methicillin-resistant Staphylococcus aureus had the F maz gene except one. The highest antibiotic resistance was related to the strains isolated from the wound and the lowest resistance was related to the strains isolated from the urine. the effect of the supernatant obtained in the death phase of Staphylococcus aureus was assessed and the antimicrobial effect of these supernatants on the logarithmic growth stage of the bacteria was measured.

Conclusion : since previous studies showed the antimicrobial effect of this supernatant on many other bacteria, a type II system was suspected that was confirmed by the results.

Keywords : Staphylococcus; MRSA; Antitoxin-toxin system; MazEF

P512-498: An update on prevalence of slow-growing mycobacteria and rapidgrowing mycobacteria retrieved from hospital water sources in Iran – a systematic review

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Background and Aim : This study aimed to assess the prevalence of slow growing mycobacteria (SGM) and rapid-growing mycobacteria (RGM) retrieved from hospital water sources in Iran from 2016 to 2020.

Methods : The review was conducted to get eligible published studies from 1st January 2016 to 25th March 2020 based on PRISMA protocol. A combination of related words from the Medical Subject Heading Terms (MeSH), with (AND, OR) were used to search for published studies reporting the prevalence of nontuberculous mycobacteria (NTM) in Scopus, MEDLINE, Web of Sciences, Google Scholar, and Iranian databases. Then data from the studies were extracted and reported.

Results : Our study showed that different water sources of hospitals were contaminated with NTMs. The prevalence of RGM isolates in hospital water samples varied between 42.2%–67.5%, and the prevalence of SGM varied between 32.5%–57.7%, respectively. M. lentiflavum (84.7%), M. avium complex (2.8%–56.4%) and M. gordonae (2.8%–56.2%) were the most prevalent NTM species amongst SGM, whereas M. fortuitum (2.9%–44.2%), M. chelonae (8%–36.8%) , M. mucogenicum (8%–25.6%) were the most leading NTM isolates among RGM

Conclusion : A high prevalence of NTM was reported from hospital environments particularly hospital water sources which can colonize medical devices, solutions, and water used for patients and cause nosocomial infection. Therefore, the hospitals should check the microbiological quality of the water used

Keywords : Nontuberculous mycobacteria, prevalence, hospital, water resources, environment

P513-500: Prevalence of Helicobacter felis and Helicobacter heilmannii and coinfection with Helicobacter pylori in gastric biopsy specimens in endoscopic ward of Shahid Beheshti Hospital, Hamadan, Iran

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Background and Aim : Helicobacter pylori (H. pylori) has various strains that are associated with human infections. H. pylori, H. heilmannii and H. feils are the most common strains in humans. H. pylori is associated with several human diseases such as chronic gastritis, peptic ulcer, mucous membrane lymphoma, and gastric adenocarcinoma. Therefore, this study aimed to determine the prevalence of H. felis and H. heilmannii and the effect of co-infection with H. pylori in gastric biopsy specimens of patients

Methods : Totally, 80 gastric biopsy specimens were taken by a physician from the patients referred to Shahid Beheshti Hospital, Hamadan province, Iran. PCR test was used to confirm the presence of H. pylori in samples that had positive rapid urease tests. Moreover, ureB gene and ureA & B gene were used for H. heilmannii and H. feils, respectively.

Results : Of the patients, 61.5% were females and 38.5% were males with a mean age of 37.8 years. Of the 80 biopsies, 50% were H. pylori-positive, 53.8% were H. heilmannii-positive and H. felis was identified in none of the sample. Results implied that smoking, having a history of gastrointestinal diseases and taking certain medications can be risk factors for H. pylori.

Conclusion : any agent contributing to gastric mucosal damage can enhance the susceptibility to bacterial contamination. Overall, the results indicated a low probability of interactions between H. pylori, H. heilmannii and H. felis.

Keywords : Helicobacter pylori, Helicobacter heilmannii, Helicobacter felis, Coinfection

P514-501: The glycerol effect on Docosahexaenoic acid production in salt-resistant bacteria

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Background and Aim : Docosahexaenoic acid (DHA) is an omega-3 essential fatty acid that cannot be produced de novo by humans. It is usually found in fish and shellfish, as well as in some marine algae. Like most omega-3 fats, DHA has many physiological functions and beneficial health effects. It is essential for proper fetal neuronal and retinal development and the normal function of the brain in adults. It has also anticancer, cardioprotective, and anti-inflammatory effects.

Methods : : In this study, the salt-tolerant strain was cultured in nutrient broth at 30°C with shaking at 170 rpm. After 24 h, the hydrochloric acid treatment was performed overnight at 4 °C. then, the sediments were collected by centrifugation. Chloroform/methanol (2:1) was used for lipid extraction. The lipids were analyzed by GC / MS spectroscopy and FTIR. Glycerol (0.1%) was used as an additive for lipid production comparison under the same conditions.

Results : The results of FTIR analysis and GC / MS showed that the strain was able to produce docosahexaenoic acid at a level of 0.26% of total fatty acids when incubated in a glycerol medium. Some other fatty acid profile changes were seen in the presence of 0.1 % glycerol.

Conclusion : Altering the conditions and using some additives can change the fatty acid profile produced by some bacteria and make them a suitable source for the production of this class of valuable materials, which of course will require optimization and more research.

Keywords : Docosahexaenoic acid, Fatty acids profile, Glycerol

P515-511: The investigation of antibacterial effects of Lawson (Henna extract)-loaded porous silica nanoparticles

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Background and Aim : Considering the increasing rise of infectious diseases and antibiotic resistance to conventional drugs, great attention is paid to the development and production of new drugs for the treatment of infectious diseases. In this context, nanotechnology plays an important role in the introduction of novel drugs, and nanoscale compounds have several advantages including high reactivity, better therapeutic properties, and more suitable physical and chemical characteristics. Porous silica nanoparticles can be used as carriers for various cargoes and increase the solubility and availability of drugs with low solubility in aqueous environments, thus improving the therapeutic properties of drugs. The aim of this study is to load Lawsone (Henna extract) into the pores of porous silica nanoparticles and to investigate its antibacterial properties in comparison with Lawsone alone.

Methods : For this purpose, nanoparticles were synthesized by the sol-gel method, and Lawsone was loaded into their pores. Then, the prepared nanoparticles were characterized by dynamic light scattering (DLS) and Fourier transform infrared spectroscopy (FTIR) methods. Finally, their antibacterial activity on Gram-positive and Gram-negative bacterial strains was evaluated and compared with Lawsone alone.

Results : The characterization results showed that the amine-functionalized porous silica nanoparticles had a hydrodynamic diameter of 143± 6 nm and a PDI of 0.31, and their zeta potential in water was +31.7±3.6 mV. FTIR analysis was performed to investigate the functional groups on the surface of the nanoparticles. A Si-O-Si absorption band was observed at 1060 cm-1 and another at 806 cm-1 which was attributed to the presence of Si-O groups in the structure of the nanoparticles. The broth microdilution method was applied to Staphylococcus aureus and Escherichia coli to determine the minimum inhibitory concentration (MIC). The results showed that the loading of Lawsone in the pores of silica nanoparticles improved the antibacterial properties and increased the solubility of Lawsone in the aqueous medium.

Conclusion : This study showed that porous silica nanoparticles are a suitable carrier for Lawsone and have the ability to improve its therapeutic properties.

Keywords : Porous silica nanoparticles, Lawsone, Antimicrobial properties, Drug solubility.

P516-513: Isolation of enterotoxigenic Escherichia coli (ETEC) from children medical center hospital, Tehran

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Background and Aim : diarrheal disease is still one of the most important causes of death among children in developing countries. The importance of these disease is due to children's weakness in response to the infectious agent on one side and sensitivity to water and electrolyte loss on the other side.

Methods : during January 2021 to February 2022, 100 sample collected and investigated for present of Escherichia coli (E. coli). Among all sample, 40 isolate identify as E. coli through biochemical test. After this step, through uidA gene, which encodes Beta-glucuronidase and is found in almost all E. coli, these isolates were confirmed as Escherichia coli. Finally, the presence of Liable Toxin (LT) in confirmed isolates indicates the presence of enterotoxigenic E. coli.

Results : among all isolates that identified as E. coli, 3 isolates were identify as enterotoxigenic Escherichia coli.

Conclusion : Escherichia coli is one of the most important bacteria causing infection and diarrheal disease. This bacterium can become an invasive bacterium by acquiring virulence genes. One of the most important of these invasive genes is the LT toxin gene. The presence of 40% of Escherichia coli in the isolate and also the isolation of 3 toxin-producing isolates is of particular importance because this bacterium has more power to cause disease, especially in children.

Keywords : Escherichia coli, E. coli heat-labile toxin, Diarrhea

P517-518: Evaluation of the effect of soil actinomycetes extracts on the growth of pathogenicity of fluconazole-resistant strains of Candida albicans

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Background and Aim : Candida species are the main cause of fungal infections in humans. Candida albicans is the most virulent and dominant, causing about 90% of all invasive yeast infections. In recent years, the importance of diseases caused by Candida species has increased due to the emergence of resistance to some antifungal drugs such as fluconazole. Therefore, attention has been directed to the screening programs of microorganisms for the production of antibiotic compounds. Among the microorganisms used to control fungal diseases, Actinomycetes have been considered due to their wide range of inhibitory activity and high viability. Our aim of this study is to find an effective substance from the source of bacteria that is effective against fluconazole-resistant Candida albicans.

Methods : In this study, we took the aqueous extract of Streptomyces isolated from the soil. Streptomyces aqueous extract in the concentration range of 1.8 micrograms to 0.0009 micrograms was effective on Candida albicans isolated from oropharyngeal candidiasis patients by micro broth dilution method. As a control, we treated Candida albicans with fluconazole at a concentration of 64 mg/ml.

Results : Streptomyces isolated from soil were effective on Candida albicans at the given concentrations, and its minimum inhibitory concentration was 0.0036 ?g. This fungus treated with fluconazole with a concentration of 64 mg/ml had significant growth and was resistant to the drug.

Conclusion : Our findings showed that the aqueous extract of Streptomyces isolated from soil affects Candida albicans while it is resistant to fluconazole, it can be considered a promising treatment and more studies should be conducted on it.

Keywords : Candida albicans, Streptomyces, candidiasis, fluconazole

P518-522: A systematic review of the antimicrobial effects of different plant extracts (Scrophularia striata) as a possible candidates in the treatment of infectious diseases

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Background and Aim : The use of herbal medicines has a long history. Today, due to the resistance of microorganisms to antibiotics and antimicrobial substances, herbal medicines have attracted attention due to their significant antimicrobial effects and low toxicity. This study aims to systematically review the antimicrobial effects of different plant extracts (Scrophularia striata) as possible candidates for treating infectious diseases.

Methods : The present study is a review study by searching reputable scientific databases such as PubMed, Google Scholar, Scopus, and Web of Science from 2000 to 2022 using the keywords Antimicrobial, Scrophularia striata, Medicinal herbal, Infectious diseases the latest information obtained.

Results : In this study, 40 articles were found and reviewed. The components used for the antimicrobial properties of this plant were root, seed, fruit, aerial parts, flowers, leaves, branches, and plant oil. The extracts used included water, hydro-alcoholic, ethanol, methanol, ethyl acetate, and chloroform. This plant had high inhibition activity and a lethal effect on gram-positive and gram-negative bacteria of ATCC strains, hospital and resistant strains Therefore, in addition to antibacterial effects, antiparasitic and antifungal effects were also observed on Leishmania major and Candida albicans. The aerial parts of the plant were the most used and the most effective antimicrobial extract among the ethanol and methanol extracts.

Conclusion : Due to the increasing antibiotic resistance in bacteria as well as the high toxicity of chemical drugs and their side effects like high mortality in patients. The use of medicinal plants is recommended. One of these plants is Scrophularia striata, which due to its effective antimicrobial substances, including Quercetin, Isorhamnetin-3-O-rutinoside, and Nepitrin and having much less toxicity is recommended for clinical trials as a possible drug candidate in the treatment of patients with various infectious diseases.

Keywords : Antimicrobial, scrophularia striata, medicinal herbal, infectious diseases.

P519-523: Phyto-Mediated Silver Nanoparticles for Antibacterial Performances by Salicornia Extract

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Background and Aim : Salicornia is a genus of succulent, halophytic (salt tolerant) flowering plants in the family Amaranthaceae that grow in salt marshes and on beaches. In this project, silver nanoparticle was synthesized using Salicornia leaves extract as a reducing and capping agent by microwave irradiation method for Antibacterial Performances.

Methods : In this project, phytosynthesis of stable silver nanoparticles was done using Salicornia extract. These phytosynthesized nanoparticles were characterized with the help of UV–Vis spectrophotometer, Fourier transform infrared spectroscopy (FTIR), X-ray diffraction (XRD), and Transmission electron microscopy (TEM). Later, their antibacterial activity was screened against both gram-negative and gram-positive microorganisms by MIC and MBC method.

Results : The formation of silver nanoparticles was confirmed by Surface Plasmon Resonance (SPR) as determined by UV-Vis spectra at 425 nm. Fourier transform infrared spectroscopy shows that the functional groups are carboxyl, amine, and phenolic compounds of seed extract which are involved in the reduction of silver ions. The XRD peaks at 38?C, 44?C, 64?C and 77?C can be indexed to the (1 1 1), (2 0 0), (2 2 0) and (3 1 1) Bragg's reflections of cubic structure of metallic silver, respectively. Silver nanoparticles of size ranging from 25-90 nm of spherical shape were characterized using transmission electron microscopy (TEM). The synthesized Ag-NPs exhibited good antibacterial potential against gram positive and gram negative bacterial strains.

Conclusion : Thus, this method can be used for rapid and ecofriendly phyto-synthesis of stable Ag nanoparticles of size range 25–90 nm possessing antibacterial activity suggesting their possible application in medical industry.

Keywords : Salicornia, Silver nanoparticles, Antibacterial Activity, MBC, TEM, Medical Industry.

P520-524: Evaluation of the antimicrobial effect of molds isolated from animel feed on gram positive bacteria

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Background and Aim : Secondary metabolites, also called specialised metabolites, toxins, secondary products, or natural products, are organic compounds produced by any lifeform, e.g. bacteria, fungi or plants, which are not directly involved in the normal growth, development, or reproduction of the organism. These compounds, isolated and have been used in modern medicine because of its antimicrobial effects.

Methods : In this study secondary metabolites of Aspergillus flavus, Aspergillus fumigatus and penicillium spp. isolated from moldy Livestock ration and its antimicrobial properties against of Staphylococcus aureus was investigated.

Results : Results of this study showed that the MIC was 416.66 ± 144.33, 333.33 ± 144.33 and 500 ± 0.00 (mg/ml) respectively for Aspergillus flavus, Aspergillus fumigatus and penicillium spp. secondary metabolites isolated. The MBC was 500 ± 0.00, 416.66 ± 144.33 (mg/ml) respectively for Aspergillus flavus and Aspergillus fumigatus; penicillium spp. had no any bactericidal effect on Staphylococcus aureus. Disk diffusion test shows no inhibitory zone in 100, 120 and 150 µl for secondary metabolites. Also There was no any inhibitory zone around secondary metabolites in well diffusion in 170, 200 and 220 µl.

Conclusion : Based on the results; secondary metabolites of Aspergillus flavus, Aspergillus fumigatus and penicillium spp. especially Aspergillus flavus and Aspergillus fumigatus have the antibacterial effects on Staphylococcus aureus and can able be newest antibiotic against this microorganism.

Keywords : Secondary metabolites, Aspergillus flavus, Aspergillus fumigatus, penicillium spp., Streptococcus pyogenes, Staphylococcus aureus.

P521-535: Investigations of Portulaca oleracea Compounds with Helicobacter pylori Virulence Factors CagA and VacA Using Molecular Docking in Gastric Cancer

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Background and Aim : Cytotoxin A-related gene (CagA) and cytotoxin A (VacA) proteins are vacuolating virulence factors of Helicobacter pylori that are associated with gastric cancer. Purslane compounds showed significant antibacterial and antitumor effects. In silico study, the identified compounds of purslane were subjected to molecular docking studies to find the effect of CagA and VacA proteins in gastric cancer using molecular docking.

Methods : Used as receptors, the selection of target proteins of CagA and VacA proteins were taken from the Uniprot database. The 3D structure of CagA protein was obtained from the PDB database chosen 4G0H. Also, The 3D structure of VacA was determined 2QV3. For ligand selection, portulaca oleracea compounds the 3D structure received from the PubChem database and downloads the SDF file. CagA and VacA proteins were edited using Chimera 1.15 software, then water molecules and ions were removed from the protein. Then, using PyRx software, molecular docking was performed and the results were defined in terms of binding energies (kcal/mol).

Results : Flavonoids as secondary metabolites and other compounds of portulaca oleracea in PyRx software, molecular docking was initiated in which the grid box was used to select the appropriate binding site. For the CagA protein, the results after molecular docking were the best binding affinity for A chain of CagA showed the highest binding affinity (-8.6 kcal/mol) for the isoschaftoside molecule. For A chain of VacA protein, the luteolin, and apigenin molecules were the highest binding affinity (-7.5 kcal/mol). other Compounds such as the Flavonoids for CagA and VacA least binding affinity interaction were (-6.5 and -6.8 kcal/mol respectively).

Conclusion : The compounds of these molecules showed negative binding affinity and hybrid affinity with Helicobacter pylori virulence factors (CagA and VacA). Therefore, these compounds can be used as prospects for the development of new drugs against Helicobacter pylori and can be potential for their development into drugs to control the pathogenicity of Helicobacter pylori for the treatment of gastric cancer.

Keywords : Helicobacter pylori, CagA and VacA, Molecular docking, portulaca oleracea, Gastric Cancer

P522-536: Evaluation of the effect of soil bacteria extracts on growth of pathogenicity of fluconazole resistant strains of Candida tropicalis.

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Background and Aim : Background: Candida tropicalis has emerged as one of the most important Candida species. It has been widely considered the second most virulent Candida species, only preceded by C. albicans. Besides, this species has been recognized as a very strong biofilm producer, surpassing C. albicans in most of the studies. the azole antifungals are the most frequent class used to treat Candida infection. Azole antifungals such as fluconazole are often preferred for the treatment of many Candida infections. However, resistance to azoles exists among several Candida species. The aim of this study is to investigate the effectiveness of the antifungal activity of the extract of bacteria isolated from the soil, which is an effective treatment against Candida tropicalis resistant to fluconazole.

Methods : Method: In this test, we cultured Streptomyces isolated from the soil. The aqueous extract of the bacteria with a concentration of 0.018 mg/ml in the range of 1.8 µg to 0.0009µg was used on fluconazole-resistant Candida tropicalis isolated from patients with Oropharyngeal candidiasis was treated with the Micro Broth Dilution method. And we also used fluconazole with a concentration of 64 mg/ml as a control.

Results : Result: Treatment with the extract of bacteria isolated from soil, genus Streptomyces, with a concentration of 0.018 mg/ml showed a great fungicidal effect on C. tropicalis resistant to fluconazole. The minimum inhibitory concentration (MIC) was 0.0072 ?g. On the other hand, fluconazole with a concentration of 64 mg/ml had no effect on this fungus and it showed significant growth.

Conclusion : Conclusion: These findings show that the aqueous extract of bacteria isolated from soil, especially Streptomyces genus, is more effective than fluconazole and is a promising treatment against fluconazole-resistant Candida tropicalis.

Keywords : Candida tropicalis, Streptomyces, oropharyngeal candidiasis, fluconazole

P523-541: In vitro Qualitative Phytochemical Analysis and Antibacterial Activity of Ethanolic Extract of Flowers of Rheum ribes L. from Tonekabon - Iran

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Background and Aim : Plants are an important source for the discovery of new products of medicinal value for drug development and plants secondary metabolites are unique sources for pharmaceuticals food additives, flavors, and other industrial values. The aim of this project was to evaluate the phytochemical activity of ethanolic extract of flowers of Rheum ribes L. belonging to the family Polygonaceae from Tonekabon, Iran.

Methods : In this project, the flowers were collected and extract prepared from ethanol by microwave assisted extraction (MAE) method. The present study revealed that the phytochemicals analysis of nine different chemical compounds terpenoids (Salkowski Test), flavonoids (Alkaline Reagent Test), phenols (Ferric Chloride Test), coumarins (sodium hydroxide Test), tannins (Ferric Chloride Test), phlobatannins (HCl Test), cardiac glycosides (Keller-Killani test), quinones (H2SO4 Test), and saponins (Foam Test) were tested in ethanolic extracts. Later, the antibacterial activity of the ethanolic extract of flowers of Rheum ribes L. was tested using both gram positive as well as gram negative bacteria i.e. (Bacillus subtilis, Staphylococcus aureus, Pseudomonas aeruginosa and Escherichia coli) respectively using minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) methods.

Results : The results of the phytochemical screening of ethanolic extract of flowers of Rheum ribes L. were (terpenoids, flavonoids, phenols, coumarins, quinones and tannins) presented. The ethanolic extract of flowers of Rheum ribes L. exhibited good antibacterial potential against gram positive and gram negative bacterial strains.

Conclusion : Conclusively, Rheum ribes L. is valuable source for new compounds and should receive special attention in research strategies to develop new antibacterial urgently required in the near future.

Keywords : Rheum ribes L., Bacillus subtilis, MIC, Flavonoids.

P524-544: Antibacterial Activity of Methanolic Extract of Pistacia atlantica Fruits using Disk Diffusion Method for the Treatment of Urinary Tract Infections

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Background and Aim : Nowadays, incidence of antibiotic-resistance among pathogenic bacteria has increased due to indiscriminate use of antimicrobial drugs for treatment of diseases, especially urinary tract infections. Medicinal plants are also of great importance as antibacterial agents. Therefore, the aim of this study was to determine the antibacterial effect of methanolic extract of Pistacia atlantica fruits from Alborz province using disk diffusion method.

Methods : Methanolic extract of Pistacia atlantica fruits was prepared by the Microwave-Assisted Extraction (MAE) method. Effect of different concentrations of the extract on Escherichia coli (PTCC 1399) and Staphylococcus saprophyticus (PTCC 1440) was evaluated using the disk diffusion method by measuring diameter of growth inhibition zone. Gentamicin and propylene glycol were used as positive and negative control, respectively.

Results : The methanolic extract of Pistacia atlantica fruits had favorable inhibitory effect on the growth of Escherichia coli and Staphylococcus saprophyticus.

Conclusion : The methanolic extract of Pistacia atlantica fruits has good inhibitory effect on the growth of Escherichia coli and Staphylococcus saprophyticus which confirms the traditional use of this plant for the treatment of urinary tract infections.

Keywords : Pistacia atlantica, Staphylococcus saprophyticus, Disk Diffusion, Urinary Tract Infections.

P525-546: Investigation of Phytase Production by a Strain of Aspergillus niger in Submerged Fermentation of Orange peel

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Background and Aim : The diet of poultry, fish and pigs is rich in phytic acid. Due to the lack of the phytic acid hydrolyzing enzymes in these animal's digestive system ,they are not able to use its phosphate, so Pi must be added separately to their diet. Phytic acid is an anti-nutrient factor that forming insoluble complexes with divalent cations, proteins and vitamins. Phytase is an enzyme capable of hydrolyzing phytic acid and releasing organic phosphate. Thus adding phytase to the feed can increase the nutritional value, leading to no need to use Pi supplements in feed.

Methods : In the present study phytase enzyme activity from a strain of Aspergillus niger was investigated for the hydrolysis of agricultural wastes such as Orange peel and wheat bran in submerged fermentation. Phytase-producing media includes (NH4)2 SO4, KCl, MgSO4, FeSO4 and MnSO4 in 100 ml purified water. As a phytic acid source to induce phytase production, wheat bran (A) and orange peel (B)were used in two different media separately(0.5 g/100 ml). A third medium containing 0.5% Sodium phytate (C) was prepared as pure source of phytic acid. Inoculation was done with 1 ml (105 spore/ml) of 72 hours cultured Aspergillus niger plate. Inoculated flasks were incubated at 30 o C at 150 rpm. After that the enzyme activity was assayed.

Results : B media containing orange peel indicated more enzyme activity(0.025 U/L) than wheat bran(0.015U/L). Moreover, enzyme production in B medium reached the maximum value in 60 hours, while this time for wheat bran was longer, 96 h.

Conclusion : It is suggested that one reason for the higher enzyme production in B medium, is the lower concentration of free phosphate in orange peel. Researches have shown that citrus peel contains little mineral phosphorus compared to wheat bran, rice bran, soy bran, etc. Since free phosphate is one of the inhibitors of phytase production by fungies.In research by spire et al., the orange peel was used to produce phytase from Aspergillus niger. In addition, in another study by Mittal et al., orange peel was used to induce Klebsiella sp.DB3 for phytase production.Considering that citrus peel utilization in poultry feed has tremendous effects on improving their growth, so adding phytase to the feed, caused the release of Pi and Consequently, by eliminating phosphate supplements, it reduced environmental pollutions.

Keywords : Aspergillus niger, Phytase , Phytic acid

P526-549: Bacterial etiology of fever episodes of splenectomised patients in three medical centers in the city of Mashhad in northeastern Iran

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Background and Aim : Many medical and surgical conditions may need to be treated with splenectomy. However, this lymphoid tissue has an important role in controlling many infections; thus, many life-threatening infections may be caused in the absence the spleen; therefore any episode of fever should be considered important. The aim of our study is to assess the bacterial etiology of fever episodes of splenectomised patients in three Medical centers in the city of Mashhad in northeastern Iran.

Methods : In a cross-sectional study on splenectomised patients in Imam Reza, Ghaem, and Dr. Sheikh hospitals between 2006 and 2017, those with episodes of fever were included. Collected data included, among others, age at splenectomy, duration of hospitalization, indications for ICU admission, recorded vital signs at admission, bacterial species causative for sepsis, times of hospitalization due to fever episodes, clinical signs and symptoms, antibiotic prophylaxis, and 6-month and one-year outcomes. The data was analyzed using SPSS Statistics 20.

Results : A total of 280 splenectomised patients were reviewed and 23 splenectomised patients with episodes of fever were included. The most common causes of splenectomy were spleen masses and idiopathic thrombocytopenic purpura (ITP) accounting for 17.4% of the cases, each. The mean age of patients was 24.2±1.6 years. 47.8% of the patients were male and 52.2% were female. The median admission duration was 7 days. The most common causes of admission were intra-abdominal infections (26.7%), pneumonia (13.3%), and bacteremia (10.0%). A total of 30 episodes of fever were recorded, of which 2 (6.7%) ultimately ended in patient death. Blood culture was positive in four cases (13.3%) for Streptococcus pneumoniae, Staphylococcus aureus, Citrobacter, and Brucella. Patients received suitable antibiotic coverage in 13.3% (i.e. ceftriaxone + vancomycin or a fluoroquinolone + vancomycin), minimum suitable empiric coverage in 10.0%, and no suitable coverage in 76.7% of episodes.

Conclusion : The present study highlights widespread inappropriate empiric therapy of fever episodes in splenectomised patients as well as a lack of due attention to timely sample collection before antibiotic administration. Despite this, the isolated organisms were varied and included S. pneumoniae, S. aureus, Coagulase Negative Staphylococci, P. aeruginosa, Brucella, and Citrobacter.

Keywords : splenectomy, fever, bacterial etiology, empiric antibiotic therapy

P527-560: Anti-biofilm potency of PepR, a viral-derived peptide, against drug-resistant Pseudomonas aeruginosa

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Background and Aim : Background: The global crisis of antibiotic resistance increases the demand for the new promising alternative drugs such as antimicrobial peptides (AMPs). Accordingly, the antibiofilm activity of the PepR peptide against P. aeruginosa isolates was investigated for first time in this study.

Methods : Two clinical MDR and carbapenem-resistant (CR) P. aeruginosa isolates, and P. aeruginosa ATCC 27853 were investigated. The MIC and MBC of PepR were determined. The MBIC was determined to evaluate inhibitory activity of PepR on biofilm formation and MBEC to dispersal activity on preformed biofilm. The relative expression levels of biofilm-associated genes including rhlI, rhlR, lasI, lasR, pelB, pilT, PA0756 and PA2070 were analyzed using qRT-PCR. In vivo evaluation of inhibitory effect of pepR on biofilm formation was performed in the mouse models of P. aeruginosa biofilm-associated subcataneos catheter infection.

Results : MIC and MBC of PepR for both MDR and ATCC 27853 P. aeruginosa strains were 8 and 16 µg/mL, respectively, while both MIC and MBC against CR strain were 4 µg/mL. MBIC was estimated to be 64 µg/ml for all strains. MBEC against MDR and ATCC 27853-P. aeruginosa strains was 128 µg/ml and against CRPA was 64 µg/ml. The bacterial adhesion was significantly inhibited at concentrations of 1/2× and 1/4× MIC in all P. aeruginosa isolates ($P < 0.05$).Following treatment with PepR at 1/2×, 1/4×, and 1/8× MIC, significant inhibition in biofilm formation was observed in all isolates ($P < 0.05$). PepR at concentration of 32 µg/mL was able to destroy 69.7% and 81.3% of MDR P. aeruginosa isolates and ATCC 27853 P. aeruginosa biofilms, respectively ($P < 0.03$). The expression levels of all genes in isolates treated with 1/2 MIC of PepR were down-regulated by more than four-fold compared to the untreated isolates ($P < 0.05$). PepR at concentrations of 2×, 4×, and 8× MIC significantly reduced the biofilm formation in catheter-associated infection model by 33%, 52%, and 67%, respectively ($P < 0.05$).

Conclusion : Considering relatively strong inhibitory and eradication effect of PepR on the P. aeruginosa biofilms in in vitro and in vivo conditions, the peptide could be considered as a promising candidate for designing an antibiofilm drug.

Keywords : Antimicrobial peptides; PepR; biofilm; Pseudomonas aeruginosa

P528-561: Microbial decolorization of acid red 18 by a novel bacterial strain

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Background and Aim : Different industries use all kinds of dyes, especially Azo dyes, including textile, leather, plastics, cosmetics, and food. These dyes cause severe problems for the ecosystem and aquatic life by preventing light and oxygen from reaching the water environment. These dyes also endanger human health because these compounds are highly toxic, mutagenic, and carcinogenic. One of the most significant discharging contaminants is the textile industry, and 280,000 tons of textile dyes are discharged in effluents annually. Hence, biological methods have played a significant role in destroying dyes rather than physical and chemical methods. The biological methods commonly use different species such as yeast, bacteria, algae, and fungi.

Methods : In this study, strain M isolated in the Kashan University laboratory was used for decolorization. At first, this strain was cultured in nutrient agar and incubated for 24 hours. Then, it was transported in a peptone yeast culture medium supplemented with 50 mg/ml glucose and 50 ppm acid red 18 and incubated in an incubator shaker. After 24 and 48 hours, the decolorization percentage was measured by certain formula and UV-VIS spectroscopy.

Results : The results revealed that strain M had a high decolorization ability of acid red 18, and the decolorization percentage reached 100% after 48 hours.

Conclusion : Bacillus sp. has a great ability to decolonize and is the usual operation for wastewater decolonization systems.

Keywords : Acid red 18, Decolorization, Wastewater, Bacteria

P529-562: High frequency of phenotypic resistance against ampicillin in Shiga toxin-producing Escherichia coli strains isolated from sheep carcasses in Kerman

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Background and Aim : Shiga toxin-producing Escherichia coli (STEC) are one of the most important food-borne pathogens associated with fecal contaminations in the foods produced by animals. The present study was carried out in order to study of phenotypic resistance to ampicillin in STEC strains isolated from sheep carcasses in Kerman.

Methods : In this study 30 STEC isolates were confirmed by conventional PCR methods. Disk diffusion technique was used to analyze STEC isolates for resistance against ampicillin.

Results : Among the 30 STECs, 22 isolates (73.3 %) were resistant to the ampicillin. Also, 2 isolates (6.6 %) was evaluated as sensitive to ampicillin and the remaining isolates (20.1%) were identified as intermediate.

Conclusion : The results of this study showed that raw sheep meat could be considered as a potential reservoir of ampicillin resistant STECs, which may threaten public health.

Keywords : Shiga toxin-producing, Escherichia coli, Sheep, Antibiotic resistance, ampicillin.

P530-565: Study of phenotypic antimicrobial resistance to cephalosporins in Shiga toxin-producing Escherichia coli strains isolated from sheep carcasses in Kerman

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Background and Aim : Shiga toxin-producing Escherichia coli (STEC) are one of the most important food-borne pathogens associated with fecal contaminations in the foods produced by animals. The present study was carried out in order to study of phenotypic resistance to cephalosporins (cefixime and cephalexin) in STEC strains isolated from sheep carcasses in Kerman.

Methods : In this study 30 STEC isolates were confirmed by conventional PCR methods. Disk diffusion technique was used to analyze STEC isolates for resistance against cefixime and cephalexin.

Results : Among the 30 STECs, 24 (80%) were resistant to the cephalexin and 17 (56.6%) were resistant to the cefixime. Also, 6 isolates (20 %) were evaluated as sensitive to cephalexin and 9 isolates (30 %) were evaluated as sensitive to cefixime.

Conclusion : The results of this study show that STEC strains obtained from raw sheep meat have significant resistance to cefixime and cephalexin, which potentially threatens public health.

Keywords : Shiga toxin-producing, Escherichia coli, Sheep, Antibiotic resistance, cephalosporins.

P531-566: Prevalence of antibiotic resistance against colistin in Escherichia coli strains isolated from sheep carcasses in Kerman

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Background and Aim : Shiga toxin-producing Escherichia coli (STEC) are foodborne pathogens that cause severe diseases, including hemorrhagic diarrhea and hemolytic uremic syndrome in human. Ruminants, especially cattle, are asymptomatic primary reservoirs. Antibiotic resistance among STECs lead to problems in treatment options. The present study was performed in order to detect the phenotypic resistance to colistin in STECs isolated from sheep carcasses in Kerman

Methods : In this study 30 STEC isolates were confirmed by conventional PCR methods. Disk diffusion technique was used to analyze STEC isolates for resistance against colistin.

Results : Among the 30 STECs, 7 isolates (23.3 %) were resistant to the colistin. Also, 9 isolates (30 %) was evaluated as sensitive and the remaining isolates (46.7%) were identified as intermediate.

Conclusion : The results of this study showed that raw sheep meat could be considered as a potential reservoir of colistin resistant STECs, which may threaten public health.

Keywords : Shiga toxin-producing, Escherichia coli, Sheep, Antibiotic resistance, colistin.

P532-567: Identification of Infectious Laryngotracheitis antibodies in broiler flocks in ce Guilan provin

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Background and Aim : Infectious laryngotracheitis (ILT) is a respiratory tract Infectious of chickens caused by Gallid herpesvirus type 1 (GaHV-1).This virus infects the upper respiratory and ocular organ of poultry and characterized by respiratory depression, dyspnea , cough, open mouth breathing and spitting blood exudate from the respiratory tract with high rates of morbidity and mortality.

Methods : In this study, 150 blood samples were collected from 15 broiler farms, so that 10 samples were taken randomly from each farm of Guilan province. Sampling was done by collecting 2 to 3 cc of blood. In the laboratory, the samples were centrifuged at 3000 rpm for 5 minutes to completely separate the serum and were evaluated by synbiotics ELISA kit. It should be noted that all the steps of ELISA test were performed according to the method and instructions of the kit manufacturer.

Results : In this study, blood samples were collected from 150 broilers in Guilan province. After separating the serum and examining the titer of each sample, it was found that all samples were negative.

Conclusion : This study was carried out to determine the seroprevalence of Infectious Laryngotracheitis virus (ILTV) in broiler flocks of Guilan province in Iran. Indirect ELISA was performed to determine the antibody titre against ILTV in broiler flocks. Total 150 blood samples were taken from 15 broiler farms.The serum prevalence of infectious laryngotracheitis virus in all samples, were negative and since the study method in the present study was ELISA, it is recommended to investigate the prevalence of infectious laryngotracheitis in native chicken flocks ,Laying flocks, broiler breeder and also in broiler flocks in different seasons, with different diagnostic methods as well as in other provinces of the country to prevent the spread of the disease and extensive economic losses caused by this disease.

Keywords : Infectious laryngotracheitis (ILT), Indirect ELISA, Seroprevalence, Guilan province.

P533-570: The Screening of Rubella Virus, Cytomegalovirus, Hepatitis B Virus, and Toxoplasma gondii Antibodies in Prepregnancy and Reproductive-Age Women in Tabriz, Iran

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Background and Aim : The organisms of Toxoplasma gondii, Rubella virus, Cytomegalovirus, and Herpes simplex virus as an acronym of TORCH are major pathogens in prepregnancy and reproductive-age women. These microorganisms are considered a serious problem and cause 2-3% of all birth defects in the fetus. Our study was aimed at screening the seroprevalence of TORCH antibodies among prepregnancy and reproductive-age women in Tabriz, Iran.

Methods : This study was carried out in 2726 prepregnancy and reproductive-age women, who were referred to the laboratory for prenatal TORCH screening. To detect the presence of IgG, IgM antibodies and Hepatitis B surface antigen against these microorganisms were carried out using a chemiluminescence immunoassay analyzer (CLIA).

Results : In the current study, the rates of anti-Toxoplasma gondii IgG, anti-Rubella virus IgG, and anti-Cytomegalovirus IgG were found in 722 cases (26.5%), 2579 cases (94.6%0), and 2718 cases (99.7%), respectively. Moreover, the rates of anti-Toxoplasma gondii IgM, anti-Rubella virus IgM, and antiCytomegalovirus IgM were discovered in 10 cases (0.4%), 13 cases (0.5%), and 16 cases (0.6%), respectively. The Hepatitis B surface antigen was found in 32 cases (1.2%). The dissemination of positive TORCH in various ages was different (P < 0:05).

Conclusion : In our study, the seroprevalence of acute TORCH infections was relatively low. Due to the probability of vertical transmission to the fetus during pregnancy and the unpleasant complication of these pathogens, it is essential to be screened for detection of specific IgG and IgM antibodies in reproductive ages.

Keywords : Rubella Virus, Cytomegalovirus, Hepatitis B Virus, and Toxoplasma gondii

P534-572: The study of the antibacterial effect of peptides obtained from the microbial degradation of feather by Bacillus Tequilensis BK206

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Background and Aim : Feather is one of the most important byproducts of the poultry industry. 90% of the feather proportion are filamentous protein structures called beta-keratin, which has a solid figure due to the presence of a high amount of cysteine and can only decompose by keratinase enzyme, which is an extracellular protease and has the ability to cut disulfide bonds. These feather hydrolysates can be used in various industries. The aim of this research is to investigate the antibacterial effect of peptides obtained from the microbial degradation of the feather by Bacillus Tequilensis BK206

Methods : B. Tequilensis was cultured in feather medium, after complete degradation of the feathers, the culture medium containing the hydrolyzed proteins was spray dried. In order to qualitatively measure the antibacterial property, concentrations of 50, 100, and 200 mg/ml of dried peptides were prepared then were transferred to agar plates containing Escherichia coli and Staphylococcus aureus bacteria, after incubation the disc diffusion was checked. For quantitative method certain concentrations of the peptides were prepared in the 96-well plate containing the mentioned bacteria and the absorption was measured by ELISA reader then MIC (minimum inhibitory concentration) was calculated. To determine the minimum bactericidal concentration (MBC) of peptides, the concentrations in the 96-well plate was inoculated in solid culture medium along with the bacteria.

Results : qualitative analysis showed that the zone of inhibition were observed only in the S. aureus bacteria plate of all the mentioned concentrations, and the diameter of the zone increased in higher concentrations of the peptide. In the quantitative method, growth of both bacteria were completely inhibited at the concentration of 100 mg/ml and as the concentration decreased the inhibition percentage also gradually decreased and reached below 50% in the lowest concentration. Also, MBC was not observed in any of the plates at any concentrations.

Conclusion : Based on the observations, it can be concluded that the microbial based feather hydrolysates have the ability to actively inhibit the growth of E. coli and S. aureus bacteria

and consequently they can be used as a safe feed additive in industries such as livestock and poultry.

Keywords : Keratinase, Feather, Peptide, Antibacterial

P535-573: Isolation and molecular identification of endophytic fungi from Licorice (Glycyrrhiza glabra L.)

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Background and Aim : It seems that plants in natural ecosystems coexist with fungal endophytes. Endophytes are ubiquitous and have high biodiversity and can affect plant communities by increasing optimum growth by increasing tolerance to abiotic and biotic stresses, increasing biomass and reducing water consumption, or reducing optimum growth by changing resource allocation. Despite more than 100 years of research that has resulted in thousands of articles, the ecological importance of these fungi has not been determined. This study aims to isolate and molecular identification of endophytic fungi from Licorice.

Methods : A sampling of healthy plants was carried out randomly in three different locations of Hamedan city (including M=Agriculture research center, D=Moradbeig Valley, and K=ImamzadehKooh Mai) in 2022. Sampling was taken from three different tissues (leaf, root, and stem). Then, isolates were identified by carrying out multiple cultures in the PDA medium based on morphological characteristics and molecular sequencing of the ITS1-5.8S-ITS2 region based on PCR products For sequencing that were carried out by Niagen Noor Medical Genetics Company.

Results : Totally, 21 endophytic fungi were isolated from this plant. There are no isolated fungal endophytes from the leaf but, It was found that the highest range of fungal endophytes is related to the root tissue (84.62%) and the area of the M (Agriculture research center) (46.15). Then, with molecular methods, it was determined with more than 95% similarity that the fungal species related to the area of the M is Aspergillus niger and Fusarium oxysporum, and the samples taken from the two mentioned areas are F. redolense species with a percentage of identification of 96%.

Conclusion : This is the first report that endophytic fungi were isolated from Licorice in Iran. F. redolence is new and the first endophytic fungus reported from Licorice in the world. It can be concluded that molecular identification is a very exact method to detect endophytic fungi.

Keywords : Licorice, endophytic fungi, Molecular

P536-575: Frequency of cagE and cagM genes in Helicobacter pylori isolated from patients with digestive disorders

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Background and Aim : Helicobacter pylori is considered one of the most important human pathogenic bacteria that has infected almost half of the world's population, which can cause a lifelong infection if not treated. However, the amount of pollution varies greatly according to the geographical area. The occurrence of infection and the outcome of the disease depend on various factors, including the pathogenic factors of bacteria, the conditions of the host and the environment. The aim of this study is to determine the frequency of CagE and cagM genes in strains isolated from gastric biopsy samples of a number of patients referred to medical centers.

Methods : In this research, 350 patients who suffered from gastrointestinal diseases were studied. DNA extraction of all biopsy samples was done using chloroform method and then using PCR method and glmM specific primer, samples containing Heliobacter pylori were identified. Also, in order to identify cagM and cagE genes, primers extracted from previous studies and PCR technique were used. At the end, the duplex PCR reaction products were electrophoresed on 1% agarose gel and the results were observed by Gel Documentation device.

Results : From a total of 350 biopsy samples from patients with an average age of 49 years, 190 women and 160 men, 123 Helicobacter pylori samples were positive based on PCR and glmM gene. The prevalence of cagE gene was 56% and cagM was 54% and 43% for both genes.

Conclusion : The frequency of this bacteria was 26% using urease test and 35% using PCR method. According to the results of previous studies, the higher specificity of molecular tests in identifying this bacterium can be pointed out. In the present study, the frequency of cagE gene was 56%. cagE can be used as a marker for healthy cag-PAI samples. R. Mattar and others reported that the cagM gene is a marker to identify people at higher risk of peptic ulcer disease in Brazil. The simultaneous presence of the two genes studied in the research It was also observed in 43% of the samples, and in general, the results of this study are consistent with the results of previous studies.

Keywords : Helicobacter pylori, cagPAI, Biopsy, Duplex PCR

P537-576: In vitro and In vivo evaluation of antiendotoxin activity of the pepR peptide against endotoxin mediated shock and invasive Pseudomonas aeruginosa Infection

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Background and Aim : Sepsis and septic shock are important medical problems with high mortality rates. Common treatment of sepsis is based of antibiotic therapy to target the bacteria, without addressing the systemic inflammatory response, which is a major contributor to mortality in sepsis. Accordingly, novel treatment options are necessary to counteract these complex sepsis pathologies. Here, antiendotoxin activity of the PepR peptide which derived from capside of dengo virus was investigated against P. aeroginosa.

Methods : The MIC and MBC values of PepR against P. aeroginosa ATCC 27853 was determined by the microtiter broth dilution method. In vitro and In vivo LPS models were prepared by affecting PepR on macrophages cells (3.5×105 cells/well) and Male Balb/c mice (8–10 weeks), respectively. The levels of IL-6, IL-10, MCP-1, IFN-γ, and TNF-α were measured in both cell culture supernatants and murine plasma using the Mouse Inflammation Kit according to the manufacturer's instructions. In addition, P. aeruginosa infection model was prepared by intra-peritoneally injection of bacterial suspension and subcutaneously injection of PepR in male Balb/c mice. Finally, bacterial dissemination to target organs including spleen, liver and kidney was determined by measuring cfu/g. Results:

Results : MIC and MBC of PepR for ATCC 27853 P. aeruginosa strains were 8 and 16 µg/mL, respectively. The results showed that PepR has antimicrobial activity against the P. aeruginosa strain. Moreover, PepR binds to LPS and thereby decrease LPS-induced pro-inflammatory responses by reducing in vitro NF-kB/AP-1 activation. In mouse models of LPS-induced shock, PepR significantly increased survival by modulating the pro-inflammatory cytokine response. Finally, in an invasive Pseudomonas infection model, the peptide inhibited bacterial growth and reduced the pro-inflammatory response, resulting in a significant reduction of mortality.

Conclusion : Given simultaneously targeting bacteria and LPS-induced pro-inflammatory responses by PepR, the peptide could be considered as a novel promising therapeutic candidate for invasive infections.

Keywords : Antimicrobial peptides; PepR; Pseudomonas aeruginosa; Anti-endotoxin; Anti-inflammatory; LPS.

P538-579: Study of Infection of Broiler Chickens in Guilan Province with Fowl cholera by ELISA Method

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Background and Aim : Fowl cholera or Pasteurellosis is an acute and highly contagious disease caused by Pasteurella multocida a gram-negative coccobacillus in the Pasteurellaceae family in a range of avian species including chickens, turkeys, and other birds. This disease is seen worldwide and can range from acute septicaemia to chronic and localised infections. The broiler flocks is more sensitive than the laying breed .The morbidity and mortality may be up to 100% and It can also occur in humans which shows the importance of investigating this bacterium .

Methods : Total 150 blood samples were taken from 15 broiler flocks of Guilan province (randomly 10 samples from each flock). Sampling was done by collecting 2 to 3 cc of blood .The samples were centrifuged at 3000 rpm for 5 minutes to completely separate the serum and Indirect ELISA was performed using by Pasteurella Multocida Antibody Test Kit IDEXX to determine the antibodies titres against Pasteurella Multocida.

Results : In this study 150 blood samples were collected from broilers in Guilan province and after examining the titer of each sample, it was found that 100% samples were positive that indicates high infection in this flocks.

Conclusion : This study was carried out to determine antibodies against Pasteurella Multocida in broiler flocks of Guilan province. Since all the studied samples had positive titers and it could be due to high humidity in Guilan province and high pollution of local poultry and non-compliance with health standards in broiler farms.Because of this, it is recommended that poultry workers should not have contact with native birds and health standards in broiler flocks should be raised .Also similar research in other provinces with similar and different climates is suggested to be done with serological and molecular methods.

Keywords : Fowl Cholera, Pasteurella Multocida Antibody Test Kit IDEXX, ELISA, Guilan provience.

P539-581: Isolation and molecular identification of two rutin-producing endophytic fungi from Caper (Capparis spinosa L.)

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Background and Aim : Flavonoids are a group of polyphenolic compounds that are naturally found in plants and many flavonoids are the basis of herbal medicines and have effective pharmacological effects. Rutin is one of the flavonoids that is used as a reagent in the study of flavonoids and is also considered an antioxidant. This study was conducted to isolate and identify rutin-producing endophytic fungi from C. spinosa.

Methods : Sampling was performed in 10 regions of Iran and was taken from different tissues (including leaves, stems, roots, and fruits). After surface disinfection, explants were placed on PDA medium and the fungal isolates were purified. Molecular identification of isolates was performed by sequencing ITS1-5.8S-ITS2. Morphological identification of fungi was performed by microscopic slide preparation and fungus identification keys. Methanolic extract of fungi was prepared by the maceration method and the presence of rutin was investigated using the HPLC technique

Results : A total of 24 fungi were identified. HPLC analysis showed that the peak of standard flavonoids including rutin, quercetin, and apigenin appeared at 3.82, 7.60, and 12.40 min, respectively. Results showed that only two isolates were able to produce rutin. A comparison of the mean production of rutin showed a significant difference between the two fungi. Alternaria alternata M28 (22.94 ppm) had the highest amount of rutin production. Results also showed that rutin production in the mycelial tissue was more than in the extracellular medium so that in A. alternata M28 and Paecilomyces maximus had rutin content of about 67.5 and 5.56 times, respectively.

Conclusion : Fungal rutin in methanolic extracts was characterized by HPLC. This is the first report that endophytic fungi have an acceptable potential for rutin production from C. spinosa and more research on these isolates can increase the amount of rutin production in them and lead to commercialization.

Keywords : Flavonoids, HPLC, Rutin, Caper

P540-584: Phenotypic resistance to fluoroquinolones (enrofloxacin and ciprofloxacin) in Shiga toxin-producing Escherichia coli isolates from sheep carcasses in Kerman against

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Background and Aim : Shiga toxin-producing Escherichia coli (STEC) are known as foodborne pathogens and are also responsible for epidemics of hemorrhagic colitis (HS) and hemolytic uremic syndrome (HUS), worldwide. The aim of this study was to investigate the phenotypic antibiotic resistance to fluoroquinolones (ciprofloxacin and enrofloxacin) in STEC strains isolated from sheep carcasses in Kerman.

Methods : In this study 30 STEC isolates were confirmed by conventional PCR methods. Disk diffusion technique was used to analyze STEC isolates for resistance against enrofloxacin and ciprofloxacin.

Results : Among 30 STECs, 9 isolates (30%) and 22 isolates (73.4%) were resistant to the antibiotics ciprofloxacin and enrofloxacin, respectively

Conclusion : The results of this study showed that STEC strains obtained from raw sheep meat have a significant amount of resistance to fluoroquinolones and resistance to enrofloxacin was more frequent in comparison with ciprofloxacin. Therefore, these ovine STECs are considered as potential risk for public health in Kerman.

Keywords : Shiga toxin-producing Escherichia coli, Sheep, Fluoroquinolones

P541-585: Investigation of antimicrobial resistance to chloramphenicol in Shiga toxin-producing Escherichia coli isolates from sheep carcasses in Kerman

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Background and Aim : Shiga toxin-producing Escherichia coli as one of the important foodborne bacteria causes diarrhea, hemorrhagic colitis (HC) and hemolytic-uremic syndrome (HUS). Present investigation was done to study phenotypic resistance to chloramphenicol in Shiga toxin-producing Escherichia coli (STEC) strains isolated from sheep carcasses in Kerman slaughterhouse.

Methods : . In this study 30 STEC isolates were confirmed by conventional PCR methods. Disk diffusion technique was used to analyze STEC isolates for resistance against chloramphenicol.

Results : Among the 30 STECs, 7 (23.3%) were resistant to the chloramphenicol whereas sensitivity to the antibiotic was determined in 17 isolates (56.6%), and intermediate resistance was detected in 6 isolates (20.1%).

Conclusion : Although prevalence of resistance to chloramphenicol was low but could be progressive. Therefore, STEC strains obtained from raw sheep meat potentially pose a food-borne risk for public health.

Keywords : Shiga toxin-producing Escherichia coli, Sheep, Antibiotic resistance, Chloramphenicol

P542-590: Antimicrobial resistance to gentamicin in Shiga toxin-producing Escherichia coli isolated from sheep carcasses in slaughterhouse of Kerman

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Background and Aim : Antibiotic-resistant Shiga toxin-producing Escherichia coli (STEC) are a zoonotic and food-born pathogen which can spread through fecal contaminated food. The purpose of this study was to investigate the phenotypic resistance to gentamicin in STEC strains isolated from sheep carcasses in Kerman

Methods : In this study 30 STEC isolates were confirmed by conventional PCR methods. Disk diffusion technique was used to analyze STEC isolates for resistance against gentamicin.

Results : Among the 30 STECs, 16 isolates (53.3%) were resistant to the gentamicin, whereas 8 isolates (26.6%) were found to be sensitive, and the remaining 6 isolates (20.1%) were in an intermediate stage of resistance.

Conclusion : The findings of this study demonstrate a considerable level of antibiotic-resistant in STEC strains isolated from raw sheep meat. As a result, these strains potentially threatens public health in kerman city.

Keywords : Shiga toxin-producing Escherichia coli, Sheep, Antibiotic resistance, Gentamicin.

P543-597: Assessment of in vitro Antibacterial Efficacy of Phytosynthesized Selenium Nanoparticles using Polylophium involucratum (Pall.) Boiss. Seeds Extract Against Pathogenic Bacteria

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Background and Aim : Biosynthesis of nanoparticles is an interdisciplinary application of metal science and technology through biology. The main reaction of this technique is oxidation or reduction using biomolecules. Biosynthesis of selenium nanoparticles (SeNPs) has gained significant interest due to their distinctive chemical and biological properties that is essential for potential application in various fields.

Methods : In this project the phytosynthesis of selenium nanoparticles using seeds Polylophium involucratum (Pall.) Boiss. extract as a reducing agent by microwave irradiation method and its antibacterial properties has been reported. Phytosynthesis of selenium nanoparticles was characterized by UV-Vis, FT-IR, XRD, TEM, FE-SEM. The antibacterial activity of the synthesized selenium nanoparticles was tested using both gram positive as well as gram negative bacteria i.e. Staphylococcus aureus and Bacillus cereus respectively.

Results : FT-IR spectroscopy revealed that SeNPs were functionalized with biomolecules that have primary amine group, carbonyl group, OH groups and other stabilizing functional groups. An absorption band centered on 330 nm was observed, this absorption corresponds to the surface plasmon resonance (SPR) of the selenium nanoparticles. The structure and composition of selenium nanoparticles were analyzed by XRD and showed that the SeNPs are crystalline in nature. The morphological study of selenium nanoparticles using TEM suggests that the nanoparticles are spherical in shape with a diameter 200 nm. The synthesized selenium nanoparticles exhibited good antibacterial potential against gram positive and gram negative bacterial strains.

Conclusion : Therefore, in the present project the phytochemical evaluation of Polylophium involucratum (Pall.) Boiss. were found to be a powerful antibacterial agent and this study can be continued for their structural elucidation and pharmacological activity.

Keywords : Polylophium involucratum (Pall.) Boiss., Bacillus cereus, Se-NPs, SPR, FT-IR, Pharmacological activity.

P544-606: Antibacterial Activity of Synthesis of Silver Nanoparticles of Methanolic Extract of Leaves of Anethum graveolens L. from Tonekabon - Iran

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Background and Aim : Currently, considerable attention has been made towards metal nanoparticles due to their unique properties that are different from their bulk metals. They have wide applicability in different areas including biology, chemistry, medicine and optoelectronics. Many methods have been developed for the synthesis of metal NPs and most of these methods are based on chemical reduction and physical methods which are expensive, toxic and non-environmentally friendly. At present, there is a growing need to use non-toxic, environmentally, and renewable materials for the synthesis of metal nanoparticles. Thus many attempts have focused on the use of green synthesis approach. Here a simple biosynthesis approach was applied and silver nanoparticles were synthesized by using Anethum graveolens L. leaves extract and its examined antioxidant and antimicrobial activity.

Methods : In this study, Anethum graveolens L. is one of the members of Apiaceae family. Anethum graveolens leaves collected from Tonekabon city were used to synthesis of silver nanoparticles and evaluation of biological properties. Methanolic extracts were investigated for antibacterial activity against six selected bacterial strains (Bacillus subtilis, Staphylococcus aureus, Pseudomonas aeruginosa, Escherichia coli, Salmonella typhi and Shigella dysenteriae) using minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) methods. Antioxidant activity of methanolic extracts was assessed by DPPH0 method. Synthesis of silver nanoparticles was evaluated by TEM, FT-IR, UV-Vis and XRD.

Results : Our research showed that synthesis of silver nanoparticles using methanolic extracts of Anethum graveolens L. had antibacterial activity on all of the investigated microorganisms. The amount of IC50 for silver nanoparticles was (181.8±4.6 mg/ml). Synthesis of silver nanoparticles and pictures captured by TEM showed that nanoparticles were spheroids which were distributed uniformly. The size of particles varied between 10 and 50.

Conclusion : Finally it can be concluded that the synthesis of silver nanoparticles of leaves extract of Anethum graveolens L. can be used effectively against certain bacteria causing disease in human beings as it is a potent antimicrobial agent.

Keywords : Anethum graveolens L., Pseudomonas aeruginosa, Silver Nanoparticles, DPPH0 Method.

P545-611: Evaluation of gene expression changes in two-component regulatory systems of Pseudomonas aeruginosa

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Background and Aim : Pseudomonas aeruginosa is an opportunistic pathogen that causes serious nosocomial-infections. The biofilm plays a critical role in the virulence of P. aeruginosa. Biofilm formation is under-regulation of two-component regulatory systems of bacteria gacA and retS. The biofilm matures during a process in 5-days, which is the outcome of equivalence in the expression of upstream regulatory genes. This study aims to evaluate the expression of two major gene-regulators gacA and retS, during biofilm maturation in Pseudomonas aeruginosa.

Methods : The biofilm producer P. aeruginosa ATCC 10145 was placed in the in-vitro conditions of biofilm production using a micro-titer plate assay. After days 1, 2, and 5, total RNA was extracted, and the expression of gacA/retS genes measured using the relative Real-Time PCR method.

Results : Both gacA and retS expression showed a time-dependent increase after two days. However, from 2nd to 5th day, a reducing expression was observed in gacA, while retS showed a continued increasing expression in this time period.

Conclusion : The results confirmed that gac and ret regulators have a direct positive effect on the expression of genes are involved in biofilm formation of P. aeruginosa.

Keywords : Pseudomonas aeruginosa, biofilm formation, quorum sensing, two-component regulatory system, gacA, retS.

P546-612: Bacterial Profile and Antibiotic Resistance in Patients with Diabetic Foot Ulcer: a meta-analysis

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Background and Aim : Diabetic foot ulcers are among the most common complications of patients who have diabetes mellitus which is not well controlled. About 15% of people with diabetes will get a foot or toe ulcer. Around 14% to 24% of people with diabetes in the U.S. need an amputation after they get an ulcer. Nowadays, the prevention of limb amputation and treatment of DFUs are known as the major health challenges. The identification and diagnosis of diabetic foot ulcer (DFU) infections remains a complex problem. Because inflammatory responses to microbial invasion may be diminished in persons with diabetes, clinical signs of infection are often absent in persons with DFUs when infection is limited to localized tissue. Therefore, we designed this study to identify the most common bacteria causing DFIs, as well as detection of their antibiotic susceptibility pattern and detection of the prevalence rate of MDR organisms with meta-analysis method.

Methods : In this research, we searched papers based on specific and relevant keywords in research databases including ISI web of science, PubMed, Google Scholar, and Persian database such as ISC and SID. The search keywords and strategies are followed; “diabetic,” “wound,” “bacteria,” “antibiotic resistance,” were used in combination with Boolean operators OR and AND.

Results : The proportion of Gram-negative bacteria was higher than Gram-positive bacteria (59.1% versus 40.9%). The most prevalent pathogens isolated were Staphylococcus aureus (27.7%), Escherichia coli (12.9%), Pseudomonas aeruginosa (10.5%), Klebsiella pneumoniae (6.2%), Staphylococcus epidermidis (5.3%) and Enterococcus faecalis (4.9%). Staphylococcus aureus (30.4%) was the most predominant MDR bacteria, followed by extended-spectrum ?-lactamase (ESBL) (19.1%). The prevalence of methicillin-resistant Staphylococcus aureus appears to be stable.

Conclusion : There is a notable local pattern of DFI bacteriology in our community. Our findings could be valuable in developing the future empirical treatment guidelines for DFIs.

Keywords : Bacterial Profile, Antibiotic resistance, diabetic foot, infections

P547-636: Comparison of bactericidal properties of argon and helium cold atmospheric plasma on multidrug resistance Pseudomonas aeruginosa

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Background and Aim : Pseudomonas aeruginosa is a gram-negative bacterium that has become resistant to many antibiotics in recent years. The most common wound infection occurs with Pseudomonas aeruginosa, and with the increasing resistance to a variety of antibiotics, new antimicrobial approachs seem necessary. One of the new approach is the use of cold plasma. Cold atmospheric plasma is an innovative, promising tool capable of inactivating bacteria. The present study aimed to investigate in vitro antimicrobial properties of cold argon plasma and cold helium plasma on Pseudomonas aeruginosa.

Methods : : Pseudomonas aeruginosa from the microbial collection of Tabriz University was selected and approved. Then antibiotic resistance was evaluated by the disk diffusion method, and the bacterium resistant to most antibiotics was selected. Then a 106 CFU/ml bacterial suspention was prepared, and used for plasma treatment. Plasma therapy was performed with Argon and helium gas for different characteristics and times. The surface culture method was used to count the colony.

Results : The results of the inactivation of Pseudomonas aeruginosa in suspension by cold plasma of Argon and helium showed that, with increasing plasma treatment time, the plasma microbicides property increases so that with 8 minutes of Argon plasma therapy, the microbial suspension is reduced 3 logs but plasma therapy with helium for 8 minutes decreased 2.5 log of bacteria in the microbial suspension.

Conclusion : The results showed that Argon and helium have bactericidal properties on Pseudomonas aeruginosa. Although the characteristics of plasma can vary, the bactericidal rate of Argon plasma is better than helium.

Keywords : Pseudomonas aeruginosa, Antibiotic resistance, Argon cold atmospheric plasma, Helium cold atmospheric plasma, Multidrug resistance

P548-640: Feasibility of Ethanol Production from Whey by Kluveromyces sp.

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Background and Aim : Yeast known as Kluyveromyces sp. is a microorganism with the potential to produce ethanol from lactose-containing compounds. The lactose sugar in whey is the main cause of spoilage of this effluent for the environment and ethanol is one of the most widely used substances in industry. The aim of this study was the production of ethanol from whey.

Methods : after macroscopic & microscopic examinations of the prepared yeast and its confirmation, sampling was performed from Labanyiate Damaneh Sarab factory. The whey prepared after protein extraction was autoclaved with the help of DNS reagent and standard diagram of lactose as the medium for yeast culture. Yeast requirements for aeration were also assassed in three states. the amount of ethanol produced was measured by sulfochromic acid reagent and spectrophotometer.

Results : based on the ethanol diagram prepared and comparing the results obtained by spectrophotometry of the tested samples, it was found that in the state without optimization, in the best state yeast growth in the aerobic state 2.25% of ethanol was produced.

Conclusion : It is possible to actually produce ethanol from whey, and the Kluyveromyces sp is a good case in point. Ethanol production efficiency from whey is at its highest.

Keywords : bioEthanol, whey, biofuel, Kluyveromyces sp., K. fragilis, K. marxianus.

P549-650: Designing of a multi-epitope vaccine candidate against Campylobacter jejuni based on bioinformatics study

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Background and Aim : Campylobacter species are widely distributed globally. Campylobacter jejuni is a Gram-negative bacteria that causes complicated diarrhea worldwide. Owing to the lack of effective vaccine against C. jejuni till now, the best way for reducing the C. jejuni infections includes developing protective vaccine for human use. Application of in silico studies for the design of vaccine candidate reduces the time duration and costs of the workflow. CadF, FlpA, Peb1A, FlaA, CiaA and Ftsk are the most important structural and non-structural proteins in the pathogenesis of this bacterium. Accordingly, the aim of this work was performing a bioinformatics study to design a multi-epitope-based protein subunit vaccine candidate.

Methods : Primary epitopes were selected using NCBI from a set of bacterial protein structures then the potential of peptide sequences in immune responding was evaluated and antigenic, non-allergenic and non-toxigenic epitopes were predicted using VaxiJen 2.0, AllerTOP, and ToxinPred servers. In the next step, the non-allergenic and non-toxic epitopes were selected and these adopted epitopes were linked to each other using appropriate linkers, followed by appending a suitable adjuvant (toll-like receptor 4 agonist) to increase the immunogenicity of the multi-epitope vaccine.

Results : The vaccine candidate was able to provoke sufficient responses of T cells and B cells and Gamma-interferon which are pivotal for the antibacterial responses of the immune system.

Conclusion : Therefore, it seems that our multi-epitope vaccine candidate was appropriate and had high potential for experimental analysis and was proven to be useful against C. jejuni infection as a concerning cause of diarrhea.

Keywords : Campylobacter jejuni, diarrhea, vaccine, CadF, FlpA, Peb1A, FlaA, CiaA, Ftsk, bioinformatics

P550-651: In silico study to design a multi-epitope vaccine against to challenges caused by Listeria monocytogenes

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Background and Aim : The Gram-positive bacterium, Listeria monocytogenes (L. monocytogenes), causing listeriosis, is a food-born infection. Although this bacterium influences on pregnant women, fetal, elderly and immunosuppressed patients, it also affects normal people. L. monocytogenes is resistant to extreme conditions such as low temperature or high salt and this represents that this species has high adaptability to their environment. L. monocytogenes has severe clinical manifestations such as abortion, meningoencephalitis, sepsis, myocarditis, hepatitis, cellulitis and etc. Despite these fatal effects, there hasn't been suitable antibiotic against this bacterium so far. One of the most promising ways against this challenge is vaccination. In silico analysis of protein shows that various structural features allow surface proteins to interact with different components of bacteria or host. This variety provides new clues about molecular basis of L. monocytogenes. Some bacterial structural and non-structural proteins include InlA, Hly, ActA, PrfA, OrfX, PlcA and InlB. This study aimed at prediction of T cells and B cells epitopes for subunit vaccine design against L. monocytogenes.

Methods : In this study, after selection of protein sequences from the NCBI and suitable epitopes detection, the antigenicity, allergenicity and toxicity of epitopes were predicted for designing an appropriate multi-epitope construct using suitable linkers. Thereafter, a suitable adjuvant (toll-like receptor 4 agonist) was added for increasing the immunogenicity, designing molecular modeling of 3D structure.

Results : This multi-epitope vaccine was shown to induce T cells and B cells responses.

Conclusion : Therefore, this vaccine candidate was effective and safe against listeriosis though future studies can validate the results.

Keywords : Listeria monocytogenes, structural proteins, in silico, multi-epitope vaccine

P551-652: Evaluation of immunological characteristics in order to design a multi-epitope vaccine candidate against shigella dysenteri

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Background and Aim : Shigellosis is an important dysenteric disease specially in under 5 year old children, elderly and immuno- compromised patients. Currently, there is no effective vaccine for shigellosis, because of this developing vaccine is necessary. In this study, the immune informatics approach was applied to design and explore a potential multi-epitope vaccine against Shigella.

Methods : First of all, optimal epitopes (antigenic, immunogenic, non-toxic, and non-allergenic) were extracted from structural proteins of the Shigella using screening web tools. Candidate epitopes were fused to each other suitably using KK, and GPGPG linkers. toll-like receptors (TLR) 4 agonist (50S ribosomal protein L7/L12) as adjuvant were then added to the amino terminal of the final epitope vaccine sequence to increase its immunogenicity. The three dimensional structure of the potential vaccine was then modeled using I-TASSER server.

Results : Molecular dynamics simulations studies verified the high stability of final free vaccines and in complex with TLR4. This construct was also antigenic, non-allergenic, nontoxic and immunogenic.

Conclusion : Although the designed vaccine traits was promising as a potential candidate against the shigellosis, experimental studies and clinical trials are required to verify the protective traits and safety of the designed vaccine.

Keywords : Shigellosis , diarrhea , multi_ epitope vaccine , bioinformatics

P552-653: Antimicrobial activity of Pediococcus acidilactici PTCC 1954 and Leuconostoc mesenteroides PTCC 1953 isolated from organic meat sausages

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Background and Aim : Organic meat products are well known for their probiotic values due to the presence of probiotic lactic acid bacteria such as Lactobacillus, Leuconostoc, Lactococcus, and Pediococcus strains. This study aimed to isolate and characterize new strains of lactic acid bacteria (LABs) from organic meat sausages and to evaluate their antimicrobial activities.

Methods : In this study, LAB strains were isolated from vacuum-packed organic meat sausages bought from Solico Group Co Ltd. (Tehran, Iran). All isolates were characterized by morphological, biochemical, and 16S rRNA analysis. The primary antibacterial activity of the isolates was evaluated against Micrococcus luteus PTCC 1408. The growth kinetics and antimicrobial activity of the strain MN-B against Lactobacillus casei ATCC 39392 were determined in MRS broth medium. In addition, bacteriocin produced by the strains MN-B revealed antimicrobial activity against selected foodborne pathogens. Bacteriocin produced by the MN-B strain was partially purified using the adsorption-desorption method followed by dialyzes.

Results : In this study, two Pediococcus spp. and three Leuconostoc spp. with antimicrobial activity were isolated from vacuum-packed organic meat sausages and designated as MN-A, MN-B, MN-A2, MN-A2-1, and MN-A3. The results showed that the isolate MN-A and MN-B belonged to the strain Pediococcus acidilactici and the MN-A2, MN-A2-1, and MN-A3 isolates were identified as Leuconostoc mesenteroides strains. Amongst the isolates, the strain MN-B showed the highest antimicrobial activity against the Micrococcus luteus PTCC 1408. The molecular weight of bacteriocin was about 5.0 KDa.

Conclusion : Pediococcus acidilactici (strain MN-B) showed significant antimicrobial activity against Salmonella enterica subsp. enterica serotype Typhimurium PTCC 1709, Staphylococcus aureus PTCC 1113, Listeria monocytogenes PTCC1302, and Listeria inovani PTCC 1303. Therefore, this strain can be considered a potential candidate in different sectors such as the food industry as a preservative.

Keywords : Antimicrobial activity, bacteriocin, isolation, characterization,

P553-654: Characterization of Razi Bovine Kidney (RBK) cell line as sensitive cell for BOHV-1 virus

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Background and Aim : Razi Bovine Kidney (RBK) cell line has been stabilized in Razi institute. RBK cell line is extremely sensitive to some viruses. This cell line was derived from primary bovine kidney cells by continuous passage. The purpose of this study is characterization of RBK cell line by identity tests (consist of karyology and molecular tests) and growth characteristics; to achieving an appropriate cell line for Bovine Herpesvirus 1(BoHV-1) virus.

Methods : In order to preparing RBK cells, the standard methods were followed based on Freshney 2016. Origin of RBK cell line was confirmed by PCR test. The RBK were incubated for different time periods such as 24, 48, 72, 96,120, 144, 168 and 192 hours, Then cell growth curve and doubling time (DT) were determined. The cell DT was calculated using formula: T = t {lg2 (lg Nt _ lg N0)_1} Cytogenetic analysis of RBK was carried out with standard procedure.

Results : According to the single band in 102 bp, the results of molecular identification revealed that cell line origin was bovine. During DT the cell line exhibited an exponential growth pattern. Cells reached stationary growth phase after 144 hours of exponential growth. Finally, the results of cell count and time of DT for RBK by using formula calculated. cytogenetic analysis revealed an aneuploid karyotype, that only 42% of the RBK cells possessed the modal diploid chromosome number of 2n=44, which consisted 4 pairs of metacentrics, 2 pairs of subtelocentrics and 16 pairs of telocentrics (2n=4m+2st+16t).

Conclusion : Sensitivity of RBK cell line to different viruses and parasites was studied and various results have been reported. In this study, we found RBK cell line as the most effective for cultivation of BOHV-1 virus, which is optimal for the propagation of BOHV-1 virus. As well as, the BOHV-1 virus titre reached 8±0.5 CCID50/mL on RBK cell line. Consider to DT and titration tests, this research work proved that RBK has a recognizable and appropriate sensitivity to BOHV-1 virus; In addition this cell line can be easily and rapidly proliferated.

Keywords : RBK, DT, cell line, cytogenetic analysis, aneuploid

P554-655: A multi-epitope vaccine candidate design against Coxiella burnetii causing Q fever

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Background and Aim : Q fever is a zoonotic and important infectious disease caused by Coxiella burnetii. Because of numerous outbreaks and the endemic potential of C. burnetii which is without any approved vaccine, the prognosis of the infection is crucial. Targeting structural and non-structural proteins is a proper strategy to reach the aim of vaccination. Com1, GroEL, Mip, OmpH, ComE, IcmG, CH60, CpoB, YbgF, YufA, SucB and RpIL are the most important proteins in the pathogenesis of this bacterium. The aim of this work was performing an immunoinformatics study to identify a multi-epitope-based subunit vaccine candidate.

Methods : In this study, designing a synthetic in silico multi-epitope vaccine against C. burnetii was followed using immunoinformatics approach. Primary epitopes were extracted from the set of bacterial protein structures and then the potential of peptide sequences in immune response was evaluated and antigenic peptides were selected. In the next step, the non-allergenic epitopes were fused to each other with appropriate linkers, followed by appending a suitable adjuvant to increase the immunogenicity of the polypeptide vaccine. Therefore it seems that these peptides have good potential for experimental analysis and can prove to be useful against C. burnetii. Antigenic proteins, and T cell epitopes were selected. Antigenicity, allergenicity, and toxicity of the selected epitopes were evaluated using the VaxiJen 2.0, AllerTOP, and ToxinPred servers, respectively.

Results : The affinity of the proposed vaccine to MHC I and II molecules was measured in a molecular docking study. Resultant vaccine had high antigenicity, stability, and a half-life compatible with utilization in vaccination programs.

Conclusion : In conclusion, the validated multi-epitope sequences had the potential as a vaccine candidate to ensure protection against Q fever agent.

Keywords : Q fever, Coxiella burnetii, peptide-based vaccine, immune informatics, epitope

P555-680: Application of Chitosan-Silver Nanoparticle as Theranostic Agents

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Background and Aim : The term Theraryostic was first created in 2002 by, John Funkrouser, president of the Farmanic company while defining his company's business strategy for diagnostic development and its direct relevance with personalized therapy. He defines the diagnosis as "the ability to define the state of the disease" and theranostics as "the ability to influence therapy or treatment with the diagnosis of disease". One of the important components that must be considered for the development of a nano-theranostics system is the design of a nanocarrier or nano-platform that can play an effective role in the theranostics system. Biosynthesized silver nanoparticles with theranostics properties have anticancer applications, targeted drug delivery, and bioimaging. Polymeric nanoparticles are another category of nanocarriers that have therapeutic and diagnostic applications. Chitosan (CS), a common cationic polysaccharide, is studied as a hopeful carrier in pharmaceutical and food industries for the improvement of delivery systems, due to its features of biodegradability, biocompatibility, and low toxicity. This review examines a new treatment method called theranostics based on the natural polymer chitosan and silver metal nanoparticles.

Methods : In order to select the articles, the papers of the years 2011-2019 were examined in the Google Scholar, PubMed, and Scopus databases with the keywords of theranostics, Ag-nanoparticles, and Chitosan. Information extraction from basic studies has been done. The keywords were selected by the MeSH browser.

Results : In general, it can be said that the primary choice of scientists for the development of new medicinal agents are natural polymers due to the mentioned advantages. Therefore, if we focus on a natural polymer and a metal nanoparticle such as gold, silver, copper, zinc, and titanium we can refer to them as new nano theranostics agents with higher activity and higher diagnostic properties, and ultimately lower adverse effects. Chitosan-silver nanoparticles have also been used for inhibition of bacterial growth, tissue regeneration process, wound healing process, etc.

Conclusion : The design of a nano-platform-based chitosan and silver nanoparticles has played an effective role as a wound healer, antibacterial and effective drug delivery system.

Keywords : Theranostics, Silver nanoparticles, Chitosan (CS)

P556-683: Studu on Antibacterial activity of extracted phycocyanin from spirulina platensis

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Background and Aim : Phycocyanin, a blue color pigment is a common pigment of cyanobacteria. Phycocyanin is used as colorant in food and cosmetics. It was known as antioxidant and has some therapeutic value such as immuno-modulating activity, anticancer activity and antimicrobial activity.

Methods : The phycocyanin of cyanobacterium, Spirulina platensis, was extracted by using two physicochemical methods and purified by ammonium sulfate precipitation and dialysis. The concentration and extraction yield of phycocyanin was calculated. Antibacterial assay were applied for against 6 type test strains consist of gram positive and gram negative bacteria. Activity was determined by using direct drop and agar well diffusion methods.

Results : It was found that the phycocyanin concentration was 2mg/mL and Extraction yield was obtained to be 4mg/g. The protein estimation of the phycocyanin pigment using Lowry method was found to be 128 µg/ml. Each extracts exhibited varying degrees of antibacterial activity against an array of all Gram-positive bacteria but no effect against Gram-negative bacteria was showed.

Conclusion : The results of this study indicate the potential use and ability of Spirulina platensis and extracted phycocyanin as a source of antimicrobial agent against some bacteria.

Keywords : Spirulina platensis, Phycocyanin extraction, Antibacterial activity

P557-706: Effects of probiotic therapy on immune system and inflammation in patients with multiple sclerosis

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Background and Aim : Multiple sclerosis (MS) is an autoimmune inflammatory disease affecting the myelin sheaths in the central nervous system (CNS). Gut microbiota dysbiosis has been implicated in a wide range of immune-mediated diseases, including MS. Regarding the interactions between immune system and gut microbiota, the aim of this paper is to review the immunomodulatory and anti-inflammatory role of probiotics in the progress and management of multiple sclerosis.

Methods : A search was conducted on PubMed, Cochrane Library, and Web of Science databases from 2011 to 2022 using the terms "probiotics", "multiple sclerosis ", "immune system", and "inflammation".

Results : Different probiotics strains showed to influence the immune system in MS patients through different mechanisms. The pro-inflammatory effects of Th1- and Th17-produced cytokines such as IL-17, IL-6, IL-1β, IL-4, IFN-γ, TGF-β, and IL-2 as well as their serum levels were attenuated by administration of L. acidipiscis, L. helveticus SBT2171 (LH2171), L. casei (Lca), lactobacilli mixture, B.coagulans, Escherichia coli strain Nissle 1917 (ECN), L. plantarum A7 and B. animalis PTCC 1631 Combination, and Vivomixx. Also, these probiotics decreased the number of pro-inflammatory cytokine-producing cells, inhibiting the differentiation of CD4+ cells into Th1 and Th17 cells. Furthermore, by increasing the production of the anti-inflammatory cytokines and transcription factors such as IL-4, IL-10, TGF-β, GATA3, and Foxp3 and increasing the responses of the regulatory T cells, ECN, L. plantarum A7 and B. animalis PTCC 1631 Combination, IRT5, L. acidipiscis, VSL3, and Vivomixx probiotics showed to suppress the inflammation and promote the anti-inflammatory gene expression in multiple sclerosis patients and animal models.

Conclusion : Collectively our findings demonstrate that the probiotics could improve immune and inflammatory factors in MS disease. Probiotics may have beneficial effects on the management and treatment of multiple sclerosis as co-therapeutic strategy, especially when administered in combined forms. However, more studies are needed to determine the most effective strains or combinations and to validate them in human studies.

Keywords : "Probiotics", "multiple sclerosis ", "immune system", "inflammation"

P558-707: The probiotic properties and potential of vaginal lactobacilli spp. Isolated from healthy women against some vaginal pathogens

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Background and Aim : During the last decade, research in probiotic has progressed considerably and significant advances have been made in the selection and characterization of specific probiotic strains. The most studied probiotics belong to Lactobacillus genera.

Methods : The potential probiotic characteristics of 970 Lactobacillus strains separated from the vagina of healthy women were evaluated in terms of some safety features such as antibiotic susceptibility and hemolytic activity; probiotic properties like resistance to acidic conditions and bile salts; antagonistic activity against pathogens; lactic acid production; hydrophobicity, auto-aggregation, and co-aggregation abilities; hydrogen peroxide production; and adhesion capacity to Hela cells.

Results : Among the isolates, five strains were identified as Lacticaseibacillus rhamnosus, Lacticaseibacillus casei, Lactiplantibacillus plantarum, Lactobacillus acidophilus and Lactobacillus gasseri, presented acceptable antibiotic susceptibility pattern. Further analysis showed antimicrobial activity of Lacticaseibacillus culture against various bacterial pathogens and real-time PCR showed all five strains were able to prevent the colonization of bacterial pathogens. All five selected strains produced organic acids, hydrogen peroxide and were resistant to the spermicide. In addition, they lacked hemolytic activity with the ability of hydrophobicity, auto-aggregation and co-aggregation with pathogens.

Conclusion : These results suggest that the vaginal microbiome could be a good source for the isolation of probiotics and the strains of this study may be considered as good probiotics candidates.

Keywords : Probiotics, lactic acid bacteria, Women, Vaginal microbiota, Lactobacillus spp.

P559-708: Isolation and identification of Lactobacillus producing Biosurfactant and investigating its antimicrobial effects on human pathogenic bacteria

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Background and Aim : Biosurfactants are amphiphilic molecules that are mainly produced by microorganisms as extracellular secondary metabolites and are of special importance due to their use in various industries. The aim of this research was to isolate and identify Lactobacillus strains producing biosurfactants from local dairy products and to investigate the antimicrobial effects of biosurfactants produced by them.

Methods : Dairy products were sampled and cultured in MRS medium. Hemolytic activity, emulsification, and measurement of surface tension were measured and the isolated strains with the ability to produce biosurfactants were identified based on biochemical and molecular tests. Then the biosurfactant produced by the selected strain was extracted from the culture medium and the effect of various factors such as Temperature (25, 50, 75, 100), pH (3-12), and NaCl concentration (5-20%) were investigated on its stability. Finally, the antimicrobial effect of the produced biosurfactants on Escherichia coli (PTCC 1330), Staphylococcus aureus (PTCC 1112), Staphylococcus epidermidis (PTCC 1856), Proteus mirabilis (PTCC 1710) and Pseudomonas aeruginosa (PTCC 1074) by measuring MIC and MBC was evaluated.

Results : In this study, 47 bacterial strains were isolated. Among them, 13 strains had hemolytic activity, and 5 strains had emulsifying activity above 70%. Finally, only 1 strain was able to bring the surface tension to less than 40 mN/m. Based on biochemical and molecular tests, the isolated strain of Lactobacillus plantarum was identified. Also, the results showed that the produced biosurfactants had antibacterial activity and the most susceptible and resistant bacteria to the produced biosurfactants were Staphylococcus aureus and Pseudomonas aeruginosa respectively.

Conclusion : The isolated Lactobacillus plantarum has a high ability to reduce surface tension and the biosurfactant extracted from it has good stability and antimicrobial effects. For this reason, it can be used in various industries.

Keywords : Lactobacillus, biosurfactant, antimicrobial effect, stability

P560-710: Isolation, Identification, and Evaluation of The Ability to Produce Xanthan Gum from Lactose by Xanthomonas campestris Isolated from Plants Infected by Bacterial Canker

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Background and Aim : Xanthan gum is a polysaccharide with many industrial uses, including as a common food additive. It is an effective thickening agent, emulsifier, and stabilizer which prevents ingredients from separating. It can be produced from simple sugars using a fermentation process and derives its name from the species of bacteria used, Xanthomonas campestris. This study aimed to isolate, identify and evaluate the amount of xanthan gum production from lactose by Xanthomonas campestris Isolated from Plants Infected by Bacterial Canker.

Methods : : Leaves of trees infected with bacterial canker were collected from an orange garden in the north of Iran. The initial isolation was done using culture in glucose-yeast extract agar medium. Then, the isolated strains with the ability to produce xanthan gum were identified based on biochemical and molecular tests. Finally, the production of xanthan gum was done using lactose as a substrate.

Results : In this study, 35 bacterial strains were isolated. Among them, 20 strains were able to produce xanthan gum. Based on biochemical and molecular tests, 6 strains were identified as Xanthomonas campestris. Among these strains, only 1 could use lactose as substrate, and the amount of xanthan gum production in this strain was 8.7g/l.

Conclusion : The results showed that the isolated bacteria have a good potential in the production of xanthan gum from lactose and this amount can be increased by optimizing different production conditions.

Keywords : Xanthan gum, Xanthomonas campestris, lactose, plant

P561-712: Molecular identification of bacteria isolated from vaginal infections of infertile women

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Background and Aim : Infertility is one of the most critical problems of human societies, which has a significant percentage all around the world. Infertility occurs due to a disorder in the reproductive system, which is defined as the inability of couples to bear children after at least 12 months of consecutive unprotected intercourse. There are many factors involved in infertility that cause defects in reproductive performance in men or women. It has been reported that female genital infections are possible causes of female infertility. In this study, bacteria causing vaginal infection in infertile women were identified by molecular method.

Methods : After sampling from the infectious vagina of infertile women, the samples were cultured in suitable bacterial culture media, such as Brain Heart Agar. Bacteria were purified, and PCR products using universal primers were sequenced. In order to identify the isolated bacteria, the obtained sequences were analyzed using bioinformatics methods.

Results : The results of bioinformatics analysis showed that Escherichia coli is the dominant bacterium causing infection in the vagina of infertile women. Also, Enterococcus was another bacterium that was isolated from the infected vagina of some women.

Conclusion : Bacterial infections of the genital tract of infertile women should be considered and treated as a possible cause of infertility.

Keywords : infertility, bacteria, vaginal infection

P562-713: Optimization of bio-decolorization Acid Red 14 using bacterial strain isolated from wastewater

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Background and Aim : Synthetic dyes are used today in textiles, food, paper, and plastics. Among the synthetic dyes, Azo dyes are the most widely used dyes in the textile industry, which enter the environment as pollutants through the wastewater of textile factories and pollute natural ecosystems such as soil, groundwater, and organisms. Therefore, it is very important to remove these contaminants from textile effluents

Methods : In this study, the ability to decolorize Acid Red 14 dye was investigated using a bacterial strain isolated from the effluent of textile factory in the presence of carbon sources of fructose, xylose, lactose, and sucrose

Results : This strain decolorized Acid Red 14 dye at 50 ppm with pH 6 and temperature of 37 ° C in the incubator and the presence of fructose, after 24 h, 48 h and 72 h, 18%, 42% and 89% respectively.

Conclusion : The analysis of the visible-ultraviolet spectrophotometer showed that the discoloration is due to a microbial analysis by the bacterial strain. The bacteria strain isolated from the effluent of textile factory decolorized Acid Red 14 dye at the especial condition

Keywords : Decolorization, Azo dyes, Bacteria, Optimization, Waste water

P563-716: Applications of Bacillus as probiotics for human use

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Background and Aim : The use of Bacterial spore formers such as Bacillus spp. in probiotic supplements and foods has increased considerably over the last decade. Bacillus species have been used as probiotics for at least 50 years with the Italian product known as Enterogermina. Spores of Bacillus spp. are heat-resistant and capable of surviving the low pH of the gastric barrier while active probiotics as Lactobacillus are susceptible to bile salts and gastric acid. Therefore, Bacillus spp. are a good choice for use as probiotics.

Methods : In this study, we searched for papers and book in electronic databases (PubMed, Medline, Google scholar, Web of Science, Scopus) using keywords such as: Bacillus, probiotic supplements, spore and commercial probiotics from their inception up to 2022.

Results : The stability during processing and storage, ease of production and therapeutic potential such as antimicrobial activities, prevent gastrointestinal disorders and immune stimulation make Bacillus spp. a suitable candidate for commercial manufacture of novel foods and supplements for human and animal feeds. Bio-KultR B. subtilis; ThorneR: Bacillus coagulans; BiosporinR; B. subtilis 2335 and B. licheniformis 2336 and MegaSporeBioticTM; B. licheniformis, Bacillus indicus, B. subtilis, B. clausii and Bacillus coagulans, are only part of probiotic supplements containing Bacillus strains in global market for human use.

Conclusion : Today, Bacillus spp. spores are being used extensively in dietary supplements as probiotics. Bacillus spp. which have GRAS status from the FDA and are included in the QPS, used as probiotics for human and animal hosts and only a few are ordinarily used as probiotics, these include Bacillus coagulans, B. clausii, B. licheniformis, B.cereus and B. subtilis.

Keywords : Bacillus, probiotic supplements, spore, commercial probiotics

P564-718: Optimization of Pectinase Production from Agricultural Waste Under Solid-State Fermentation by Bacillus pumilus

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Background and Aim : As a large group of enzymes, pectinases break down pectin into simpler molecules such as galacturonic acid. These enzymes are widely produced by many microorganisms. Today, many agricultural wastes are used as pectin-rich sources to induce pectinase production by many microorganisms. The aim of this study was to optimization of pectinase production from agricultural waste under solid-state fermentation by Bacillus pumilus.

Methods : Bacillus pumilus PTCC 1319 was obtained from the Iranian Research Organization for Science and Technology (IROST). In this work, Response Surface Methodology (RSM) was applied to evaluate the influence of different solid substrates (rice bran and wheat bran), nitrogen sources (peptone, yeast extract, ammonium sulfate), and pH (6,7,8) on pectinase production. The fermentation process was held for 96 hours. Measurement of the enzyme activity was carried out by measuring the amount of D-galacturonic acid liberated from pectin.

Results : The highest pectinase activity (31.28 U/ml) was observed when wheat bran as solid substrate, yeast extract as nitrogen source, and pH of 8.

Conclusion : Microbial sources of pectinase enzymes are great importance in several industries. The use of agricultural waste for the production of pectinase has been found to be economical and effective.

Keywords : pectinase, Bacillus pumilus, Agricultural wastes, Response Surface Methodology

P565-728: Efficacy of alcoholic extract of Heracleum persicum (Golpar) on the survival of Lactobacillus plantarum and Lactobacillus kazei in probiotic dough,

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Background and Aim : In this study, the efficacy of Golpar alcoholic extract on the survival of Lactobacillus plantarum and Lactobacillus kazee in probiotic dough was investigated.

Methods : The probiotic bacterium Bifidobacterium bifidum and Lactobacillus acidophilus were inoculated to samples of dough which is without alcoholic extract of golapr (control) and dough containing of alcoholic extract of golpar. Produced dough were stored in refrigeratore at 4C during 4 weeks. During one week in terms of microbial count, changes in pH, acidity and survival during shelf life and organoleptic properties of the product were examined.

Results : Results of statistical analysis showed significant differences in the survival of Lactobacillus plantarum and Lactobacillus kazei among ordinary dough and dough containing alcoholic extract of golpar ($p < 0.05$) . regarding the taste , the results of the study showed, there is a significant difference between different kinds of taste($p < 0.05$). Examination of organoleptic properties in dough of Golpar alcoholic extract showed that the taste of dough was improved compared to ordinary dough. The highest and lowest pH values were related to the sample containing 1% and 2% of the extract, respectively.

Conclusion : Also, the study of the main effect of the amount of extract on the acidity showed that the highest and lowest acidity were related to the sample containing 2% and 1%, respectively. Therefore, the production and consumption of dough containing Golpar extract is recommended as a pragmatic food product while maintaining organoleptic properties along with probiotic bacteria.

Keywords : Alcoholic extract of Angelica, Lactobacillus plantarum, Lactobacillus kazai, Probiotic dough

P566-735: Detection of enteroviruses in children with acute gastroenteritis in Iran

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Background and Aim : Acute gastroenteritis is one of the common causes of morbidity and mortality around the world. It has been estimated that more than 700 million cases of acute gastroenteritis (AGE) occur in children below 5 years old per year. Enteric viruses have been identified as the most important etiological agent of AGE. Beside common and well-known enteric viruses such as rotaviruses, noroviruses, adenoviruses, and astroviruses, there are other viral agents which are associated with AGE. Latest molecular techniques allow us to discover novel viruses from AGE patients such as enterovirus. The aim of this study was to determine the frequency of enterovirus infection in Iranian children suffering from AGE

Methods : Stool samples were collected from 100 children with diarrheal symptoms. viral RNA was extracted from 10% stool suspensions and after the reverse transcription process, a PCR assay was done to detect the enterovirus genome. Then, positive samples were sequenced to confirm the results.

Results : The study population comprised 60 males and 40 females. The mean age of the studied patients was 10.12+8.19 years. Among the 100 analyzed stool samples from children with acute gastroenteritis, 2 positive samples (2%) were recognized, and sequencing results were confirmed by BLAST online tool.

Conclusion : The importance of viruses in children's gastroenteritis has been underestimated in many reports worldwide. this study describes the detection of enterovirus associated with acute diarrhea in children. according to the results, the number of the patients who have the enterovirus is about 2%. However, this number is less than other enteric viruses but the critical role of this virus must be considered in viral diagnosis to help to improve patient treatment.

Keywords : Acute gastroenteritis , enterovirus , Detection , children

P567-741: A Mathematical Probabilistic Modelling for the Single Molecule Kinetics Problem

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Background and Aim : In the past decades, advances in microscopy have made it possible to study the dynamics of individual biomolecules in vitro and to resolve intra-molecular kinetics that would otherwise be hidden in ensemble averages. Recently, single-molecule methods have been used to image, localize, and track individually labeled macromolecules in the cytoplasm of living cells, allowing the investigation of intermolecular kinetics under physiologically relevant conditions.

Methods : Assume that a protein A bind to protein B. Also, the bound coplex AB can be converted into C. In this article, we try to derive time probability distributions for single-molecule kinetics. Assume that the probability of spices reacting in the time t is p. Also, consider that this probability is independent of any past history.

Results : If in n consecutive intervals with the same amount as t, there is no reaction, the probability of surviving is 〖(1-kt)〗^n. Where, k represents the avarage frequency of te reaction. Notice that when n→∞, 〖(1-kt)〗^n→e^(-kt).

Conclusion : It is known that there exists connection between single-molecule techniques when studying kinetics in living cells and solutions to specific challenges associated with these methods. For Example recently, single molecule kinetics of bacteriorhodopsin by HS-AFM is discussed by Alma P. Perrino.

Keywords : Single-molecule kinetics, probability distributions, Modeling

P568-742: Simple One-step Synthesis of Carrageenan Coated-Silver Nanoparticles with Antibacterial Properties

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Background and Aim : In recent years, the prevalence of infectious diseases has increased due to the presence of multidrug-resistant pathogens, and the development of novel drugs is attracted more attention for the treatment of infectious diseases. Nanotechnology has emerged as a potent area in the introduction of novel antibiotics. Among the metallic nanoparticles, there is impressive interest in the antibacterial activity of silver nanoparticles (AgNPs) against diverse microorganisms. Green synthesis of AgNPs has been studied with different biological sources as an alternative to chemical synthesis.

Methods : This study aims to synthesize AgNPs in the presence of carrageenan polymer and investigate its antibacterial properties. For this purpose, nanoparticles were synthesized by a simple one-step method with 0.3% carrageenan solution and 0.01 M silver nitrate solution at 60 °C for 1 h. The characterization was performed by dynamic light scattering (DLS) after 20, 40, and 60 min of the synthesis process to measure particle size and polydispersity index (PDI) and Fourier transform infrared spectroscopy (FTIR) methods to investigate surface chemical groups. Finally, the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) of NPs were evaluated on Gram-positive (Staphylococcus aureus) and Gram-negative (Escherichia coli) bacterial strains.

Results : The characterization results showed that carrageenan coated-AgNPs had a hydrodynamic diameter of 277.12±4.7 nm and a PDI of 0.336±0.002 after 20 min. FTIR analysis was performed to investigate the functional groups on the surface of the nanoparticles and it was confirmed that functional groups in carrageenan are involved in the synthesis and stability of AgNPs. The broth microdilution method was applied to Staphylococcus aureus and Escherichia coli to determine MIC and MBC. The results showed that the MIC and MBC were 14.6 µg/mL and 29.3 µg/mL for E.coli and 58.6 µg/mL and 117.2 µg/mL for S. aureus, respectively.

Conclusion : This study indicates that carrageenan coated-AgNPs exhibit strong antibacterial activity against both gram-positive and gram-negative bacteria and might be administrated for the treatment of infectious diseases.

Keywords : Silver nanoparticles, Carrageenan, Antimicrobial properties, Green Synthesis.

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