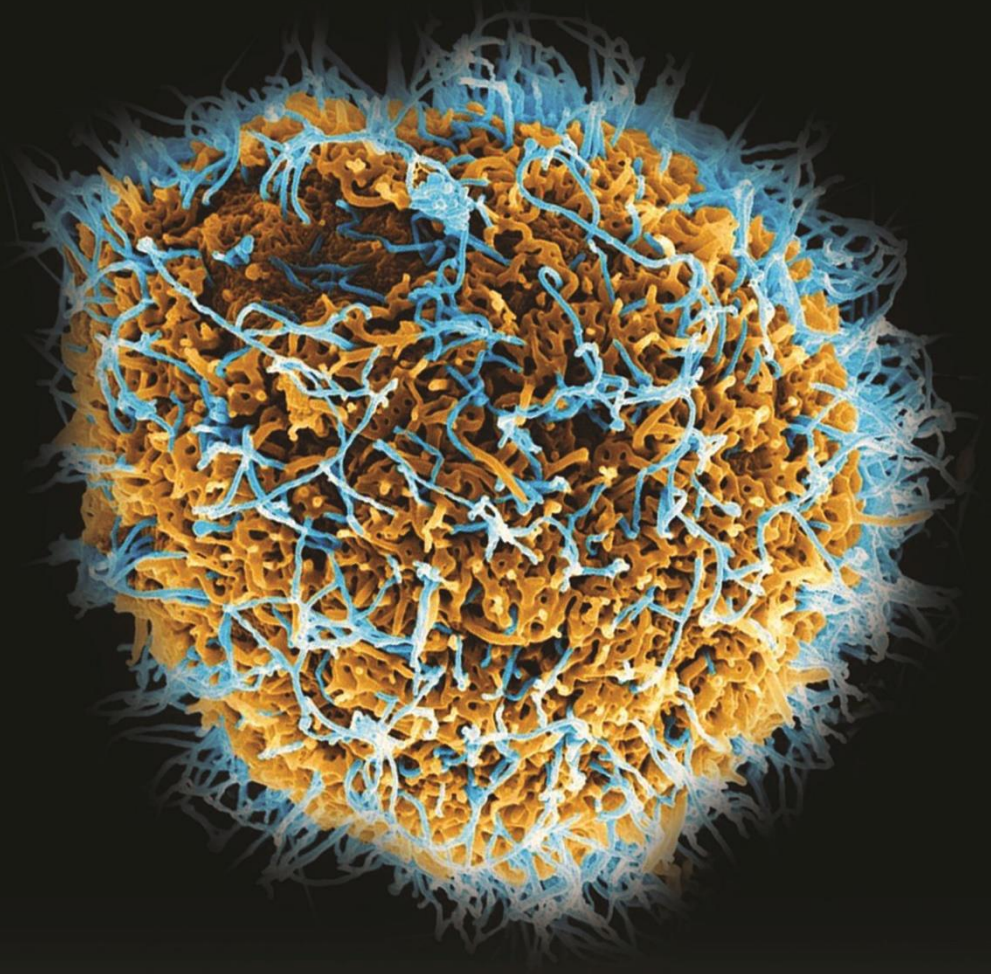
# IRAN'S 22nd INTERNATIONAL VIRTUAL CONGRESS OF MICROBIOLOGY



28 AUGUST _ 2 SEPTEMBER 2021

TEHRAN - IRAN

https://ismcongress.ir/

Iranian Society of Microbiology

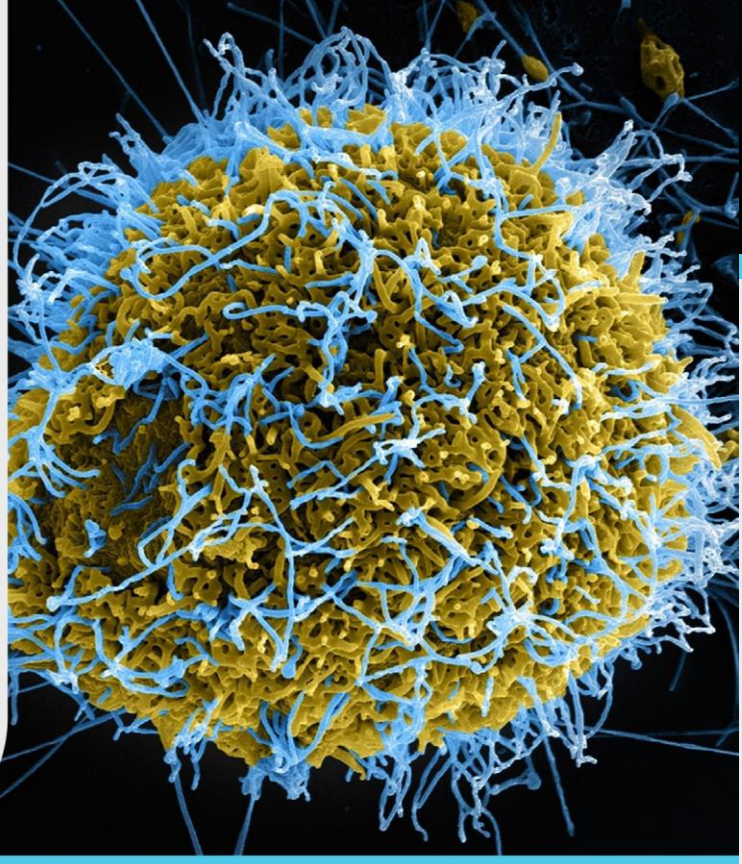
Tehran University of Medical Sciences


بسم الله الرحمن الرحیم

## فهرست مطالب

TEHRAN UNIVERSITY OF MEDICAL SCIENCES

Iranian Society of Microbiology



# Iran's 22nd International Virtual Congress Of Microbiology

## 28 August - 15 September

President
Dr. Mohammad Mehdi Faizabadi
Professor of Microbiology, Tehran University of Medical Sciences; Chairman of the Iranian Society of Microbiology

Secretary
Dr. Abbas Abdollahi
Assistant Professor of Microbiology, Fasa University of Medical Sciences

| | | |
|---|---|---|
| Urinary Tract Infection: Complication in Treatment<br>28 August | New Findings in COVID-19 Treatment<br>29 August | Food and Beverage Microbiology - Part 1<br>30 August |
| Antimicrobial Resistance<br>31 August | New Methods in the Diagnosis and Treatment of Infectious Diseases<br>1 September | Emerging and Re-emerging Infectious Diseases - Part 1<br>2 September |
| Food and Beverage Microbiology - Part 2<br>13 September | Detection Methods of COVID-19: Achievements, Challenges & Opportunities<br>14 September | Emerging and Re-emerging Infectious Diseases - Part 2<br>15 September |

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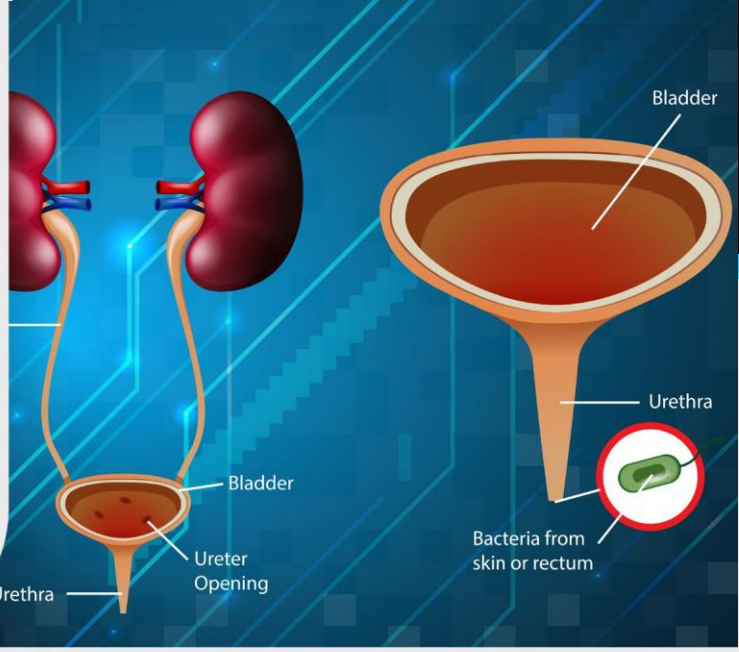
# Urinary Tract Infection: Complication in Treatment




**28 August, 2021** **03:30 PM (IRST), 11:00 AM (GMT)**


**Dr. Erfan Amini**
Department of Urology, Tehran University of Medical Sciences, Iran
**Moderator**

**Dr. Kurt G. Naber**
Associate Professor of Urology, School of Medicine, Technical University of Munich, Germany

**Dr. Reinhard E.M. Fünfstück**
Department of Medical Health Care, Weimar, Germany

**Dr. Florian Wagenlehner**
Clinic for Urology, Pediatric Urology and Andrology, Justus Liebig University, Germany

**Dr. Fereshteh Ghiasvand**
Department of Infectious Diseases, Tehran University of Medical Sciences, Iran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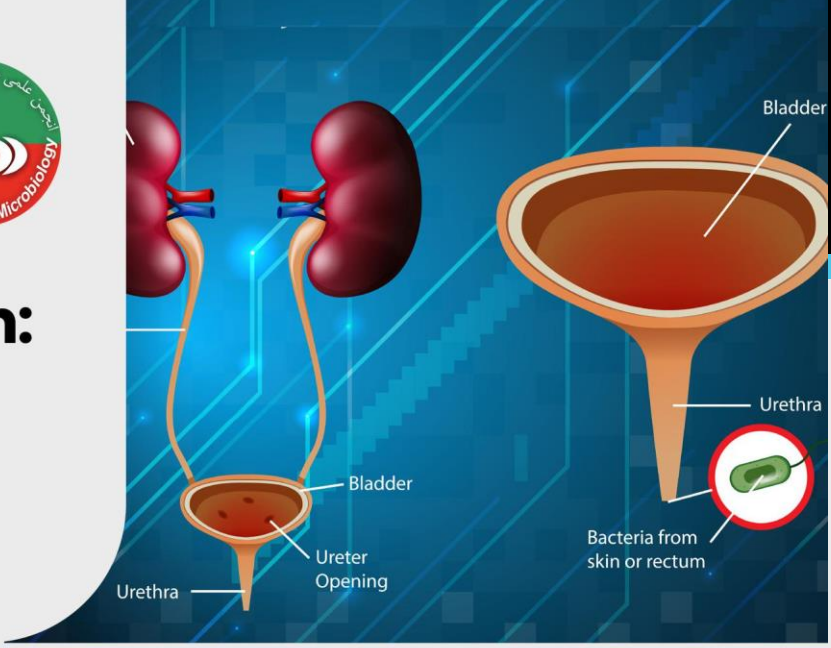
# Urinary Tract Infection: Complication in Treatment




**28 August, 2021** **03:30 PM (IRST), 11:00 AM (GMT)**

| | |
|---|---|
| Uncomplicated UTI – New Approach for Diagnostics and Treatment | **Dr. Kurt G. Naber** |
| Urinary Tract Infections in Patients With Renal Insufficiency | **Dr. Reinhard E.M. Fünfstück** |
| Complicated UTI and Urosepsis | **Dr. Florian Wagenlehner** |
| Discussion on Urinary Tract Infection | **Dr. Erfan Amini** |
| Asymptomatic Bacteriuria | **Dr. Fereshteh Ghiasvand** |

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# New Findings in COVID-19 Treatment

**29 August, 2021** **03:30 PM (IRST), 11:00 AM (GMT)**

**Dr. Mehrnaz Asadi Gharabaghi**
Associate Professor of Respiratory Medicine, Imam Khomeini Hospital, Tehran University of Medical Sciences, Iran
**Moderator**

**Dr. Yazdan Yazdanpanah**
Infectious Disease Department at Bichat Claude Bernard Hospital, Aviesan Institute of Immunology, Inflammation and Microbiology, Paris Diderot University, France

**Dr. Seyed A. Dehghan Manshadi**
Department of Infectious Diseases and Tropical Medicine, Imam Khomeini Hospital, Tehran University of Medical Sciences, Iran

**Dr. Shervin Shokouhi**
Department of Infectious Diseases, Shahid Beheshti University of Medical Sciences, Iran

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# New Findings in COVID-19 Treatment

**29 August, 2021** **03:30 PM** (IRST), **11:00 AM** (GMT)

| | |
|---|---|
| COVID-19 Treatment | **Dr. Yazdan Yazdanpanah** |
| Challenges in Management of Patients with Covid-19 | **Dr. Seyed Ali Dehghan Manshadi** |
| Challenges in Treatment of Patients with Covid-19 | **Dr. Shervin Shokouhi** |
| Immunosuppresion Challenge in Treatment of COVID Patients | **Dr. Mehrnaz Asadi Gharabaghi** |

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# Food and Beverage Microbiology Part 1

**30 August, 2021** **05:30 PM** (IRST), **01:00 PM** (GMT)

**Dr. Nahid Rahimifard**
Food and Drug Administration (FDA), Ministry of Health and Medical Education, Iran
**Moderator**

**Dr. Mohammad Katouli**
Associate Professor in Microbiology, University of the Sunshine Coast, Queensland, Australia

**Dr. Seyed Reza Mohebbi**
Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Iran

**Dr. Keith Warriner**
Department of Food Science, University of Guelph, Guelph, Ontario, Canada

**Dr. Shila Safaeian**
Department of Food and Scince Technology, North Tehran Branch, Islamic Azad University, Iran

**Dr. Ruth Eden**
Department of Food Engineering and Biotechnology at Bio-Experts, Greater, Boston, USA

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# Food and Beverage Microbiology Part 1

**30 August, 2021** **05:30 PM** (IRST), **01:00 PM** (GMT)

| | |
|---|---|
| The Efficacy of a Cocktail of Probiotics on The Inhibition of Adherent-Invasive Escherichia Coli in an Improved Co-Culture Of Caco-2:HT29-MTX Cells | **Dr. Mohammad Katouli** |
| Detection of Viral Contamination in Ready-To-Eat Food Products | **Dr. Seyed Reza Mohebbi** |
| Vapor Phase- Hydroxyl Radical Process for Decontaminating Food and Non- Food Surfaces | **Dr. Keith Warriner** |
| Detection Methods of Food Borne Pathogen Viruses | **Dr. Shila Safaeian** |
| Evolution in Food Pathogen Detection | **Dr. Ruth Eden** |
| Nutritional Support in Covid-19 | **Dr. Nahid Rahimifard** |

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# Antimicrobial Resistance

**31 August, 2021** **03:30 PM (IRST), 11:00 AM (GMT)**

**Dr. Fereshteh Shahcheraghi**
Department of Microbiology, Pasteur Institute, Iran
**Moderator**

**Dr. Christian Giske**
Department of Laboratory Medicine, Karolinska Institute and Karolinska University Hospital, Sweden

**Dr. Mohammad Reza Salehi**
Infectious Diseases and Tropical Medicine Specialist, Imam Khomeini Hospital, Tehran University of Medical Sciences, Iran

**Dr. Hamid Solgi**
Department of Laboratory Medicine, Amin Hospital, Isfahan University of Medical Sciences, Iran

**Dr. Mohammad Javad Nasiri**
Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Science, Iran

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# Antimicrobial Resistance

**31 August, 2021** **03:30 PM** (IRST), **11:00 AM** (GMT)

| | |
|---|---|
| Gram Negative Pathogens and Covid-19 Co-Infection | **Dr. Christian Giske** |
| MDR Bacterial and Fungal Co-Infection in Covid-19 Patient | **Dr. Mohammad Reza Salehi** |
| Infection-Prevention and Control Measures to Reduce Colonization and Infection of ICU-Acquired Infections | **Dr. Hamid Solgi** |
| Drug Resistant Tuberculosis and Covid-19 Co-Infection | **Dr. Mohammad Javad Nasiri** |
| Enterobacterial Clinical Isolates Resistant Reports From Iran | **Dr. Fereshteh Shahcheraghi** |

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Iranian Society of Clinical Laboratory Sciences

Tehran University of Medical Sciences

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# New Methods in the Diagnosis and Treatment of Infectious Diseases

**1 September, 2021** **09:00 AM (IRST), 04:30 AM (GMT)**


**Dr. D. Kalantar-Neyestanaki**
Kerman University of Medical Sciences, Kerman, Iran
**Moderator**

**Dr. J. R. Morones-Ramirez**
Full Professor, Chemical Engineering Department, Universidad Autonoma de Nuevo Leon, Mexico

**Dr. Mahmoud Osanloo**
Department of Nano-Technology, Fasa University of Medical Sciences, Iran

**Dr. Masoud Dadashi**
Ph.D in Clinical Microbiology, Alborz University of Medical Sciences, Iran

**Dr. Hossein Pourghadamyari**
Clinical Biochemistry Department, Kerman University of Medical Sciences, Iran

**Dr. Ali Afgar**
Department of Parasitology and Mycology, School of Medicine, Research Center for Hydatid Disease, Kerman University of Medical Sciences, Iran


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# New Methods in the Diagnosis and Treatment of Infectious Diseases

**1 September, 2021** **09:00 AM** (IRST), **04:30 AM** (GMT)

| | |
|---|---|
| Pathways to Develop Smart Antimicrobials and Combat Antimicrobial Resistance | **Dr. Jose Ruben Morones-Ramirez** |
| Use of Biosensors in Medical Microbiology | **Dr. Davood Kalantar-Neyestanaki** |
| The Use of Nanotechnology in Development of Essential Oil-Based Antibacterial Agents | **Dr. Mahmoud Osanloo** |
| miRNAs as Biomarkers In Infectious and Non-Infectious Diseases | **Dr. Masoud Dadashi** |
| CRISPR-Based Diagnosis of Infectious Disease | **Dr. Hossein Pourghadamyari** |
| Bioinformatics steps and approaches in drug discovery | **Dr. Ali Afgar** |

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# Emerging & Re-emerging Infectious Diseases

## Part 1

**2 September , 2021** **03:30 PM (IRST), 11:00 AM (GMT)**

**Dr. M. Mehdi Gouya**
Center for Communicable Disease Control, Ministry of Health and Medical Education, Iran
**Moderator**

**Dr. Mathieu Picardeau**
Biology of Spirochetes Unit, Pasteur institute of Paris, France

**Dr. Lucia Moro**
Centre for Tropical Diseases, Sacro Cuore Hospital, Italy

**Dr. Katja Mertens-Scholz**
Institute of Bacterial Infections and Zoonoses, Friedrich Loeffler Institute, Germany

**Dr. Ehsan Mostafavi**
Research Centre for Emerging and Re-emerging Infectious Diseases, Pasteur Institute, Iran

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# Emerging & Re-emerging Infectious Diseases

## Part 1

**2 September , 2021** **03:30 PM** (IRST), **11:00 AM** (GMT)

| | |
|---|---|
| A Review of the Situation of COVID-19 in Iran | **Dr. Mohammad Mehdi Gouya** |
| Taxonomy, Ecology and Pathogenesis of the Genus Leptospira Revisited Byggenomics | **Dr. Mathieu Picardeau** |
| Tropheryma Whipplei: A Neglected Bacterium | **Dr. Lucia Moro** |
| Coxiella Burnetii: Epidemiological Situation and New Approaches in Diagnostics | **Dr. Katja Mertens-Scholz** |

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# Food and Beverage Microbiology Part 2

**13 September, 2021** **10:00 AM (IRST), 05:30 AM (GMT)**

**Dr. Nahid RahimiFard**
Food and Drug Administration (FDA), Ministry of Health and Medical Education, Iran
**Moderator**

**Dr. Greetje Castelijn**
Food Microbiology Department, Wageningen University, Gelderland, Netherlands

**Dr. Zohreh Mashak**
Department of Food Hygiene and Quality Control, Karaj Branch of Islamic Azad University, Iran

**Dr. Masoud Alebouyeh**
Pediatric Infections Research Center, Research Institute for Children Health, Shahid Beheshti University of Medical Sciences, Iran

**Mr. Hesam Karimi**
Department of Hepatitis and AIDS, Pasteur Institute, Department of Virology, Faculty of Medical Sciences, Tarbiat Modares University, Iran

**Ms. Razieh Sadat Banijamali**
Food and Drug Control Laboratories, Ministry of Health and Medical Education, Department of Virology, Faculty of Medical Sciences, Tarbiat Modares University, Iran

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# Food and Beverage Microbiology Part 2

**13 September, 2021** **10:00 AM (IRST), 05:30 AM (GMT)**

| | |
|---|---|
| Interpretations of Antimicrobial Effectiveness Standard Methods of Disinfectants and Antiseptics | **Dr. Nahid RahimiFard** |
| Real-time WGS Monitoring Identifies L. Monocytogenes Outbreaks in The Netherlands and Contributes to A Rapid Detection of the Source | **Dr. Greetje Castelijn** |
| Study of Prevalence Rate; Phenotypic and Genotypic Pattern of Staphylococcal Antibiotic Resistance in Ready-To-Eat Foods | **Dr. Zohreh Mashak** |
| Rapid Test in Food Microbiology | **Dr. Masoud Alebouyeh** |
| Vaccine Industry: An Overview of Coronavirus Vaccine Platforms | **Mr. Hesam Karimi** |
| Types of Mutations and Strains of Coronavirus | **Ms. Razieh Sadat Banijamali** |

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# Detection Methods of COVID-19: Achievements, Challenges and Opportunities


**14 September, 2021** **03:30 PM (IRST), 11:00 AM (GMT)**

**Dr. Abbas Ali Imani Fooladi**
Applied Microbiology Research Center, Baqiyatollah University Medical of Sciences, Iran
**Moderator**

**Dr. Leonardo Antonio Sechi**
Biological Sciences Department, University of Sassari, Italy

**Dr. Rouhollah Keshavarz**
Diagnostic Laboratory, Tuberculine Department, Razi Vaccine & Serum Research Institute, Iran

**Dr. Bizhan Nomanpour**
Department of Microbiology, Kermanshah University of Medical Sciences, Iran

**Dr. Samira Khodai**
Senior Data Scientist and Innovation Lead, Thermo Fisher Scientific, Carlsbad California, USA

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# Detection Methods of COVID-19: Achievements, Challenges and Opportunities


**14 September, 2021** **03:30 PM** (IRST), **11:00 AM** (GMT)

| | |
|---|---|
| Humoral Immune Response Against SARS-CoV-2 | **Dr. Leonardo Antonio Sechi** |
| Detection of Covid-19; Molecular and Serological Tests | **Dr. Abbas Ali Imani Fooladi** |
| Validation of Highly Specific SARS-CoV-2 Neutralizing Antibodies Detection Kit (RBD Razi ELISA Kit) | **Dr. Rouhollah Keshavarz** |
| Peripheral Laboratory-based Surveillance of COVID-19 in Tehran Metropolitan; a Population- based Study | **Dr. Bizhan Nomanpour** |
| Application of Data Scientist and Machine Learning in Covid-19 Diagnosis | **Dr. Samira Khodai** |

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# Emerging and Re-emerging Infectious Diseases

**15 September , 2021** **03:30 PM (IRST), 11:00 AM (GMT)**


**Dr. Ehsan Mostafavi**
Research Centre for Emerging and Re-emerging Infectious Diseases, Pasteur Institute, Iran
**Moderator**

**Dr. Alireza Sazmand**
Department of Pathobiology, Faculty of Veterinary Science, Bu-Ali Sina University, Iran

**Dr. Saber Esmaeili**
Research Centre for Emerging and Re-emerging Infectious Diseases, Pasteur Institute, Iran

**Dr. Saeid Reza Naddaf**
Department of Parasitology, Pasteur Institute, Iran


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# Emerging and Re-emerging Infectious Diseases

**15 September , 2021** **03:30 PM (IRST), 11:00 AM (GMT)**

| | |
|---|---|
| A Review of the Situation of Tularemia in Iran | **Dr. Ehsan Mostafavi** |
| Canine Vector-Borne Diseases of Zoonotic Concern in Iran | **Dr. Alireza Sazmand** |
| Challenges and Approaches to Diagnosis of Culture-Negative Endocarditis in Iran | **Dr. Saber Esmaeili** |
| Lyme Borreliosis and Relapsing Fever Spirochetes in Hard Ticks of Caspian Sea Littoral, Iran | **Dr. Saeid Reza Naddaf** |

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# پیام رئیس انجمن

## President of Committee of Iranian Society for microbiology

Scientific advancement and the presentation of the latest achievements of faculty members, researchers and students in the field of Microbiology is the main objective of the Iranian Microbiology Association. As previous years, the association will organize and host the 22nd Iranian International Microbiology Congress, which is especially noteworthy bearing in mind the experience gained from last year's congress that was held during the Corona pandemic.

Considering the importance of advancing the scientific knowledge of Microbiologists in the country and facilitating interaction with international experts in the field, the association is fully dedicated to its responsibilities in reaching these goals. Thus, we are very pleased to announce that the 22nd Iranian International Microbiology Congress will be held from the 28 August-2 September, 2021. We invite faculty members, researchers and students to participate in the event.

Individuals involved in the medical field ( general practitioners, dentists, pharmacists, laboratory technicians, nurses and healthcare managers) who participate in the 22nd Iranian International Microbiology Congress, which is sponsored by universities and scientific institutes, will be awarded retraining points.

In addition, points shall be awarded to participating Microbiologists, laboratory experts and infectious disease specialists, and the latest technological advances in various fields of Microbiology will be presented and discussed by experts in seminars and symposiums.

I hope the support provided by various organizations and scientific institutes enables us to create an atmosphere where the latest scientific achievements by prominent Iranian and foreign experts can be presented.

Dr. Mohammad Mehdi Feizabadi

# پیام دبیر کنگره

## Executive Secretary of the Congress

The 22nd Iranian international Microbiology Congress will be held despite the fact that the Corona pandemic and related problems are still having an impact on a global scale. In spite of the challenges created by the pandemic and numerous problems faced by the organizers and participating faculty members, researchers and students, the 21st Iranian Microbiology congress was held in an online format and was warmly received by both domestic and foreign participants.

Bearing in mind the positive outcome of last year's congress, the 22nd Iranian International Microbiology Congress will be held from the 28 August-2 September, 2021, at Tehran University of Medical Sciences. Similar to previous years, the latest scientific achievements in the field of Microbiology from prominent Iranian and foreign experts will be presented through lectures, educational panels and posters. Special prizes will be awarded to the best lectures, posters and retraining programs. In addition, lifetime achievement awards shall be presented to distinguished faculty members.

Dr. Abbas Abdollahi

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- دکتر احسان مصطفوی
- دکتر فرشته شاهچراغی
- دکتر ناهید رحیمی فرد
- دکتر داود کلانتر نیستانکی
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# خلاصه مقالات سخنرانی

## O1-133: Molecular Typing and Antimicrobial Susceptibility of Acinetobacter baumannii Isolates in Kermanshah City with Pulse Field Gel Electrophoresis (PFGE)

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**Background and Aim :** Acinetobacter baumannii (A. baumannii) in the last decade has been identified as one of the opportunistic pathogens and an important cause of nosocomial infections. Molecular typing plays an important role in studying the epidemiology of Acinetobacter. The aim of this study was to investigate the genomic pattern which was performed by Pulse Field Gel Electrophoresis (PFGE) and antimicrobial susceptibility of the isolates from patients in various hospitals in the city of Kermanshah, the city which is located in the west of Iran.

**Methods :** 33 isolates of A. baumannii were collected from clinical samples in four general hospitals of Kermanshah. Isolates were identified by biochemical tests and API 20NE kit. The antimicrobial susceptibility of isolates was determined by Kirby-Bauer disk diffusion method. The clonal connection was estimated by PFGE and DNA patterns were analyzed by Gel compare II 6.5 software.

**Results :** All isolates showed high-level of resistance, but resistance which was observed against Colistin and Minocycline was low, while no resistance to Polymyxin B and Tigecycline was observed. The PFGE analysis revealed the existence of 10 different genetic patterns among the 33 strains including: I (n = 12), II (n = 2), III (n = 4), IV (n = 3), V (n = 3), VI (n = 4), VII (n = 2). Clone I was the dominant clone. In terms of antibiotic resistance, no significant difference was observed among the different genetic patterns.

**Conclusion :** Isolates were obtained from a large variety of patterns genetically. This study could represent the wide range of isolates of A. baumannii that were gathered from different parts of the hospital. Diverse sources of infection may, therefore, appear to control these infections, according to various sources, which are not simple.

**Keywords :** Antimicrobial resistance; Acinetobacter; pulsed-field gel electrophoresis; Kermanshah

# O2-13: Study of fosfomycin and colistin resistant in accordance to ESBL production among E. coli isolates from UTI after kidney transplantation

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**Background and Aim :** The aim of this study was phenotypic and molecular evaluation of fosfomycin and colistin resistant in accordance to ESBL production among E. coli isolates from UTI after kidney transplantation.

**Methods :** 60 E. coli isolates from urine samples of kidney transplant patients with UTIs from 3 different Kidney transplant centers in Tehran were collected during 2018-19. Antimicrobial susceptibility test(AST) was done based on the CLSI 2018. Minimum inhibitory concentration (MIC) of fosfomycin was performed by E-test. Further ESBL phenotypic screening by double disk synergy test(DDST) was evaluated. Molecular survey of ESBL genes ( including; CTX-M, TEM, SHV), some of fosfomycin resistance (uhpT, murA) genes and mcr-1 gene as plasmidic colistin resistance were detected by PCR after DNA extraction. As control, K. pneumonia ATCC 700603, a fosfomycin resistant and a colistin resistant E.coli isolates which were bestow from Dr. C. Giske (Karolinska, Sweden) were evaluated simultanously. Sequencing was done by Bioneer Korean company and further analysis and blasting was done in data bank/NCBI.

**Results :** Based on AST, highest susceptibility was to: doripenem, ertapenem (100%) and Imipenem 95%, and the highest resistant rate was to: ampicillin (86%), cefotaxime (80%), cefazolin and cefpodoxime (77%). Of 60 E. coli isolates, 27(45%) were associated with multidrug resistance (MDR) phenotype. Only (3.3%) of E. coli isolates showed intermediate resistant (MIC 128µg/ml) to fosfomycin based on the E- test. By DDST, 46% of isolates were identified as ESBLs producer. The frequency of ESBL genes were: blaTEM (54%), blaCTX-M (51%) and blaSHV (40%) and mcr-1 (3.3%) respectively by PCR. Mutation in different points of uhpT and murA genes were detected after sequencing analysis.

**Conclusion :** Frequency of fosfomycin resistant was not high in this study, but, coexistence of ESBL and fosfomycin plasmidic resistance genes in E. coli isolates among kidney transplant patients, show the importance of awareness among infection-control practitioners and physicians during prescription. Also, colistin is not a recommended antibiotic for treatment and during AST for E. coli isolates by CLSI. But detection of mcr-1 gene among 3.3% of isolates is alarming because it can be exchange between different bacteria and may increase globally soon.

**Keywords :** colistin, ESBL, Fosfomycin, E. coli

# O3-58: Differentiation of methiclin resistant staphylococcus aureus MRSA from the coagulase negative staphylococcus aureus MRCoNS using the PCR methods in teaching hospitals of shiraz.

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**Background and Aim :** Staphylococcal related infections is one of the major causes of nosocomial infections which leads to wide range of health problems, including skin lesions, invasive infections, such as osteomyelitis and also bacteremia. Hence, the aim of this study was to evaluate the frequency of methicillin resistant staphylococcus aureus (MRSA) isolates and methicillin resistant coagulase negative staphylococcus aureus (MRCoNS) isolates due to the fact that their resistance frequency to methicillin and other antibiotics is increasing. Additionally, it is important to determine pvl genes which are associated with respiratory tract and skin infections.

**Methods :** We have performed a cross-sectional study on a total of 221 staphylococci isolated from clinical specimens in two hospitals in Shiraz-Iran during a one year period. (2016-2017). Moreover, antibiotic susceptibility profiles of isolates were evaluated by the disk diffusion methods according to CLSI protocols. Also, DNA extraction was performed by boiling method and we used polymerase- chain-reaction (PCR) for the detection of mecA, femA, pvl gene.

**Results :** Among 221 isolates, about 168 isolates (76%) were determined as staphylococci, 53 isolate (24%) were coagulase negative staphylococci (CoNS), also 70 isolates were confirmed as MRSA and 53 CoNS and about (49.5%) 26 isolate were MRCoNS. Molecular investigations showed that among all isolates, 96 isolates (43.4%) was carrying mecA gene, 168 (76%) femA gene and interestingly,6 isolates was carrying pvl gene. Antibiotic resistance pattern of MRCoNS isolates showed 70% resistance to erythromycin, 69.2% to gentamicin, and 65% to chloramphenicol, while MRSA isolates showed (82.8%) resistance to chloramphenicol , (68.5%) to gentamicin, and also (64.2%) to tobramycin.

**Conclusion :** We can concluded that the frequency of CoNS isolates and especially MRCoNS isolates in southwest of IRAN (Shiraz) is remarkably increasing. Hence, prevention and control of MRSA isolates in order to prevent the gene transfer and antibiotic resistance are important factors to decrease the mortality rates and also infections.

**Keywords :** Nosocomial infections, MRSA, MRCoNS, antibiotic, IRAN.

# O4-70: Antimicrobial susceptibility testing and molecular characterization of Neisseria gonorrhoeae in Tehran, Iran

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**Background and Aim :** Antimicrobial resistance (AMR) surveillance in Neisseria gonorrhoeae and associated molecular epidemiological studies are crucial to ascertain the spread of antibiotic-resistant gonococci at national and international levels. AMR data are essential for developing or refining the local treatment guidelines. The current study was carried out to determine antimicrobial susceptibility and molecular epidemiology of N. gonorrhoeae isolates in Tehran, Iran.

**Methods :** In 2018 – 20, 500 urogenital swab specimens were collected. Specimen swabs were cultured and examined for the presence of N. gonorrhoeae isolates by biochemical tests. MIC Test Strip determined the MICs of ceftriaxone, azithromycin, and ciprofloxacin. Neisseria gonorrhoeae multi-antigen sequence typing (NG-MAST) was also performed.

**Results :** A total of 38 N. gonorrhoeae isolates (from 37 females and 1 male) were obtained during the study period. The proportions of resistant N. gonorrhoeae isolates were as follows: ceftriaxone (MIC ≥ 0.125 mg/L) 10.5% (4/38), azithromycin (MIC > 1 mg/L) 34% (13/38) and ciprofloxacin (MIC ≥ 1 mg/L) 31.5% (12/38). In total, 25 different NG-MAST STs were identified. The STs comprised 1 to 4 isolates each, and the predominant ST was ST266 (n=4).

**Conclusion :** This is the first multi-center surveillance study on antibiotic susceptibility and molecular epidemiology of N. gonorrhoeae in Iran. Our study demonstrates a diverse gonococcal population with high rates of resistance to azithromycin and evidence of resistance to ceftriaxone. The results have potential implications for antibiotic choice for the treatment of gonorrhea and highlight the need to broaden gonococcal AMR monitoring in Iran to prevent the transmission of resistant strains.

**Keywords :** Neisseria gonorrhoeae, Gonorrhoea, Antimicrobial resistance, NG-MAST, Ceftriaxone, Ciprofloxacin

# O5-105: Antimicrobial resistance patterns and prevalence of integrons in Shigella species isolated from children with diarrhea in southwest Iran

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**Background and Aim :** Shigellosis is a major healthcare concern in the world, especially in developing countries with poor hygiene particularly among children under 5 years old. To investigate the antimicrobial resistance patterns and prevalence of integrons in Shigella species isolated from children with diarrhea in southwest Iran.

**Methods :** In this study, 1530 stool samples were collected from children under 15 years with diarrhea referred to teaching hospitals in Ahvaz and Abadan, southwest Iran. Shigella spp. were identified by standard biochemical tests and PCR. The antibiotic resistance pattern of all Shigella isolates was determined by the disk diffusion method and minimum inhibitory concentration (MIC) by E-test.

**Results :** Of 1530 stool samples, 91 (5.9%, 91/1530) were positive for Shigella spp. the most common Shigella isolates were Shigella flexneri 47 (51.6%, 47/1530). Antibiotic susceptibility tests showed that the highest antibiotic resistance was related to trimethoprim-sulfamethoxazole (87.9%, 80/91) and ampicillin (86.8%, 79/91). Multiplex PCR results revealed that 56% and 86.9% of Shigella isolates carried integron class I and integron class II genes, respectively. None of the isolates included the integron class III gene.

**Conclusion :** The high prevalence of multi-drug resistance in Shigella isolates in our area increases the concerns about the dissemination of the antibiotic-resistant isolates in this bacterium.

**Keywords :** Integrons; Shigella spp.; Multi-drug resistance; PCR

# O6-106: Whole-Genome Sequencing of a Clinically isolated Antibiotic-Resistant Enterococcus faecium EntfacYE

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**Background and Aim :** Enterococcal infections are considered the most common nosocomial infections. Nowadays, enterococci show high resistance to antibiotics, especially vancomycin. Vancomycin-resistant Enterococcus faecium is one of the most common nosocomial infections, including in the World Health Organization priority pathogens list for research and development of new antibiotics. The study of bacterial genes can be effective in understanding the antibiotic resistance of bacteria.

**Methods :** In this study, a multidrug-resistant Enterococcus faecium EntfacYE strain was isolated from a human blood sample. The isolated Enterococcus faecium strain was verified using Sanger partial sequencing of the bacterial elongation factor Tu. EntfacYE strain was assessed for antibiotic resistance and the bacterial genome was extracted and completely sequenced. The sequenced genome was analyzed and the genes were annotated in the DNA Data Bank of Japan.

**Results :** Totally, EntfacYE genome subsystems included 23 various categories with 59 genes belonging to antimicrobial resistance genes such a way that 49 antibiotic resistance genes were included in specific subsystems, while ten genes lacked specific subsystems. Moreover, cadmium, cobalt, copper, zinc and mercury resistance genes were identified in the EntfacYE genome.

**Conclusion :** In conclusion, studies on bacterial genomes help researchers identify characteristics of common pathogens, including virulence and antibiotic-resistance genes, and hence better understand bacterial pathogenesis to provide novel solutions for the treatment of common infections.

**Keywords :** Whole-genome Sequencing, Enterococcus faecium, Antibiotic resistance, Clinical sample

# O7-163: Decrease of methicillin-resistance in Staphylococcus epidermidis in Iran: A Systematic Review and Meta-Analysis over 5 years

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**Background and Aim :** One of the most prevalent drug-resistant bacteria is Methicillin-resistant Staphylococcus epidermidis (MRSE) causing health care infections. Previously, a meta-analysis study on the frequency of MRSE was conducted from Mar 2006 to Jan 2016 in Iran. The present study aimed to evaluate the changes in this prevalence in the last 5 years in different cities of Iran.

**Methods :** Published articles on the frequency of MRSE were collected from Web of Science, PubMed, Scopus, Google Scholar, Cochrane Library, and Iranian databases from the beginning of 2016 to the end of 2020. Of the 503 records identified 17 studies met the inclusion criteria, that their extracted data were analyzed using comprehensive meta-analysis version 2.0 (Biostat).

**Results :** The results of the analysis showed that the frequency of MRSE has decreased significantly in the last 5 years and has reached 60.8 [95% confidence interval (95% CI) 54.2-66.9] among culture-positive cases of S. epidermidis in Iran.

**Conclusion :** The noticeable reduction in the prevalence of MRSE in Iran could be due to the improvement of infection control programs to disrupt the pathogen transmission cycle. Another influential reason is the significant reduction in methicillin prescriptions by physicians for infections caused by staphylococci.

**Keywords :** Meta-Analysis, Methicillin-Resistant Staphylococcus epidermidis, MRSE, Iran

# O8-190: The high frequency of genes encoding VIM and NDM among isolates of Acinetobacter baumannii involved in nosocomial infections

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**Background and Aim :** Background: Acinetobacter baumannii, as one of the most important pathogens in nosocomial infections, causes a wide range of respiratory, urinary tract and blood infections. The high prevalence of antibiotic resistance mechanisms in this bacterium has caused widespread health concerns in various countries around the world. One of the mechanisms of resistance in this bacterium is the production of carbapenemases and metallobetalactamases, which makes this bacterium resistant to almost all beta-lactams. In this study, the frequency of genes encoding metallobetalactamases and carbapenemases was investigated by PCR.

**Methods :** Materials and Methods: 74 isolates of Acinetobacter baumannii involved in nosocomial infections were examined for phenotypic and genotypic identification of isolates producing metallobetalactamase and carbapenemase. Isolates were selected from Ilam and Tehran teaching hospitals. After identifying the isolates by biochemical methods, screening and confirmation methods according to the 2020 CLSI guidelines were used to identify the phenotypic isolates of metallobetalactamase producing isolates. In the next step, DNA of isolates was extracted and PCR method was used to evaluate the frequency of genes encoding metallobetalactamase including NDM, OXA23, OXA48, KPC, IMP and VIM

**Results :** Results: Out of 74 isolates studied by screening method, 67 isolates were identified as metallobetalactamase resistant which in the confirmation phase the number of isolates was reduced to 61 isolates. Based on PCR results, 40 isolates (54%) encoded NDM, 58 isolates (78.4%) encoded VIM and 52 isolates (70.3%) encoded OXA23. The frequencies of genes encoding IMP, OXA48 and KPC were 1.35%, 2.7% and 2.7%, respectively.

**Conclusion :** Conclusion: The results of this study showed that a high percentage of Acinetobacter baumannii isolates are phenotypically and genotypically producing metallobetalactamase. Among the 6 genes encoding metallobetalactamase, the highest frequency was observed in VIM, OXA23 and NDM genes.

**Keywords :** Keywords: Acinetobacter baumannii, resistance to carbapenems, metallobetalactamase

# O9-208: Molecular evaluation of methicillin-resistant staphylococci isolated from dogs

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**Background and Aim :** The dog is the main host of Staphylococcus pseudintermedius. This is the leading cause of otitis, pyoderma, and urinary tract infections; although as an opportunist, any site with compromised host defenses is susceptible. The high prevalence of methicillin-resistant Staphylococcus pseudintermedius (MRSP) within such infections is a growing concern. The goal of this study was detection of the frequency of genes encoding different antibiotic resistance (blaZ, mecA) ,hemolysins (hIa and hId) and leucosidines (lukF and lukS) in each of the isolates of methicillin-resistant S. pseudintermedius isolated from the studied dogs.

**Methods :** The samples (43 canine Staphylococcus pseudintermedius) were collected by sterile swabs from vertical part of the outer ear of 65 dogs referring to the Small animal Veterinary Hospital, University of Tehran. The mecA and blaZ which are genes related to resistance to methicillin and penicillin respectively, also toxin production related genes such as hIa and hId for hemolysis and lukF, LukS for leukocidins were investigated by PCR.

**Results :** 40 of the 43 isolates were considered methicillin-resistant and carried mecA gene. 35\40 MRSP isolates were positive for blaZ while15\40 harbored hla whereas, in 14\40 MRSP isolates hld existed. However, 34 of the 40 MRSP isolates contained both lukF and lukS genes.

**Conclusion :** These results highlight the importance of risk and prevalence of MRSP as well as intercepting overuse of antibiotics.

**Keywords :** Staphylococcus pseudintermedius; Methicillin resistance; Antimicrobial resistance; Dog

# O10-256: Prevalence of mcr-producing Klebsiella pneumoniae among clinical isolates around the world: A systematic review

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**Background and Aim :** currently, colistin (Polymyxin E) is considered a last-line therapeutic choice for severe human infections caused by multi-drug and carbapenem-resistant Gram-negative bacteria. Recently, the number of colistin resistance Klebsiella pneumoniae (CoRKP) has increased worldwide. In this systematic review, we present the frequency distribution, Prevalence of mcr-type genes and most prevalent sequence types (STs) of mcr-producing K. pneumoniae among CoRKP clinical isolates around the world.

**Methods :** Several international databases, including PubMed, Web of Science, Embase and Google Scholar were searched (1987 - 2020) to identify studies addressing the frequency of CoRKP strains worldwide.

**Results :** 280 studies were included in our study. A systematic review of prevalence studies showed that the overall resistance of CoRKP strains worldwide was 11.65%. Oceania had the highest percentage of colistin resistance with a frequency of 45.45%, which is due to the low number of studies conducted on this continent. After Oceania, the America, Europe, Asia, and finally Africa, respectively, had the most CoRKP among the clinical specimens. The most common mcr gene was mcr-1 with a frequency of 83.17%. After that, mcr-8.2 and mcr-8.1 (7.47% and 3.73%) had the most reports around the world. According to the results of articles published during the years 1987-2020, 106 different types of ST were obtained worldwide. The highest number of ST reports (56%) was in European articles. Interestingly, the highest variation of ST was recorded in Asia. In this study, the most common ST among the studied samples was ST101 with a frequency of 26% worldwide.

**Conclusion :** Finally, it can be concluded that the significant increase in the prevalence of CoRKP strains in recent years in various countries, especially in Asia, requires more attention by health care providers, physicians and microbiologists. Due to the high rate of CoRKP clinical strains reported in articles published worldwide and the lack of detailed analysis of K.

pneumoniae strains in terms of typing methods in many studies, therefore, CoRKP clinical strains are recommended to be examined by techniques such as MLST and PFGE for epidemiological studies and typing of strains as well as for the presence of mcr gene.

**Keywords :** colistin ,mcr, Klebsiella pneumoniae, sequence types

# O11-330: Evaluation of the antioxidant and antibacterial effect of Inula aspera various extracts

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**Background and Aim :** Inula aspera, belongs to Asteraceae family, is a perennial medicinal herb native to Asia and southeastern Europe. The aim of this study was to investigate the antioxidant and antibacterial activities of Inula aspera various extracts.

**Methods :** Inula aspera plants were collected from North Khorasan Province, Iran and dried in shade. The aerial parts of I. aspera were extracted using various solvent systems, including water, methanol, and hexane. Antioxidant activity of the plant extracts was measured using 1,1-diphenyl-2-picrylhydrazyl (DPPH) spectrophotometry. The microdilution technique was used to evaluate the antibacterial assay and minimum inhibitory concentration (MIC) against four potential pathogenic bacteria strains including Escherichia coli, Staphylococcus aureus, Pseudomonas aeruginosa and Enterococcus faecalis.

**Results :** According to the preliminary findings of this study, aqueous extract of I. aspera in comparison to the other extracts, had the highest antioxidant activity. IC50 values of aqueous, methanol, and n-hexane extracts were found to be 416.41, 661.02 and 1464 µg/ml. Aqueous and methanol extracts demonstrated significant antibacterial activity against all tested bacterial strains, with MIC values ranging from 25 to 100 mg/mL. The most sensitive strain was E. coli (MIC= 25 mg/ml), and the most resistant strain was P. aeruginosa (MIC= 100 mg/ml).

**Conclusion :** The results of this study showed that I. aspera can be considered as a potential source of a natural antioxidant and antibacterial product in food, medicine and cosmetic industries.

**Keywords :** antioxidant, antibacterial, Inula aspera, MIC, DPPH

# O12-334: Evaluation of resistance to fluoroquinolones and molecular analysis of resistance genes among Enterobacteriaceae isolated from clinical samples in Iran

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**Background and Aim :** Fluoroquinolones (FQs) resistance due to their extensive clinical use has been a major problem in clinical settings that lead to limitation of treatment. This study aimed to investigate the resistance genes to FQs in Enterobacteriaceae isolates in Azerbaijan, Iran.

**Methods :** In this descriptive-analytical study, eighty-eight Enterobacteriaceae isolated from clinical samples were collected. The biochemical and molecular diagnosis were evaluated for resistance to different antibiotics by disk diffusion agar according to CLSI recommendations and screening for ciprofloxacin-resistant isolates. The presence of mutations in quinolone resistance genes were detected by the PCR and direct sequencing.

**Results :** Overall, 63 isolates (71.6%) were resistant to at least one of the FQ antibiotics. The highest resistance rate was against ampicillin (88.6%) followed by trimethoprim-sulfamethoxazole (70.5%), ciprofloxacin (54.5%), and moxifloxacin (53.4%). All FQ-resistant Enterobacteriaceae had a mutation in gyrA. We found 100% and 76% mutation at Ser83Leu and Asp87Asn of gyrA, respectively. Mutations of gyrB were including Ser359Ala+ Ser367Thr (1.5%) and Ser366Pro+ Arg478Trp (1.5%). Forty-eight (92%) of FQ-resistant Enterobacteriaceae were positive for plasmid-mediated quinolone resistance (PMQR) genes. A total of 64.2% (27/42) FQ-resistance Enterobacteriaceae that containing 68.5% (24/35) E. coli and 57% (4/7) E. cloacae isolates presented a reduction in ompF expression level.

**Conclusion :** The rate of resistance to FQ and multidrug resistance is high in Enterobacteriaceae clinical isolates in the northwest of Iran and the double mutations in gyrA and parC result in high-level FQ resistance.

**Keywords :** Enterobacteriaceae, DNA Gyrase, Quinolone resistance

# O13-338: The efficacy of a bacteriophage against food-derived Salmonella Typhimurium isolates

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**Background and Aim :** Salmonellosis is of major foodborne bacterial gastroenteritis and an important zoonosis worldwide. Nontyphoidal salmonellae are estimated to cause approximately 153 million cases of gastroenteritis and 57,000 deaths globally each year. Bacteriophages are viruses that specifically kill bacteria. Phage-based biocontrol is a natural approach to combat food-borne bacteria at different stages of the food production chain. This study aimed to isolate and characterize novel bacteriophages as a potential candidate for biocontrol of Salmonella Typhimurium in food.

**Methods :** Fifty-two samples collected from different poultry and cattle farms in northern Germany. Soft-agar overlay technique was applied for isolating Salmonella-specific phages by using S. Typhimurium LT2. Host range determination was conducted using 16 food-originated Salmonella isolates, two E. coli O157:H7, and S. LT2. Three hosts were selected for further investigations. For one-step growth analysis, SP1 was incubated at 37 °C with the three hosts. Phage concentration was measured at 5 or 10 min-intervals for 2 h. The inhibitory effect of SP1 at different titers was tested in liquid medium at 37 °C. The absorbance at 595 nm was measured every 10 min for 10 h. The phage inhibitory effect was also tested at 4 °C, at MOIs of 104 and 105.

**Results :** Nine bacteriophages were isolated from chicken fecal samples. One bacteriophage was isolated from a nasal swab of a cow. Based on the stability and growth of the isolated phages, four bacteriophages were selected for host range determination. Among the isolated phages, SP1 demonstrated broader host range and strong lytic effects on S. LT2 and three food-derived Salmonella Typhimurium isolates. S. LT2, S1 and S2 were selected as the most susceptible hosts for further investigations. One-step growth curve analysis of the phage demonstrated a 60-min latent period and a burst size of 50-61 PFU/infected cell in the three

hosts. Phage-host interaction investigations in liquid medium showed that SP1 can suppress the growth of Salmonella isolates at 37 °C for ten hours. At 4 °C, a reduction of 1.4 to 3 log units was observed in the three hosts.

**Conclusion :** SP1 phage can be a promising candidate for biocontrol of Salmonella Typhimurium in food.

**Keywords :** Salmonella Typhimurium, bacteriophages, biocontrol, antimicrobial

# O14-394: Knowledge, attitudes and practices of broiler chicken farmers toward antimicrobial resistance

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**Background and Aim :** One important issue in food safety in veterinary medicine is the emergence of antimicrobial resistance (AMR) due to using antibiotics on the farm. Understanding farmers' knowledge, attitudes and practices could highlight the factors that influence decision-making in using antibiotics by farmers. The purpose of the present study was to determine the level of knowledge of poultry farmers about antibiotic use and antibiotic resistance, and to evaluate their attitudes and practices toward this subject.

**Methods :** A total of 94 broiler chicken farmers from Fars province, southern Iran were asked to complete a structured questionnaire regarding antibiotic use and AMR. Knowledge, attitudes and practices of respondents were measured and data were entered into statistical software. In addition to descriptive statistics, association of explanatory variables such as age and education with knowledge, attitudes and practices of farmers was determined using univariable and multivariable ordinal logistic regression analyses.

**Results :** One third of farmers failed to recognize the relationship between antibiotic use in poultry and AMR in human, and the majority failed to acknowledge the high importance of antibiotic usage for growth promotion in inducing AMR. Less than half always adhered to using recommended dosage of drugs; and selecting the antibiotics without culture and susceptibility testing was practiced to some extent by 52% of farmers. Statistical analyses showed that farmers with history of completing official training for poultry production had more positive attitudes and better practices compared with farmers who had not history of training. Most farmers cited veterinarians as their main favorite source of information to learn more about the concept of AMR.

**Conclusion :** This study establishes baseline estimates for knowledge, attitudes and practices of poultry farmers toward AMR. Program planning for transfer of relevant information to farmers, in particular association of antibiotic use in poultry and AMR in human, and importance of antibiotic use for growth promotion in inducing AMR, are highly warranted. These tasks are preferentially better to be implemented by the veterinary practitioners, the favorite source of information of the farmers.

**Keywords :** antibiotic. Attitudes. Broilers. Iran. Knowledge. resistance.

# O15-408: Isolation and characterization of lytic bacteriophage against Extensively-Drug Resistant (XDR) Escherichia coli

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**Background and Aim :** According to the reports of World Health Organization, increased use of antibiotics and bacterial resistance has become a global problem. Using alternative methods instead of antibiotic therapy would help to solve this problem. Phage therapy can be an appropriate method because the phages are completely safe and do not damage eukaryotic cells. The aims of this study were the isolation and characterization of specific bacteriophage against Extensively-Drug Resistant (XDR) Escherichia coli.

**Methods :** Thirty-one XDR E. coli isolates collected from Vali-Asr hospital, Arak, Iran. A lytic phage against E. coli was isolated by standard method and its host range (against 31 XDR E. coli, and some strains of Staphylococcus aureus, Pseudomonas aeruginosa, Acinetobacter baumannii, Lactococcus lactis) as well as its thermal and pH stability in 40-80oC and pH 1-12 were determined.

**Results :** Of 31 E. coli isolates, 20 isolates (64.5%) were lysed by bacteriophage suspension. The bacteriophage was completely specific against E. coli and the other strains were no susceptible to it. After one-hour incubation of bacteriophage suspension at 40-70oC, the titers of phage were completely preserved. But at 80oC the titer was reduced from 1012 to 1010. Phage titers were completely preserved after incubation of phage suspension (37oC, 1h) at pH 4-10, but at pH 1, 2, 3, 9, 10, 11, 12 the phage titer was reduced from 1012 to 109 respectively.

**Conclusion :** Temperature and pH tolerance of this phage was appropriate and it also specifically lysed E. coli. It also had great potential for lysing the XDR E. coli. According to the results, this phage has a good potential for wound phage therapy, food preservation and biocontrol of the environment.

**Keywords :** bacteriophage, phage therapy, XDR, E. coli

# O16-37: Exposed immunogenic loops of BauA and Omp34 displayed on the loopless C-lobe of the TbpB surface lipoprotein of Neisseria meningitidis trigger antibodies against Acinetobacter baumannii in a murine model

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**Background and Aim :** The complexity of treating Acinetobacter baumannii infections due to the emergence of resistant strains has led researchers to design different types of vaccines. Omp34 is one of several pathogens of Acinetobacter baumannii that its important role in the pathogenesis and survival of this bacterium has been proven. According to studies and understanding the important role of protein BauA (Baumannii Acinetobactin Utilization), which is produced under iron deficiency conditions and is required for the transfer of acinetobactin (iron-containing siderophore) to bacterial cells, makes it necessary to use BauA and Omp34 to make vaccines.

**Methods :** A new hybrid antigen approach was used in which the superficial epitopes of the TbpA receptor protein of Neisseria meningitidis were displayed on the C-lobe derivative of the TbpB surface lipoprotein, named the loopless C-lobe (LCL). The nucleotide sequences of the immunogenic loops were amplified and cloned into the LCL. After designing specific primers from the desired genes and regions and gene amplification, for replication, the amplified fragment was treated with a vector in the desired enzymatic digestion reaction. Then, using ligase enzyme, the digested fragment was SOE-PCR into the LCL at the designated position, and the resulting fragment was inserted into the expression vector. The recombinant proteins were expressed and purified using a Ni-NTA column. After the immunization of the laboratory animal, the production of antibodies against the recombinant proteins was assessed by indirect ELISA. The hybrid antigens were used to immunized mice followed by challenge experiments with a clinical isolate of A.baumannii (ABI022).

**Results :** Mice immunized with the hybrid antigen of the BauA loop7 (BauAL7P3) and Omp34 loop 3 (Omp34L3P1) brought protection against A. baumannii infection.

**Conclusion :** The findings support the use of multiantigens to induce broadly reactive antibody responses against heterologous A. baumannii strains.

**Keywords :** Immunogenicity., Vaccine. , BauA., Omp34., Acinetobacter baumanni., Hybrid antigen

# O17-45: Evaluation of the antibiotic resistance pattern and prevalence of oxacillinase genes in clinical isolates of Acinetobacter baumannii from hospitals in Shiraz. (2013-2014)

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**Background and Aim :** Acinetobacter baumannii is one of the main factors of nosocomial and pneumonia infections. Most of the major difficulties related to the treatment of Acinetobacter baumannii infections is the emergence of MDR-strains (multi-drug resistant). In majority of medical centers, the best choice for the treatment of Acinetobacter baumannii infections is carbapenems. However, in the last years, resistance to these antibiotics due to the production of carbapenem-hydrolysing beta-lactamases such as OXA-carbapemase genes has been increased. Hence, the goal of this study was to investigate the presence of Oxacillinase genes in isolated acinetobacter baumannii strains from clinical samples.

**Methods :** This study has been done in four Shiraz teaching hospitals( Namazi, Faghihi, Ali-asghar, Ghotbo-aldin).we were gathered about 200 Acinetbacter baumannii clinical samples during the six-months. All the isolates were investigated through the disk diffusion tests in order to antibiotic resistance patterns. Also, the MIC concentration of imipenem and colistin antibiotics were evaluated by E-test methods. Additionally, the polymerase chain reaction (PCR) and multiplex PCR was used to survey the presence of blaOXA-23-like, blaOXA-24-like ,blaOXA-51-like and blaOXA-58-like genes.

**Results :** First, all the isolates were positive for the presence of blaOXA-51-like genes and 71 isolates were harbored blaOXA-23-like genes. Among the tested antibiotics through the disk-diffusion methods, all the isolates were susceptible to Colistin and polymixin B antibiotics, however, all isolates had shown resistance to the ampicillin,pepiracilin, pepiracili-tasobactam, ceftazidime, and cefotoxin. According to the results of E-test of 86 isolates of Acinetobacter baumannii, 85 isolates were susceptible to Colistin antibiotics, and only one isolate (1/2%) was resistant to this antibiotic.

**Conclusion :** According to the data we were gathered through the mentioned tests, the rate of resistance to Colistin and polymixin B was significantly high. Also, resistance rate of isolates to imipenem and meropenem were remarkably high. Among the Oxacillinase genes, blaOXA-23-like and bla-OXA-24-like genes had the most frequency.

**Keywords :** Acinetobacter baumannii, antibiotic resistance, OXA-carbapenemase, Oxacillinase.

# O18-57: Frequency and antibiotic susceptibility of non-fermenting Gram-negative bacteria isolated from hospitalized patients in Hazrat Zeinab hospital, 2016-2017.

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**Background and Aim :** Antimicrobial resistance to the available antibiotics has been emerged as a serious problem in treatment worldwide which causes high rates of morbidity and mortality. The aim of this study was to investigate the frequency and antibiotic resistance patterns of non-fermenting Gram-negative bacteria including Acinetobacter baumannii and Pseudomonas aeruginosa.

**Methods :** This was a cross-sectional study that was conducted in a referral hospital, by using a questionnaire including patients' age, gender, and the sampling site, severity of bacterial growth, type of organism which was found on the medium, and also the result of antibiogram tests.

**Results :** Of 210 patients including (7 adults and 203 neonates) were evaluated in this study. The most prevalent resistance of Acinetobacter baumannii was related to amikacin (89.4%), ceftazidime (86.5%), gentamicin (70%), imipenem (70.9%),cefepime ( 67.4%), ciprofloxacin (60.3%),cotrimoxazole (36.2%), tetracycline( 9.9%), and cefotaxime (5.7%). Also,the most resistance frequency of P.aeroginosa was associated were these antibiotics: amikacin (31.9%), gentamicin (31.9%), ceftazidime (29%), cefepime (24.6%), ciprofloxacin (11.6%), and imipenem( 10.1%).

**Conclusion :** It was concluded that the lowest rate of resistance was associated with tetracycline in A.baumannii, however, the lowest resistance rate of P.aeroginosa was associated with ciprofloxacin and imipenem.

**Keywords :** Acinetobacter baumannii, pseudomonas aeruginosa, neonate, antibacterial resistance, Iran.

# O19-189: Investigation of gastrointestinal Escherichia coli phylogenetic linage in immunocompromised pediatrics

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**Background and Aim :** Multiple stays in hospital considered as a risk factor for hospital acquired infection (HAI), especially in immunocompromised pediatrics. Dysbiosis of the fecal microbiota could occur in these children with bacteria originating from the hospital environment. To show this relationship, phylogenetic homology of Escherichia coli isolates among admitted pediatrics to the bone marrow transplantation and oncology wards was investigated in a hospital in Tehran, Iran.

**Methods :** A total of 56 immunocompromised children were included in this investigation. Culture of fecal samples and characterization of E. coli isolates was done according to standard methods. ERIC-PCR genotyping method was used to identify the phylogenetic relationship and clonal diversity of the strains.

**Results :** Out of 31 E. coli isolates, homology of ERIC-PCR patterns was detected between 21 pairs of them. The isolates with identical patterns were related to hospitalized patients in the oncology (25.8%, 8/31), transplantation (9.6%, 3 /31), or oncology/transplantation wards (22%, 7/31), respectively. We detected 21 different clones of E.coli with considering 100% of homology in both wards. Nearly 100%, 90%, 75% homology in ERIC-PCR patterns was detected in 41.9%, 54.8%, and 25% of the E. coli strains with identical, similar, and related clones, respectively.

**Conclusion :** Homology of the E. coli isolates among immunocompromised children at different wards of the hospital was shown in this study. Control programs are necessary to avoid transmission of resistant clones of pathogenic bacteria between different hospital wards and from the hospital environment to the community.

**Keywords :** Escherichia coli, Dysbiosis, microbiota, ERIC-PCR, phylogenetic relationship

# O20-220: Phylogenetic analysis of uropathogenic Escherichia coli isolates recovered from kidney transplant patients

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**Background and Aim :** Worldwide phylogenetic analyses have demonstrated that virulent extraintestinal Escherichia coli strains belong mainly to group B2 and, to a lesser extent, to group D. In contrast, most of the commensal strains are associated with group A or group B1. This study aimed to investigate the phylogenetic characterization of uropathogenic Escherichia coli (UPEC) isolated from kidney transplant patients (KTPs) as well as non-KTPs.

**Methods :** To this end, we determined the phylogenetic characterization of UPEC in non-KTPs (n=65) and KTPs (n=46) collected at the three laboratory centers as well as two nephrology private clinics affiliated to Isfahan University of Medical Sciences (IUMS) between June 2019 to October 2019. The non-KTPs were considered the control group of the study.

**Results :** According to the quadruplex PCR assay results, most (38.7%) of the UPES isolates belonged to phylogenetic group B2, followed by group D (18.9%), group A (13.5%), B1 (9%), C (5.4%), E (4.5%), and F (3.6%). The remaining 6.3% of the isolates were found to be un-typeable. This study also revealed that the major phylogenetic group in KTP isolates was B2 (39.1%), followed by D (21.7%), and A (19.6%), while the predominance of phylogenetic groups in non-KTP isolates were B2 (38.7%), followed by D (18.9%), and B1 (9%).

**Conclusion :** There was no significant difference between phylogenetic dissemination in KTPs and non-KTPs, except for phylogenetic group C that was significantly predominant in the control group. However, it should be pointed out that this study's findings suggested that UTIs can have extraintestinal origin even in immunosuppressed patients such as KTPs.

**Keywords :** Uropathogenic Escherichia coli, phylogenetic group, kidney transplant patients

# O21-374: BauA and Omp34 surface loops trigger protective antibodies against Acinetobacter baumannii in a murine sepsis model

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**Background and Aim :** The complexity of treating Acinetobacter baumannii infections due to the emergence of resistant strains has led researchers to confront this pathogen by developing vaccines. In this study, we used two important virulence factors of A. baumannii to elicit immunity against the A. baumannii. The immunogenic loops were from Baumannii acinetobactin Utilization A (BauA) and 34kD outer membrane protein (Omp34).

**Methods :** A new hybrid antigen approach was used in which the superficial epitopes of the TbpA receptor protein of Neisseria meningitidis were displayed on the C-lobe derivative of the TbpB surface lipoprotein, named the loopless C-lobe (LCL). The nucleotide sequences of the immunogenic loops were amplified and cloned into the LCL. The hybrid antigens in the LCL scaffold were expressed in the E. coli cytoplasm as soluble antigens. The hybrid antigens were used to immunized mice followed by challenge experiments of murine sepsis with a clinical isolate of A.baumannii (ABI022).

**Results :** Mice immunized with the hybrid antigen of the BauA loop7 in position 3 and Omp34 loop 3 in position 1 of LCL ( BauAL7P3Omp34L3P1) brought protection against A. baumannii infection.

**Conclusion :** The findings support the use of multiantigens to induce broadly reactive antibody responses against heterologous A. baumannii strains.

**Keywords :** Immunogenicity., Vaccine. , BauA., Omp34., Acinetobacter baumanni., Hybrid Antigen

# O22-41: Exposed loops of BauA and ZnuD provide immunity protection against Acinetobacter baumannii in mice sepsis model

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**Background and Aim :** Acinetobacter baumannii causes severe nosocomial infections and is a difficult-to-treat pathogen due to the development of multidrug-resistant strains. Vaccines represent an alternative promising strategy for the control of infections caused by A. baumannii.

**Methods :** Antibody therapy may be an alternative option for treatment of infections caused by the multi-drug resistant (MDR) A. baumannii. As this pathogen possesses multiple capsular serotypes, a universal antibody therapy would need to target conserved protein antigens rather than the capsular polysaccharides. In this study, we targeted iron and zinc acquisition systems by selecting immunologically active loops from Baumannii acinetobactin Utilization A (BauA) and Zinc uptake component D (ZnuD) in A.baumannii. The surface epitopes were displayed and a hybrid antigen from the loopless C lobe of the TbpB protein of Neisseria meningitides referred to as LCL was constructed. The nucleotide sequences of the immunogenic loops of BauA and ZnuD were amplified and implanted in the LCL. The recombinant genes were expressed and purified. The purified proteins were administered to BALB/c mice. Both active and passive immunizations were carried out. The mice were then challenged with a clinical isolate of A.baumannii.

**Results :** Indirect ELISA confirmed significant antibody rise to the antigens. In the active immunization, the survival rates of 42.8%, 14%, and 42.8% were achieved with the loops derived from BauA, ZnuD, and combination of both loops respectively. Significant decrease in the bacterial loads were noted in the spleen, liver and lungs of the immunized mice groups.

**Conclusion :** Loop 7 of BauA plays an effective role in immunoprotectivity against A.baumannii infections.

**Keywords :** Acinetobacter baumannii- BauA- ZnuD- Immunogenicity- Siderophore- Vaccine

# O23-43: Study of the amino acid sequence of Enterotoxigenic Escherichia coli Flagellin as a vaccine candidate

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**Background and Aim :** Enterotoxigenic Escherichia coli (ETEC), is the most common cause of travelers' diarrhea and the main cause of diarrheal disease particularly among the younger in low-income and developing countries. Food and water contaminated with animal or human feces is a source of ETEC transmission. Although there are several whole germ-attenuated, killed, or recombinant vaccines. But the bacteria still lead to infection and vaccines have failed.

**Methods :** In this study, we analyze ETEC Flagellin as a major immunogenic protein in ETEC by multiple sequence alignment. For this purpose, we used the NCBI protein database to collect samples (all of which were obtained from diarrhea) from various countries. Samples were analyzed by Vector NTI software to identify conserved and consensus sequences.

**Results :** The results show these proteins had 46.5% similarity and they had only 25% conserved sequence. Moreover, the main position of the conserved sequence is 1 to 139 and 646 to 717.

**Conclusion :** Therefore, it can be clear one of the reasons for vaccine failure is the major difference in bacterial flagellin proteins. Together, this study suggested that these positions are good candidates for future study in the vaccine field.

**Keywords :** ETEC, Flagellin, diarrhea, vaccine failure

# O24-176: Evaluation of opsonic effect of LytA antibodies on common pneumococcal serotypes in Iran

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**Background and Aim :** Vaccination is an effective strategy to prevent pneumococcal diseases. Currently, licensed vaccination against Streptococcus pneumoniae uses vaccines based on capsular polysaccharides from selected serotypes and has led to non-vaccine serotype replacement disease Therefore, it is important to find new immunogenic candidates for developing pneumococcal vaccines. the cell wall hydrolase LytA protein is the major neuraminidase that is immunogenic and conserved in all S. pneumoniae serotypes.

**Methods :** The LytA protein was significantly expressed in the vector pET28a E. coli BL21 host the lytA recombinant protein was purified by the Ni-NTA affinity chromatography based on denaturation-renaturation method then the expression and quality of lytA protein was surveyed by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and the recombinant protein was confirmed by Western blotting method. In this study we have characterized the antibody responses after immunization of rabbit with LytA in the presence of alum as an adjuvant. Enzyme-linked immunosorbent assays measuring the titer of antibody lytA in serum. then, the function of anti- LytA antibodies in the opsonophagocytosis of 1, 4, 6A and 19F S. pneumoniae serotypes were evaluated by using a flow cytometry assay.

**Results :** The results showed that there was a significant difference between the control and test groups in 1:50 and 1:200 dilutions (p-value<0.05).

**Conclusion :** Therefore Vaccination with LytA induced protection demonstrating that LytA might be a good candidate to be considered in a future protein-based vaccine against S. pneumoniae.

**Keywords :** LytA protein, Streptococcus pneumonia, opsonophagocytosis, Vaccine candidate

# O25-211: Investigation of the presence of OmpL1, LipL41 proteins' in the outer membrane of Leptospira

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**Background and Aim :** Leptospirosis is zoonotic disease which caused by pathogenic leptospires in humans. The disease is one of the most common diseases in humans and animals. The outer membrane of leptospira contains lipopolysaccharide and several lipoproteins known as OMP, which play an important role in the pathogenesis process. The aim of this study was to investigate the presence of LipL41 and OmpL1 proteins

**Methods :** The sequences used for cloning and expression were based on the serovars in the collection of Razi Serum and Vaccine Institute and were designed using snapgen software. The construct was prepared based on the pathogenic serovars. The target construct was then transferred into Ecoli PlysS bacteria and the expressed protein was confirmed using SDS page test.

**Results :** In total, the presence of LipL41 and Ompl1 in the existing serovars was well cloned and expressed and confirmed by SDS page test with clear wind at 43 kDa.

**Conclusion :** This study shows that the recombinant antigen produced may be used in the future as a recombinant vaccine as well as the design of an ELISA kit for diagnosis.

**Keywords :** Leptospira, SDS page, OmpL1, LipL41

# O26-257: Designing of puf4 gene knockout in Leishmania major as an attenuated vaccine candidate using CRISPR/Cas9 gene edition system

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**Background and Aim :** Introduction: Leishmaniasis is a neglected tropical disease that is caused by Leishmania (L.) parasites that transmits by the bite of infected sandflies. As a next generation of live vaccines, genetically attenuated parasites are more attention. PUFs are conserved RNA-binding proteins in eukaryotes that are responsible for regulation of RNA processing. Leishmania has 11 members of PUFs that lead to regulate gene expression post-transcriptionally. The main goal of this study is disruption of puf4 gene in L. major and generation an attenuated vaccine through CRISPR/Cas9 system.

**Methods :** Method: In the first step, sgRNA and donor DNA primers have designed using different software (LeishGEdit, EuPaGDP, CCTop, CRISPOR and CHOPCHOP) to increase the accuracy of designed primers.

**Results :** Results: Between 100 bp region from the beginning of the puf4 gene, four suitable sgRNA sequences (including: 5'- AAGACACAGGTGCAGATGCA-3', 5'-CAGCTCTTCGCTCTCGGATT-3', 5'-GCTCTCGGATTGGGCAAACA-3' and 5’-AGGTGCAGATGCACGGATGA-3’) can be considered to have the highest efficiency in cutting the 5' of the puf4 gene. In addition, four appropriate sgRNAs for 3'-end cutting of gene have recognized (including: 5’-GCACGCATGCAAAATGCTAA-3’, 5’-AGACGGAGCTCGCCTTGCTG-3’, 5’-TAGTTGCGCGAGCTCAGCAG-3’ and 5’-GACGGAGCTCGCCTTGCTGA-3’). GC content of primers is ranging from 33 to 64.8. In addition, to increase MMEJ (Microhomology-Mediated End Joining) rate and substitution of puf4 gene with antibiotic markers, two specific short nucleotide sequences (~30 nt) in upstream and downstream of the gene (5’-ACGTTGTGCAGCTCCCTTCACCGTCATCCG-3’ and 5’-GAGTGCAGCGGCCGGGAACGGTGGCCACAC-3’, with GC content 60% and 73%, respectively) have selected.

**Conclusion :** Conclusion: In the next step, sgRNA and donor DNA sequences will be used to create DSB within flanking puf4 target region and replace of two alleles with two drug resistance genes.

**Keywords :** Attenuated vaccine, Leishmania major, PUF4, CRISPR/Cas9.

# O27-306: The immunoprotective effect of a hybrid antigen from Omp34 against A.baumannii in a murine model of pneumonia

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**Background and Aim :** Acinetobacter baumannii is one of the most troublesome human infections. Researchers are looking for alternative therapeutic options, including immunization against the nosocomial bacterium, due to the emergence of antibiotic-resistant strains. Although no vaccine for this infection is currently available, various attempts have been made to develop one. Omp34 is known as a specific antigen in Acinetobacter.

**Methods :** In this study, the most immunogenic loop of Omp34 protein was found to be loop 3. The gene in the query was amplified and cloned into a predetermined position in loopless C lobe (LCL) of Neisseria meningitides and the construct was cloned into the 5044 plasmid. The purified recombinant protein was subsequently administered to mice.

**Results :** According to an indirect ELISA test on the serum of mice given 20 µg of Omp34 protein and adjuvant , there was a substantial rise in antibody to Omp34 compared to the control group. The active immunized mice were subjected to A.baumannii challenge. The mice group challenged with A.baumannii ATCC 19606 showed 80, 100, and 60% survival rate in mice after nasal inoculation with loop3 in positions 1, 3, and combination of the two positions while the clinical strain exhibited 100, 100, and 80% survival rate at the same LCL positions respectively. In addition, the bacterial load in the lung was significantly reduced in all immunized groups.

**Conclusion :** Our results showed that protein omp34 as an immunogen can protect against A.baumannii.

**Keywords :** Acinetobacter baumannii, Omp34, Immunogenicity

# O28-319: Mouse model study of a PTX inactivated clinical strain of Bordetella pertussis in Iran

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**Background and Aim :** Despite high vaccination coverage of whole cell and acellular vaccines against pertussis, new vaccination strategies are under investigation. Genetically inactivated Bordetella pertussis is one of the new strategies to generate live attenuated vaccine against whooping cough. S1mBPIP91 is a PTX inactivated B. pertussis strain derived from BPIP91 that was selected based on predominant profile of circulating Iranian isolates. The aim of this study was to confirm immune response of this engineered clinical strain in mouse models.

**Methods :** Colonization and immune response of S1 mutant strain (named S1mBPIP91) was determined in a mouse model. The 8-wk-old female Balb/C mice were intranasally infected with approximately 4 × 106 bacteria in 30-µl PBS, and the number of colony-forming units (CFU) in the lungs were measured. Sera were collected, and antibody titers were estimated by enzyme-linked immunosorbent assays (ELISA). For challenge infections with Bordetella, mice were intranasally infected 1 month after vaccination with approximately 4 × 106 BPIP91 in 30-µl PBS.

**Results :** The PTX mutant strain of B. pertussis in this study remained in mouse lunge for one month after intranasal infection of the mouse and also produced IgG antibodies against PTX. The S1mBPIP91 strain also provided protection against infection with Bordetella after one month infection of mice.

**Conclusion :** A PTX inactivated B. pertussis strain with predominant genomic and virulence profile in Iran was able to colonize and immunize the mice and will be useful to further studies of both whole cell and acellular pertussis vaccines strategies.

**Keywords :** Bordetella pertussis, attenuated vaccine, pertussis toxin, mouse model

# O29-344: Serotype Distribution, Antibiotic Susceptibility and Family Typing of Pneumococcal Surface Protein A (PspA) among Iranian Streptococcus pneumoniae Isolates

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**Background and Aim :** Streptococcus pneumoniae is a major cause of morbidity and mortality worldwide and an etiological agent causing various infectious diseases ranging from non-invasive to invasive diseases. The high prevalence of multidrug-resistant pneumococci has become a global concern. Available vaccines are serotype dependent and protect against only a limited number of pneumococcal serotypes. One of the virulence factors of pneumococci is pneumococcal surface protein A (PspA). This protein is highly conserved and an attractive candidate antigen for the development of new effective vaccines. PspA is classified into 3 families and 6 clades based on its structure. The distribution of pneumococcal serotypes among the different PspA families and clades varies from country to country. The purpose of this study is to investigate of the serotype distribution, antibiotic susceptibility, and the diversity of PspA family types from pneumococcal isolates from nasopharyngeal swab samples of children under 6 years of age, referred to medical centers in Tehran.

**Methods :** A total of 100 S. pneumoniae isolates from nasopharyngeal swab samples were characterized for PspA family typing, antibiotic resistance, and capsular typing. The antibiotic susceptibility test was performed based on the Clinical and Laboratory Antimicrobial Standards Institute (CLSI). Pneumococcal serotyping was performed using multiplex polymerase chain reaction methods, and PspA family typing was also done using PCR with specific primers for family typing.

**Results :** Our results showed that serotype 6A/6B is the most prevalent in all isolated pneumococcal strains. All strains were sensitive to Levofloxacin, while 88.64% were resistant to gentamycin. Our studies also demonstrated that all of these strains were positive for the presence of the cpsA and pspA genes. This study also indicated that the majority and minority of the isolates belonged to PspA family 2 and PspA family 3, respectively. Also, 23.37% of the strains were placed in both PspA families 1 and 2.

**Conclusion :** This study, along with other studies, demonstrated the presence of the pspA gene in all strains. Since most isolates were classified as PspA family 2, PspA family 2 can be

attractive candidate antigens for the development of novel, effective protein-based pneumococcal vaccines.

**Keywords :** Streptococcus pneumoniae, Antibiotic Susceptibility, Pneumococcal Surface Protein A, Genetic Diversity, Iran

# O30-446: Immunological effect of conjugated alginate-exotoxin A Pseudomonas aeruginosa on the titer of G antibody subclasses in Mice

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**Background and Aim :** Pseudomonas aeruginosa is an opportunistic pathogen and alginate is its most important factor in pathogenicity. The objective of study is the immunogenicity evaluation of P. Pseudomonas aeruginosa alginate conjugated to exotoxin A as a vaccine candidate in mice

**Methods :** mucoid strain of Pseudomonas aeruginosa 6494 was used to prepare alginate and the separation of exotoxin A was done with the standard strain of PAO1. Alginate was extracted by the means of sedimentation with cold ethanol, dialysis, enzymatic digestion and chromatography. To improve immunogenicity, purified antigen was coupled to exotoxin A with ADH as a spacer and EDAC as a linker. Based on confirmation tests, resulting conjugate was devoid of specific toxicity and pyrogenic effect. Four groups of BALB/c female mice (each group was included 15 mice) were selected in the next step. The first group with the ALG, the second group with the D-ALG-ETA and the third one with the ETA were vaccinated. The fourth group as a control group was vaccinated with normal saline. Vaccination was performed in three injectable doses with two-week intervals. Subsequently, serum samples were collected and antibody responses were measured by the ELISA method, for total IgG, IgG1, IgG2a, IgG2b, IgG3

**Results :** After the second and third doses with ALG-ETA showed a significant increase in antibody titer against ALG-ETA in comparison with pure ALG. The titers of IgG2a, IgG2b, IgG, IgG1, IgG3 antibodies that produced against alginate increased in the third injection compared to the first conjugate injection which was 2/9, 9/2, 10, 5/2 and 3 respectively.

**Conclusion :** These results show that ALG from Pseudomonas aeruginosa increases antialginate antibodies in conjugate form with exotoxin A and can be considered an appropriate effective adjuvant.

**Keywords :** Pseudomonas aeruginosa, Alginate, Exotoxin A, conjugate, ELISA

# O31-23: Isolation and Characterization of bacteriophage against Methicillin- resistant Staphylococcus aureus isolated from bedsore and diabetic wounds

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**Background and Aim :** Methicillin-resistant Staphylococcus aureus (MRSA) is a major human pathogen causing a variety of diseases. The potential of bacteriophages as an alternative treatment for MRSA infections has recently gained lots of attention. The purpose of this study was to isolate and characterize bacteriophages effective against clinical isolates of MRSA.

**Methods :** Bacteriophage was isolated from Mofid children's hospital sewage in Tehran. Lytic activity was determined with a spot test, while the titers of phage lysates were measured using the Double-Layer Plaque Assay. The phage characterization was determined through transmission electron microscopy (TEM), adsorption rate, and stability tests to various agents such as the pH, temperature, NaCl concentration, and chloroform. The spot test was used for host range determination and the latent period and burst size were estimated from a one-step growth curve. The effect of bacteriophage against 1-3-5-day old preformed MRSA biofilm was determined using TTC assay.

**Results :** The isolated lytic bacteriophage formed small clear plaques. TEM results revealed that the phage resembled the Cystoviridae family. The latent period of phage was 30 min, corresponding to about 71/43 phage particles per infected cell. The phage was resistant to chloroform and was most stable at 37 °C, pH 7. By increasing the NaCl concentration, the rate of phage survival decreased. Furthermore, in the first 5 minutes, the phage exhibited rapid adsorption to the bacteria. This phage had a broad host range and infected 80% of clinical isolates of MRSA. The phage dispersed preformed MRSA biofilm.

**Conclusion :** The isolated phage has the potential to be used as a therapeutic agent against MRSA infections.

**Keywords :** Methicillin-resistant Staphylococcus aureus, Bacteriophage, Phage therapy, Wound

# O32-209: Pseudomonas bacteriophages

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**Background and Aim :** Today, multidrug resistance has increased with the spread of nosocomial infections caused by gram-negative and opportunistic human pathogens such as Pseudomonas aeruginosa, abuse in the prescription and overdose of antibiotics has increased. During the increase in antibiotic resistance, alternative antimicrobial therapies such as phage therapy, which is an intelligent remedy for pneumonia and acute and chronic nosocomial infections, have been used. In this study, the effective phage against Pseudomonas aeruginosa was isolated and used as an effective phage against this bacterium.

**Methods :** First, different clinical strains of Pseudomonas aeruginosa were identified and used to isolate phage affecting Pseudomonas by examining disk diffusion tests and biochemical tests. Then, using high bacterial load-rich effluent against Pseudomonas aeruginosa, plaque formation was evaluated using the point method, and then after purification and enrichment of phage affecting Pseudomonas aeruginosa, phage samples were used for transmission electron microscopy.

**Results :** Isolated Pseudomonas aeruginosa phages were able to fully toxicize the target bacterial cell, these phages are capable of treating antibiotic-resistant bacterial infections. The bacteriophages in question belong to the family Myoviridae, Podoviridae and Siphoviridae, which can be used instead of treating ineffective antibiotics.

**Conclusion :** Phage therapy as a new antibacterial treatment that has the least side effects during treatment. Hence, isolated phage from different families has been effective for phage therapy against multidrug resistant Pseudomonas aeruginosa strains.

**Keywords :** phage therapy, Bacteriophage, Pseudomonas

# O33-213: Changes of microbial cell survival, metabolic activity, efflux capacity, and quorum sensing ability of Aggregatibacter actinomycetemcomitans due to antimicrobial photodynamic therapy-induced bystander effects

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**Background and Aim :** The bystander effects, whereby naive (bystander) microbial cells near microbial cells directly exposed to certain treatment show responses that would not have happened in the absence of the directly targeted microbial cells, is recently documented in the field of microbiology. In this article, we discuss that substantial bystander responses are also observed after antimicrobial photodynamic therapy (aPDT) using curcumin (Cur).

**Methods :** Bystander effects induced by whole bacterial cell suspension (WBCST), cell-free supernatants fluid (CFSFT), and bacterial cell pellet (BCPT) obtained from A. actinomycetemcomitans culture treated with Cur-aPDT on cell survival, quorum sensing (QS) ability, metabolic activity and efflux capacity of A. actinomycetemcomitans were determined using microbial viability assay, Escherichia coli-based bioassay, XTT reduction method, and ethidium bromide (EtBr) accumulation assay, respectively.

**Results :** A. actinomycetemcomitans cell survival reduced by 82.7% (P=0.001) and 76.2% (P=0.01) after exposure to WBCST and CFSFT, respectively. The A. actinomycetemcomitans population increased by 5.5% (P=0.7) after exposure to BCPT. Bacterial metabolic activity decreased by 42.6% (P=0.02), 35.3% (P=0.03), and 9.4% (P=0.5) after exposure to WBCST, CFSFT, and BCPT, respectively. A. actinomycetemcomitans exposed to WBCST, CFSFT, and BCPT showed a reduction of 83.2% (P=0.001), 77.2% (P=0.01) and 21.9% (P=0.09) in the QS mediator compared to the WBCSU, CFSFU, and BCPU of untreated A. actinomycetemcomitans, respectively. No significant change of the EtBr accumulation was observed in the three preparations of the Cur-aPDT-treated culture (i.e. WBCST, CFSFT, and BCPT) compared to their respective controls.

**Conclusion :** The results of the current study revealed that Cur-aPDT could significantly reduce microbial cell survival, cell metabolic activity, efflux capacity, and QS ability through the bystander effects. As a result, the bystander effects of Cur-aPDT along with the direct effect of Cur-aPDT can enhance the efficiency of aPDT as an adjunct therapeutic strategy for treatment of local infections

**Keywords :** Aggregatibacter actinomycetemcomitans, Curcumin, Bystander, Periodontitis, Peri-implantitis, Antimicrobial photodynamic therapy

# O34-217: Isolation and identification of bacteriophage affecting Pseudomonas aeruginosa isolated from Patients with cystic fibrosis (CF)

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**Background and Aim :** Now days, due to the increasing of antibiotic resistance in Pseudomonas aeruginosa and the global decrease in the effectiveness of antibiotics treatment of bacterial infections, a novel approach has been developed to use bacteriophages in treatment of infections. Pseudomonas aeruginosa is an opportunistic hospital bacterium that causes acute infections of Respiratory system in patients with cystic fibrosis, which due to appearance of antibiotic-resistant strains in this bacterium, phage therapy is an effective approach to control this phenomenon.

**Methods :** Initially, from the hospital wastewater, Bacteriophage was isolated by double layer method and also purified and enriched by the same method. After titration and determination of phage host spectrum by spot test, Phage stability assay against different temperatures and pH values, and determination of phage absorbance time to bacteria by double layer method has been done. Phage morphology was determined by TEM electron microscopy. Phage was used for Prevention of biofilm formation by titration assay with microplate.

**Results :** For isolation, transparent areas of plaque indicate the presence of phage in the wastewater sample and the ability of bacteria for lysis, which after purification and enrichment, TEM images indicate that phage belongs to Myoviridae family. Isolated phage had limited host spectrum and had good function in temperature range of -20 ° C to 50° C and the pH value range of 4 to 10.

**Conclusion :** According to the effectiveness and the desired results in all tests, it can be said that Isolated phage against Pseudomonas aeruginosa is effective and can be used for treatment of Infections caused by this bacterium.

**Keywords :** Pseudomonas aeruginosa, cystic fibrosis , bacteriophage , Myoviridae

# O35-275: The evaluation of the antibiotic activity of sultamicillin-colistin eluting noisome nanoparticles against biofilm of Acinetobacter isolates.

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**Background and Aim :** Acinetobacter baumannii is a multi-drug resistant bacterial pathogen causing nosocomial outbreaks worldwide. The particular ability of this pathogen is to form biofilms that demonstrate greater protection against antibiotics, host immune defense, and adverse environmental conditions than the free-living cells. The purpose of this study was to evaluate the antibiofilm activity of sultamicillin-colistin eluting noisome nanoparticles against biofilm of Acinetobacter isolates.

**Methods :** In this study, 40 pre-isolated strains were used. Niosomes were prepared using thin-film hydration method and were characterized by zeta potential measurement and Field Emission Electron Microscope (FE-SEM). The release rate of sultamicillin and colistin from the niosome was evaluated using the dialysis method. The Sultamicillin and colistin entrapment efficiency were determined. antibiofilm activity of sultamicillin-loaded niosomes, colistin-loaded niosomes, and sultamicillin-colistin-loaded niosomes was determined using crystal violet method . The MIC of niosomes was determined using the agar diffusion method.

**Results :** The round-shaped sultamicillin-colistin-loaded niosomes were 230 nm and had -25mV zeta potential. The percentage of sultamicillin and colistin encapsulation in the niosomes was 91% and 94%,respectively. Release of the sultamicillin and colistin from niosomes occurred over a longer period of time than the non-niosome form. The sultamicillin-colistin containing niosomes removed 1, 3, and 5 day old biofilms at the concentration of 0.00625 µg ml-1, 0.03125 µg ml-1, and 0.0625 µg ml-1, respectively. The MIC of colistin loaded niosomes and sultamicillin-colistin loaded niosomes were 0.5 mg ml-1 , and 0.25 mg ml-1,respectively.however,sultamicillin-loaded niosomes didn’t show antibacterial activity.

**Conclusion :** Niosome nanoparticles containing sultamicillin-colistin could be considered as a promising candidate for the treatment of biofilm-mediated infections of A.baumannii.

**Keywords :** Acinetobacter baumannii- biofilm – noisome nanoparticles

# O36-38: Prevalence of Human Papillomavirus(HPV), Cytomegalovirus(CMV), Epstein-Barrvirus(EBV) and Herpes Simplexvirus(HSV) in human bladder cancer biopsy samples in comparison with the control groups in East Azerbaijan province

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**Background and Aim :** Bladder cancer is one of the most common cancers of the epithelial cells and the second most common cancer of the urogenital tract. The incidence of bladder cancer is higher in men than women. Viral infections are one of the most effective factors in causing cancer. Therefore, the aim of this study was to investigate the prevalence of oncogenic viruses in biopsy samples of patients with bladder cancer in comparison with the control groups in East Azerbaijan province.

**Methods :** 120 biopsy samples including 80 samples obtained from patients with bladder cancer and 40 control samples were collected from hospitals of East Azerbaijan province and after deparaffinized, DNA was extracted and using specific primers by PCR method, the frequency of oncogenic viruses was determined.

**Results :** Out of 80 cancer samples, 28 (35%) samples from patients with bladder cancer were infected with HPV virus, 17 (21.25%) samples were infected with CMV virus and 11 (13.75%) samples were infected with EBV virus. In the control group, 3 samples were infected with HPV, but no positive samples of CMV and EBV were observed in the control group. Two cancer samples were infected with all three HPV, CMV and EBV viruses simultaneously. HSV was not observed in any of the samples. No significant relationship was observed between age group, cancer and oncogenic viruses.

**Conclusion :** Considering the significant presence of oncogenic viruses in bladder cancer compared to the control group, it seems that there is a significant relationship between bladder cancer and viral infection.

**Keywords :** Bladder cancer, Human papilloma virus, Cytomegalovirus, Epstein-Barr virus, Herpes simplex virus, PCR

# O37-42: Molecular detection of Coxiella burnetii in horse blood sera in West Azarbaijan, Iran

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**Background and Aim :** Coxiella burnetii is a zoonotic bacterium that has been reported in humans and a broad range of animal species, including wild and domestic mammals and arthropods such as ticks. However, the involvement of horses in Q fever epidemiology remains unclear. The objective of our work was to investigate the presence of C. burnetii DNA by nested PCR method in the horse blood sera in the West-Azarbaijan province.

**Methods :** DNA Extraction Kit (Bioneer, South Korea) was followed to extract total DNA from 1 milliliter of horse blood serum. In this study, we used 2 sets of genomic primers targeting IS1111 genes, The primers and thermal cycling condition for both trans and nested PCR were previously described by Parisi et al. The PCR products were electrophoresed on a 2% agarose gel containing safe stain and then visualized using gel documentation system. Also, the information regarding the age, sex, and breed of the animals was recorded. The obtained data were statistically analyzed by the Chi-square test using SPSS software Ver. 23 (SPSS Inc., Chicago, IL). The P value< 0.05 was considered significant.

**Results :** Of the 320 horse serum samples tested for Nested-PCR, (8.12%) serum samples were positive for C. burnetii bacterium which (42.3%) serum samples belong to stallion, and also (57.69%) serum samples were Mares specimens. In this study, there was no significant difference between the study areas, sex, and breed associated with seroprevalence to C. burnetii, however, Horses older than 3 years had a significantly higher seroprevalence to C. burnetii.

**Conclusion :** We demonstrated that Nested PCR assay is a valuable technique for surveillance of C. burnetii in serum samples, emphasizing the emerging aspect of Q fever in the equine population as a reservoir of the disease.

**Keywords :** Horse blood sera, Q fever, Coxiella burnetii, west-Azarbaijan

# O38-97: Electrochemical immunosensor for determination of Staphylococcus aureus bacteria by IgY immobilized on glass carbon electrode with electrodeposited

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**Background and Aim :** S. aureus is known to be an important infectious agent worldwide. One of the most important virulence factors of S. aureus is 42 kDa protein that is called surface immunoglobulins (Ig)-binding protein A (SpA). This protein binds to the Fc region of IgG antibodies and prevents disrupting the bacteria via opsonization and phagocytosis. This study aims at developing a new electrochemical immunosensor for the measurement of S. aureus based on chicken anti-protein A IgY as a dedicated receptor.

**Methods :** The chicken IgY was obtained by injecting the purified recombinant protein A into hen and, then, IgY was extracted and purified from yolk eggs. In order to construction of the immunosensor for ultrasensitive detection of S. aureus, the electrodeposited AuNPs modified GCE was used to immobilization of the IgY, as recognition element. The performance of the proposed immunosensor and its application for analysis of S. aureus was carried out by the use of CV and EIS techniques with [Fe(CN)6]4−/3− as the redox probe. In order to characterize AuNPs' modified electrode, the scanning electron microscopy (SEM) was applied. In addition, the application of the immunosensor was evaluated by detecting S. aureus in milk and human blood serum as real samples.

**Results :** The Proposed immunosensor displayed a wide linear dynamic range from 10 to 107 CFU mL−1 with a detection limit of 3.3 CFU mL−1 with RSD 3.0% and was capable of accurately detecting and determining the S. aureus in milk and human blood serum as a complex matrix sample with satisfactory recovery rate of ~97-103%. In addition, the immunosensor displays high selectivity over other bacteria as high sensitivity and acceptable stability were achieved by this immunosensor.

**Conclusion :** Presumably, our study can be regarded as the first one to report hen IgY in order to detect S. aureus based on the electrochemical method and the suggested methodology can be potentially used to construct other effective and sensitive nanotools and easily miniaturized

to develop other electrochemical biosensor-based assays in order to facilitate clinical diagnosis and environmental applications.

**Keywords :** Staphylococcus aureus; Immunosensor; Anti-protein A antibody; Gold nanoparticles

# O39-120: Green synthesis and characterization of alfalfa (Medicago sativa) leaves extract capped silver nanoparticles (MSL@AgNPs): Antibacterial, antifungal, antioxidant, catalytic, and cytotoxic activities

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**Background and Aim :** Nowadays, nanoparticles are used effectively for targeted drug delivery, diagnosis, treatment of various diseases including heart disease, wound healing and antimicrobial compounds. The aim of this study was to obtain a suitable method for the green synthesis of silver nanoparticles using alfalfa extract and to investigate its antibacterial, antifungal, anticancer, antioxidant and catalytic properties of it.

**Methods :** Using a nontoxic, low-cost and rapid approach in presence of alfalfa (Medicago sativa) leaves extract, green silver nanoparticles were synthesized as MSL@AgNPs and characterized in terms crystalline, morphology and structural with XRD, EDS, FESEM, TEM, FT-IR, DLS and UV-Vis techniques. Antimicrobial activities of AgNPs was assessed using MIC, MBC and MFC on standard strains of Escherichia coli, Klebsiella pneumoniae, Staphylococcus aureus, Staphylococcus epidermidis, Enterococcus faecalis and Candida albicans. The antioxidant activity was calculated by scavenging free radicals of DPPH. The cytotoxic effects were assessed on human fibroblasts using MTT staining method. To assess the catalytic feature, photocatalytic activity for the degradation of the methylene blue (MB) and methyl orange (MO) was applied.

**Results :** FESEM, TEM and XRD analysis results revealed that the product was homogeneous, uniformly, spherical-like morphology regular and small size with face-centered cubic structure. MSL@AgNPs showed strong antimicrobial effects against the tested microorganisms. The antioxidant results revealed that with increasing the concentration of nanoparticles, the percentage of DPPH inhibition increases (25% to 78%). Treatment of human fibroblasts with different concentrations of the nanoparticles for 24 hours showed that the cytotoxicity of synthesized silver nanoparticles was dose-dependent and at concentrations of 50 and 100 ?g/ml showed the most cytotoxic effects and the amount of inhibitory concentration (IC50) showed

18.22 ?g/ml. Furthermore, the biosynthesized AgNPs exhibited a highly significant photocatalytic activity for the degradation of MB and MO.

**Conclusion :** For the first time, we synthesized silver nanoparticles in presence of alfalfa leaves extract with strong antimicrobial, anticancer, antioxidant and catalytic features applicable in medicine and pharmacological industry.

**Keywords :** Silver nanoparticles, Antibacterial, Antifungal, cytotoxic, antioxidant, Medicago sativa

# O40-197: Physico-mechanical properties, antimicrobial activities, and anti-biofilm potencies of the orthodontic adhesive containing graphene oxide nanoparticles against Streptococcus mutans

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**Background and Aim :** In fixed orthodontics, the formation of white spot lesions, enamel demineralization, and tooth decay around appliances are common complications, which mars the outcome. The aims of this study were the determination shear bond strength (SBS) and adhesive remnant index (ARI) of orthodontic adhesive doped with N-GO, as well as the assessment of antimicrobial activities of the modified orthodontic adhesive against Streptococcus mutans.

**Methods :** N-GO was characterized by Scanning electron microscope (SEM), Fourier transformation infrared (FT-IR), X-ray diffraction (XRD), and Zeta potential. The SBS and ARI of modified orthodontics adhesive containing different concentrations of N-GO (0, 1, 2, 5, and 10 wt%) were then measured. The influences of adding N-GO on antimicrobial properties of orthodontic adhesive were determined against S. mutans by disc agar diffusion (DAD) testing and biofilm formation inhibition assay.

**Results :** The SEM, FTIR, XRD, and Zeta potential analysis indicated the successful synthesis of N-GO. Orthodontics adhesive doped with 5 wt% N-GO showed the highest concentration of N-GO and SBS value (21.71 ± 7.45 MPa, $P < 0.05$) simultaneously with no significant differences in adhesive remnant index compared with the control group. SBS in the 1, 2, and 5% N-GO were significantly higher than that in 10% N-GO (P=0.025, P=0.036, P=0.041, respectively). The disinfection ability of the modified orthodontic adhesive doped with N-GO against S. mutans in the DAD and biofilm formation inhibition assays were positively associated with increase in N-GO concentrations ($P < 0.05$). However, the 5 and 10 wt% N-GO showed a statistically significant decrease in the CFU/mL of the test microorganisms in biofilm structures ($P < 0.05$).

**Conclusion :** It could be concluded that 5 wt% N-GO can consider as an orthodontic adhesive additive to reduce the microbial count and biofilm with no adverse effect on SBS and ARI.

**Keywords :** Nano-Graphene Oxide, Orthodontict adhesive, cariogenic bacteria

# O41-116: Facile green synthesis and characterization of Pistacia khinjuk leaves extract capped silver nanoparticles (PKL@AgNPs): Antibacterial, antifungal, anti-cancer, antioxidant and catalytic activities

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**Background and Aim :** In recent years, green nanoparticles have found many applications especially as alternative antimicrobial approaches due to their unique physicochemical, biological, mechanical, optical, electrical and thermal properties characterized by their small size and high surface-to-volume ratio. This study aimed to synthesis a green capped silver nanoparticle using Pistacia khinjuk leaves and evaluate its antimicrobial, antioxidant, anticancer and catalytic activities.

**Methods :** In this study for the first time, biogenic silver nanoparticles were synthesized using nontoxic, low-cost and rapid approach in presence of Pistacia khinjuk leaves extract (P. khinjuk) as PKL@AgNPs. The biosynthesized AgNPs were characterized in terms crystalline, morphology and structural with XRD, EDS, FESEM, TEM, FT-IR, DLS and UV-Vis techniques. Antibacterial and antifungal activities of biosynthesized AgNPs were investigated using MIC, MBC and MFC. The antioxidant activity of PKL@AgNPs was calculated by scavenging free radicals of DPPH (1,1-diphenyl-2-picrylhydrazyl hydrate). Anticancer activity was evaluated on k562 as a human leukemia cancer cell line by MTT assay. To assess its catalytic feature, photocatalytic activity for the degradation of the methylene blue (MB) and methyl orange (MO) as hazardous contaminants was applied.

**Results :** FESEM, TEM and XRD analysis results revealed that the product was homogeneous, uniformly, spherical-like morphology regular and small size (about 35-45 nm) with face-centered cubic structure. PKL@AgNPs showed strong antibacterial and antifungal activities against Escherichia coli, Klebsiella pneumonia, Staphylococcus aureus, Streptococcus mutans, Streptococcus mitis, Enterocuccus faecalis, and Candida albicans. The antioxidant results revealed that with increasing the concentration of nanoparticles, the percentage of DPPH inhibition increases (3.8% to 69.9%). The PKL@AgNPs also revealed significant anticancer

activity on k562 (IC50 = 2.69 µg/ml). Furthermore, the biosynthesized AgNPs exhibited a high photocatalytic activity for the degradation of MB and MO.

**Conclusion :** PKL@AgNPs as a novel facile green synthesized nanoparticle by Pistacia khinjuk leaves has highly significant antimicrobial, anti-cancer, anti-oxidant and catalytic activity which can be in medicine and biotechnology industry.

**Keywords :** Silver nanoparticles, Antibacterial, Antifungal, Anticancer, Pistacia khinjuk

# O42-225: Production of Bovicin HC5 in two strains of E. coli, Rosetta gami and Rosetta plysS

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**Background and Aim :** Introduction: Bacteriocins are antimicrobial peptides that are produced by ribosomes in bacteria and some archaea. Evidence suggests that these peptides could be used to treat cancer disease. Bovicin HC5 is a bacteriocin produced by Streptococcus bovis HC5 and was used in the treatment of liver cancer. Objective: The expression of recombinant bovicin HC5 was performed for the first time in two bacterial strains of E. coli, Rosetta gami, and Rosetta plysS.

**Methods :** The cDNA of Bovicin HC5 was cloned in the pET21a vector. For protein expression, IPTG with 0.5 and 1 mM concentrations was used. Also, cultivation temperature of 35 °C and post-induction times of 2, 4, and 8 hours were selected for incubation. For protein expression analysis, the dot blot method was used and then the data were quantified by ImageJ software.

**Results :** : The highest expression level, 20.49%, in the Rosetta gami strain was achieved at 0.5 mM IPTG and a post-induction time of 4 hours. Also, the maximum expression rate, 21.50%, was observed in Rosetta plysS at 0.5 mM IPTG and a post-induction time of 8 hours.

**Conclusion :** According to the results, both strains had appropriate protein expression levels.

**Keywords :** bovicin HC5, E. coli, protein expression

# O43-303: Prediction of potential drug targets and vaccine candidates against antibiotic-resistant Pseudomonas aeruginosa

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**Background and Aim :** Pseudomonas aeruginosa is one of the leading causes of nosocomial infections, characterized with increasing antibiotic resistance, severity and mortality. Therefore, numerous efforts have been made nowadays to identify new therapeutic targets. The aim of this study was to find novel and common bacterial targets in drug resistant strains of Pseudomonas aeruginosa.

**Methods :** Extensive antibiotic resistant and carbapenem-resistant strains of Pseudomonas aeruginosa with complete genome were selected and ten common hypothetical proteins (HPs) containing more than 200 amino acids were obtained. The structural, functional and immunological predictions of these HPs were performed with the utility of bioinformatics approaches.

**Results :** Two common HPs (Gene ID: 2877781645 and 2877781936) among other investigated proteins were revealed as potential candidates for pharmaceutical and vaccine purposes based on structural and physicochemical properties, functional domains, subcellular localizations, peptide signals, toxicity, virulence factor, antigenicity, allergenicity and immunoinformatic predictions.

**Conclusion :** The consequent of this predictive study will assist in novel drug and vaccine design through experimental investigations.

**Keywords :** Pseudomonas aeruginosa, hypothetical proteins, drug resistance

# O44-137: Liver transplantation from deceased donors with Coronavirus-disease 2019

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**Background and Aim :** The transplant patients should be considered a main high-risk population during the COVID-19 outbreak . However, the rejection of all (SARS-CoV-2) positive donors leads to the loss of remarkable numbers of transplantable organs, which can save the lives of many patients. Since there is no enough evidence on COVID-19 transmission through organ transplantation, this study aimed to evaluate the possibility of COVID-19 transmission by liver transplantation from a donor with a late complication of COVID-19 to the recipients.

**Methods :** This descriptive study was conducted on all the recipients of liver transplantation who had an acute liver failure or were the models for the End-Stage Liver Disease (MELD) higher than 20. From March 2020 to March 2021.

**Results :** 153 brain deaths were reported in our center due to trauma (n=43), anoxia (n=41), and brain tumor (n=8); however, 14 candidates were excluded due to respiratory failure. Furthermore, hemorrhagic strokes were diagnosed in 61 cases. It is worth mentioning that lung involvement compatible with the late phase of COVID-19 was observed in all of these cases. In general, 36 liver transplantation was performed during the study period. Out of these patients, only 14 cases (deceased donors) had hemorrhagic cerebrovascular accidents, and other donors died of trauma (n=7) and anoxia (n=15). All patients showed negative results for polymerase chain reaction (PCR) (two negative 24 h PCR), whereas their high-resolution computed tomography (HRCT) test revealed that they had previously lung involvement with COVID-19 as the late complication of the disease. All recipients (n=14) had normal chest CT scans and negative COVID-19 PCR 48 h before transplantation, while after transplantation,

three patients (21.4%) showed positive PCR in the early phase (one week after transplantation) and had lung involvement.

**Conclusion :** This study supports the safety of continuing donation and transplant process during the outbreak even the transplant donor be infected previously with the COVID-19, which is reinforced by other similar pieces of evidence

**Keywords :** Brain death, COVID-19, Donors, Liver transplantation

# O45-196: Nano antimicrobial photodynamic therapy: An in vitro therapeutic application in plasma containing SARS-CoV-2

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**Background and Aim :** The ability of antimicrobial photodynamic therapy (aPDT) as a treatment approach and adjuvant therapy using Curcumin-Poly (Lactic-co-Glycolic Acid) nanoparticles (Cur@PLGA-NPs) was investigated to inactivate Coronavirus disease 2019 (COVID-19) in plasma.

**Methods :** Following synthesis and characterization of Cur@PLGA-NPs, the treated plasma samples with Cur@PLGA-NPs plus blue laser were exposed to Vero cells. Eventually, cell cytotoxicity and apoptotic effects of treated Vero cells were evaluated.

**Results :** Different concentrations of Cur@PLGA-NPs (3, 5, 7, and 10% wt.), the irradiation times of blue laser (1, 3, and 5 min), and aPDT with the maximum dosed of blue laser light (522.8 J/cm2) plus 10% wt. Cur@PLGA-NPs had no cytotoxicity. Although there were significant cell degradation and apoptotic effects in treated Vero cells with treated plasma using 10% wt. Cur@PLGA-NPs, and a blue laser at an energy density of 522.8 J/cm2, no visible changes in cells and apoptosis were observed following aPDT.

**Conclusion :** aPDT exhibited in vitro anti-COVID-19 activities in the treated plasma containing SARS-CoV-2 without Vero cell apoptosis and any adverse effects on plasma quality in aPDT-exposed plasma.

**Keywords :** Antimicrobial photodynamic therapy, Coronavirus, COVID-19, Curcumin, PLGA, SARS-CoV-2

# O46-235: Review of the Diagnostic techniques for COVID-19

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**Background and Aim :** Coronaviruses are important viral pathogens that most commonly cause respiratory and gastrointestinal complications in humans and animals. Due to the high-speed spreading of COVID-19, the diagnostic methods are very important for screening and controlling the virus and managing patients. Different methods around the world are used for identification and confirmation of infected patients with COVID-19. This article reviews the different methods used for the diagnosis of this virus since the beginning of the outbreak.

**Methods :** A comprehensive search was conducted using the electronic databases of PubMed, Scopus, and Google Scholar. The keywords coronavirus, COVID-19, SARS-CoV-2, RT-PCR, CT scan, molecular tests and serology tests were used to identify diagnostic methods articles of COVID-19.

**Results :** Since the beginning of the pandemic, various methods have been used with different efficiencies for screening and final identification of cases. But given that most of these methods have advantages and disadvantages, using just one method doesn't seem reasonable for this aim. The diagnostic protocols vary according to economic conditions and the severity of epidemics in different countries. Currently, methods such as CT scans for screening and RT-PCR for final confirmation of infected cases have been approved. However, because these methods are not widely available everywhere, the performing of simpler methods with reliable efficiency can be used in countries with more limited facilities.

**Conclusion :** Molecular and serological diagnostic techniques plays a critical role in identifying and isolating patients. Recently, with the pandemics of the COVID-19, the design and application of methods with high efficiency and cost-effectiveness should have priority for healthcare providers worldwide for rapid detection, preventing the spread of the pandemic disease, and acceleration of treatment.

**Keywords :** COVID-19, SARS-CoV-2, Molecular test, serological test, laboratory

# O47-27: Transcriptional alteration of genes linked to gastritis concerning Helicobacter pylori infection status and its virulence factors

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**Background and Aim :** Helicobacter pylori infection and heterogeneity in its pathogenesis could describe diversity in the expression of inflammatory genes in the gastric tissue. We aimed to investigate the transcriptional alteration of genes linked to gastritis concerning the H. pylori infection status and its virulence factors.

**Methods :** Biopsy samples of 12 infected and 12 non-infected patients with H. pylori that showed moderate chronic gastritis were selected for transcriptional analysis. Genotyping of H. pylori strains was done using PCR and relative expression of inflammatory genes was compared between the infected and non-infected patients using relative quantitative real-time PCR.

**Results :** Positive correlations between transcriptional changes of IL8 with TNF-α and Noxo1 in the infected and TNF-α with Noxo1, MMP7, and Atp4A in the non-infected patients were detected. Six distinct genotypes of H. pylori were detected that showed no correlation with gender, ethnicity, age, endoscopic findings, and transcriptional levels of host genes. Irrespective of the characterized genotypes, our results showed overexpression of TNF-α, MMP7, Noxo1, and ATP4A in the infected and IL-8, Noxo1, and ATP4A in the non-infected patients.

**Conclusion :** Complexity in the transcription of genes respective to the characterized H. pylori genotypes in the infected patients was detected in our study. The observed difference in co-regulation of genes linked to gastritis in the infected and non-infected patients proposed the involvement of different regulatory pathways in the inflammation of the gastric tissue in the studied groups.

**Keywords :** Helicobacter pylori. Gastritis. Inflammation. virulence genotype. NF-κB pathway

# O48-223: Effect of fungal endophytes isolated from Nepeta crispa on human pathogenic fungi in vitro conditions

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**Background and Aim :** Nepeta crispa (Lamiaceae) is one of the endemic plants of Hamedan. This plant grows wild and parts of the heights of Hamadan province. Therapeutically, it has anti-flatulence, anti-inflammatory, analgesic and antibacterial properties. Endophytic fungi are often referred to asymptomatic fungi that can be present in all plants. They live in the intracellular space of plant stems, roots and leaves without any obvious negative effects. Some endophytes may improve host growth, nutrient uptake, and improve plant ability to tolerate abiotic stresses such as drought and salinity and reduce biological stress by increasing plant resistance to insects, pathogens and pests.

**Methods :** In this study, endophytic fungi isolated from N. crispa were used and the their biocontrol and antagonistic ability was evaluated by cross-culture on PDA against human pathogenic fungi such as Candida glabrata, Aspergillus niger and Pseudallescheria boydii. Test was performed Based on a randomized complete block design with 5 treatments and three replications. Statistical test was performed by SPSS 20.0 software.

**Results :** The results were evaluated seven days after test. The results showed that the effect of endophytic fungi on pathogenic fungi was significant ($p<0.01$) and Penicillium paneum FB11 and Curvularia inaequalis FB7 showed similar effects on A. niger (NS) and Fusarium oxysporum FB10 and P. paneum FB11 showed similar effects on C. glabrata (NS). Also P. paneum FB11 and Ceratobasidium sp. FB13 showed similar effects on C. glabrata (NS). Examination of the percentage of inhibition showed that Paecilomyces maximus FB8 had the highest percentage of inhibition on C. glabrata, A. niger and P. boydii (63.33%, 52.50% and 77.42%, respectively) in compared to other endophytes.

**Conclusion :** P. maximus FB8 (an endophytic fungi) could be a promising for future as a biocontrol and antagonist on studied human pathogenic fungi.

**Keywords :** Nepeta crispa, Endophyte, Pathogen, Biocontrol, Antagonist

# O49-272: Enhanced Macrophage Activity against Methicillin-Resistant Staphylococcus aureus on Exposure to Glucomannan: An in-vitro study

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**Background and Aim :** Methicillin-resistant Staphylococcus aureus (MRSA) causes a wide range of diseases and is one of the main causes of nosocomial infections. Carbohydrate glucomannan has adjuvant and immune regulating properties, which is an ideal candidate for immunological development. The aim of this study was to evaluate the level of macrophage gene expression and phagocytic activity against Methicillin-Resistant S. aureus in the presence of glucomannan.

**Methods :** The effect of different concentrations of glucomannan were assessed on the phagocytic activity of macrophage cells by colony count method. The expression of tumor necrosis factor-alpha (TNF-α) and Inducible nitric oxide synthase (iNOS) genes were evaluated by Real-Time PCR.

**Results :** The concentration of glucomannan significantly reduced the colony-forming units (CFUs) of MRSA and increased the phagocytosis of macrophages. The high level of iNOS and TNF gene expression was observed at 100 g/mL concentration of glucomannan.

**Conclusion :** The glucomannan may introduce as a stimulant of the immune system. It increases the expression of TNF-α and iNOS genes which are involved in the phagocytosis pathway of macrophages against MRSA.

**Keywords :** Glucomannan, Macrophage Activity, Methicillin-Resistant Staphylococcus aureus, In-Vitro Study, iNOS, TNF-alpha

# O50-295: Antagonistic ability of endophytic fungi isolated from Saffron (Crocus sativus) against human pathogenic fungi

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**Background and Aim :** Saffron (Crocus sativus) is a perennial plant that belongs to Liliaceae family. Since saffron has been used in traditional medicine in the treatment of various infectious diseases, the antimicrobial and antifungal effects of saffron has also been investigated in new studies. Endophytic fungi are ubiquitous and are found in almost all plant genera even plant-like protists. Two ecological groups of endophytic fungi have been identified including: narrow-leaf endophytes and woody plant endophytes. Endophytes represent a chain of variable relationships including collaboration, coexistence, and latent pathogenicity. It is believed that the environment plays an important role in the biodiversity of endophytes and the diversity of their species that endophytic fungi of woody plants are very abundant and diverse, especially in the tropics. Therefore, the antagonistic effect of saffron endophytic fungi with human pathogenic fungi was considered.

**Methods :** In this study, endophytic fungi isolated from saffron were used and the antagonistic ability of them was evaluated by cross-culture method against human pathogenic fungi such as Candida glabrata, Aspergillus niger and Pseudallescheria boydi on PDA medium. This test was performed as randomized complete block design with 6 treatments (5 endophytic fungi +Control) and three replications.

**Results :** The results were evaluated seven days after culture and inhibitory percentage showed that A. niger FT14 (endophytic fungus) had effect on C. glabrata, A. niger and P. boydii with inhibitory percentage of 38.89%, 86.25%, 84.81%, respectively. The analysis of variance showed that the effect of endophytic fungi on these human pathogens was significant ($p<0.01$). Means Comparing based on Duncan test showed Penicillium canescens FT17 had highest effect (55.56%) on C. glabrata. Also, Aspergillus europaeus FT11, Penicillium canescens FT17 and Cadophora malorum FT19 showed similar effect on P. boydii (NS).

**Conclusion :** A. niger FT16 and P. canescens FT17 (endophytic fungi) could be promising microorganisms for future as a biocontrol and antagonist on studied human pathogenic fungi.

**Keywords :** Saffron, Fungal endophyte, Human pathogenic fungus, Antagonist

# O51-340: MADS-box transcription factor Mcm1 is involved in the virulence of the fungal wheat pathogen Zymoseptoria tritici

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**Background and Aim :** Zymoseptoria tritici is an economically important fungal pathogen responsible for Septoria tritici blotch (STB), the most destructive disease of wheat worldwide, threatening global food security. Due to the pivotal importance of STB, it is necessary to design new and environmentally safe measures to manage STB effectively. Gaining new insight into the biology of this damaging fungal pathogen plays a pivotal role in developing novel management measures.

**Methods :** In this study, we investigated the instrumental function of the ZtMcm1 encoding a MADS-box transcription factor in the infection process of the Z. tritici. To aim this, we deleted this gene from the genome of Z. tritici IPO323 (reference isolate) through the Agrobacterium tumefaciens–mediated transformation (ATMT) technique. The User-friendly cloning technique was employed to generate the ZtMcm1 deletion construct in such a way about 2,000 bp upstream and downstream of ZtMcm1 was amplified through PfuTurbo® DNA polymerase. Subsequently, the resulting PCR amplicons and the digested vector were mixed and treated with the USER enzyme mix and incubated at 37 °C for 30 min followed by 25 °C for 30 min.

**Results :** The developed deletion construct was applied in the ATMT procedure to eliminate the ZtMcm1 from the IPO323 genome through the homologous recombination event. The obtained mutant lacking ZtMcm1, ectopic strain, and wild type (WT) strain were used in the infection assay. Our results demonstrated that mutant strains failed to infect the susceptible wheat cultivar Taichung 29, whereases the WT and ectopic strains caused STB on the same cultivar.

**Conclusion :** This study adds to a better understanding of Z. tritici biology and may be applied to develop novel strategies to effectively manage this damaging fungal pathogen.

**Keywords :** STB, Wheat, Transcription factor, virulence

# O52-393: The Link Between Specific Haplotype of Tumor Necrosis Factor Alpha and Interleukin-1β Polymorphisms in Promoter Region with Helicobacter Pylori Infection and Gastric Carcinogenesis

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**Background and Aim :** The infection with Helicobacter pylori (H. pylori) and cytokine-mediated inflammatory responses plays significant roles in the pathogenesis of gastric cancer (GC). To determine a link between the risks of GC and genetic polymorphisms in tumor necrosis factor-alpha (TNF-α), and interleukin (IL)-1β, this study was performed.

**Methods :** The polymorphisms of IL1B and TNFA genes were analyzed by PCR-RFLP in 290 patients who underwent endoscopy. H. pylori infection was affirmed by rapid urease test, histological analysis, and gastric biopsy PCR. The quantitative real-time PCR was performed to determine the relative mRNA expression levels.

**Results :** There were no significant differences in allele frequencies and genotype for all explored polymorphisms between chronic gastritis, GC and healthy individuals. Interleukin 1β mRNA was down-regulated in both the gastritis group (Relative Quantification (RQ)=0.447) and the GC group (RQ=0.151). In contrast, the expression of TNF-α were increased in the GC group (RQ=2.817) in relation to the gastritis group, which was down-regulated (RQ=0.861).

**Conclusion :** The studied single-nucleotide polymorphisms are not risk factors for development of chronic gastritis and GC. However, the H. pylori infection causes a huge increase in the expression of TNF-α in GC patients.

**Keywords :** gastric cancer; cytokines; chronic gastritis; gene polymorphisms; Helicobacter pylori

# O53-417: Detection of human papillomavirus (HPV) infections in Iranian women with and without abnormal cervical cytology by dot blot hybridization

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**Background and Aim :** Infection with certain human papillomaviruses (HPV) is strongly associated with the development of dysplasia and cancer of the cervix uteri. The average global prevalence of HPV infection has been reported to be almost 1.4–25.6% in different geographical regains. To date, more than 200 HPV genotypes have been identified, and more than forty of these have been shown to cause anogenital infections in humans. The aim of this study was to estimate the prevalence of HPV in 540 cervical samples from patients who underwent annual routine gynecological exams by dot blot hybridization from different geographical regions in Iran.

**Methods :** Cervical cells were collected from 14 different city and were stored at 4°C until DNA extraction. The extraction of total DNA was performed according to the manufacturer's instruction (Add bio, Korea) 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 :** Five hundred and forty women between 18 and 77 years (mean age: 34 years) and 217 (40.18 %) were HPV-DNA positive. A total of 143 low-risk and 143 high-risk HPV isolates were identified. HPV high-risk type 31 showed the highest prevalence (16.58%), while in low risk samples, HPV type 6 showed the highest prevalence 30.41%. Demographic data of positive HPV patients showed that 3.22%, 4.14%, 4.60%,1.38%, 4.60% and 2.30% with

presence of raised lesions/discharge, abnormal bleeding, history use oral contraceptives pills, abnormal pap smear, menstrual irregularities and abortion, respectively.

**Conclusion :** Due to the high prevalence of HPV is important for the selection of prevention strategies and improving approaches to combating cervical cancer. Our dot blot hybridization assay will be useful to address questions related to viral persistence at the genotype level, the kinetics of viral load and disease recurrence.Evidence is accumulating that HPV genotyping may be useful for patient management in the future.

**Keywords :** Hybridization, Human papillomavirus, cervical cancer

# خلاصه مقالات پوستر

## P1-53: Evaluation of Candidemia in Mashhad, Iran

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**Background and Aim :** Candida species are the most prevalent cause of invasive fungal infections such as candidemia. There are at least 15 distinct Candida species that cause human disease, but mostly invasive disease is caused by C. albicans, C. glabrata, C. tropicalis, C. parapsilosis, and C. krusei. Each of these organisms has unique virulence potential, antifungal susceptibility, and epidemiology, but taken as a whole, significant infections due to these organisms are generally referred to as invasive candidiasis. Candidemia is a significant public health problem among patients with certain condition, such as mucosal membrane disruption, immunodeficiency, malignancies, renal failure, uncontrolled diabetes, post-surgical procedures, low birth weight or prematurity, and long-term antibiotic use. In this study, we identify Candida spp. obtained from candidemia by Multiplex PCR methods to assessed species distribution and clinical features of patients with candidemia, to understanding the epidemiology of this infection in Mashhad, Iran.

**Methods :** From 2016 to 2018, 175 Candida isolates from blood cultures were collected from patients in Emam Reza, Ghaem and Doctor Shikh hospitals in Mashhad, Iran. All yeast isolates were identified using a Multi-plex PCR & sequencing.

**Results :** One hundred and seventy-five episodes of yeast were diagnosed in patients with ages ranging from 5 days to 89 years old, with 59.5% of the patients (n=104) being ≥16 years of age. Candida parapsilosis (n = 64; 36.5%) was the most prevalent yeast species identified, followed by C. albicans (n = 50; 28.5%), C. glabrata (n = 34; 19.5%), C. tropicalis (n = 20; 11.5%) and C. krusei (n = 7; 4%).

**Conclusion :** C. parapsilosis was the main cause of yeast-derived fungemia in north-West of Iran and mortality rate was 42.8%. Because of the affordability of PCR devices, the YEAST PANEL multiplex PCR assay has the potential to be integrated in large-scale epidemiological studies. On the other hand, routine laboratories in developing countries can take the advantage of supplementation of biochemical assays with YEAST PANEL multiplex PCR assay.

**Keywords :** Candidemia, Candida, Mashhad, Iran

# P2-69: Application of artificial intelligence based algorithms in microbiology: challenges and benefits

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**Background and Aim :** Artificial intelligence (AI) as a proven technique has the potential to make us more accurate, more efficient, and even could help us draw new conclusions from data generated in microbiology area. AI algorithms has been applied to every microbiology domain including virology, bacteriology, mycology and parasitology. Therefore, it is important to study the challenges and benefits of these intelligence and expert systems.

**Methods :** This review article aims to discuss the opportunities and challenges associated with application of AI algorithms in Microbiology. PubMed, Ovid Medline, and Embase were the sources of research in this article.

**Results :** Using treatment or diagnostic datasets in microbiology, the machine learning algorithms recognize patterns and underlying data structure for prediction or classification in disease outbreaks, diagnosing microorganisms causing infectious diseases, and antimicrobial drug resistance. The use of intelligence algorithms (such as artificial neural networks) has been rapidly advancing in the automated blood culture instruments, colony morphology recognizing, colony counting and genome sequencing. The current development efforts are focused on automating the interpretation of primary cultures. The cost, technology limitations, modeling of medical knowledge, clinical data entry, accuracy of the systems and the methods to validate the systems are some challenges in this field.

**Conclusion :** Artificial intelligence as a golden opportunity is beginning to be used in microbiology and is already assisting laboratory staff and researcher with certain aspects of diagnostic, prediction and classification of disease. However, increased research efforts need to be made to solve the limitations of this fields.

**Keywords :** Artificial Intelligence, Algorithm, Microbiology

# P3-79: Evaluation of loop mediated isothermal amplification method (LAMP) for detection of Mycoplasma hominis in vaginal swab samples in comparison whit Real time PCR

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**Background and Aim :** : Mycoplasma hominis as one of the etiologic agent of non-gonococcal urethritis in women, should be identified in order to early treatment that led to the patient does not suffer from serious complications such as pelvic inflammatory disease and infertility. With regard to the importance of M. hominis in genitourinary diseases, there's need for development of reliable, simple and repeatable laboratory method in diagnosis. The aim of study was to establish a 16srRNA-based LAMP method for identification of M. hominis from vaginal samples in comparison with Real Time PCR.

**Methods :** The eighty vaginal samples were taken from patients and were evaluated by culture, Real-time PCR and LAMP diagnostic assays.

**Results :** Totally, 13 (16.3%), 14 (17.5%) and 25 (31.3%) samples were positive for M. hominis by culture, Real-time PCR and LAMP methods, respectively. The one of negative culture results diagnosed by real-time PCR, while the LAMP assay detected twelve positive among negative cultures. Also, the sensitivity, specificity, positive and negative predictive value for LAMP were calculated as 100%, 83.3%, 56% and 100%,respectively.

**Conclusion :** Based on our results, LAMP technique was more specific and sensitive than both Real time PCR and culture methods for diagnosis of M. hominis.

**Keywords :** Mycoplasma hominis; LAMP; 16srRNA, vaginal samples, Real-Time PCR.

# P4-83: Identification of common bacteria in oropharyngeal samples from cystic fibrosis patients using multiplex PCR

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**Background and Aim :** Cystic fibrosis (CF), is the most common fatal multisystem genetic disease in Caucasian populations, results from mutations in the CF transmembrane conductance regulator (CFTR) gene and affects almost all of the body's function exocrine glands. This causes the secretion of thick and sticky mucus in the lungs, which leads to narrowing of the airways and, as a result, traps of viruses, bacteria, and fungal spores in the air in this mucus, leading to various infections. CF Patients have chronic and recurrent lung infections, which is why lung problems are often the leading cause of death in those with the disease. In this study, a multiplex PCR method was developed to identify Haemophilus influenzae non-typeable, Burkholderia cepacia complex, and Pseudomonas aeruginosa, in oropharyngeal samples from CF patients.

**Methods :** Forty-four oropharyngeal samples were collected from CF patients (25 male, and 19 female) in Children's Medical Center Hospital. Samples were studied by culture and multiplex PCR method. SDS and chloroform-isoamyl alcohol were used for cell lysis and DNA purification. Multiplex PCR was done using three pairs of primers targeting specific genomic sequences of each species.

**Results :** Multiplex PCR results revealed 72.2 % P. aeruginosa and 36.4 % B. cepacia complex, as well as 22.7 % of H. influenzae. Multiplex PCR was able to detect CF patients cloned with P. aeruginosa who were not identified by standard culture. Multiplex PCR detected P. aeruginosa in 21 participants, H. influenzae in 10 participants, and B. cepacia complex (BCC) in 16 participants, that were not detected in culture-dependent technique. Comparing to culture results, the sensitivity and specificity values of multiplex PCR for P. aeruginosa identification were, respectively, 100% and 36.4%. Specificity values of multiplex PCR for BCC and H.

influenzae were 100%. The sensitivity of the multiplex PCR for B. cepacia complex and H. influenzae cannot be assessed because no positive results have been recorded for these two bacteria by culture method.

**Conclusion :** we conclude that multiplex PCR provides a rapid method for detecting these 3 bacterial species in CF patients' samples with greater accuracy and sensitivity than the culture method

**Keywords :** Cystic Fibrosis, Multiplex PCR, Infections, Pseudomonas aeruginosa, Burkholderia cepacia complex, Heamophilus influenzae

# P5-108: Evaluation a gold nanorods based nanobiosensor for rapid detection of Mycobacterium Tuberculosis

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**Background and Aim :** Mycobacterium tuberculosis (MTB) is a deadly pathogen, causing the disease tuberculosis (TB) in human. The IS6110 gene is specific to members of the Mycobacterium tuberculosis complex (MTBC). MTB diagnosis has been increasingly relying on the molecular identification. Today, the use of biosensors based on metal nanoparticles, especially gold nanoparticles due to their optical properties in the detection of bacteria has become widespread. In this study a gold nanoparticle (AuNPs) probes to detect IS6110 of MTB, that based on the colorimetric differentiation of specific DNA sequences aggregation in the presence or absence of specific target hybridization.

**Methods :** At first, gold nanoparticles were synthesized by the seed mediated growth method, and confirmed with transmission electron microscope (TEM) and Dynamic Light Scattering (DLS). The ssDNA probes designed for IS6110 were attached to the gold nanoparticles. By preparing serial dilutions from recombinant plasmid (pUc57/IS6110), the Limit Of Detection (LOD) was determined for biosensor and TaqMan-Real Time PCR. In this study, 220 sputum specimen of subjects suspected tuberculosis was used. Final biosensor results were compared with TaqMan Real-time PCR method.

**Results :** The size and morphology of the synthesized Gold Nanorods (GNRs) were confirmed by TEM and DLS techniques. From 220 sputum specimen of subjects suspected tuberculosis, 42 cases by TaqMan- Real Time technique and 41 cases by nanobiosensor method, were detected. Based on the vector used, limit of detection for biosensor 10-7ng/µl and This value for TaqMan real-time assay 10-10ng/µl was determined. Also, the specificity of both methods was 100%.

**Conclusion :** It was received that sensitivity of IS6110 TaqMan real-time PCR assay more than biosensor. But the specificity of both methods was the same. High speed and simplicity of biosensor method are its advantages. The DNA biosensor provides a new strategy for clinical MTB diagnostics and probably also for pathogenic bacteria. According to the importance of

rapid diagnosis of tuberculosis, this technique can play an important role in developing novel optical biosensors for MTB detection.

**Keywords :** Mycobacterium tuberculosis, gold nanoparticles, biosensor, detection

# P6-192: Development of a nano-biosensor for direct detection of Helicobacter pylori

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**Background and Aim :** Helicobacter pylori is the leading cause of gastritis, stomach ulcers, gastric cancer, and mucosa-associated lymphoid tissue (MALT). However, it is still diagnosed by conventional methods and urea breath test (UBT) is often considered as the gold standard. Due to the importance of rapid specific diagnosis of H. pylori, we developed a nanoprobe-based method for direct detection of the target in the cells.

**Methods :** A specific target region in the genomic DNA of the microorganism was selected and a specific complementary probe was designed and modified for further particle attachment. The probe was used to functionalize gold nanoparticles. The genomic DNA contents of the samples were accessed by the boiling method. The nucleic acid content of the cells was used for the further detection procedure. After a denaturation and annealing stage, magnesium chloride salt was used for induction in the colorimetric assay. The specificity and limit of detection were analyzed.

**Results :** The results show that the designed Au-nanoprobe could attach to the target region specifically among ten different bacteria, providing a specific colorimetric detection approach in less than six minutes. Furthermore, the optimized concentration of the salt yields an optimum color differentiation between the positive and the negative samples. In positive samples, the nanoparticles stayed dispersed (red) due to a successful hybridization while in negative samples, aggregation occurred due to the absence of a complementary sequence resulting in a blue shift.

**Conclusion :** The direct gold nanoprobe-based method could be employed as a simple, rapid, and affordable method to nano-diagnosis of H. pylori and help restraining the spread of H. pylori infection.

**Keywords :** Helicobacter pylori; Amplification-free; Rapid diagnostic test; gold nanoparticle; biosensing

# P7-193: A specific diagnostic method for differentiation of Citrobacter freundii based on target amplification

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**Background and Aim :** Citrobacter freundii is able to cause dangerous diseases such as neonatal meningitis associated with brain abscesses, diarrhea, sepsis, and nosocomial infections in humans. Therefore, rapid identification is essential for effective treatment. In this study, we detected bacteria using a specific molecular polymerase-based method.

**Methods :** The bacterial cells were cultured in tryptic soy broth medium followed by genomic DNA extraction. We designed specific oligonucleotides targeting the gene and amplified the region with the polymerase chain reaction. The target gene was a protein coding of YdcF family with unique sequence in Citrobacter freundii. The assay was tested by analyzing different bacteria from various genera and species. The products are visualized and confirmed by gel electrophoresis. The specificity and limit of detection (LOD) were analyzed.

**Results :** DNA extraction has been performed and the quality of the extracted DNA was evaluated by spectroscopy and 2% agarose gel electrophoresis. The target gene was amplified and a 266 bp product was expected. The specificity was analyzed using different bacteria namely Yersinia enterocolitica, Morganella morganii, Serratia marcescens and Shigella sonnei. A unique amplicon band was detected for Citrobacter freundii while there was no observable amplification for other bacteria. For evaluating the sensitivity of the method, the extracted genomic DNA of Citrobacter freundii was subjected to serial dilution. Amplification occurred at up to 10^(-5) dilution of initial concentration.

**Conclusion :** As a diagnostic system, the used technique could identify target microorganism efficiently with high sensitivity in a few hours. By making the identification process easier, faster, and more affordable, the difficulties associated with the late diagnosis of infectious diseases could be facilitated.

**Keywords :** Citrobacter freundii; Molecular Diagnostics; Pathogen; Nucleobiomarker; PCR

# P8-226: Deep learning model for predicting COVID-19 in x-ray images

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**Background and Aim :** COVID pandemic has been one of the most severe and life-threatening phenomena, causing many deaths worldwide. Despite the discovery of various vaccines, nations have not yet been able to control COVID. Therefore, rapid detection at its early onset is one of the most crucial steps toward preventing its prevalence. Lung is the first endangered organ during this infection. Therefore, urgent diagnosis and treatment of this organ are of the main concerns currently. Chest radiography is one of the practical steps to achieve this purpose. The only challenge in diagnosing CXR-based COVID-19 patients is that trained physicians may not always be available, especially in remote areas. Moreover, the radiological manifestations of COVID-19 are new and unfamiliar to many professionals who have no previous experience with COVID-19-positive CXRs.

**Methods :** In this paper, we introduce one of the newest methods in deep learning science using advanced models in data mining and the detection of complex patterns to detect damaged lungs. A database including 2000 images of healthy lungs and 84 images of patients was used to train the system. However, due to the lack of data for the training system, the data volume was increased using data generation methods. After that, a dataset including 2000 images of healthy lungs and 100 images of patients was used to test the model. It should be noted that to increase the accuracy of our model, in addition to healthy people, patients with other kinds of diseases have been added to this database.

**Results :** Using the DenseNet structure, a model with an accuracy of 98.5% in diagnosing this disease is presented in this study.

**Conclusion :** The results show that this model is accurate enough in diagnosing Covid disease along with other diseases. The program can be easily used on any computer and mobile phone by any medical staff to diagnose COVID patients using chest X-ray images in seconds.

**Keywords :** COVID-19-deep learning-DenseNet structure-x-ray images

# P9-278: Expression of bap Gene in Acinetobacter baumannii by Real-Time PCR assay from Clinical Specimens in Khorramabad, Iran

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**Background and Aim :** Biofilm-associated protein (Bap) in Acinetobacter baumannii is a major factor in biofilm production and persistence in the hospital environment. Therefore, the aim of this study was detection of bap gene in Acinetobacter baumannii by Real-Time PCR from Clinical Specimens in Khorramabad, Iran

**Methods :** In this cross-sectional study from April 2017 to April 2018, A. baumannii strains from clinical samples were collected and identified by microbiological and biochemical tests. Expression of Bap gene was evaluated by Real-Time PCR method. Data were analyzed with statistical package for the social science (SPSS) version 24.

**Results :** In our study 43 A. baumannii isolated from teaching hospitals in Khorramabad, Iran. Out of them, 23 sample isolated from phlegm, 8 sample isolated from wounds, 3 sample isolated from urine, 3 sample isolated from tissue, 3 sample isolated from blood, and3 sample isolated from chest sputum. According to PCR results all isolates had Bap gene, except one isolate. Real-time PCR results of the expression of bap gene showed significant difference among A. baumannii isolated from different clinical sample.

**Conclusion :** The expression of bap gene in phlegm and wound samples showed the highest value and had a significant difference compared to other samples (P <0.0001).

**Keywords :** Acinetobacter baumannii; Biofilm-associated protein (Bap); Real-time PCR

# P10-294: Specific early identification of Morganella morganii based on polymerase chain reaction (PCR) method

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**Background and Aim :** Morganella morganii is considered as an opportunistic pathogen and cause of some clinical infections in human with a high degree of mortality. Identification of the organism is mainly performed by tedious conventional biochemical assays or time-consuming culture techniques. Therefore, we developed a molecular method based on conventional PCR assay for the specific detection of M. morganii.

**Methods :** The bacterial strains were purchased in lyophilized form and cultured in the respected bacterial media overnight to reach the log phase in their growth curve. Nucleic acid extraction was performed by a DNA extraction kit. After the analysis of the quality and quantity of the extracted DNA using spectroscopy at 260 nm, the target gene was amplified by an optimized PCR protocol using previously designed primers. Furthermore, the specificity of the primers and the developed method was assessed using eight gram-negative bacteria. Finally, the amplification products were investigated by agarose gel electrophoresis and hydroxy naphthol blue indicator.

**Results :** The quantity of the extracted nucleic acid was measured as 101 µg mL-1 which was appropriate for further experiment. A 237 bp target product was expected to be amplified by the designed primers. The specificity of the method was determined by observing the supposed band for M. morganii on gel electrophoresis while no amplification product was detectable for any of the other tested bacteria (Shigella boydii, Yersinia enterocolitica, Citrobacter freundii, Klebsiella pneumonia, Enterobacter aerogenes, Pseudomonas aeruginosa, Burkholderia cepacia, Serratia marcescens). The Limit of detection (LOD) was attained to be 101 ng ml-1 of the amplified genomic DNA of M. morganii.

**Conclusion :** The developed method is a molecular amplification-based detection technique to expedite the whole detection process of M. morganii in urgent circumstances.

**Keywords :** Nucleic acid testing (NAT); Morganella morganii; PCR; microbial detection; diagnosis

# P11-402: The role of microRNA in the control and treatment of Covid-19

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**Background and Aim :** Coronavirus disease 2019 (COVID-19) is the seventh member of the bat severe acute respiratory syndrome family. COVID-19 can fuse their envelopes with the host cell membranes and deliver their genetic material. COVID-19 attacks the respiratory system and stimulates the host inflammatory responses, enhances the recruitment of immune cells, and promotes angiotensin-converting enzyme 2 activities. Nowadays, the SARS Coronavirus 2 (SARS-CoV-2) infection is recognized as the primary cause of mortality in humans. SARS-CoV-2 is transmitted through human-to-human contact and is asymptomatic in most patients. In addition to approved vaccines against SARS-CoV-2 infection, miRNAs may also be promising options against this new virus.MicroRNAs (miRs) as small non-coding RNAs (21–25 nt) regulate gene expression.

**Methods :** Indeed developing nanoformulations of the COVID-19-related miRNAs can successfully transfer the miRNAs to the cells. Also, miRNAs-based therapeutics could be used in the nanovaccines that are specific with minimal off-target effects. Furthermore, nanobased miRNAs vaccines can be used as nasal spray or drops. In the case of COVID-19 disease, nanovaccine in the form of nasal spray seems to be more effective due to the activation of the immune response in the respiratory tract as the common initial site for SARS-CoV-2 virus entry.

**Results :** Over expression/inhibition of miRs might result in cell cycle irregularity, impaired immune response, or cancer. In this manner, the exact role of each miR should be specified. Mimic encodedmiRs like antagomirs showed the successful result in phases of clinical trial prevent from negative effects of viral encoded-miRs.

**Conclusion :** Products of mimic miRs are inexpensive correspond to the synthesis of primer; they are short and nanoscale in size. Although the SARS-CoV-2 genome is undergoing evaluation, detection of exact molecular pathogenesis open up opportunities for vaccine development. Salivaomics can evaluate the SARS-CoV-2 genome, transcriptome, proteome, and biomarkers like miRs in oral related and cancer disease. In this review, we studied the

challenge and opportunities of miRs in the therapeutic approach for SARS-CoV-2 infection, then overviewed the role of miRs in saliva droplets during SARS-CoV-2 infection and related cancer.

**Keywords :** microRNA , Covid-19, treatment , SARS-CoV-2

# P12-437: Is saliva suitable as an accurate SARS-CoV-2 diagnostic tool?

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**Background and Aim :** Salivary tests for the new coronavirus (SARS-CoV-2) diagnosis have been suggested as alternative methods for the nasopharyngeal and oropharyngeal tests. Saliva is a non-infectious fluid, therefore it can be a useful material for the detection of RNA/DNA of viruses. Rapid and accurate diagnosis of Covid-19 is crucial in controlling the outbreak in the community and in hospitals. Nasopharyngeal and oropharyngeal swabs are the recommended specimen types for Covid-19 diagnostic testing. Diagnosis of viral infections presently depends on salivary biomarkers, such as viral DNA and RNA, antigens, and antibodies. Saliva has a high consistency rate of greater than 90% with nasopharyngeal specimens in the detection of respiratory viruses, including coronaviruses.

**Methods :** Coronavirus disease 2019 (COVID-19) is a serious and potentially deadly disease. Early diagnosis of infected individuals will play an important role in stopping its further escalation. Recently, researchers have successfully validated saliva as being a viable biosample source for COVID-19 detection.

**Results :** Saliva testing will help with the global shortage of swabs for sampling and increase testing of patients. The use of saliva also reduces the time and cost associated with the collection of specimen. Further studies are needed to evaluate the potential diagnostic of Covid-19 in saliva and its impact on the transmission of this virus, which is pivotal to develop rapid diagnostic tests and effective strategies for prevention.

**Conclusion :** Saliva is a promising new source in the diagnosis of SARS-CoV-2 in some recent studies. The use of nasopharyngeal swabs for sampling is worrying in this disease due to the problems it creates for the patient and the health professionals. In addition to patient and health professionals safety in this type of sampling, low cost is another advantage of this method. In addition, saliva samples are a good alternative to epidemiological studies and the diagnosis of asymptomatic or pre-symptomatic infections and can be useful in screening and dental care systems.Current studies from different groups have shown promising results on the possible use of saliva for detection of SARS-CoV-2 RNA. Saliva seems to be a good candidate for the

detection of SARS-CoV-2 for cases with moderate-to-severe symptoms, and for asymptomatic or mild cases.

**Keywords :** SARS-CoV-2, Saliva, dental care, diagnostic tool, RNA

# P13-4: Determination of uhpT gene expression in E. coli isolates of UTIs among kidney transplant patients

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**Background and Aim :** E.coli is the main gram negative responsible for urinary tract infections (UTIs) specially in kidney transplant patients(KTPS Defects in one or both of the transport systems caused by mutations in the uhpT and glpT structural genes or the regulators can confer fosfomycin resistance. Our aim is to investigate uhpT gene expression in the presence of glucose 6 phosphate among E.coli isolates from UTIs of kidney transplant patients.

**Methods :** A total of 60 clinical isolates of uropathogenic E. coli were collected from 3 kidney transplant centers from April to May 2019. Antimicrobial susceptibility testing was performed by the disk diffusion method as recommended by the CLSI. Fosfomycin resistant isolates were determined by E-test. The serotyping of E. coli isolates was performed by the slide agglutination method. PCR and further sequencing was performed for ESBL genes (SHV, TEM and CTX-M genes), fosA3, fosC2, uhpT, glpT and cyaA genes and then real-time PCR was performed for genes uhpT in the presence of glucose 6 phosphate and lack thereof. A fosfomycin resistant E.coli isolate dedicated from Prof. C. Giske (Karolinska Institute, Sweden) was evaluated simultaneously.

**Results :** The frequency of ESBL-producing E. coli in KTPs was found to be 33.4%. All of the 60 E. coli were found to be susceptible to doripenem and ertapenem (100%). High resistance rates to ampicillin (86%), cefotaxime (80%), and cefazolin (77%) were also documented. We identified mutations in murA, uhpT, glpT genes in resistant samples after sequencing and gene bank alignment. No fosA3 and fosC2 genes were identified. According to the E-test, the resistance to fosfomycin in our samples was 1.6% and including 2 intermediate and a resistant isolates. According to the real-time PCR test, the expression of one of the two sensitive samples increased 32 times in comparison to intermediate and resistant isolates.

**Conclusion :** There is a discrepancy between the data from in vitro and clinical studies regarding development of resistance. This may be because of the complex biological phenomenon of infection, in which there is interplay between bacteria, antibiotics, site of

infection, presence of foreign materials and function of the immune system. Ultimately, the current fosfomycin activity seems to be more than satisfactory and justifies its use as monotherapy or in combination with other antibiotics for treatment of infections caused by susceptible and multidrug-resistant bacteria.

**Keywords :** E .coli , Urinary tract infections, Fosfomycin

# P14-12: Rapid identification of extensive drug resistant (XDR) gram negative bacterial isolates in Payvand clinical and specialty laboratory, a six month survey

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**Background and Aim :** Background The aim of this study was to evaluate the frequency of extensive drug resistant (MDR) gram negative bacterial isolates from different clinical samples in Payvand clinical and specialty laboratory.

**Methods :** All gram negative bacteria isolated from different clinical samples from March to Sept 2020 were included. Blood agar, chocolate agar and MacConkey agar were used to access pure cultures .A bacterial suspension was prepared based on Vitec 2 system for identification and Antimicrobial Susceptibility test (AST) using special cards. Statistical analysis was done by SPSS Version21 software.

**Results :** : 4125Urine, 34 sputum samples and 1 tracheal tube were included in this study. Of them 486 Urine, 32sputum and a tracheal tube was culture positive. 31 XDR gram- bacteria were isolated from 18 urine, 12sputum and 1 tracheal tube. The identified gram negative bacteria were: K. pneumonia (pneumonia (20) and ozonai(2)), E. coli (3), Pseudomonas aeruginosa(5) and Acinetobacter baumannii (1). Also, 6/22 K. pneumonia (27.27%), 1/3 E. coli (33.3%), 1/5 P. aeruginosa (20%) and 1/1 A. baumannii (100%) were ESBL producers.

**Conclusion :** In XDR cases the illness severity is higher than other situations and availability of effective antibiotics are more limited. So, rapid identification of XDR patients by using automated systems such as Vitec 2 in less than 72h can decrease the cost and mortality rate.

**Keywords :** Drug resistance, XDR, gram negative bacterial infections

# P15-26: Prevalence, molecular epidemiology and risk factors of carbapenem-resistance Enterobacteriaceae (CRE)

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**Background and Aim :** During the last decade, the forceful increase and spread of carbapenem resistance Enterobacteriaceae (CRE) has become a significant public health concern through the complete world, that has caused various outbreaks of severe hospital acquired infections (HAI), and it is become endemic in several countries. Enterobacteriaceae because the supply of community- and hospital-acquired infections (HAI) will spread simply between humans by horizontal resistance gene transfer, mediate principally by plasmids and transposons. Based on Ambler classification system, the carbapenemases that confer carbapenem resistance in Enterobacteriaceae belong to three classes: category A (K. pneumonia carbapenemases, KPC), category B (metallo-b-lactamases (MBL), as well as New Delhi metallo-b-lactamases (NDM)) and category D (Oxacillinase like OXA-48). It's shown CRE has distinctive genotypes patterns in numerous countries. During this review, we have a tendency to describe the last decade prevalence, molecular epidemiology and different risk factors of CRE in Iran and therefore other countries.

**Methods :** In this study we investigated through the last studied about frequency of carbapenem resistance genes based on reports from different countries, we also investigated the clonal source of reported genes in all of the articles by finding carbapenem resistance genes sequences and building a phylogenetic tree by MEGA X software and finally we focused on risk factors of spread of these genes and consequences of infection by them in patients.

**Results :** Based on 49 articles that we studied, the most prevalent genes were OXA-48, NDM, KPC and VIM in countries such as Iran, China, Turkey, Scandinavian countries, Spain and other European countries. Carbapenem resistance typically mediate by the assembly of carbapenemase enzymes which principally write in code by plasmids and transposons and that they will unfold by horizontal transfer, in order that they are often found in multiple totally different species of Enterobacteriaceae, similar to Klebsiella pneumoniae and Escherichia coli.

**Conclusion :** The conclusion of this review showed the increasing existence of carbapenem resistance isolates through the entire world. The high existence of resistance genes in these isolates and ease of resistance genes spread among other strains, can raise therapeutic challenges and concerns in case of systemic infections in vulnerable patients.

**Keywords :** Carbapenem resistance Enterobacteriaceae. Molecular epidemiology. Carbapenemase. Phylogenetic tree.

# P16-47: Identification of oxa and ndm genes by Multiplex-PCR method and determination of drug resistance pattern of Acinetobacter baumannii isolates isolated from clinical samples

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**Background and Aim :** Acinetobacter baumannii is the cause of a wide range of nosocomial infections. Antibiotic resistance of this organism is a major challenge worldwide. The aim of this study was to identify oxa and ndm genes by multiplex-PCR and to determine the pattern of drug resistance.

**Methods :** This study was performed in a period of 8 months by collecting 25 bacterial isolates. Antibiotic susceptibility testing was performed on Müller Hinton agar medium by disk diffusion method. MPprimer software was used to design the primers. After data collection, the level of significance was assessed at $P<0.05$ using SPSS 22.

**Results :** Except for gentamicin, cefpime, ciprofloxacin and tobramycin, there is a significant relationship between resistance pattern and sensitivity. All Acinetobacter baumannii isolates were sensitive to ceftazidime. Also, 20% of the isolates were resistant to imipenem, which are considered carbapenem-resistant isolates of Acinetobacter baumannii. Of the 25 isolates studied, 5 isolates (20%) had oxa58 gene, 5 isolates (20%) had oxa23 gene and only three isolates (12%) had ndm gene.

**Conclusion :** The results of this study showed a high widespread of antibiotic resistance among Acinetobacter baumannii isolates, which emphasizes the need to develop programs in the control and treatment of this powerful pathogen. Also, the frequency of beta-lactamase-producing isolates in hospital isolates has been growing, which indicates the need for more attention of health centers in prescribing drugs.

**Keywords :** Acinetobacter baumannii, Antibiotic resistance, Multiplex-PCR, Nosocomial infection.

# P17-48: Prevalence of antibiotic resistance and related genes in clinical isolates of Stenotrophomonas maltophilia in the North of Iran

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**Background and Aim :** Stenotrophomonas maltophilia has emerged as an important opportunistic nosocomial pathogen due to its intrinsic and acquired resistance to a wide range of antimicrobial agents. The present study aimed to investigate the occurrence of antibiotic resistance and resistance mechanisms among clinical isolates of S. maltophilia from Iranian patients.

**Methods :** This cross-sectional study was performed on 60 S. maltophilia isolates that were recovered from different clinical specimens during 2019-2020 in Tehran. Conventional microbiologic methods were used for primary identification of isolates and confirmed by specific polymerase chain reaction (PCR) primers. Minimum inhibitory concentrations (MICs) were determined by the E-test. PCR was applied to determine antibiotic resistance genes.

**Results :** Sixty clinical isolates of S. maltophilia were obtained in this study that most of them isolated from Intensive Care Units (ICU) with 90% (n=54). Antibiotic susceptibility results revealed that 15% of isolates were resistant against minocycline followed by 30% intermediate-resistant. Moreover, MIC results showed that the resistant rates of isolates toward ceftazidime, cotrimoxazole and levofloxacin were 46.7%, and 1.7% and 5%, respectively. PCR amplification of integrons gene showed that fifteen (25%) of isolates carried int1. Moreover, the prevalence of antibiotic resistance genes sul1, sul2, and Smqnr were found in 15 (25%), 6 (10%), and 28 (46.7%) isolates, respectively.

**Conclusion :** In summary, the prevalence of sul and Smqnr genes in integrons-contained isolates point out the significant risk of sulfonamides and fluoroquinolones resistance among clinical isolates of S. maltophilia in our region.

**Keywords :** Stenotrophomonas maltophilia , Drug resistance, integron genes, Guilan

# P18-55: Antibiotic resistance in Escherichia coli isolates from broiler chickens in Chaharmahal and Bakhtiari province during 2018-2020

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**Background and Aim :** Escherichia coli is a gram negative, non-spore forming bacillus and it is a common inhabitant in the intestinal tract of poultry. During the last decades, excessive reliance on antibiotics in human and animal medicine has contributed to creating favourable conditions for the selection, persistence and spread of antibiotic resistant bacteria. To prevent of Escherichia coli infection, it's necessary to determine resistance of bacteria to antibiotics. Disk diffusion method is one of the most common antibiogram methods. In this study we measured antibiotical resistance of E. coli isolates from broiler chickens in Chaharmahal and Bakhtiari province during October 2018 to October 2020.

**Methods :** Sampling was made out of pericardial sac and liver of 458 dead birds referred to clinical department of Shahrekord University, which were affected to colibacillosis and then cultured according to standard operation method. Antibiotical resistance to a panel of antibiotics was determined through disk diffusion method for 100 E. coli isolates. Due to bacterial resistance to antibiotics, diameter of lack growth halo varies. Results of antibiogram is reported to sensitive, intermediate and resistant.

**Results :** The percentages of isolates that were resistant to 10 antibacterial agents during 2018-2020 were as follows: Erythromycin: 92.7%, oxcytetracycline: 89.4%, Danofloxacin:79.2%, Difloxacin: 82.8%, Enrofloxacine: 75.6%, Doxcycycline: 77.5%, Ciprofeloxacin: 68%, Lincospectin: 53.6%, Sultrim: 72% and Florfenicole: 56.2%.

**Conclusion :** The association between the occurrence of resistance and the consumption of the antimicrobial agents is discussed. The present study highlights the prevalence of multiple drug resistant E. coli among healthy broiler chickens in mentioned province. The comparison of resistance patterns reported here with pervious investigations indicated that the resistance to some antibacterial agent among E. coli isolates from avian colibacillosis is on the rise and this may be of concern for poultry specialists.

**Keywords :** Antibiotic Resistance, antibiogram, Escherichia coli, Chaharmahal and Bakhtiari province, Iran

# P19-82: Frequency of ACC, GES and PER genes in Acinetobacter baumannii clinical isolates by multiplex-PCR method

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**Background and Aim :** Acinetobacter baumannii is the cause of a wide range of nosocomial infections. Antibiotic resistance of this organism is a major challenge worldwide. The aim of this study was to identify ACC, GES and PER genes and to determine the pattern of drug resistance.

**Methods :** Antibiotic susceptibility testing was performed on 25 bacterial isolates in plates collected from ICU samples using Müller-Hinton agar medium and disk diffusion method. MPprimer software was used to design the primers. After data collection, the level of significance was assessed at $P<0.05$ using SPSS 22.

**Results :** There was a significant relationship between resistance pattern and sensitivity in all isolates with the type of antibiotic (except carbenicillin). All isolates (100%) were sensitive to colistin Also, one isolate (4%) had PER gene, 4 isolates (12%) had GES gene and 7 isolates (28%) had ACC gene.

**Conclusion :** The results of this study indicate the identification of Acinetobacter baumannii isolates with high resistance to piperacillin, streptomycin, carbenicillin and aztronam. The abundance of resistance genes emphasizes the need for continuous monitoring to reduce the spread of resistance genes and prevent the emergence of resistant isolates, and this shows the necessity for more attention to health centers in prescribing appropriate drugs and avoiding the arbitrary consumption of antibiotics.

**Keywords :** Acinetobacter baumannii, ACC, GES and PER antibiotic resistance genes, Multiplex-PCR, Nosocomial infection.

# P20-87: Phage therapy; a novel way to prevent antibiotic resistance

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**Background and Aim :** Today, with the increasing use of antibiotics, we are witnessing antibiotic resistance and the treatment of bacterial infections has faced a serious challenge. Phage therapy, the use of bacteriophage viruses in the treatment of bacterial infections can be an effective way to combat antibiotic resistance. The purpose of this study was to review phage therapy; Is a solution to combat antibiotic resistance.

**Methods :** This research is a review. After searching for the keywords phage therapy, antibiotic resistance, drug resistance, microbiology, and using AND and OR variables, from 2015 to 2020, 63 related articles were extracted from Embase, Scopus, and PubMed databases.

**Results :** The findings indicate that this treatment method is being developed and recently has positive results in controlling bacterial infections and is a suitable alternative to antibiotic therapy. Bacteriophages specifically kill the target bacteria and have many applications in killing pathogenic bacteria.

**Conclusion :** Bacteriophages are bacterial viruses that are the most abundant biological species on Earth with several about 1032 and play a vital role in regulating the bacterial population. Recently, phage therapy in the control of bacterial infections is increasing. Bacteriophage can also be considered an excellent antibiotic because it does not cause problems such as drug resistance and has greater drug safety. This treatment is also being developed and requires further research.

**Keywords :** phage therapy, antibiotic resistance, drug resistance, microbiology

# P21-94: Prevalence and antibiotic resistance pattern of Gram-positive bacteria isolated from burn patients in the North of Iran: A three year retrospective study

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**Background and Aim :** Bacterial contamination of patients' wounds is a severe problem, and this issue is the most crucial difficulty in curing burn cases. Gram-positive organisms are more predominant in new hospitalized burn cases at first. This study aimed to survey the prevalence and antibiotic resistance pattern of Gram-positive bacteria isolated from burn patients in the North of Iran.

**Methods :** This cross-sectional study was conducted on burn cases who had a positive culture for Gram-positive isolates from clinical samples during 2018-2020 in the North of Iran. The Gram-positive bacteria were identified with biochemical and routinely microbiological tests. Moreover, antibiotic resistance pattern was performed by the disk diffusion method.

**Results :** During the study period, a total of 16 Gram-positive isolates were detected from burn patients. The isolation rate was as follows: 68.7% (11/16) Coagulase Negative staphylococci (CoNS), 18.8% (3/16) Staphylococcus aureus, and 12.5% (2/16) Enterococcus isolates. Antibiotic susceptibility results of CoNS revealed that the high level of resistance was against trimethoprim/sulfamethoxazole. S. aureus isolates showed the highest resistance rate was observed to penicillin, while Enterococcus isolates showed a high level of resistance to ampicillin, erythromycin, tetracycline, gentamicin, and ciprofloxacin. Also, all of the isolates was susceptible to teicoplanin. Moreover, the rate of methicillin-resistant Staphylococcus aureus (MRSA) isolates were 66.7%.

**Conclusion :** Due to the rising of the drug resistance pattern and the importance of antibiotic resistance, especially in susceptible burn patients, it is imperative to analyze the bacterial etiology of nosocomial infections periodically and epidemiologically.

**Keywords :** Staphylococcus aureus, Burn infection, Enterococcus, Coagulase-negative staphylococci

# P22-95: Two years study of microbiological characteristics of catheter-related bloodstream infection in the North of Iran

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**Background and Aim :** A significant part of healthcare-associated infections (HCAIs) is usually associated with the use of devices such as indwelling intravascular and urinary catheters, which can cause an increase in long-term hospitalization, cost, and morbidity and mortality. This study was performed to survey the microbiological characteristics of catheter-related bloodstream infection in the North of Iran.

**Methods :** This retrospective study was carried out on inpatients with catheter-related bloodstream infection (CRBSI) over two years during 2018 and 2019. Standard microbiological and biochemical methods were followed for bacterial isolation and identification. Antimicrobial susceptibility test was performed by disk diffusion method.

**Results :** Out of 287 examined catheters, 95 (33.1%) cases were positive with significant bacterial growth. The most prevalent causes of CRBSI were coagulase-negative staphylococci (28.4%), followed by Staphylococcus aureus (15.8%), Klebsiella pneumoniae (14.7%), and Pseudomonas aeruginosa (12.6%). Antibiotic susceptibility test showed that amikacin, co-trimoxazole, and tetracycline were the most effective antibiotics against staphylococci as the predominant cause of CRBSIs. Meanwhile, 33.3% of S. aureus isolates and 56% of coagulase-negative staphylococci were methicillin-resistant. Ciprofloxacin, piperacillin-tazobactam, and gentamicin were the most effective antibiotics against K. pneumoniae isolates. Among non-fermentative Gram-negative bacilli (NFGNB), P. aeruginosa isolates showed the highest susceptibility to ofloxacin and imipenem. While gentamicin was the most effective antibiotic against Acinetobacter baumannii isolates.

**Conclusion :** Our study showed a remarkable rate of catheter-associated infection, which demanded a more restricted and effective infection control policy. Moreover, our results provided important information for suggestions of proper antibiotics administration based on the local antibiotic susceptibility patterns.

**Keywords :** Healthcare-associated infection, Catheter-related infections, Antibiotic resistance

# P23-101: Two years study of prevalence and antibiotic resistance pattern of Gram-negative bacteria isolated from surgical site infections in the North of Iran

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**Background and Aim :** Surgical site infections (SSIs) are a devastating complication of hospitalization and one of the global health problems The present study aimed to investigate the frequency and antibiotic susceptibility pattern of Gram-negative bacteria (GNB) isolated SSIs in the North of Iran.

**Methods :** This cross-sectional study conducted over a two-year period during 2018-2020 on all cases of SSIs who had a positive culture for a GNB. Standard microbiological tests were followed for the bacterial isolation and identification. Antimicrobial susceptibility profiles were determined using disk diffusion method.

**Results :** During the study period, a total of 78 nonduplicated GNB isolated from SSIs. The most prevalent surgical procedures were fracture fixation (37.2%), and tissue debridement (23.1%). Klebsiella isolates showed the highest isolation rate (29.5%) followed by Enterobacter (28.2%), and Acinetobacter (16.7%). Antibiotic susceptibility results showed that Acinetobacter isolates were almost resistant to all of the tested antibiotics, except gentamicin, co-trimoxazole, and meropenem. Enterobacteriaceae isolates showed the lowest resistance against amikacin, co-trimoxazole, and imipenem. Overall, 49 (62.8%) of isolates were multiple drug-resistant (MDR).

**Conclusion :** In summary, a remarkable rate of MDR isolates which showed an increasing trend during recent years is a serious alarm for the management of SSIs caused by GNB. Moreover, the results of regional assessments, provide good epidemiological background for comparing our situation with other regions.

**Keywords :** Surgical site infection, Gram-negative bacteria, Antibiotic resistance, MDR

# P24-107: Prevalence of MDR, XDR and PDR Pseudomonas aeruginosa strains isolated from clinical specimens in Ardabil (2020-2021)

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**Background and Aim :** Pseudomonas aeruginosa (P. aeruginosa) is a highly virulent and drug resistant gram-negative pathogen responsible for several hospital- and community-acquired infections. Furthermore, treatment of multidrug-resistant (MDR) P. aeruginosa infections is difficult and according to the Centers for Disease Control and Prevention (CDC) assessment, MDR P. aeruginosa is considered as serious threat against public health worldwide. Therefore, the current study aimed to evaluate the prevalence of MDR, extremely drug-resistant (XDR) and pandrug-resistant (PDR) P. aeruginosa strains isolated from clinical specimens in Ardabil in 2020-2021.

**Methods :** Fifty isolates of P. aeruginosa was collected from various specimens in five hospitals in Ardabil during April 2020 to April 2021. Kirby-Bauer disk diffusion method was used for P. aeruginosa drug susceptibility testing and the interpretation of results was done based on the CLSI guideline.

**Results :** The prevalence of MDR P. aeruginosa strains was 30 (60%). In addition, 23 (76.6%) and 1 (3.3%) of MDR P. aeruginosa strains were XDR and PDR, respectively. Multidrug-resistant P. aeruginosa strains were isolated from sputum specimens (40%, n=12), urine (36.6%, n=11), wound (13.3%, n=4) and blood (10%, n=3).

**Conclusion :** Our results revealed an increasing trend of the prevalence of MDR and XDR P. aeruginosa in comparison with 2019-2020 in Ardabil hospitals. Therefore, annually monitoring of P. aeruginosa drug resistance in order to choice the best therapeutic regimen and prevent treatment failure is completely needed.

**Keywords :** Pseudomonas aeruginosa; antibiotic resistance; infection

# P25-111: Determination of capsule serotypes and antibiotic resistance of Streptococcus agalactiae isolated from urine samples of patients referred to medical centers in Yazd

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**Background and Aim :** Streptococcus agalactiae (group B streptococcus, GBS) is commonly found in the vagina, rectum and urinary tract of pregnant and non-pregnant women. This bacterium not only causes neonatal infections but also causes invasive diseases including urinary tract infections in pregnant women and non-pregnant adults. Penicillin and macrolides are the main antibiotics in the treatment of GBS infections but the prevalence of resistant strains is increasing. On the other hand, the distribution of bacterial capsule serotypes varies depending on the sampling time, geographical location and type of sample. The aim of this study was to investigate the antimicrobial resistance and capsular serotypes in group B streptococci isolated from urine samples of patients referred to Yazd medical centers.

**Methods :** This descriptive cross-sectional study was performed on 85 GBS isolates from 6068 urine positive culture samples for phenotypic survey and determine pattern of antibiotic resistance to antibiotic disks by Kirby-Bauer method. Also, capsular serotypes of isolates were determined by multiplex PCR.

**Results :** The frequency of GBS in urinary samples was 1.4%. Antibiotic resistance of GBS to tetracycline, erythromycin, clindamycin and levofloxacin was 97.6%, 38.8%, 31.8% and 9.4%, respectively. All GBS isolates were sensitive to penicillin. The predominant capsular serotype was serotype III (50.6%) followed by serotypes Ib (14.1%), V (12.9%), IV (7.1%) and II (5.9%). 9.4% of isolates were non-typeable.

**Conclusion :** The prevalence of GBS in urinary specimens was low and capsular serotype III was predominant as in previous studies. Antibiotic resistance is increasing in urinary GBS isolates.

**Keywords :** Group B streptococcus, Urinary tract infection, Serotyping, Antibiotic susceptibility

# P26-125: Molecular and phenotypic characterization of carbapenemase-producing Klebsiella pneumoniae in a tertiary university hospital in Bandar Abbas, Iran

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**Background and Aim :** Infections with carbapenem-resistant Klebsiella pneumoniae (K. pneumoniae) are emerging as an important challenge in healthcare settings, which are most commonly encountered in hospitals. The aims of this study were to identify the antibiotic susceptibility and genes coding for carbapenemases in K. pneumoniae isolates in the Bandar Abbas, Iran.

**Methods :** Two hundred K. pneumoniae isolates were obtained from clinical samples from Shahid Mohammadi Hospital, in Bandar Abbas. Identification and antimicrobial sensitivity test were performed with the disk diffusion method. The isolates were examined to determine the presence of selected antibiotic-resistant genes including NDM, IMP, VIM, SPM, and OXA48 by PCR method. All of the isolates were DNA extracted by boiling method.

**Results :** K. pneumoniae isolates were obtained from clinical samples including urine (66.5%; n = 133), trachea (9%; n = 18), wound (7.5%; n = 15), blood (6%; n = 12), sputum (5%; n = 10), discharge (2%; n = 4), BAL (1%; n = 2), eye infection (2%; n = 4), pleural fluid (0.5%; n = 1), and ascites (0.5%; n = 1). The disk diffusion results showed that 107 (53.5%) of the isolates were resistant to piperacillin, 100 (50%) to sulfamethoxazole-trimethoprim, 92 (46%) to ceftazidime, 93 (46.5%) to cefepime, 89 (44.5%) to ampicillin-sulbactam, 87 (43.5%) to aztreonam, 64 (32%) to ciprofloxacin, 53 (26.5%) to piperacillin-tazobactam, 57 (28.5%) to gentamicin, 54 (27%) to tetracycline and 32 (16%) to meropenem. PCR assays revealed that six isolates possessed the NDM gene. None of the isolates were possessed IMP, VIM, SPM, and OXA48 genes.

**Conclusion :** Based on the results, the prevalence of NDM-producing K. pneumoniae is higher compared to others carbapenemases genes (IMP, VIM, SPM, and OXA48) in the Bandar Abbas, Iran.

**Keywords :** Klebsiella pneumoniae; Antibiotic resistance; Carbapenemase

# P27-126: Prevalence of extended-spectrum β-lactamases in Klebsiella pneumoniae clinical isolates in Bandar Abbas, Iran

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**Background and Aim :** Klebsiella pneumoniae (K. pneumoniae) is an important pathogen that causes several infections in hospitalized immunocompromised patients with severe underlying diseases. Extended-spectrum β-lctamases (ESBLs) are enzymes that hydrolyze the beta-lactam ring of β-lactam antibiotics such as penicillins, first, second and third-generation cephalosporins, and monobactams. This study was conducted to identify the ESBL-producing K. pneumoniae genes and the antibiotic susceptibility of clinical isolates in Shahid Mohammadi Hospital, Bandar Abbas, Iran.

**Methods :** A total of 300 K. pneumoniae were isolated from various clinical samples from 2018-2019. The antimicrobial susceptibility patterns were analyzed using the disk diffusion test. Multiplex PCR was carried out to determine the presence of the resistance-conferring genes blaCTX-M, blaSHV, and blaTEM.

**Results :** K. pneumoniae isolates were obtained from urine (51.3%; n = 154), trachea (16.3%; n = 49), wound (11%; n = 33), blood (7.3%; n = 22), sputum (7%; n = 21), discharge (3%; n = 9), BAL (2%; n = 6), eye infection (1.3%; n = 4), pleural fluid (0.3%; n = 1), and ascites (0.3%; n = 1). The disk diffusion results showed that 197 (65.7%) of the isolates were resistant to piperacillin, 181 (60.3%) to sulfamethoxazole-trimethoprim, 164 (54.7%) to ceftazidime, 158 (52.7%) to cefepime, 150 (50%) to ampicillin-sulbactam, 148 (49.3%) to aztreonam, 133 (44.3%) to ciprofloxacin, 106 (35.3%) to piperacillin-tazobactam, 104 (34.7%) to gentamicin, 89 (29.7%) to tetracycline and 81 (27%) to meropenem. The blaSHV gene was the most prevalent gene 258 (86%). The other genes including blaCTX-M and blaTEM genes were detected in 129 (43%) and 81 (27%) isolates, respectively.

**Conclusion :** These results showed a high prevalence of genes encoding ESBL and antibiotic resistance in the K. pneumoniae isolates.

**Keywords :** Klebsiella pneumoniae; Antibiotic resistance; beta-Lactamases

# P28-139: Study of antimicrobial effect of Zataria multiflora, Thymus daenensis Celak, Alcea and Urtica on the growth of Escherichia coli in vitro

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**Background and Aim :** The use of medicinal plants for treatment has a long history of human life. In recent years, the use of medicinal plants has increased due to the lower side effects and costs and patients' adaptation to these drugs and due to the existence of known side effects for chemical drugs.

**Methods :** To evaluate the antibacterial effect of the plant extracts, susceptibility assay was performed by disk diffusion method. First, Escherichia coli was cultured uniformly on the Müller-Hinton agar medium. Then, sterile blank disks containing different dilutions of the extract (100, 50, 25, 12.5 and 6.25) were placed on the agar medium. The culture media were then incubated for 24 hours at 37 ° C.

**Results :** The results showed that the highest diameter of growth inhibition zone among different treatments is related to the use of fluorophenicol 10%. In the next priority, Zataria multiflora and Thyme extract were concentrated in Escherichia coli culture medium at concentrations of 100 and 50%, respectively. . The diameter of the growth inhibition zone was related to the commercial drugs Enrofloxacin 10% and sulfadiazine-trimethoprim (Soltrim 48%), concentrations of 25, 12.5% of thyme and Dena, and concentrations of 100 and 50% of nettle and marshmallow in one range and There was no significant difference with each other, but the diameter of the halo created by each of the treatments was significantly less than Zataria multiflora and Denai extracts in concentrations of 100 and 50% and also fluorophenicol ($P < 0.05$).

**Conclusion :** to compare the observed results on the antibacterial properties of different plant extracts, which can be explained by the differences in different laboratory methods of antibacterial properties of essential oils, method of preparation of essential oils, strain and type of plant and their sources. , Pointed out the growth stage of the plant as well as the bacterial strains used

**Keywords :** Zataria multiflora-Thymus daenensis Celak-Alcea - Urtica -Escherichia coli

# P29-155: Frequency of pilus islands and antibiotic resistance in Streptococcus agalactiae isolated from urine of pregnant women

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**Background and Aim :** Group B Streptococcus (GBS) is one of the most important causes of neonatal mortality and postpartum fever. Group B Streptococcus infection can be transmitted from the infected mother to her baby during delivery. Pilus island is one of the most important virulence factors of Streptococcus agalactiae after capsule. The aim of this study was to evaluate the frequency of pilus islands and antibiotic resistance in Streptococcus agalactiae isolated from urine of pregnant women in Yazd, Iran.

**Methods :** In this cross-sectional study, 33 GBS samples isolated from the urine of pregnant women were studied by the multiplex polymerase chain reaction (PCR) method for the presence of pilus islands PI-1, PI-2a and PI-2b. Antibiotic resistance phenotype of tetracycline, penicillin, gentamycin, erythromycin, levofloxacin and clindamycin antibiotics was determined by disk diffusion method. Data analysis was performed using SPSS, version 16.

**Results :** PI-1+PI-2a was most frequent pilus island in the GBS isolates (28 [84.8%]) and the frequency of PI-2b was 5 (15.2%). The frequency of PI-1+PI-2a was 83.33% in serotype III and 100% in serotypes II, Ia, Ib and V (P=0.492). All the GBS isolates were susceptible to ceftriaxone (100%) and cefotaxime (100%) antibiotics. However, GBS isolates showed the highest resistance to erythromycin (79%) and clindamycin (76%).

**Conclusion :** Our results showed that most of the GBS isolates examined carried the PI-1+PI-2a gene, which increases bacterial potency in colonization and resistance to the immune system. The PI-2b gene was also observed in a lower frequency. Pilus is suggested as a unique vaccine candidate.

**Keywords :** Group B Streptococcus; Pregnant women; Pilus islands; Antibiotic resistant

# P30-157: Antibiotic susceptibility pattern of Pseudomonas aeruginosa isolates, collected from patients in Tabriz hospitals.

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**Background and Aim :** Pseudomonas aeruginosa is an opportunistic pathogen that is a leading cause of morbidity and mortality in patients and immunocompromised individuals. Eradication of P. aeruginosa has become increasingly difficult due to its remarkable capacity to resist antibiotics. The pattern of Pseudomonas aeruginosa antibiotic susceptibility varies geographically, and Antibiotic susceptibility testing should be performed to select the correct antimicrobial treatment. The aim of this study was to determine the pattern of antibiotic resistance in Pseudomonas aeruginosa strains isolated from patients in Tabriz

**Methods :** A total of 78 Pseudomonas aeruginosa isolates, collected from Sina, Madani and Emam Reza Hospitals in Tabriz. To determine the pattern of antibiotic susceptibility by disk diffusion method using discs, common used antibiotics in hospitals were examined

**Results :** In this study the most effective antibiotics against isolates were amikacin and colistin with 95% susceptibility whereas the highest resistance was to Amoxicillin and Co-trimoxazole and with 92% and 91%

**Conclusion :** Continuous monitoring of antibiotic susceptibility pattern of Pseudomonas aeruginosa is essential and rational treatment regimens prescription by the clinicians is required to limit the spread of antimicrobial resistance.

**Keywords :** : Antibiotic resistance; Pseudomonas aeruginosa; Antibiogram

# P31-158: Prevalence of Extended-spectrum beta-lactamase-producing Pseudomonas aeruginosa in Clinical samples, collected from patients in Tabriz hospitals.

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**Background and Aim :** Pseudomonas aeruginosa is one of the most bacteria involved in nosocomial infections. Presence of Extended-spectrum Beta-lactamases (ESBLs) genes, play an important role in induction of resistance in beta-lactamase producing species to beta lactam antibiotics. Frequency of resistance to these antibiotics is increasing. The aim of this study was to determine the antimicrobial susceptibility pattern and prevalence of ESBLs in clinical isolates of Pseudomonas aeruginosa collect from Tabriz hospitals by phenotypic methods

**Methods :** In this analytic-descriptive study, 78 Pseudomonas aeruginosa isolates, collected from different clinical specimens in Tabriz Sina, Madani and Emam Reza Hospitals, were used. The pattern of antimicrobial resistance was determined by disk diffusion (Kirby-buer) method. The ESBL production was determined by combination disk method using disks containing ceftazidim and cefotaxim alone and in combination with Clavulanic acid.

**Results :** In this study the most effective antibiotics against isolates were amikacin and colistin with 95% susceptibility whereas the highest resistance was to Amoxicillin and Co-trimoxazole and with 92% and 91%. Combine disc test s results indicated that 47 of isolates (61%) were ESBL producers

**Conclusion :** Considering high resistance rate of Pseudomonas aeruginosa to majority of antibiotics and increasing frequency of ESBLs producing isolates, we need for infection control criteria and use of appropriate therapeutic protocols according to antibiogram

**Keywords :** Pseudomonas aeruginosa; Antibiotic resistance; ESBL

# P32-166: Antibiotic resistant pattern and biofilm formation ability of chlorine adapted Salmonella enterica cells

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**Background and Aim :** Adaptation phenomenon could takes place over time and with increasing contact of microorganisms to progressive concentrations of stresses such as disinfectants. Any exposure of bacteria to sub-lethal concentrations of disinfectants may be constitute a critical public health such as emergence of higher invasive pathogens with reduced susceptibility to antibiotics and ability to form biofilm.

**Methods :** In this study, we obtained minimum inhibitory concentration (MIC) of Salmonella enterica against sodium hypochlorite disinfectant containing 50000 ppm chlorine, then bacterium was adapted to progressive concentrations of chlorine (from 125 ppm to 3000 ppm with 25 ppm daily increase of chlorine concentration) to the extent that could tolerate MIC. Antibiotic resistance (against ampicillin, amikacin, trimethoprim, ceftriaxone, and nalidixic acid) and biofilm formation ability was determined before and after chlorine adaptation. Biofilm formation ability was done in sterile 96 well microtiter plates using TSB media and by optical density measuring at 600 nm using an Elisa reader.

**Results :** Antibiotic susceptibility findings on Mueller-Hinton agar revealed highest and significance ($p<0.05$) resistance to ceftriaxone after stress adaptation, so that sensitivity from 30 mm inhibition zone before adaptation reached to 0 mm after chlorine adaptation. Findings showed moderate ability of salmonella enterica before adaptation that remained stable after chlorine adaptation.

**Conclusion :** Finally, we could conclude chlorine disinfectants with regular use in food industry have potential for the development of bacterial adaptation and in this way induction of antibiotic resistance and increase in biofilm formation ability must be taken into account.

**Keywords :** Salmonella enterica, Chlorine adaptation, Antibiotic resistant pattern, Biofilm formation

# P33-177: Prevalence of MLSB Resistance Gene among Clinical Isolates of Staphylococcus aureus in Mashhad, Iran

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**Background and Aim :** Development of drug resistance to Staphylococcus aureus has led to the use of older antibiotics such as macrolide-lincosamide-streptogramin B (MLSB) for the treatment of infections. .The objective of this study is to determine the prevalence of erm and msr genes and the frequency of constitutive MLSB (cMLSB), inducible MLSB(iMLSB) phenotypes using D-test and polymerase chain reaction (PCR) methods.

**Methods :** The present study was done for a period of 6 months (September 2019- March 2020). During this period a total of 100 S. aureus were isolated from different clinical samples such as urine, blood, swabs from different sites etc, by the standard laboratory procedures collected from selected hospitals in Mashhad, Iran. Methicillin resistant Staphylococcus aureus (MRSA) detection was done by using cefoxitin 30µg (BD; USA). Disk induction test was performed to detect the presence of inducible clindamycin resistance among erythromycin resistant S. aureus isolated from clinical samples. Three types of phenotypes were observed by the disk induction test (D-test). After sampling, DNA extraction was performed by simple boiling method and prevalence of erm and msr genes were detected by PCR and electrophoresis.

**Results :** Phenotypic analysis revealed that 52 percent were MRSA and resistance to cefoxitin and 48 percent were methicillin-susceptible S.aureus(MSSA). The result of this study revealed that among 100 S. aureus isolates examined, frequency of cMLSB, iMLSB resistant phenotypes were 30, 15 percent respectively and sensitive phenotypes were 29 percent. In addition erm C, erm B and erm A were detected in 52, 13 and 27 percent respectively also msr A and msr B genes were detected 35 and 8 percent S.aureus isolates.

**Conclusion :** This study demonstrated that cMLSB was the most common phenotype among isolated S. aureus and resistant to erythromycin was mainly due to presence of erm genes.

**Keywords :** Staphylococcus aureus, Resistance gene, MRSA

# P34-179: Evaluation of antibiotic resistance pattern of Klebsiella pneumoniae isolates, collected from patients in some Tabriz 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 resistance of Klebsiella pneumoniae isolates collected from Tabriz hospitals.

**Methods :** In this cross-sectional descriptive study, 180 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.

**Results :** Out of 180 samples collected from different specimens, 72 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 ?-Lactamase phenotypically.

**Conclusion :** High resistance and multidrug resistance among Klebsiella pneumoniae isolates should be considered as an alarm in all hospital wards. High resistance and multidrug resistance among Klebsiella pneumoniae isolates should be considered as an alarm in all hospital wards. An antibiogram should be done before treating Klebsiella pneumoniae infections with antibiotics.

**Keywords :** Klebsiella pneumoniae,Tabriz hospitals

# P35-183: Prevalence of aac(6') - Ie / aph (2") and aph (3') - IIIa genes among clinical isolates of Staphylococcus aureus isolated from patients of selected hospitals in Mashhad

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**Background and Aim :** Staphylococcus aureus is considered as one of the most important pathogenic bacteria and the most common type of nosocomial infections. Enzymatic inactivation of aminoglycosides by aminoglycoside-modifying enzymes (AMES) is the main mechanism of resistance to these antibiotics in S. aureus. The aim of this study was to investigate the prevalence of aac (6 ') - Ie / aph (2") and aph (3') - IIIa resistance gene among clinical isolates of S. aureus.

**Methods :** Clinical staphylococcus aureus isolates were isolated during September 2019-March 2020 from selected hospitals in Mashhad. The pattern of antibiotic susceptibility to gentamicin, tobramycin, and amikacin were determined by disc diffusion method. DNA was extracted and prevalence of aac (6 ') -Ie / aph (2") and aph (3') - IIIa resistance genes were detected by PCR and electrophoresis

**Results :** The results of this study showed that among 100 isolates of S. aureus 19, 27, and 45 percent of these isolates were resistant to gentamicin, tobramycin and amikacin respectively. Also, 62 and 44 of S. aureus isolates had the aac (6 ') - Ie / aph (2 ") and aph (3') - IIIa genes.

**Conclusion :** Due to the high percentage of genes encoding aminoglycoside resistance in S. aureus isolates which were isolated from hospital sources, continuous monitoring of nosocomial infection control processes is necessary to prevent the spread of resistant bacteria in the environment and its transmission to patients

**Keywords :** Aminoglycoside resistance, Polymerase chain reaction, S. aureus

# P36-184: The first study of the effect of vaborbactam on Enterobacteriaceae-producing ESBL in Iran

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**Background and Aim :** K.pneumoniae and E. coli are two important bacteria that cause urinary tract infections. Which have become resistant to β-lactam antibiotics by obtaining plasmids encoding β-lactamases. This study was designed to investigate the effect of vaborbactam on ESBL producing strains.

**Methods :** Antimicrobial susceptibility tests were performed on 165 strains of K. pneumoniae and E. coli using the disk diffusion method. The abundance of genes related to ESBL was assessed by PCR. . The effect of vaborbactam on ESBL producing strain was performed by the combined disk method.

**Results :** Our results showed that out of 75 strains of K. pneumoniae, 30 (40%) were ESBL-producing, of which blaSHV gene in 29 strains (96.6%), blaCTX-M gene in 23 strains (76.6%) and blaTEM gene in 20 strains (66.6%) were identified. Of 90 E. coli strains, 37 strains (41.1%) produced ESBL, of which blaTEM gene in 36 strains (97.2%), blaCTX-M gene in 31 strains (83.7%) and blaSHV gene in 11 strains (29.7%) Were identified.. The results of phenotypic study of the effect of vaborbactam on ESBL strain in K. pneumoniae were as follows: the total resistance to ceftazidime and cefotaxime from 48 (64%) and 46 (61.3%) to 22 (29.3%) and 23 (30.6%) respectively decreased. This decrease in E. coli was from 76 (84.4%) and 81 (90%) to 41 (45.5%) and 41 (45.5%), respectively.

**Conclusion :** As a result, our study provided valuable information regarding the vaborbactam inhibitor on ESBL producing strains.

**Keywords :** vaborbactam, ESBL, Enterobacteriaceae, K. pneumoniae, E. coli

# P37-186: Investigation of Susceptibilities to benzalkonium chloride and distribution of antiseptic-resistance genes qacA/B and smr in clinical isolates of Staphylococcus aureus in Mashhad, Iran

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**Background and Aim :** Staphylococcus aureus is one of the most important pathogens that causes hospital-acquired infections. Quaternary ammonium compounds as antiseptics were used in healthcare facilities for the prevention of nosocomial infections . methicillin-resistant S. aureus is one of the most important causes of nosocomial infections. The objective of this study is to determine antibiotic pattern of isolates , investigation of Susceptibilities to benzalkonium chloride and distribution of the qac and smr genes frequency in clinical isolates of S. aureus.

**Methods :** Bacterial samples were collected from several parts of hospitals in Mashhad. Diagnostic tests were performed to identify S. aureus isolates. Antibiogram tests were performed by disk diffusion method by some of common antibiotics and MRSA isolates were detected by using cefoxitin disk . MIC test was done to evaluate the sensitivity of the isolates to benzalkonium chloride. Finally, the presence of qac A/B and smr genes as antiseptic resistance genes were investigated in all isolates by PCR method.

**Results :** Among 150 collected Staphylococcus isolates, 100 isolates were identified as S. aureus that 52 isolates were MRSA. Among all S. aureus isolates, resistance to erythromycin, clindamycin, gentamicin, tobramycin, trimethoprim sulfamethoxazole, doxycycline, penicillin, amikasin, ciprofloxacin and cefoxitin were respectively 50, 33, 19, 27, 23, 36, 85, 45, 38 and 52 percent. The MIC range of benzalkonium chloride for all 100 S. aureus isolates were 0.01 – 2 µg/mL. Molecular analysis revealed that qac A/B and smr genes were detected respectively in 37 and 49 percent of S. aureus isolates.

**Conclusion :** This study showed that benzalkonium chloride is still effective for disinfection purpose. But, Penicillin resistance in Staphylococcus aureus has greatly increased over time and it is no longer as efficient as before. Also, It was found that smr genes are more common than qac A/B genes in S. aureus isolates.

**Keywords :** Staphylococcus aureus, resistance genes, benzalkonium chloride

# P38-205: Evaluation of antibiotic resistance pattern of Escherichia coli isolates causing urinary tract infections referred to the laboratory of Imam Khomeini Hospital in Shirvan in 2020

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**Background and Aim :** The second most common infection in the human body is a urinary tract infection with a different pattern of antibiotic resistance in each region. Escherichia coli is the most common cause of urinary tract infections in humans. The aim of this study was to evaluate the antibiotic resistance of Escherichia coli strains that were referred to the laboratory of Imam Khomeini Hospital in Shirvan in 2020.

**Methods :** This descriptive study was conducted on 43 isolates of E. coli. After identifying the bacteria by antibiotic sensitivity tests Biochemical and microbiological evaluation of isolates was performed by disk diffusion method according to CLSI guidelines.

**Results :** Out of 43 samples, 79% of isolates belonged to women and 21% to men. Antibiotic resistance was evaluated as follows: cotrimoxazole 58%, ceftriaxone 56%, ampicillin sulbactam 54%, imipenem 52%, ciprofloxacin 35%, gentamicin 19.5%, nitrofurantoin 5.3%.

**Conclusion :** According to the results of this study, the most common cause of urinary tract infection is Escherichia coli and it is recommended to use nitrofurantoin and gentamicin to treat urinary tract infections and avoid prescribing antibiotics cotrimoxazole and cefriaxone.

**Keywords :** Urinary tract infection, Antibiotic resistance, Escherichia coli, Shirvan

# P39-210: Emergence of extensively drug-resistant and colistin resistance Klebsiella pneumoniae Isolated from hospitalized patients in Isfahan, Iran

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**Background and Aim :** The current study was performed to investigate the antibiotic resistance pattern, the prevalence of colistin resistance and its molecular mechanisms in clinical isolates of Klebsiella pneumoniae obtained from hospitalized patients in teaching hospitals in Isfahan, Iran.

**Methods :** This cross-sectional study was performed during the 2019-2020 year at several teaching hospitals in Isfahan, Iran. All K. pneumoniae isolates were screened against 14 antimicrobial agents based on standard disk diffusion method. Moreover, the minimal inhibitory concentration (MIC) of colistin was determined by the E-test strips

**Results :** In the present study, a total of 79 strains of multidrug-resistant K. pneumoniae were isolated. Among the 79 K. pneumoniae isolates, 52 (65.8%) were obtained from females and 27 (34.2%) from males. Most of K. pneumoniae strains were isolated from patients between 46-60 years old. Of these, 35 colistin-resistant clinical K. pneumoniae isolates were obtained. These isolates were resistant to all classes of antibiotics, including colistin, and were classified as extensively drug-resistant (XDR). Antibiotic susceptibility pattern showed a high rate of antibiotic resistance to ceftazidime (94.9%) followed by cefepime and aztreonam (91.1%), while, the lowest resistance rate was observed against tigecycline (2.5%).

**Conclusion :** Due to the fact that the last line of treatment for infections associated with K. pneumoniae is colistin, therefore, increasing resistance to this antibiotic causes many concerns and problems in the treatment of patients. Detection of colistin-resistant strains can greatly help in the treatment of diseases. Also in our study, a low level of resistance to tigecycline was observed, which can be used to treat patients.

**Keywords :** Klebsiella pneumoniae, colistin, MDR, XDR

# P40-212: Evaluation of aminoglycoside modifying enzymes and tetracycline resistance genes in clinical isolates of staphylococcus isolates in Shiraz teaching hospitals 2020-2021

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**Background and Aim :** Methicillin resistant Staphylococcus aureus (MRSA) and methicillin resistant coagulase-negative staphylococci (MRCONS) are one of the important pathogens of nosocomial infections and has shown a frequent and rapid development of antibiotic resistance.The goal of the present study was to evaluate the aminoglycoside modifying enzymes and tetracycline resistance genes in clinical isolates of staphylococci in Shiraz teaching hospitals.

**Methods :** A total of 113 staphylococci isolates were recovered from different clinical samples. Antimicrobial susceptibility of isolates against aminoglycoside and tetracycline antibiotics was tested by the Kirby-Bauer disk diffusion method align with CLSI guidelines. Polymerase chain reaction (PCR) for the presence of tet and AMEs genes were carried out among staphylococci isolates.

**Results :** Of 113 Staphylococcus isolates, 34.5% were MRSA, 32.7% were methicillin sensitive Staphylococcus aureus (MSSA), 26.5% were MRCONS and 6.2% were methicillin resistant coagulase-negative staphylococci (MSCONS). The resistance rates toward tetracycline antibiotics were: 46% to tetracycline, 12.4% to doxycycline and 8% to minocycline. Also, the resistance to aminoglycoside antibiotics were: 43.4% to tobramycin, 32.7% to amikacin and 31.9% to gentamicin. The highest frequency in tetracycline resistant genes were among tetM about 42.5% isolates, followed by tetK in 34.5% isolates, tetL and tetO in 2.7% and 0.9% isolates, respectively. The frequency of detected AME genes were aac (6')-Ie/aph (2"), aph (3')-IIIa and ant(4')-Ia in 39.8%, 30.1% and 16.8% isolates, respectively.

**Conclusion :** Our results showed a high rates of resistance to aminoglycoside and tetracycline antibiotics among MRSA and MRCONS isolates from hospitals in Shiraz. The aac (6′)/aph (2″) and aph (3')-IIIa genes were the most identified genes related to aminoglycoside resistance

and tetM and tetK genes were the most frequent genes associated with tetracyclines resistance. Therefore implementation of policies in order to prevent arbitrary consumption of antibiotics that would decrease the emergence of resistance to aminoglycoside and tetracycline among MRSA and MRCONS isolates is needed in Iran.

**Keywords :** Methicillin resistant Staphylococcus aureus, methicillin resistant coagulase-negative staphylococci, Aminoglycoside modifying – enzymes, Tetracycline, Drug resistance

# P41-214: Investigation of Integron resistance pattern to Carbapenems and existance of class I to III integrun genes in Pseudomonas aeroginosa, in shiraz Nemazee Hospital

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**Background and Aim :** Pseudomonas aeruginosa is a nosocomial opportunistic pathogen and responsible for 10-15% of nosocomial infections. P. aeruginosa is known as an acute problem in nosocomial infections due to innate resistance to many antibiotics, great capability to become resistant to all effective antibiotics, cause complications in treatment and also increase mortality rates.

**Methods :** The samples were bacterial archive of microbiology department of medical university, and then were distinguished as P. aeruginosa by common microbiological methods, biochemical tests and type-specific primers by polymerase chain reaction (PCR) method. Antibiotic sensitivity test against carbapenems (imipenem and meropenem), was done for all the isolates with the Kirby-Bauer disk diffusion method according to CLSI guidelines. At the end the phenotypic tests were performed for the identification of class I- III integron genes for each isolate and also the genotypic analysis including pcr was done.

**Results :** From 75 samples of the recent study, 32 isolates (42.67%) were resistant to imipenem. According to PCR results among 39 imipenem resistant isolates, 29 isolates (90.6%) harbored class I integron, 8 isolates included class II integron and none of them harbored class III integron. It is considerable that 2 imipenem resistant isolates (6.25%) were missing any integron and 2 resistant isolates just included class II integron but had no class I integron. Also, from 22 meropenem resistant isolates, 19 isolates (86.3%) harbored class I integron, 7 isolates (31.8%) included class II integron and one isolate harbored none of the integrones. Additionaly, none of the isolates carried class III integron. Among meropenem resistant isolates, 6 isolates (27.2%) were positive for class I and II integrons, while 3 sensitive isolates (9.4%) also harbored both class I and II integrons.

**Conclusion :** According to the results of spearman's test, resistance to imipenem and meropenem among P. aeruginosa isolates is increasing and this resistance has a remarkable relationship between existence of class I and II integrons. Hence, preventive measurements are necessary in order to control the distribution of resistant isolates.

**Keywords :** Pseudomonas aeruginosa, Integron, Imipenem, Meropenem, PCR, Disc diffusion.

# P42-216: Prevalence and antibiotic susceptibility pattern of fluoroquinolone and cephalosporin-resistant uropathogenic Escherichia coli isolates in Nemazee hospital during 2018-1019

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**Background and Aim :** Urinary tract infection is one of the most important bacterial infections among all ages and sexes. Delays in diagnosis and treatment can cause remarkable complications. So the early diagnosis of symptoms by a physician and also determination of causative urinary tract infection microorganism, and the effective antibiotic choice in a geographical region can help to prescription of the right antibiotics. The goal of the present study was to determine the pattern of sensitivity and resistance to major antibiotics among Escherichia coli causing urinary tract infections in Namazi Hospital in Shiraz.

**Methods :** This retrospective cross-sectional studied was performed on 1910 positive urine samples including Escherichia coli bacteria which was isolated from patients referred to Namazi Hospital in 2108 and 2019.

**Results :** A total of 1910 Escherichia coli strains were isolated, 64% were female, and the rest were male. During these two years, the mean age was 56.57 ± 29.36 for men and 50.65 ± 25.62 for women. Altogether, 86.9% and 89.7% of the isolates were resistant to at least one quinolone and cephalosporin antibiotic during the two years of study, respectively. During these two years, the great resistance rate were detected against cephalexin (87.9%) and nalidixic acid (86.1%), respectively. Also, the highest susceptibility were observed in the strains to amikacin (88.3%), nitrofurantoin (76.8%), and gentamicin (70.6%), respectively. Incidence of resistance to ciprofloxacin (P-value = 0.004), norfloxacin (P-value = 0.008), tetracycline (P-value = 0.038), cefotaxime (P-value = 0.015) and nitrofurantoin (P-value <0.001) during these two years have increased significantly.

**Conclusion :** In conclusion, the rate of resistance to antibiotics such as ciprofloxacin, norfloxacin, tetracycline, cefotaxime, and nitrofurantoin is increasing, and physicians should

consider the antibiotic resistance patterns according to results of antibiogram tests to prescribe the effective antibacterial agents.

**Keywords :** Antibiotic resistance, sensitivity, Escherichia coli, Urinary tract infection, Pattern

# P43-218: Determination of Antimicrobial Resistance Pattern among clinical isolates of Escherichia coli collected Bagheralolulom hospital in Ahar

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**Background and Aim :** Escherichia coli (E. coli) are a group of gram-negative bacteria that normally reside in the intestine of healthy people, but some strains can cause infection in the digestive tract, urinary tract, or many other parts of the body. Antibiotics are used to treat infections caused by this bacterium. Unfortunately, antibiotic resistance has become an increasingly critical problem in many countries like Iran. Since there are very few published data on antibiotics resistance in Ahar, the aim of this study was to survey the pattern of antimicrobial resistance among clinical isolates of Escherichia coli collected Bagheralolulom hospital in Ahar

**Methods :** This cross-sectional descriptive study was performed on 100 clinical Escherichia coli strains collected from Ahar s Bagherololum hospital. The selective culture media and biochemical test were used for the identification of Escherichia coli isolates. Antimicrobial susceptibility test was performed using Kirby-Bauer disk diffusion method against common antibiotics.

**Results :** Isolates showed the highest resistance to amoxicillin (97%), whereas gentamaycin was the most effective drug, with only 8.4% resistance. The frequency of multi drug resistance (MDR) to more than 5 antibiotics was 79%.

**Conclusion :** As the results of this study indicate, multidrug resistance is an increasing therapeutic concern and treatment requires further attention to the results of susceptibility tests. Antibiogram is recommended before starting antimicrobial treatment.

**Keywords :** : Antimicrobial Resistance Pattern, Escherichia coli, antibiogram

# P44-229: Invitro investigation of the effect of Aztreonam and Ceftazidime on NDM producer Klebsiella pneumonia isolates.

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**Background and Aim :** NDM is novel board-spectrum Metallo B lactamase with the capability to grant resistance to almost B- lactam antibiotics. Its widespread dissemination made treatment options a major challenge to combat, causing threat to public health worldwide. Due to antibiotic resistance problems, development of effective therapeutics for infections caused by NDM producing strains is urgently required. The present work was aimed to assess the effectiveness of current CPE detection guidelines we analyzed the Aztreonam and Ceftazidime MIC distribution for NDM producer Klebsiella pneumonia isolates.

**Methods :** THIS study was conducted in 2021 under the supervision of Arak University of Medical Sciences. Samples used in this study are from a surveillance study with doi: 10.1186/s12941-020-00349-z. 122 Klebsiella spp. isolates were cultured from extraintestinal specimens such as blood, urine , etc of patients admitted to the tertiary referral hospital in Semnan that 16 of them were NDM positive. The microdilution broth method was performed to analyze the minimal Inhibitory Concentration

**Results :** In this study, in 16 NDM producer Klebsiella pneumonia appeared the susceptibility to Aztreonam in 12 isolates were 64mg/ml and in 4 isolates were 32mg/ml and susceptibility to Ceftazidime in 11 isolates were 128mg/ml and in 5 isolated were 64mg/ml. To determine microbial resistance, MIC method was used on NDM samples, while in some studies, disk diffusion method was used. It seems that the use of microdilution method to determine the MIC leads to more accurate results than the E-test method.

**Conclusion :** Given paucity to treatment options there is a critical need to stop the spread of CPE in laboratory setting has been challenging. This study indicated Aztreonam is more effective antibiotic than Ceftazidime. A synergistic effect may be observed due to the combination of these two antibiotics that I will consider in future research this.

**Keywords :** Ceftazidime, Aztreonam, Klebsiella pneumonia, Microbial resistance, New Delhi Metallo-β-lactamase

# P45-230: High frequency of genes KPC in Klebsiella pneumoniae strains isolated from clinical samples of a tertiary hospital

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**Background and Aim :** Due to the increasing prevalence of antibiotic resistance to beta-lactam and Carbapenem producing bacteria, Identification of the gene isolates of these enzymes is essential for the timely treatment of such isolates as KPC-type Klebsiella strains. Therefore, the aim of this study was to identify and investigate the frequency of Klebsiella pneumonia strains producing KPC carbapenemase in clinical samples from Valiasr Hospital Arak, Iran

**Methods :** In this cross-sectional study, 100 samples of Klebsiella pneumoniae were isolated from clinical samples of Valiasr Hospital. After confirmation by biochemical tests, the susceptibility of all isolates to imipenem was determined by disk diffusion method Then, carbapenemase inhibitory method(CIM) method was performed to evaluate the carbapenemase resistance and to confirm the MIC by E-test. To confirm the metallo-beta-lactamase resistance, the combined disk test (CDDT) IMP / EDTA was performed. Finally, using PCR method, blaKPC gene was investigated in Klebsiella strains with carbapenemase resistance

**Results :** In this study, out of 100 strains of Klebsiella pneumoniae, 84 (84%) samples were identified as Carbapenem resistance by disk test and MIC method. Out of 84 isolates 30 (36%) were carbapenemase resistance and 54(64%) metallo-beta-lactamase resistance were observed. Among isolates with carbapenemase resistance, all samples carried the blaKPC gene.

**Conclusion :** The results of the present study showed that Klebsiella strains isolated from clinical samples of Valiasr Hospital Arak are associated with to carbapenems resistance along with the expression of blaKPC gene. Because the present gene can be spread among bacteria through genetically engineered elements, it is a serious warning sign in the treatment of infections caused by Klebsiella pneumoniae.

**Keywords :** Klebsiella pneumoniae , carbapenemase Resistance , KPC gene

# P46-249: Evaluation of colistin antibiotic resistance gene in k. pneumoniae

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**Background and Aim :** increase antibiotic resistance in multidrug- resistant gram negative bacteria (MDR- GNB), presents significant health problems worldwide, since the vital available and effective antibiotics, including; penicillins, fluoroquinolones, aminoglycosides, and β-lactams; often fail to fight MDR Gram-negative pathogens as well as the absence of new antibiotics that can defeat these 'superbugs'. All of these has prompted the reconsideration of old drugs such as polymyxins which have potential clinical toxicity, especially hepatotoxicity. However, although the polymyxins, especially colistin, are used as the last line of antimicrobial defense, the resistance against polymyxin in pathogens

**Methods :** using disk diffusion method, we tried to Determining the prevalence of various types of resistance in Klebsiella pneumoniae, which causes many nosocomial infections, Use of the Phoenix device to determine the minimum inhibitory concentration for 16 antibiotics and also using PCR method to try to identify its molecular mechanisms in different strains of bacteria isolated from several hospitals in Isfahan, including chromosomal coded resistance, mutated chromosomal mechanisms and transposon genes involved in the development of antibiotic resistance such as the MCR gene group, the synergistic effect of the compounds Antibiotics and non-antibiotics to the isolated strains of colistin resistant

**Results :** All 68 strains of the bacterium were isolated mdr, of which 16 were colistin-resistant bacteria, indicating that the prevalence of colistin resistance among these bacterial strains was increasing, causing high mortality among hospitalized patients.

**Conclusion :** All K. pneumoniae showed a multidrug-resistant phenotype, particularly to colistin. Colistin resistance was mainly associated with deleterious mutations and transposon in the mgrB gene and it is necessary to prevent the spread of these genes as much as possible by using new strategies such as the use of probiotics, etc.

**Keywords :** Gram-negative bacteria, antibiotic resistance, colistin, MCR

# P47-258: Evaluation of fos A3 and simultaneous CTX-M genes among fosfomycin resistance Pseudomonas aeruginosa isolates .

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**Background and Aim :** Respiratory secretions of cystic fibrosis (CF) patients provide an environment to the colonization of opportunistic pathogens. The aim of this study was to evaluate the resistance to fosfomycin and the frequency of fos A3 in simultaneous to CTX-M gene which is responsible to extended spectrum beta-lactamase (ESBL) production among Pseudomonas aeruginosa isolates from patients with CF

**Methods :** In this study, 40 P.aeruginosa isolates from sputum of patients with cystic fibrosis in Mofid hospital were collected 2020 .All isolates were reconfirmed by standard bacteriologic methods and kept in 10% glycerol +TSB at -70°C.Antimicrobial susceptibility test(AST)was performed by disk diffusion method and resistance to fosfomycin and colistin evaluated by E-test. PCR was used for the abundance of fos A3 and bla CTX-M genes.

**Results :** Based on the AST, the most resistant was to Amikacin (52.5%). By E- test, resistant to fosfomycin and colistin was (57/5%) and (2.5%) respectively. The frequency of bla CTX-M and FosA3 plasmid genes was (42.5%) and (67.5%) respectively by PCR.

**Conclusion :** Simultaneous existence of fosA3 gene (67.5%) and bla CTX-M (42.4%) among P. aeruginosa isolates, show the importance of distribution of resistant to other bacteria via plasmidic carrier. So, to decrease the resistance rate, doing AST before any prescription and no arbitrarily consumption of antibiotics is recommended. Also, evaluation of the role of chromosomal genes such as glpT and the role of presumptive mutations in the fosfomycin resistant P. aeruginosa isolates in further studies is mandatory.

**Keywords :** : P. aeruginosa, bla CTX-M, fosfomycin, fosA3 gene

# P48-266: Detection of Plasmid-mediated Amp-C β-Lactamases in Klebsiella pneumoniae Clinical Isolates

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**Background and Aim :** The aim of this study was to investigate the prevalence of plasmid-mediated AmpC β-lactamases (pAmpCs) in clinical isolates of Klebsiella pneumoniae using phenotypic and genotypic methods.

**Methods :** A total of 228 K. pneumoniae isolates were collected from 6 hospitals in Bushehr province, Iran, over a period of 14 months (December 2017- January 2019) and confirmed using polymerase chain reaction (PCR) of the malate dehydrogenase gene. Cefoxitin insusceptibility was used for screening AmpC production. Three phenotypic confirmatory tests including combination disk test (CDT) with 3-aminophenylboronic acid (BA), double disk synergy test (DDST) and modified three dimensional test (M3DT) were conducted. The genes encoding pAmpC were investigated by multiplex PCR as the gold standard.

**Results :** Out of 228 isolates, 38 were resistant to cefoxitin in screening test while only 18 (7.9%) isolates were confirmed as pAmpC producer by multiplex PCR: 12 DHA (66.6%) and 6 CMY (33.3%). In addition, 72.2% of PCR-positive isolates harbored both AmpC and ESBL ?-lactamases.

**Conclusion :** In this study DHA was the most prevalent pAmpC β-lactamases in our collection of K. pneumoniae clinical isolates. Comparing the results of three phenotypic tests, M3DT represented the best overall performance (92% efficiency). It is notable that despite the low prevalence of pAmpC in Bushehr, the spread of clinical isolates harboring both pAmpC and ESBL β-lactamases requires regular monitoring and careful surveillance.

**Keywords :** AmpC β–lactamase, Klebsiella pneumoniae, CDT, DDST, M3DT

# P49-277: Inhibitory effect of hydroalcoholic extract of native plants of Dysphania botrys and Artemisia khorassanica on some Gram-positive and Gram-negative bacteria

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**Background and Aim :** Following the development of drugs, microorganisms become resistant to them through a variety of mechanisms. In recent years, the prevalence of antibiotic resistance has increased dramatically and the treatment of diseases caused by them has become more difficult. In this regard, new drugs are being developed. The aim of this study was to study the inhibitory effect of hydroalcoholic extracts of Dysphania botrys and Artemisia khorassanica on some bacteria.

**Methods :** Artemisia khorassanica (Family: Asteraceae) and Dysphania botrys (Family: Amaranthaceae) were collected from suburbs of Quchan (Khorasan Razavi province). After extracting the hydroalcoholic extract of the mentioned plants, blank discs impregnated with 2 mg of the extract were prepared using DMSO. Inhibitory effect of the extracts was determined by disk diffusion method based on Kirby Bauer standards. Klebsiella pneumoniae (ATCC 700603), Micrococcus, Staphylococcus aureus (PTCC111) and Staphylococcus epidermidis (ATCC12228) and 15 clinical isolates of K. pneumoniae were inoculated on Mueller-Hinton agar. Clinical isolates were previously identified using differential biochemical tests and confirmed with 16S rRNA primer and polymerase chain reaction. Standard gentamicin disk and blank disk were placed on the plate as positive and negative controls.

**Results :** The results showed that the highest effect of D. botrys on S. aureus (18 mm) and the highest effect of A. khorassanica on K. pneumoniae (12 mm). The minimum inhibition concentration (MIC) of D. botrys was 500 ?g/ml against S. aureus.

**Conclusion :** The results of this study showed that these two plants or their effective compounds can be a good candidate for the more effective treatment of bacterial infections.

**Keywords :** Dysphania botrys, Artemisia khorassanica, Antimicrobial activity, Diffusion disk

# P50-305: Antimicrobial effect of aqueous and methanolic extracts of white tea on standard and clinical strains involved in wound infection

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**Background and Aim :** Skin health is important as the body's first line of defense. Treatment of skin wound infections is one of the major concerns of medical science. The use of antibiotics is a common treatment method, but today, due to the increase in antibiotic resistance, in most cases, early treatment is not achieved. Therefore, efforts to reduce the use of antibiotics by replacing natural active ingredients can be worthwhile. Medicinal plant extracts are considered due to having active ingredients with antimicrobial, anti-inflammatory, and antioxidant properties, as well as their easy availability and reasonable price. The aim of this study was to investigate the antimicrobial effect of white tea extract on standard and clinical strains isolated from purulent wound secretions.

**Methods :** In this study, aqueous and methanolic extracts of Iranian white tea leaves were prepared by maceration method and their antimicrobial activity was evaluated by disk diffusion and agar well diffusion methods. The minimum inhibitory concentration (MIC) and the minimum bactericidal concentration (MBC) were evaluated by microdilution method. Bacteria included standard strains of Staphylococcus aureus (ATCC 25923), Pseudomonas aeruginosa (ATCC 27853), Klebsiella pneumoniae (ATCC 13883) and Escherichia coli (ATCC 25922), and their clinical strains isolated from purulent wound secretions.

**Results :** Aqueous and methanolic extracts of white tea showed antimicrobial effect on all strains. The most antimicrobial effect was related to aqueous extract of white tea on standard Staphylococcus aureus and the concentration of 50 mg / ml of this extract resulted in an average diameter of growth inhibition zone in the disk diffusion method and agar well diffusion method of 24.3 mm and 29.6 mm, respectively. The MIC and MBC of this extract on this bacterium were 25 and 50 mg / ml, respectively.

**Conclusion :** The aqueous extract of white tea had the most antimicrobial effect on the studied strains, especially gram-positive bacteria. Therefore, it can be used in the preparation of medicinal ointments with topical application at the site of wound infection after assessment of its efficacy and safety in the laboratory mice and then volunteer patients having purulent wound.

**Keywords :** extract white tea - maceration - Antimicrobial effect - Wound infection

# P51-308: Comparison of antibacterial activity of aqueous and methanolic extracts of Dracocephalum kotschyiboiss against some standard and clinical strains involved in wound infection

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**Background and Aim :** It is necessary to develop new efficient antibacterial agents because of the growing antibiotic resistance as a major public health problem. Medicinal plant extracts have a good antimicrobial potential against the resistant/non-resistant pathogenic bacteria due to their secondary active metabolites such as phenolic compounds. These natural agents are more compatible with the body and have fewer unwanted side effects. The aim of this study was to compare the antimicrobial effect of aqueous and methanolic extracts of Dracocephalum kotschyiboiss aerial parts against Staphylococcus aureus and Pseudomonas aeruginosa as two important bacterial pathogens causing burn wound infections.

**Methods :** Aqueous and methanolic extracts of Iranian Dracocephalum kotschyiboiss (aerial parts) were prepared by maceration and their antimicrobial activity was evaluated by disk and agar well diffusion methods against standard strains of Staphylococcus aureus (ATCC 25923) and Pseudomonas aeruginosa (ATCC 27853) and their clinical strains isolated from purulent wound secretions. The minimum inhibitory concentration (MIC) and the minimum bactericidal concentration (MBC) of extracts were determined using microdilution method.

**Results :** Methanolic extract, unlike aqueous extract, showed good antimicrobial effect on all strains. Methanolic extract showed the most antibacterial effect on clinical Staphylococcus aureus with MDR resistance pattern. The concentration of 50 mg/ml of this extract resulted in an average diameter of growth inhibition zone of 18.3 and 18.6 mm against Staphylococcus aureus in disk diffusion and agar well method, respectively. The MIC and MBC of this extract on this bacterium were 6.25 and 25 mg / ml, respectively. Methanolic extract (50 mg/ml) also showed an acceptable effect on Pseudomonas aeruginosa with an average diameter of growth inhibition zone of 18.6 and 16.6 mm in disk diffusion and agar well method, respectively. The MIC and MBC of this extract on this bacterium were 12.5 and 25 mg / ml, respectively. The aqueous extract had no antimicrobial effect on the strains of this study.

**Conclusion :** Due to the antimicrobial effect observed against both gram-positive and gram-negative pathogenic bacteria, the methanolic extract of Iranian Dracocephalum kotschyiboiss

(aerial parts) has great potential for use in the treatment of wound infections, which of course requires further research in this area.

**Keywords :** methanolic extract - Aqueous extract - Dracocephalum kotschyiboiss -Maceration - Wound infection - Antibacterial activity

# P52-317: Prevalence of colistin Resistance in MDR Escherichia coli and Klebsiella pneumoniae strains isolated from clinical infections in selected hospitals in Isfahan

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**Background and Aim :** The increasing prevalence of colistin resistance in multidrug-resistant(MDR) gram-negative bacteria which caused nosocomial and serious infections , is now an important clinical problem worldwide.The main objective of this study was to determine the antibiotic resistance pattern especially the rate of colistin resistance isolates.

**Methods :** In this cross-sectional study, 141 clinical isolates of E. coli (n=78)and K. pneumoniae (n =63) have been obtained from hospitalized people with severe infections in Isfahan. All isolates were identified using standard microbiology tests. The disk diffusion susceptibility testing and the Minimum Inhibitory Concentration(MIC) of colistin were performed according to the Clinical and Laboratory Standards Institute (CLSI 2020) guidelines. Antibiotic disks used in this study included aztreonam ,amikacin ,ciprofloxacin, levofloxacin ,cefepime , ceftriaxone ,ceftazidime ,cefoxitin ,imipenem ,piperacillin/tozabactam.

**Results :** MDR isolates were found in E. coli (55.31%)and K. pneumoniae (44.68%).The results of antibiogram tests showed that most of the MDR isolates were resistant to ciprofloxacin, cefepime, ceftazidime ; however, the most susceptibility among the isolates were to imipenem ,piperacillin/tozabactam, aztreonam .The colistin resistance among E.coli and K. pneumoniae was 5% and 52.5% respectively .

**Conclusion :** In this study, high frequency of colistin-resistant E. coli and K. pneumoniae isolates was seen . Also , the increased rate of MIC pattern of colistin resistant bacteria in our severe infections. As respects to that colistin is the last line of severe infections treatment, increasing resistance to this antibiotic lead to higher mortality and hospital costs. It is necessary more sensitivity in early diagnosis and control of nosocomial infections.

**Keywords :** MDR, E. coli , K. pneumoniae ,Resistance, colistin .

# P53-320: Inhibitory effect of onion juice and eucalyptus essential oil against antibiotic-resistant clinical isolates of Klebsiella pneumoniae and Escherichia coli

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**Background and Aim :** Finding the right drug to treat bacterial infections has always been a challenge for researchers. This challenge has become more difficult due to the increasing development of bacterial resistance and the emergence of antibiotic-resistant strains. In this study, white onion juice (family: Amaryllidaceae) and eucalyptus essential oil (family: Eucalyptus) (Barij Esans Company, Iran) were tested against 15 clinical isolates of Klebsiella pneumoniae and onion juice against 6 clinical isolates of antibiotic-resistant Escherichia coli.

**Methods :** Clinical isolates were previously identified using conventional biochemical tests and confirmed by polymerase chain reaction using 16S rRNA gene primers. The pattern of sensitivity of isolates to onion juice and eucalyptus essential oil was determined by two methods of disk diffusion and the agar well diffusion, according to CLSI standards. Gentamicin antibiotic disc was used as positive control and sterile distilled water was used as a negative control. After 24 hours of incubation at 37 °C, the diameter of the bacterial growth inhibition zone was examined. The results of this study showed that eucalyptus essential oil had the highest growth inhibitory effect against K. pneumoniae isolates. Also, the growth inhibition of eucalyptus essential oil in the agar well diffusion method was higher than the disk method.

**Results :** So that the growth inhibition zone of K. pneumoniae compared to eucalyptus essential oil was 23 mm in the agar well diffusion method and 9 mm in the disk diffusion method. All clinical isolates of K. pneumoniae and E. coli were resistant to the onion juice.

**Conclusion :** According to the results of this study, it can be concluded that eucalyptus essential oil can be a suitable alternative to chemical drugs against K. pneumoniae as the herbal medicine with a high antimicrobial effect.

**Keywords :** Eucalyptus, Onion, Diffusion disk, Antimicrobial activity

# P54-321: Evaluation of the BD Phoenix automated identification & susceptibility testing system in antibiotic resistance pattern of Acinetobacter strains isolated of hospitalized patients in ICU from Mashhad Hospitals in 2020

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**Background and Aim :** Infection with antibiotic resistance bacteria such as Acinetobacter is one of the most important problems in treatment in the world. This non-fermentative Gram negative bacteria can cause nosocomial infections (NI) in hospitalized patient after 48 to 72 hours especially in the intensive care unit (ICU). The incidence rate of NI infections in the ICU in developed countries is up to 50%. Using the Phoenix Automated Microbiology system can be a suitable tool in identifying bacteria and determining the exact pattern of microbial resistance of bacteria, especially Acinetobacter as one of the most common agent in NI in the ICU. The objective of this study was to evaluate the Phoenix system in the antimicrobial susceptibility testing of Acinetobacter isolates collected from hospitalized patients in ICU from Mashhad hospitals in one year in Iran.

**Methods :** The Phoenix system in the identification & antimicrobial susceptibility testing using one Phoenix panel type, NMIC/ID-5 used for 160 gram-negative isolates collected different samples of ICU patients from Mashhad hospitals in 2020.

**Results :** The results produced by the system identified 60 Acinetobacter strains. A category agreement value was found for the susceptibility of Acinetobacter to Colistin (90%). The antibiotic resistance pattern showed the highest resistance to Aminoglycosides (55%), Carbapenemase (55%), Quinolones (55%), Cephalosporin (54%), Macrolides (54%), Beta Lactamase (54%), Sulfonamides (43%) and Monobactams (40%), respectively. The results indicated the increasing of antibiotic resistance of Acinetobacter to those antibiotics group which has been sensitive, previously.

**Conclusion :** This study demonstrates the development of antibiotic-resistance of Acinetobacter strains in ICU in Mashhad. The use of prophylactic antibiotics in high-dose for ICU patients appears to increase drug resistance. It is highly recommended to antibiotic stwartetship in Acinetobacter infections. Decided to provide appropriate solutions to control the increase in resistance as well as provide a suitable new line for treatment according to MIC it seems necessary.

**Keywords :** Acinetobacter spp, ICU, nosocomial infections, antibiotic resistant pattern, Phoenix system

# P55-322: Isolation, identification and antibiotic susceptibility pattern of peripheral isolates of Klebsiella during Corona

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**Background and Aim :** Klebsiella species are found everywhere in nature. They can be found in water, soil, plants, animals and humans. Klebsiella is commonly found in the intestines and feces of humans. These bacteria enter other areas of the body and cause opportunistic infections. The aim of this study was to isolate, identify and investigate the antibiotic susceptibility of Klebsiella peripheral isolates in the Corona period.

**Methods :** Samples were collected from the sanitary services of parks and university (Faculty of Basic Sciences, Islamic Azad University) in Mashhad. Of the 120 samples collected, 16 Klebsiella isolates were collected by transferring swabs in a nutrient broth and transferred to McConkey agar. Isolates were identified using tests of oxidase, indole, sugar fermentation, gas production, motility, MRVP, and citrate. Also they were confirmed by molecular method using specific primers of Kp16S rRNA and PCR. Of the 16 Klebsiella isolates, 14 were K. pneumoniae. The pattern of antibiotic susceptibility was determined by disk diffusion method based on Kirby Bauer standards.

**Results :** 69.23% of the isolates were resistant to quinolone. The highest and lowest antibiotic resistance of isolates were related to cefotaxime and aztereonam (76.92%) and nalidixic acid (31.53), respectively. The highest and lowest antibiotic susceptibility of the isolates were related to norfloxacin (61.54%) and cefotaxime and aztereonam (23.08), respectively. Nine isolates (69.23%) were multi-drug resistant.

**Conclusion :** The results showed that despite observing hygiene and disinfection of places in corona era, Klebsiella isolates can be isolated from the environment. The resistance of these

isolates to antibiotics was relatively high, which indicates the rotation of resistant strains in the community and environment.

**Keywords :** Klebsiella, Identification, Peripheral isolates, 16S rRNA

# P56-357: Phenotypic and genotypic study on presence of M-bla-CTX and OXA-10 genes in clinical isolates of Acinetobacter baumannii

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**Background and Aim :** Acinetobacter baumannii is an opportunistic pathogen that is mainly important in causing nosocomial infections, especially in ICU wards. This bacterium causes many infections such as sepsis, pneumonia and urinary tract infections following hospitalization. In addition, Acinetobacter baumannii and Pseudomonas aeruginosa are the most common organisms isolated from burns. One of the most important problems with this bacterium is the increase in isolates with multidrug resistance, which can be due to the widespread use and without control of antimicrobial agents, especially in developing countries. Studies show that this bacterium has the ability to acquire external DNA sequences, including antibiotic resistance genes and can survive in environments that are harmful to bacteria. Therefore, there is the potential for resistance to different classes of antibiotics, including aminoglycosides, broad-spectrum cephalosporins, and fluoroquinolones.

**Methods :** Bacterial samples were collected from educational and medical centers in Tehran and microbiological tests were used to confirm the strains and then the pattern of drug resistance was determined using disk diffusion method according to 2020 CLSI guidelines. The presence of OXA-10 and bla CTX-M genes was investigated by polymerase chain reaction.

**Results :** 38 isolates of Acinetobacter baumannii had high resistance to 10 antibiotics used in this study and the results of polymerase chain reaction showed that out of 38 samples of Acinetobacter baumannii, 12 strains had OXA-10 gene and 32 strains had bla- CTX-M gene.

**Conclusion :** The results revealed a very high resistance of Acinetobacter baumannii to antibiotics, which requires the use of multidrug therapy and the discovery of new antibiotics chemically or using plant extracts or nanoparticles.

**Keywords :** Acinetobacter baumannii, Drug resistance, Disc diffusion, PCR

# P57-360: Alteration of Enterobacteriaceae microbial composition, drug resistance pattern and resistance spectrum to broad-spectrum beta-lactams in pediatric gastrointestinal tract during hospitalization

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**Background and Aim :** Infections caused by extended-spectrum β-lactamase (ESBLs)-producing organisms have been described as an emerging worldwide public health problem. Transmission of these pathogens from the community to hospitals and vice versa is considered as a public health threat. Although secondary infections from the hospital environment is critical for patients, administration of antibiotics in hospital settings is considered as an important risk factor for selection and enrichment of ESBLs-producing bacteria.

**Methods :** In this study, 78 pairs of fecal samples from hospitalized children in PICU ward were examined in two different time periods, <48 hours and 3-5 days after hospitalization in Mofid Children's hospital. Bacterial isolates were identified by standard diagnostic and biochemical methods and antimicrobial susceptibility testing and ESBL phenotype were performed using DOUBLE DISK method.

**Results :** Among the samples studied in the first and second stages, the presence of Escherichia coli, Klebsiella and Enterobacter species was detected in 81.9% and 69.4%, 11.1% and 18.1%, and 6.9% and 12.5%, respectively. Comparison of drug resistance patterns confirmed the highest changes in resistance to cefotaxime-clavulanic acid (from 24% to 34%) and the lowest to amoxicillin-clavulanic acid (From 84% to 82%). ESBL phenotype was detected in 59% of primary isolates and 51.3% of isolates obtained afterwards. In total, 28.6% of patients did not have strains with ESBL resistance pattern.

**Conclusion :** These findings highlight that changes in the intestinal colonization of members of the Enterobacteriaceae family and drug resistance patterns occur in the pediatric gastrointestinal tract following the hospitalization and antibiotic use.

**Keywords :** Enterobacteriaceae, Extended-spectrum β-lactamase, pediatric,drug resistance

# P58-361: Prevalence of carriers of family members of Enterobacteriaceae producing Extended-spectrum β-lactamase in the feces of hospitalized children

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**Background and Aim :** Children are at risk for disease, and this is especially true for those admitted to the NICU. Extended-spectrum β-lactamase-producing enterobacteriaceae are one of the bacterial species that can spread to wards of these hospitalized children. The aim of this study was to evaluate the prevalence of enterobacteriaceae producing Extended-spectrum β-lactamase in the feces of children admitted to the intensive care unit of a pediatric hospital.

**Methods :** In this experimental study, patient's information including age, sex, type of disease, history of hospitalization, duration of hospitalization, etc. was first collected by a questionnaire. The collected stool samples were examined by culture and antibiogram and a drug resistance pattern was determined for them.

**Results :** In this study, fecal samples of 74 patients were examined. 92% of patients in the first culture had at least one of three families of Enterobacteriaceae (69.4% Escherichia, 18.1% Klebsiella and 12.5% Enterobacter). Fifty-nine percent of patients in the first culture and 51.3% in the second culture were positive for ESBL phenotype. Resistance pattern of 50 patients was studied. 66% had different pattern and the remaining 34% had the same drug resistance pattern in the first and second cultures and the highest frequency was related to CEFOTAXIM-CLAVULANIC ACID (24.2%).

**Conclusion :** Extended-spectrum β-lactamase-producing enterobacteriaceae have a high prevalence and high antibiotic resistance in the feces of neonates admitted to the NICU care unit. This resistance has correlation with the age and sex and previous antibiotics taking. The ESBL gene can change the degree of antibiotic resistance from susceptible to resistant, even during hospitalization.

**Keywords :** Enterobacteriaceae, Extended-spectrum β-lactamase, pediatric, drug resistance

# P59-362: Profile of drug resistance in Staphylococcus saprophyticus strains causing urinary tract infection in Women from Gorgan, Northern of Iran

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**Background and Aim :** S.saprophyticus is a Coagulase-negative staphylococci that was reported in a 1962 Torres Pereira study to be associated with a urinary tract infection. Intrinsic resistance to novobiocin disc is a laboratory characteristic that distinguishes it from other species.The pathogenicity of S.saprophyticus is related to some major surface proteins that have been characterized as important for the pathogenesis and attachment to host tissues, and some enzymes, such as D-serine deaminase (DsdA), urease. Today, increasing antibiotic resistance has become a major challenge in the treatment sector. This study aimed to investigate the pattern of antibiotic resistance of S.saprophyticus isolates from urine samples in northern Iran (Gorgan)

**Methods :** This study was performed from May 2018 to September 2020. The antibiotic susceptibility pattern of Staphylococcus saprophyticus isolates evaluation was carried out using the disc diffusion method (Kirby Bauer) according to (CLSI2019)Clinical and Laboratory Standards Institute. For identification of the isolates, 16S rRNA gene were amplified. Some PCR products were sequenced and deposited in the GenBank.

**Results :** Thirty-five isolates of S.saprophyticus had novobiocin disk resistance, Examination of growth in mannitol salt agar medium showed that 22 isolates (62.9%) were able to ferment mannitol sugar. All isolates belonged to women (100%) with urinary tract infections. Patients ranged in age from 4 to 65 years. (Mean ± SD) (35 ± 11/8). The results of the antibiogram showed that All strains (100%) were sensitive to the linezolid, Gentamicin, and Nitrofurantoin. the High sensitivity was also observed to Cotrimoxazole and Levofloxacin(94/3%). urinary tract infections caused by this bacterium have reported the existence of a seasonal distribution pattern. In the present study, 24 isolates (68.6%) were related to the summer season.There is no clear reason for this seasonal variation.

**Conclusion :** the choice of a solution to reduce resistance or use complementary or alternative therapies with antibiotics such as the use of bacteriophages in the treatment of urinary tract infections has been considered. The authors have also Isolation and Identification of

S.saprophyticus Lytic bacteriophages from Urban and Hospital Wastewaters in Gorgan city ، The results will be published soon.

**Keywords :** Urinary tract infection, Staphylococcus saprophyticus, Antibiotic resistance

# P60-363: Study of antimicrobial effect of ethanol extract of Cnicus benedictus and Parietaria judaica, on the bacteria A.baumannii and S.aureus

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**Background and Aim :** Infectious diseases caused by resistant infectious agents have led to serious complications.This study was designed to determine the antimicrobial efficacy of the hydroalcoholic extracts of Cnicus benedictus and Parietaria judaica against Staphylococcus aureus and Acinetobacter baumannii.

**Methods :** hydro alcoholic extract of medicinal plant collected from The scope of Chaharmahal va Bakhtiari; Extraction produced by soaking method then The MIC values and MBC of the Cnicus benedictus and Parietaria judaica extract against the bacterial strains Staphylococcus aureus ATCC 25923, Acinetobacter baumannii PTCC 1855) were determined by a micro broth dilution method based on instructions CLSI.

**Results :** The MIC value for the hydro alcoholic extract of Cnicus benedictus was 4 mg/mL for Acinetobacter baumannii and 2 mg/mL for S. aureus. The MIC value of the ethanol extract of Parietaria judaica was 4 mg/mL for Acinetobacter baumannii and 4 mg/mL for S. aureus. The MBC value of the ethanol extract of Cnicus benedictus was 8 mg/ml for S. aureos and 8 mg/ml for A. baumannii. The MBC value of the ethanol extract of Parietaria judaica was 16 mg/ml for S. aureos and 16 mg/ml for A. baumannii.

**Conclusion :** According to antibacterial effects of alcoholic extracts, The best inhibitory effect on S. aureus for Cnicus benedictus and The best inhibitory effect on A. baumannii for Parietaria judaica. the necessity of further research on this plant in order to extract its effective compounds and its effects on a variety of pathogens is suggested.

**Keywords :** Antimicrobial effects, Cnicus benedictus, Parietaria judaica, Staphylococcus aureus, Acinetobacter baumannii

# P61-376: Evaluation of Antibiotic Resistance in Isolates from UTI in Department of Pediatrics, Shohada Hospital, Izeh, in Khuzestan province

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**Background and Aim :** One of the most important infections in children is urinary tract infection. It is essential to prevent serious complications of urinary tract infections in children, such as high blood pressure and kidney failure, and definitive diagnosis and immediate treatment is needed. Since the Enterobacteriaceae family is the most common cause of urinary tract infection, the aim of this study was to evaluate the antibiotic resistance in isolates from the UTI in department of pediatrics in Shohada hospital at Izeh in 2017.

**Methods :** This cross-sectional study was performed on urine specimens of children with UTI who were admitted to the pediatric ward of Shohada hospital at Izeh during 3 months (from April to June). Urine specimens were cultured on selected media and isolates were identified by biochemical tests. Antibiotic resistance pattern was studied by disk diffusion.

**Results :** From 110 urine samples related to the children admitted to the pediatric ward of Shohada Hospital at Izeh, 53 were female (48/2) and 57 were male (51/8). Escherichia coli with 15/5% outbreak, was the most prevalent bacterium isolated among Enterobacteriaceae family. Clinical isolates were most susceptible to amikacin (76/4%) and imipenem (64/7%) and had the highest resistance to ceftriaxone (100%).

**Conclusion :** Considering the prevalence of urinary tract infections in children, for preventing its serious complications, evaluation of regional pattern and timely treatment must be done. For experimental treatment of urinary tract infections in children, amikacin and imipenem antibiotics are recommended.

**Keywords :** UTI, Pediatrics, Escherichia Coli, Antibiotic Resistance, Diffusion Disc

# P62-380: Analysis of the presence of genes conferring resistance to aminoglycosides in Acinetobacter baumanii isolates belonging to global clone1 (GC1) and determination of the location of resistance genes

Atena Nemati[1] *

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**Background and Aim :** A. baumannii (Acinetobacter baumannii) is a nosocomial pathogen known as a global worry because of high levels of resistance to many antibiotics. Aminoglycoside resistance has increased in these bacteria due to the expression of AMEs (Modifying Enzymes Genes). The cause of resistance to the aminoglycosides in A. baumannii isolates belongs to GC1 (Global Clone1), and the location of these genes, namely aphA6, aphA1b, aadB, aacA1, aacA4, and aadA1, have been determined.

**Methods :** PCR was used to characterize isolates, detect antibiotic resistance genes, and the location of AMEs genes on the mobile genetic elements. Plasmid pRAY* has been isolated and examined by restriction digestion to identify features. The clonal type was determined by Multiplex PCR and MLST (Multilocus sequence typing).

**Results :** Fourteen isolates that belong to GC1 were found among 253 A. baumannii isolated between 2012 and 2018 from 5 Hospitals in Tehran. Exhibited resistance to gentamicin, kanamycin, and tobramycin have related to AMEs. Present (100%) of aadB gene, 11 (78.57%) aadA1, 9 (28/64%) aphA6, 3 (42/21%) aacA1, 3 (42/21%) aphA1b, 3 (42 /%) 21) aacC1 were detected. aacA4 gene was not found in any of the isolates. These isolates all carried the aadB gene cassette on pRAY*.

**Conclusion :** Substantial diversity was observed among aminoglycoside-resistant genes in GC1 that increase antibiotic resistance and Lead to phenotypic resistance to the antibiotics amikacin, neomycin, gentamicin, and tobramycin. Therefore, molecular surveillance and providing Appropriate antibiotic prescribing for preventing infections is the most important to control the spread of these genes among GC1 isolates.

**Keywords :** Antibiotic Resistance Genes; Aminoglycosides; Global Clone; Acinetobacter baumannii; pRAY*

# P63-395: Expression of RND efflux pumps mediated antibiotic resistance in Pseudomonas aeruginosa Clinical Strains

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**Background and Aim :** Resistance-Nodulation-Division (RND) efflux pumps are responsible for multidrug resistance in Pseudomonas aeruginosa. The present study aimed to evaluate the overexpression of RND efflux pumps and its role in the antibiotic resistance of P. aeruginosa clinical isolates. A number of 122 isolates were obtained from three military hospitals in Tehran, Iran.

**Methods :** In order to determine the antibiotic resistance, the isolates were identified and assessed by the disk diffusion and agar dilution methods. This study investigated the gene expression of four multi-drug efflux pump systems (MexAB-OprM, MexCD-OprJ, MexEF-OprN and MexXY (-OprA)) and its correlation with antibiotic resistance.

**Results :** The isolates indicated that the highest resistance rate was against ticarcillin (80%), followed by ciprofloxacin (74%) and meropenem (71%). Most of them expressed mexB (69%), mexC (28.7%), mexE (43.4%), and mexY (74.6%), suggesting that mexB and mexY were highly expressed in the studied strains.

**Conclusion :** The overexpression of mexB and mexY was significantly more prevalent in the ICU wards (p=0.033). Furthermore, there was a significant correlation between the expression of RND-type efflux pumps and the resistance to most anti-pseudomonal antibiotics.

**Keywords :** Pseudomonas aeruginosa; Efflux pump inhibitor; MexAB-OprM; MexXY-OprA; MexCD-OprJ; Gene expression

# P64-428: Evaluation of the Frequency of mcr-1 Gene in Clinical Isolates of Escherichia coli in a Zanjan Educational Hospital (Valiasr)

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**Background and Aim :** Responsible for most of the gram negative blood and urinary tract infections in humans, Escherichia coli is one of the most debated microorganisms in the world. This study aimed to investigate the prevalence of the colistin resistance gene mcr-1 and the associated susceptibility profiles in E. coli isolates obtained from patients in an Iranian educational hospital.

**Methods :** In this cross-sectional study, a total number of 100 PCR-confirmed E. coli isolates were collected at an educational hospital in Zanjan, Iran in June 2021. Disk diffusion antimicrobial susceptibility disk diffusion was used to determine in the isolates. Minimum inhibitory concentrations were evaluated in the colistin resistant isolates and PCR was used to assess the presence of mcr-1 gene in them. Data analysis was performed using SPSS 26.

**Results :** Multidrug resistance (MDR) and ESBL production were observed in 72 and 56 isolates, respectively. Colistin resistance was observed in 70 isolates. The mcr-1 gene was detected in 30 (41%) MDR E. coli isolates. Resistance to other classes of antibiotics was less in these isolates, with the majority of them being susceptible to carbapenems.

**Conclusion :** The results indicate that colistin resistance is alarmingly rising among E. coli clinical isolates, including resistance mediated by the mcr-1 gene in Zanjan, Iran and controlling measures should be taken regarding this.

**Keywords :** Escherichia coli, Colistin. mcr-1

# P65-438: Antimicrobial Resistance and Fimbrial Virulence Genes of Uropathogenic Escherichia coli Isolated from Iran

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**Background and Aim :** Urinary tract infections (UTIs) are one of the most common bacterial infections with global expansion. These infections are predominantly caused by uropathogenic Escherichiacoli (UPEC).The present investigation was performed to study the fimbrial virulence factors and Antimicrobial Resistance of UPEC isolated from Iranian patients.

**Methods :** This cross sectional investigation was performed on 210 urine samples collected from hospitalized patients in Boroujerd, Sanandaj and Tehran hospitals, Iran. A totally 150 UPEC isolates were subjected to detect antibiotic resistance genes and bacterial fimbrial virulence factors. Also, antimicrobial susceptibility testing was performed according to the instruction of Clinical Laboratory and Standard Institute.

**Results :** We found that 26% of males and 74% of females had positive results for Escherichiacoli. High resistance levels to tetracycline (68%),sulfonamide (60%) and trimethoprim (58%) were also observed. 7.33% of tested strains were resistant to 8 antibiotics. The incidence of genes encoding resistance against aminoglycosides (aadA1 and aac(3)-IV), sulfonamide (sul1), beta-lactams (blaSHVand CITM), tetracycline (tetAand tetB), trimethoprim (dfrA1), chlor¬amphenicol (cat1 and cmlA) and quinolones (qnr) were (8%,5.33%), 44.66%, (42.66%, 8%), (58.66%, 55.33%), 48.66%, (8%, 3.33%)and 30%, respectively. The most commonly detected fimbrial virulence factors were fim(96.66%), pap(93.33%), papGII(42.66%) and papGIII(34%).

**Conclusion :** Resistant strains of uropathogenic E. coli had the high incidence of uropathogenic fimbrial virulence factors. In the current situation, it seems that the administration of tetracycline, sulfonamide and trimethoprim for the treatment of UTIs is vain.

**Keywords :** Uropathogenic Escherichia coli; Fimbrial Virulence Factors. Antimicrobial Resistance

# P66-439: Study of mutations in the quinolone resistance determinant regions of gyrA and parC among clinical isolates of Escherichia coli

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**Background and Aim :** Extensive consumption of quinolones and fluoroquinolones in the urinary tract infections (UTIs) have led to the increasing rate of resistance to these drugs. Occurrence of mutations in the QRDR region in the gyrA and parC genes encoding the target enzymes for fluroquinolones is the reason for resistance to them. The purpose of this study was conducted to determine the antibiotic resistance profile and mutations occurred in gyrA and parC genes among Escherichia coli (E. coli) isolates causing UTIs.

**Methods :** One-hundred E. coli isolates causing UTIs were obtained for the study. The isolates were identified following standard microbiology procedures as described everywhere. The antibiotic resistance profile was done according to the clinical laboratory standards institute (CLSI) protocol. Next, the quinolone-resistant isolates were evaluated regarding the mutations in the gyrA and parC genes with sequence analysis.

**Results :** of the total 100 isolates, 66% and 27.4% were resistant to nalidixic acid and ciprofloxacin, respectively. The sequencing results showed the presence of at least one mutation in each isolate, by occurrence of 83 (Ser Leu), 87 (Asp Asn) in gyrA gene and 80 (Ser Leu/Arg) and 84 (Glu Lys/Gly) in the parC gene as the main mutations detected here.

**Conclusion :** results from sequencing of gyrA and parC genes in the present study highlights the occurrence of those mutations leading to the high level resistance to quinolones and there was a significant relation between resistance to quinolones and these mutations. In order to overcome this issue, there is a need for restriction of indiscriminate prescribing antibiotics and performance and following the antibiotic susceptibility pattern of infectious agents.

**Keywords :** Escherichia coli, gyrA, parC, urinary tract infections, quinolones, fluroquinolones

# P67-443: Antibiotic Resistance and Virulence Factors Properties of Escherichia coli K1 Recto-vaginal Colonized Pregnant Women in Iran

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**Background and Aim :** Neonatal invasive infections caused by E. coli K1 are still major health problems and effective preventive strategies at the maternal level can be a concern. The aim of this study was to determine the prevalence of recto-vaginal colonization, related risk factors, virulence factors and antibiotic resistance properties of E. coli K1 among pregnant women.

**Methods :** In this cross-sectional study vaginal and rectal swabs were collected among 400 pregnant women. The identification of E. coli isolates was performed by microbiological tests. A PCR assay was used to identify the E. coli K1 strains. The antimicrobial susceptibility patterns were determined by the Kirby-Bauer disk diffusion. Two duplex PCR assays were developed separately to detect virulence determinants (fimH, hlyF, ibeA and iucC) in the E. coli strains.

**Results :** The vaginal and rectal maternal E. coli K1 colonization rates were reported 3.7% and 19.25%, respectively. There is no significant association between demographic-obstetric factors and vaginal E. coli colonization. The most effective antibiotics against E. coli K1 strains were Imipenem, Gentamycin, Ciprofloxacin and Ceftazidime. In our study the E. coli K1 strains were significantly more likely to possess the fimH (90.9 vs. 60.7%) and iucC (90.9 vs. 53.6%) than E. coli Non-K1 strains.

**Conclusion :** This study demonstrates that E. coli K1 seems to be more virulent than Non-K1 strains. Our findings highlight the importance of screening pregnant women for vaginal colonization by E. coli K1 and the appropriate antibiotic prophylaxis for the prevention of early onset E. coli -neonatal infection and co-morbidity.

**Keywords :** Escherichia coli K1, Pregnant women, Antibiotic resistance, Risk factors, Polymerase chain reaction, Virulence factors.

# P68-444: Antibiotic Resistance Patterns and Molecular Characteristics of Metallo-beta-lactamase Producing Non-fermentative Gram-negative Bacilli in Birjand, South-East Iran

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**Background and Aim :** Non-fermentative Gram-negative Bacilli (NFGNB) is known as a major cause of healthcare-associated infections with high levels of antibiotic resistance. The aim of this study was to investigate the antibiotic resistance profiles and the existence of blaIMP, blaVIM, and blaNDM genes among metallo-beta-lactamase (MBL)-producing NFGNB isolates.

**Methods :** In this cross-sectional study, the antibiotic resistance profile of 122 clinical NFGNB isolates was determined by the Kirby-Bauer disk diffusion and microdilution broth methods. Bacterial isolates were investigated for the detection of MBLs production using the combination disk diffusion Test (CDDT). The existence of blaIMP, blaVIM, and blaNDM genes in all carbapenem-resistant isolates was determined employing polymerase chain reaction (PCR) assays.

**Results :** High resistance in P. aeruginosa was reported to Cefotaxime and Minocycline, whereas A. baumannii isolates were highly resistant to all antibiotics except Colistin. Multidrug resistance (MDR)-NFGNB (66% vs. 12.5%, P=0.0004) and extensively drug resistant (XDR)-NFGNB (55.7% vs. 12.5%, P=0.001) isolates were significantly more common in hospitalized patients than in outpatients. The production of MBL was seen in 40% of P. aeruginosa and 93.3% of A. baumannii isolates. It was found that 33.3% and 46.7% of carbapenem-resistant P. aeruginosa isolates, and 13.3% and 28.9% of carbapenem-resistant A. baumannii isolates were harboring blaIMP-1 and blaVIM-1 genes, respectively. The incidence of MDR (98.2% vs. 28.3%, P<0.001) and XDR (96.4% vs. 11.7%, P<0.001) in MBL-producing NFGNB isolates was significantly higher than non-MBL-producing isolates.

**Conclusion :** This study demonstrated a higher rate of resistance among NFGNB isolates with an additional burden of MBL production within them, warranting a need for robust microbiological surveillance and accurate detection of MBL producers among the NFGNB.

**Keywords :** Gram-negative Bacteria, Carbapenems, Anti-bacterial agents, Metallo-beta-lactamase, Carbapenem resistance.

# P69-46: Evaluation the virulence factors and biofilm formation ability of isolated Acinetobacter baumannii strains from the teaching hospitals in Shiraz-Iran.

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**Background and Aim :** Acinetobacter baumannii as an opportunistic pathogen with the ability to form biofilm on biotic and abiotic surfaces and is one of the concerns related to nosocomial infections and hospital outbreaks worldwide. The aim of this study was to evaluate the presence of various virulence factors and the ability of isolated Acinetobacter baumannii bacteria from the hospitalized patients in Shiraz- Iran.

**Methods :** In this study the prevalence of A. baumannii isolates in clinical samples were investigated through the conventional biochemical tests. Also polymerase chain reaction (PCR) was used to evaluate the presence of virulence factors. Moreover, the biofilm formation ability was determined by microtiter plate methods.

**Results :** Out of 120 samples, about 100 isolate were confirmed as Acinetobacter baumannii. Although the presence of iutA (10%) and papC (5%) genes were affirmed by PCR method, the isolates were negative for the presence of cnf1, cnf2, fbn and kpsMT2. Additionally, the phenotypic biofilm formation (microtiter plate) showed that 61% of the Acinetobacter baumannii isolates had the ability to form biofilm. (p=0.028). Besides, there was no significant relationship between the presence of iutA and papC genes and biofilm formation.

**Conclusion :** the remarkable rates of Acinetobacter baumannii isolates were able to form biofilm which promotes their survival and growth in various environments and also in hospitals. Furthermore, we confirmed that iron uptake and fimbriae production plays an important role in virulence and adherence of Acinetobacter baumannii in order to initiate its pathogenesis.

**Keywords :** Acinetobacter baumannii, Polymerase chain reaction, Biofilm, iutA, papC.

# P70-59: A retrospective study of the prevalence of bacteria causing joint infection and their antibiotic resistance in Shiraz Shahid Chamran Hospital from 2018 to 2020.

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**Background and Aim :** Infectious arthritis is one of the bacterial inflammation factors of the joints that causes by bacterial spread in blood stream, and commonly after a trauma or surgery and also infection of bone or bone marrow. Therefore, early diagnosis and treatment of related septic arthritis plays an important role in control of arthritis infections. Hence, the aim of this study was to investigate the frequency of causative pathogen of joint infections and their antibiotic resistance profile in Shahid Chamran Hospital of Shiraz during 2018-2020.

**Methods :** Patient's records who were admitted to Shahid Chamran Hospital of Shiraz during 2018-2020 were reviewed. The information such as age, sex, inpatient ward and antibiogram were extracted and then analyzed for more information. Therefore, the statistical analysis was performed using SPSS mord software.

**Results :** Out of 249 samples, 29 were positive in bacterial culture. The most commonly used antibiotics were ciprofloxacin, cefazolin, cephalexin. Moreover, the antibiotic resistance to ciprofloxacin and cefazolin was increased during the three-year period of study.

**Conclusion :** Although the joint infections are common disease, it is not always possible to diagnose. So, early arthrotomy with along the onset of antibiotic treatment plays a vital role in reducing the incidence of related complications.

**Keywords :** Infectious arthritis, joint infections, bacteria, antibiotic resistance.

# P71-85: Detection of bla TEM and bla CTX-M in Klebsiella oxytoca isolated from patients in Khorramabad, Iran

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**Background and Aim :** Klebsiella oxytocan is a gram-negative bacillus and an opportunistic pathogen belonging to the Enterobacteriaceae family. The aim of current study was to identify the prevalence of bla TEM and bla CTX-M genes in Klebsiella oxytoca isolated from clinical specimens (Burns, wounds, urinary tract infections, and respiratory tract infections).

**Methods :** Klebsiella oxytoca strains screened from Klebsiella spp collected from hospitals of Khorramabad, Iran during the period from January 2019 to January 2020. After DNA extraction from all Klebsiella oxytoca clinical strains bla TEM and bla CTX-M genes detected by PCR technique.

**Results :** A total of 142 Klebsiella spp isolated 32 Klebsiella oxytoca were collected. The results showed that 19(59.3%) and 16(50 %) of isolates were carried bla TEM and bla CTX-M genes.

**Conclusion :** Due to the high prevalence of bla TEM and bla CTX-M genes, their tracing in clinical specimens for infection control measures by PCR-based molecular typing method is essential for rapid and reliable identification.

**Keywords :** Klebsiella spp; Klebsiella oxytoca; bla CTX-M gene; bla TEM; Enterobacteriaceae family

# P72-88: Investigation, identification, and antimicrobial resistance of Salmonella spp. isolated from Imam Khomeini hospital, Tehran

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**Background and Aim :** Salmonella is a facultative anaerobic gram-negative rod-shaped bacteria that belong to the Enterobacteriaceae family. Extensive use of antimicrobial agents such as Cotrimoxazole in medicine and veterinary has been associated with the rising of antimicrobial resistance. In the current study, we focused on the assessment of the frequency of cotrimoxazole resistance genes among Salmonella spp.

**Methods :** forty-one isolates were identified from Mar.2019 to Apr.2020 in Imam Khomeini hospital of Tehran. Antibiotic susceptibility of isolates was done through the Kirby-Bauer method. The sul1, sul2, sul3, dfrA1, dfrA5, and Int1, genes were detected by Multiplex-PCR.

**Results :** among 41 isolates, 14 isolates (29%) were resistant to the cotrimoxazole. The frequency of dfra1 and dfra5 is 10% (4 isolates) and 10% (4 isolates) respectively. The frequency of other genes includes sul1, sul2 and sul3 are 25% (10 isolates), 19% (8 isolates) and 0% (0 isolates) respectively.

**Conclusion :** data have shown that the antimicrobial resistance increased and one-third of Salmonella isolates have a Cotrimoxazole resistance gene that illustrated the accumulation of resistance genes among Salmonella spp.

**Keywords :** cotrimoxazole, Salmonella, antimicrobial resistance

# P73-93: Investigation of bacterial contamination of medical surfaces and equipment in the neonatal and NICU wards of Shahid Beheshti Hospital In Isfahan

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**Background and Aim :** Nosocomial infection is an important cause of mortality in neonatal and NICU wards.continuous monitoring and care for microbial contamination of these wards is one of the effective strategies to prevent nosocomial infections.The aim of this study was to determine the bacterial contamination of equipment in the neonatal and NICU wards of shahid Beheshti Hospital in Isfahan

**Methods :** In a descriptive study of 63 devices in the neonatal and NICU departmens sampling was performed before and after routin disinfction ,samples were taken with a sterile swab impregnated with TSB medium and placed inside a tube containing TSB.Identification of isolates was performed first by conventional biochemical tests and then by 16SrRNA gene amplification and molecular sequencing

**Results :** Of the 63 items before disinfection, 38 (60.3% )were positive for bacterial contamination . of the 63 items after disinfection, 12 (19.04% )were positive for bacterial contamination.The most abundant bacterial isolate before and after disinfection Negative coagulase Staphylococcus respectively inabundance (57.14% )and (19.04% ) was .The highest contamination of non-medical devices before and after disinfection related to the patients cartable is 100 and 50 respectively and the highest contamination of medical devices before and afte disinfection related to the Lrayngoscope blade is 100 and 50 respectively

**Conclusion :** This study showed that bacterial contaminatin is significant .Periodic culture and use of standard guidelines and prevention have an effective rolein reducing contamination

**Keywords :** Bacterial contamination ,NICU, Negative coagulase Staphylococcus,Neonation

# P74-130: Identification and characterization of Staphylococcus aureus isolated from Imam Reza hospital, Kermanshah

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**Background and Aim :** Staphylococcus aureus (S. aureus) almost can cause disease in all organs such as osteomyelitis, pneumonia, sepsis, and superficial skin infection. S. aureus through many factors include toxin, cell wall-associated proteins, and protein modulators can resist immune response. S. aureus can be categorized into two types based on resistance to the Methicillin, Methicillin-resistance Staphylococcus aureus (MRSA) and Methicillin-sensitive Staphylococcus aureus (MSSA).

**Methods :** 95 isolates were collected from November 2020 to June 2021. Differentiation of these two types is done through the presence of mec gene. In the next step antibiotic resistance is done through Kirby-Bauer Method on the Muller-Hinton agar.

**Results :** among 95 isolates, 65 number were identifying as MRSA, and 30 isolate as MSSA. The highest level of resistance among the studied antibiotics was related to Cefoxitin. Other antibiotics that investigated in this study include Oxacillin and Cefotaxime.

**Conclusion :** most of the isolates are MRSA that concludes that the percent of bacteria that carrier the antibiotic resistance are in progress. Abusing of medication of course is one of the major roles in this enhancement.

**Keywords :** Staphylococcus aureus, antibiotic resistance, MRSA, Oxacillin

# P75-185: Antifungal drug susceptibility of yeast isolated from blood samples of patients with Severe COVID-19 Admitted to ICUs Patients

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**Background and Aim :** As a novel risk factor, COVID-19 has led to an increase in the incidence of candidemia and an elevated mortality rate. Despite being of clinical importance, there is a lack of data regarding COVID-19-associated candidemia (CAC) among Iranian patients. Therefore, in this retrospective study, we assessed CAC epidemiology and Antifungal susceptibility in the intensive care units (ICUs) of two COVID-19 centers in Mashhad, Iran, from early November 2020 to late January 2021

**Methods :** Yeast isolates from patients' blood were identified by 21-plex polymerase chain reaction (PCR) and sequencing, then subjected to antifungal susceptibility testing according to the CLSI M27-A3 protocol.

**Results :** The mortality of the limited CAC cases was high and greatly exceeded that of patients with COVID-19 but without candidemia (100% vs. 22.7%). Among 1988 patients with COVID-19 admitted to ICUs, seven had fungemia and nine yeast isolates were collected, five Candida albicans, three C. glabrata, and one Rhodotorula mucilaginosa. Half of the patients infected with C. albicans (2/4) were refractory to both azoles and echinocandins. None of the C. glabrata isolates were resistant to the tested antifungal drugs. The R. mucilaginosa isolate showed high MICs of all azoles and echinocandins tested but a low MIC of AMB.

**Conclusion :** In conclusion, our study revealed a high mortality rate among critically ill patients with COVID-19 and candidemia in Iran, thus underscoring the importance of rapid diagnosis followed by the timely initiation of appropriate antifungal therapy.

**Keywords :** Antifungal; COVID-19; candidemia; multidrug resistance

# P76-263: Investigation the antibacterial effect of Inola aspira extract on bacteria isolated from Urinary tract infection.

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**Background and Aim :** Increasing bacterial resistance against antibiotics, used in urinary tract infection (UTI) is an emerging problem for human health. This study amied to investigate the antibacterial effect of the Inola aspira extract on bacteria isolated from urinary tract infections.

**Methods :** In this cross-sectional study, 50 samples were collected from patients with urinary tract infections referring to a medical diagnostic laboratory in Mashhad, Iran. Then bacteria were confirmed by standard biochemical tests. The antibacterial effect of the Inola aspira extract was investigated by the using microdilution method, and the minimum inhibitory concentration (MIC) of bacterial growth was determined.

**Results :** Out of 50 samples of urinary tract infections, Escherichia coli was the most frequent strain 21(42%), followed by Klebsiella pneumoniae 10 (20%), Staphylococcus aureus 8 (16%), Enterobacter spp. 7 (14%), Pseudomonas aeruginosa 2 (4%), and Enterococcus spp. 2 (4%). The Inola aspira extract demonstrated its highest antimicrobial activity against Escherichia coli, Staphylococcus aureus, Enterobacter spp., Enterococcus spp. with a MIC of 50 mg/ml. On the other hand, the lowest antimicrobial activity of the Inola aspira extract was reported to be against Pseudomonas aeruginosa and Klebsiella pneumoniae with MIC 100 mg/ml.

**Conclusion :** The result suggests that extract of Inola aspira can be used as a source of cheap and accessible replacing chemical drugs to treat some bacterial infections.

**Keywords :** Inola aspira, UTI, MIC.

# P77-264: The most common bacterial pathogens associated with nosocomial infections

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**Background and Aim :** Nosocomial infections are infections that people usually get 48 to 72 hours after hospitalization. These infections increase mortality, disability, prolong hospital stays, and financial costs and damage to health care systems. The present study was designed to determine the most common bacterial pathogens associated with nosocomial infections.

**Methods :** The present study was a brief review study designed in 2021. PubMed / Medline and Scopus databases were used to search for similar studies and extract content. Selected keywords for the search included “bacterial”, “Pathogen” and “nosocomial infection”. The articles were retrieved using advanced search and using AND - OR operators. The one researcher examined the extracted articles and included Latin articles on the bacterial pathogens associated with nosocomial infections. Summaries of articles published in congresses and conferences were excluded from the study. Initially, 15 articles were finally evaluated.

**Results :** Bacteria are the most common pathogens in nosocomial infections, which are divided into two categories: gram-positive and gram-negative: Common gram-positive pathogens include C. difficile, the most commonly reported pathogen in US hospitals, coagulase-negative staphylococcus, Staphylococcus aureus, Enterococcus and Streptococcus species; Also the most common gram-negative bacterial pathogens include species of the family Enterobacteriaceae including: Klebsiella pneumoniae and Klebsiella oxytoca, E.coli, Proteus Mirabilis and enterobacteria species including: Pseudomonas aeruginosa, Acinetobacter baumanii and Burkholderia cepacia that E.coli and Klebsiella are the most common pathogens associated with urinary tract infections.

**Conclusion :** The results of the present study showed that bacteria are the most common nosocomial pathogens and since the most common way of transmission of these microorganisms is through contact, then hand hygiene is the most important way to prevent nosocomial infections. Also, medical equipment and the patient environment should be kept clean regularly, hospital waste is an important source for the spread of pathogenic microorganisms, so proper monitoring of the transport and disposal of these substances is

essential. Excessive use of antibiotics and antimicrobials increases the resistance of pathogens to these drugs, so their use should be limited and prescribed by a doctor.

**Keywords :** Nosocomial infection, Pathogen, Bacterial, Hospital

# P78-265: The most common fungal and viral pathogens associated with nosocomial infections

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**Background and Aim :** Nosocomial infections affect a significant number of patients worldwide and lead to increased mortality and financial impact on health care systems. The present study was designed to determine the most common fungal and viral pathogens associated with nosocomial infections.

**Methods :** The present study was a brief review study designed in 2021. PubMed / Medline and Scopus databases were used to search for similar studies and extract content. Selected keywords for the search included “fungal”, “viral”, “Pathogen” and “nosocomial infection”. The articles were retrieved using advanced search and using AND - OR operators. The one researcher examined the extracted articles and included Latin articles on the fungal and viral pathogens associated with nosocomial infections. Summaries of articles published in congresses and conferences were excluded from the study. Initially, 11 articles were finally evaluated.

**Results :** Fungi are among the most common pathogens in nosocomial infections. Candidia species including C. albicans, C. parapsilosis, and C. glabrata are the most common fungal microorganisms associated with nosocomial infections. Candia auris is also a multidrug-resistant microorganism that is associated with high mortality due to difficulty in diagnosis and high failure rate in treatment. Also, species of Aspergillus, Mucor and Fusarium are involved in nosocomial infections. Among the pathogens, viral infections are the least reported. However, HIV and hepatitis B and C are common in medical and health care centers due to contact with unsafe needles. Rhinovirus, cytomegalovirus, herpes simplex virus, rotavirus, influenza are other common types of viral pathogens associated with nosocomial infections.

**Conclusion :** The results of the present study showed that fungi and viruses are among the most common pathogens associated with nosocomial infections, so the patient environment and medical equipment should be kept clean regularly; The use of safe disposable syringes as well as prophylaxis with antifungal drugs for patients at risk for invasive fungal infections should be considered during periods when the patient has a weakened immune system.

**Keywords :** Nosocomial infection, fungal infection, viral infection

# P79-267: In Vitro Susceptibility of clinical Rhodotorula mucilaginosa isolates from animal source to antifungal agents

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**Background and Aim :** Rhodotorula species are common non-virulent environmental yeasts and emerged as opportunistic pathogens, causing catheter associated fungemia among immunocompromised hosts. Rhodotorula mucilaginosa is considered the most common species involved in human and animal infections. The aim of the present study was to evaluate antifungal susceptibility patterns of Rh. mucilaginosa strains isolated from animal.

**Methods :** The 37 isolates of Rh. mucilaginosa obtained from Chicken (7 isolates), cat (12 isolates), Horse (5 isolates), Canary (7 isolates) and Camel (6 isolates) were tested for susceptibility to standard antifungal drugs.

**Results :** The Geometric Mean of minimum inhibitory concentration (MIC) values of Amphotericin B, 5-Fluorocytosine and Caspofungin were 1.10 µg/ml (Range; 0.125-32), 0.20 µg/ml (Range; 0.06-1) and 5.82 µg/ml (Range; 2-32), respectively. These values of Fluconazole, Itraconazole, Voriconazole and Posaconazole calculated ranged from 0.125-32 µg/ml. Comparing the MIC90 for all Rh. mucilaginosa strains, the lower MIC90 were observed for 5-Fluorocytosine (0.2 µg/ml) and Posaconazole (0.49 µg/ml).

**Conclusion :** Rhodotorula's infections are usually resistant to treatment with antifungal drugs especially triazoles and echinocandins.Our results indicated that Fluconazole does not effective against the Rh. Mucilaginosa isolates from animal source. Furthermore, 5-Fluorocytosine and Posaconazole is the best drug against this genus in comparison to other azole drugs.

**Keywords :** Rhodotorula mucilaginosa, 5-Fluorocytosine amphotericin B, itraconazole, voriconazole, antifungal susceptibility

# P80-269: Prevalence of bacterial Hospital-Acquired Infections in ICU ward of shohaday ashayer Hospital of khorramabad, 2019

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**Background and Aim :** Nosocomial infections are one of the most important health problems that always affect the quality of health services in hospitals and increase hospitalization costs, duration of treatment, the spread of various infections in the community and even the mortality of hospitalized patients. In recent years, it has increased all over the world. Therefore, the present study was designed and conducted to investigate the epidemiological aspects of bacterial nosocomial infections in the intensive care unit of Khorramabad shohadaye Ashayer Hospital in the first 9 months of 2019.

**Methods :** This study was a cross-sectional study that was performed on all patients admitted to Khorramabad shohadaye Ashayer Hospital in Khorramabad shohadaye Ashayer Hospital for 9 months from the beginning of April 2019 to the end of December 2019. He was tested in the intensive care unit of this hospital with suspected nosocomial infection. The collected information was entered into SPSS software version 22 and to determine the descriptive objectives of the study, frequency calculation as well as mean and standard deviation according to the type of variable were used.

**Results :** In this study, out of 917 patients admitted to ICUs and intensive care units of Shohada-e-Ashayer Hospital, 92 patients contracted nosocomial infections with a prevalence of 10%. 64.1%) and 33 women (35.9%) with a mean age of 61.23 18. 18.64 years. The youngest patient was 18 years old and the oldest was 95 years old. The highest prevalence of nosocomial infection was due to catheter infection (40.3%) followed by urinary tract infection (33.7%). The highest antibiotic resistance to cotrimoxazole (80.4%), ceftriaxone (72.8%), ceftazidime (72.8%) and the highest antibiotic susceptibility to ciprofloxacin (26.1%) and amikacin (23.9%). ) Was seen. The highest frequency of bacteria isolated from the culture of the studied patients was related to Acinetobacter (28.3%).

**Conclusion :** According to the results of the present study, it can be concluded that the prevention of nosocomial infections requires careful and calculated activities and programs

that can be used for the correct and timely use of medical interventions to limit the transmission of microorganisms through washing. Hands were especially noted by medical staff, infection monitoring and epidemic diagnosis and control, health education and ongoing hospital-level monitoring, proper use of disposable items, controlled use of antibiotics, and careful wound care.

**Keywords :** Nosocomial infections, bacterial infections, intensive care unit

# P81-285: Distribution of blaTEM, blaCTX-M and blaSHV genes and biofilm-forming capacity among Stenotrophomonas maltophilia clinical isolates

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**Background and Aim :** Stenotrophomonas maltophilia known as one of the major contributor to nosocomial infections. Extended-spectrum ßlactamase (ESBL)-producing S. maltophilia is spreading worldwide particularly in the immunocompromised patients. We aimed to determine the frequency of ESBL encoding genes, blaTEM, blaCTX-M and blaSHV among clinical isolates of S. maltophilia.

**Methods :** In this descriptive cross-sectional study, a total of 97 S. maltophilia isolates were collected from five tertiary-care hospitals affiliated to Tehran and Qazvin University of Medical Sciences between September 2019 and March 2020 and were identified through standard biochemical tests and PCR amplification of the 23S rRNA gene. Antibiotic susceptibility was investigated by disk diffusion test. Biofilm formation was determined by microtiter plate assay. The blaTEM, blaCTX-M and blaSHV were detected by PCR and sequencing

**Results :** All isolates were resistant to imipenem and meropenem. Levofloxacin, minocycline and trimethoprim/sulfamethoxazole exhibited the highest susceptibility of 97.9 %, 88.7% and 85.6 %, respectively. The resistance rates to other antibiotics were as follow: ceftazidime (76.3 %); ticarcillin/clavulanate (60.9%); chloramphenicol (39.2%); tigecycline (13.4%). Among the isolates examined, 93 (95.9%) were able to produce biofilm, of which 45 (46.4%) were strong biofilm-producers, whereas 41 (42.3%) and 7 (7.2%) were moderate and weak biofilm-producers, respectively. The existence of blaTEM and blaCTX-M was detected in 10 (10.3%) and 4 (4.1 %) isolates respectively, whereas none of the isolates carried blaSHV gene. One of the isolates harbored both the blaTEM and blaCTX-M genes.

**Conclusion :** The prevalence of β-lactamase-producing genes in S. maltophilia detected by our study is of great concern and highlights the need of appropriate infection control protocols including screening isolates with beta-lactamase-producing genes to prevent further infection.

**Keywords :** Stenotrophomonas maltophili, ESBL, Biofilm

# P82-335: Distribution and antibiotic susceptibility pattern of Hypervirulent Klebsiella pneumoniae (HvKp) strains isolated from hospitalized patients in North of Iran

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**Background and Aim :** Hypervirulent Klebsiella pneumoniae (hvKp) is an increasingly recognized pathotype of K. pneumoniae characterized clinically by its ability to cause organ- or life-threatening infections in healthy hosts from the community. One of the concerns of physicians and health communities about the recent pathogen is the emergence of multidrug resistance (MDR) and Extended-Spectrum β-Lactamase (ESBL) phentotype. Therefore, the aim of this study is to isolation, identification and determination of antibiotic susceptibility pattern of HvKp strains isolated from hospitalized patients in North of Iran

**Methods :** In this study, 90 clinical samples of K. pneumoniae were collected randomly from three teaching hospitals affiliated to Babol University of Medical Sciences in the form of microbial plates. Stringent tests were used to identify HVKP strains. In this study, K. pneumoniae ATCC 13883 and Escherichia coli ATCC25922 were used as positive and negative control, respectively. Antibiotic susceptibility of HvKp isolates was determined according to CLSI standards. Antibiotics used in disk diffusion test include ciprofloxacin, amikacin, trimethoprim /sulfamethoxazole, cefotaxime, ampicillin, aztreonam, imipenem, tetracycline, gentamicin, ceftazidime and cefepime. Finally, multiple resistance phenotypes (MDR) were identified.

**Results :** From 90 clinical samples of K. pneumoniae, 40 isolates of HvKp strains were isolated according to specific tests. According to susceptibility test, the highest resistance rate was observed against ampicillin (100%) followed by trimethoprim /sulfamethoxazole (67/7%), cefotaxime (56/6%), ceftazidime (52/2%), aztreonam (47/7%), tetracycline (44/4%), gentamicin (43/3%), cefepime (36/6%), amikacin (35/5%), ciprofloxacin (25/5%) and imipenem (12/2%). Moreover, all isolates were MDR.

**Conclusion :** HvKp, especially ESBL-hvKp and MDR-hvKp, is emerging in the hospitalized patients. It is essential to enhance clinical awareness and management of hvKp infections.

**Keywords :** Klebsiella pneumoniae; Antibiotic resistance ; Hypervirulent; HvKp

# P83-337: Evaluation of Antibiotic Susceptibility Pattern of Uropathogenic Escherichia coli Isolates obtained from Patients with Urinary Catheter in North of Iran

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**Background and Aim :** Antibiotic resistance in Uropathogenic Escherichia coli (UPEC) isolates, especially in hospitalized patients with nosocomial infections such as urinary catheters, is a growing problem and challenge. Resistance genes exist for all known antibiotics in use today, and extremely resistant pathogens are becoming more common. E. coli bacteria have developed the broadest spectrum of resistance due to multiple structural adaptations and antibiotic degradation enzymes. Therefore, the aim of this study was to investigate the pattern of antibiotic resistance of UPEC isolates obtained from patients with urinary catheter in North of Iran.

**Methods :** In this cross sectional study, 60 UPEC isolates were collected from urine samples taken from patients admitted to a teaching hospital from May 2021 to August 2021 in Babol, North of Iran. After confirmation of UPEC isolates using standard microbiology tests, the disk diffusion method was used to determine antibiotic susceptibility pattern.

**Results :** According to susceptibility test, UPEC strains was most resistant against followed by ceftriaxone (80%), trimethoprim-sulfamethoxazole (72%), amikacin (65%), cefotaxime (60%), nalidixin acide (59%), gentamicin (55%), nitrofurantoin (51%), imipenem (50%), ciprofloxacin (40%). Moreover, all isolates were MDR.

**Conclusion :** The risk of urinary tract infection increases with increasing duration of catheterization. So for avoiding to the increasing resistance of antibiotics, infection control or antibiotic administration should be done with more caution and laboratory confirmation

**Keywords :** E. coli; urinary catheter; carbapenem resistance

# P84-347: The main bacteria in wound infection- A review article

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**Background and Aim :** Wound infection is one of the health problems that are caused and aggravated by the invasion of pathogenic organisms. Wound Infections are continuous to be a major complication with significant increase in costs, morbidity and potential mortality. The aim of study was introduced the main bacteria exist in wound.

**Methods :** To investigate the main bacteria in wound we used Embase, PubMed/Medline, Scopus, Google Scholar and Web of Sciences data base with keywords such as prevalence, bacterial isolates, wound infection and antibiotic resistance

**Results :** A total of 28 studies on more than 5000 patients (female and male) with the age of 10 days - 100 years and various form of the wounds like: acute traumatic injury, wound infection, surgical wound, post operation wound, burns and abscess were included in our review. A total of about 4,300 bacteria were isolated from different patients, of which about 1,900 were gram-positive and 2,400 were gram-negative. The gram positive ones are including: Staphylococcus spp, Coagulase-negative staphylococci (CoNS), Streptococcus spp, Also E.coli as the commonest gram negative bacteria, Klebsiella spp, Pseudomonas .aeruginosa, and Proteus were determined as the main gram negative isolated bacteria.

**Conclusion :** In order to reduce wound infections and the time of hospitalization of patients, it is better to determine the type of bacteria in the wound so that the use of antibiotics appropriate to the type of bacteria

**Keywords :** main bacteria, wound infection, surgery injury,traumatic injury

# P85-359: Comparison of the expression of Enterococcus faecium biofilm-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 biofilm-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 virulence-associated gene 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, and among the six genes associated with biofilm formation, the expression of the efaA gene has the highest expression. Expression increased in five isolates and decreased in only one isolate. The four genes fsr, asa, esp and gelE increased in expression in the four isolates. The lowest gene expression of the hyl gene increases the expression of only one isolate. The increase expression of 5 selected virulence genes (asa1, fsr, gelE, efaA and esp) 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

**Keywords :** Enterococcus faecium, biofilm, Gene expression, real-time PCR

# P86-370: Prevalence of colistin resistance and its molecular mechanisms in clinical isolates of Klebsiella pneumoniae obtained from hospitalized patients in teaching hospitals in Isfahan, Iran.

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**Background and Aim :** The current study was performed to investigate the prevalence of colistin resistance and its molecular mechanisms in clinical isolates of Klebsiella pneumoniae obtained from hospitalized patients in teaching hospitals in Isfahan, Iran.

**Methods :** This cross-sectional study was performed during the 2019-2020 year at several teaching hospitals in Isfahan, Iran. The minimal inhibitory concentration (MIC) of colistin was determined by the E-test strips. Also, PCR assay was carried out to detect genes encoding resistance to colistin, including mcr-1, mcr-2, pmrA, pmrB, crrB.

**Results :** In the present study, a total of 79 strains of multidrug-resistant K. pneumoniae were isolated. Of these, 35 colistin-resistant clinical K. pneumoniae isolates were obtained from hospitalized patients in Isfahan. All colistin-resistant isolates were classified as extensively drug-resistant (XDR). PCR results on K. pneumoniae isolates showed that mcr-1 and mcr-2 genes were not detected in any of the strains, while, 8 isolates (10.1%) contained pmrA gene and 8 isolates (10.1%) also carried pmrB gene. In addition, the frequency of crrB gene among our isolates was 3.8%.

**Conclusion :** Due to the fact that the last line of treatment for infections associated with K. pneumoniae is colistin, therefore, increasing resistance to this antibiotic causes many concerns and problems in the treatment of patients. Detection of colistin-resistant strains and reporting of occurrence of genes associated with this resistance can greatly help in the treatment of diseases.

**Keywords :** Klebsiella pneumoniae, colistin, MDR, XDR

# P87-407: Investigation of antibacterial properties of borage extract

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**Background and Aim :** Nowadays, finding of alternative antibacterial agents in essential, because of spreading of resistant bacteria compared to antibiotic drugs and problems of their use. The purpose of this investigation is determination of borage (Echium amoenum) antibiotic effects on two human pathogenic bacteria including Staphylococcus aureus and Salmonella typhimurium and four plant pathogenic bacteria including Brenneria nigrifluens, Pseudomonas syringae, Serratia marcescens and Erwinia amylovora in vitro condition.

**Methods :** In the present study, first prepared the extract of aqueous and alcoholic for samples of borage in three dilution (50 mg/ml, 100mg/ml and 200 mg/ml) of dimethyl sulfoxide (DMSO) solvent. Evaluation of antibacterial properties borage extracts was performed by disk diffusion. Diameter of the transparent halos caused by inhibition of bacterial growth was evaluated.

**Results :** The extract of borage caused a growth inhibition zone in all studied bacterial species in this survey. The smallest diameter zone was related to concentration of 50 mg/ml in both of aqueous and alcoholic extracts. The results of evaluation of zone indicated that in higher concentrations of borage extract, the diameter of growth zone will be increased.

**Conclusion :** The results of this study showed the borage extract has antibacterial properties and we can be hopeful to make some useful drugs mixed with plant origin and much less side effects to confronting of bacteria.

**Keywords :** Antibacterial - Bacteria - Borage - Antibiotics

# P88-424: Types of Nosocomial Infections: A Summary Review

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**Background and Aim :** Nosocomial infections have always been one of the major problems of health centers and its importance is increasing day by day and the health system of countries has faced a serious challenge. Increasing and diverse needs for medical services, emerging and re-emerging diseases and increasing microbial resistance have made the occurrence of these types of infections inevitable.

**Methods :** The present study was a summary review study designed in 2021. PubMed / Medline and Scopus databases were used to search for similar studies and extract content. Selected keywords for the search included “Nosocomial”, “Infection”. Summaries of articles published in congresses and conferences were excluded from the study. Initially, 12 articles were finally evaluated.

**Results :** The most common types of nosocomial infections are: Surgical wound infection that may develop during or a few weeks after surgery and lead to serious problems such as defects in the surgical repair process, sepsis, organ damage, or even death. Bloodstream infection or sepsis Infection causes clots and reduced blood flow, and as a result, nutrients and oxygen do not reach the organs properly or even lead to tissue necrosis of some organs. In the worst case, a blood infection can cause a rapid drop in blood pressure, known as an infectious shock, which can lead to lung, kidney, liver and eventually death. Urinary tract infection is the most common nosocomial infection and occurs in 80% of cases due to catheters and in about 20% of cases due to manipulation of the urinary tract. Pneumonia is the most deadly nosocomial infection caused by ventilators. The risk of pneumonia is very high in people who are in the intensive care unit and are intubated.

**Conclusion :** Given that nosocomial infections can affect anyone, the first step in preventing it is to implement special training programs for patients, their companions and hospital staff.

**Keywords :** Infection, nosocomial, hospital staff

# P89-425: Epidemiology of Urinary Tract Infection and Antibiotic Resistance Pattern in Patients Referred to Amiralmomenin Hospital of Gerash City in 2018

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**Background and Aim :** Urinary tract infections are one of the most common human infections seen in all age groups and both sexes. Inappropriate use of antibiotics to treat urinary tract infection causes the resistance of the pathogens to the drug. The present study aimed to determine the frequency of gram-negative and gram-positive bacteria and antibiotic resistance patterns in patients with urinary tract infection.

**Methods :** Samples were ultured on Blood Agar and Eosin Methylene Blue. Colonies' growth was identified by biochemical tests and standard microbiological and antibiotic sensitivity tests, which were performed with the disc diffusion method according to the Clinical and Laboratory Standards Institute 2016 Standard.

**Results :** The isolated bacteria showed the highest susceptibility to imipenem (89.66%) and meropenem (87.21%) and the highest resistance to sulfamethoxazole (50.00%) and nalidixic acid (44.09%).

**Conclusion :** So, using imipenem is recommended as the most effective antibiotic for the treatment of infection.

**Keywords :** Antibiotics, Resistance, Urinary tract infections

# P90-441: Detection of Metallo-β-Lactamase Producing Pseudomonas aeruginosa Isolated From Patients in Gorgan, Iran

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**Background and Aim :** Pseudomonas aeruginosa has recently emerged as one of the main causes of nosocomial infections due to vast antibiotic resistance potency. The production of metallo-β-lactamases (MBLs) is 1 of the resistance mechanisms in Pseudomonas aeruginosa . : Imipenem is a member of Carbapenem with stability against most t -lactamases.It is of particular use in the treatment of infections associated with drug resistant gram negative bacteria harboring ESBL and AmpC genes. The aim of this study was to determine antimicrobial resistance pattern and the imipenem resistance in Pseudomonas aeruginosa and the presence of metallo- -lactamases (MBLS) in resistant isolates.

**Methods :** In this study, the prevalence of MBL-producing strains was determined among 50 P. aeruginosa isolated from patients inGorgan, Iran. Also, resistance to various antibiotics was determined by disk diffusion test.Minimum inhibitory concentration (MIC) of imipenem was determined for Pseudomonas aeruginosa. Disk diffusion method with disks containing imipenem and imipenem+10µl EDTA (0.5 M) was used for determination of the presence of metallo- -lactamases. An increase of ≥7 mm in the inhibition zone diameter of EDTA containing imipenem disk compared to imipenem disk was considered MBL positive.

**Results :** A high rate of resistance to antibiotics was seen in the 50 strains. Most of the isolates were resistant to, ceftazidime, cefotaxime and tobramycin. 16 isolates (32%) were MDR. Also Among these, MBL activity was detected in 3 of 19 imipenem-resistant strains. 19 isolates showed MIC≥8 µg/ml for IPM. Based on the DDST results, 3 isolates were confirmed to be MBL producers.

**Conclusion :** Carbapenem resistance and production of the metallo-beta-lactamase enzyme in Pseudomonas aeruginosa are increasing According to the presence of metallo - lactamases in bacterial strain in the region, resistance to this valuable therapeutic agent is not unexpected

**Keywords :** imipenem, metallo-β-lactamase, Pseudomonas aeruginosa

# P91-31: Simultaneous colonization of non-Helicobacter and Helicobacter pylori in patients with gastritis

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**Background and Aim :** Understanding the bacterial community composition of gastric microbes and the relationship between its differences in the development and progression of gastritis can be of great help in the perception of the mechanism of this disease and designing preventive treatment pathways for its progression. We aimed to investigate the simultaneous colonization of bacterial agents in patients with chronic gastritis.

**Methods :** The study was performed on 168 gastric biopsy specimens of patients with gastric complaints who were referred to the endoscopic ward of Firoozgar hospital in Tehran. Biopsy specimens in the pathology department were examined histologically by the hematoxylin-eosin staining method and in the specific culture medium of Helicobacter under microaerophilic growth conditions and in general culture medium under aerobic conditions for the presence of Helicobacter and other bacteria. Identification of Helicobacter pylori (H. pylori) isolates was performed by analyzing colony morphology, gram staining, positive reactions of oxidase and catalase, rapid urease test, and polymerase chain reaction (PCR). Other bacteria were identified by biochemical and phenotypical analysis.

**Results :** In our study, the recovery rate of H. pylori infection was 27.4 %. The mean age of patients in the two groups with and without H. pylori infection was almost the same. 87.5% of all patients had chronic gastritis, which showed significant associations with H. pylori infection (p-value: 0.00). We identified 140 bacterial colonies that belonged to 12 genera and 3 phyla. At the genus level, Streptococcus and Staphylococcus were predominant followed by Micrococcus, Escherichia coli, Bacillus, Enterococcus, Klebsiella, Pseudomonas, Enterobacter, Citrobacter, and Providencia. The predominant phyla were Proteobacteria and Firmicutes while Actinobacteria was less frequent. Co-infection of H. pylori with other isolated bacteria, especially Streptococcus and Staphylococcus was observed.

**Conclusion :** The presence of different bacterial genera in the gastric tissue of patients with gastritis in the absence of H. pylori suggests their possible role in the occurrence or progression of this disease. Additional studies to determine the association of the persistence of these bacteria with the use of drugs that modulate gastric acidity and pathological changes can be useful in the prevention and treatment of gastritis.

**Keywords :** Gastritis; Helicobacter pylori; gastric microbiota

# P92-66: DRUG MICROBIOM INTRACTION –A Short Review

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**Background and Aim :** The human microbiome plays an important role in controlling vital hemostatic mechanisms in the body. It is known as a major mediator of pharmacological activity. Microbiota chemistry produces drugs and toxicity, intestinal bacteria produce a wide range of enzymes and metabolites that may alter chemicals. The intestinal microbiome can be an active, inactive, or toxic drug. This can directly affect drug metabolism through biotechnology, which converts organic compounds into other chemical forms or metabolites and is done by microorganisms. The most common mechanisms of intestinal microbiota metabolism are hydrolytic and reactive reactions. In addition, many other chemical reactions such as acetate, demineralization, dehydroxylation, decarboxylation, methylation, solution decomposition, and proteolysis have been reported. In addition to environmental drugs, the microbiota can indirectly control the effect of the drug by altering the host metabolism and producing metabolites that compete with the drug-receptor. This study examines the effects of drugs on people with different microbes. Here we review recent studies for better investigation, based on the mechanism of drug-microbiome interaction and their response.

**Methods :** search and study in databases and papers

**Results :** As discussed in this short review, a large number of drugs already in the market are substrates for microbial metabolism, and this highlights the importance of including the microbial metabolism of the drug during the development phase. most of the drugs changed with microbiome metabolic. it may become better or worse or toxicity for our body

**Conclusion :** An understanding of the implications of microbial metabolism is expected to increase with time as more and more drugs are being identified as substrates for gut Microflora. As discussed in this short review, a large number of drugs already in the market are substrates for microbial metabolism, and this highlights the importance of including the microbial metabolism of the drug during the development phase. most of the drugs changed with microbiome metabolic. it may become better or worse or toxicity for our body

**Keywords :** key word; Drugs, microbials, microbiota, bacteria, grazing, drug More about this source textSource text required for additional translation information

# P93-72: Review Article: Microbiota and Nutritional Interventions in Covid-19

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**Background and Aim :** With the onset of Covid-19 epidemic in the world, scientists are looking for a specific treatment and prevention for this disease. One of the ways to deal with Covid-19 is to support and strengthen the immune system and respond to it. This study aimed to review microbiota-mediated nutritional interventions in Covid 19.

**Methods :** This is a review study that by searching the electronic sources of PubMed, Science Direct, and Embase, using the keywords Probiotic, Covid 19, Microbiota from 2015 to 2021, 55 related articles were found and then analyzed.

**Results :** The results indicate that lifestyle and nutrition affect the modulating effects of the immune system induced by microbiota against viral infections including Covid 19. Factors such as air pollution, smoking, and toxic inhalable chemicals can reduce the abundance of microbiota.

**Conclusion :** Airway microbiota and Covid 19 are related to each other and the rate of host immune responses determine the pathogen microbiota. Foods such as colored vegetables, probiotics, and plant elements also support the gut microbiota. This study demonstrates the association between the airways and intestinal microbiota and the host's diet and lifestyle in preventing Covid 19.

**Keywords :** Probiotic, Covid 19, Microbiota.

# P94-112: Gut Microbiota Relationship with Lewy Body Dementia

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**Background and Aim :** One of the most challenging issues among psychiatrists is differentiating between neurological diseases and psychiatric disorders. Side effects of even a low dose of antipsychotic drugs may aggravate the patient's mental disease. The subject in this study has shown jealousy delusions, which may suggest primary delusional disorder. The disease is associated with the destruction and death of nerve cells. Lewy body disease is similar to Alzheimer's and Parkinson's disease (PD) in many ways and this disease is sometimes difficult to distinguish from PD. Many studies of neurological disorders have examined patients' Gut microbiota, but we have no evidence of Lewy body. Since PD is similar to Lewy body and we have evidence of Gut microbiota in these patients, can we hypothesize the study of Gut microbiota in Lewy body patients?

**Methods :** A 58-year-old married woman without the previous medical illness and no vascular risk factors referred to a neuropsychiatry clinic. She was examined comprehensively by neuropsychiatrists in examining with dementia; also she underwent laboratory tests and standard neuropsychological examination such as Mini-Mental State Examination (MMSE). Brain magnetic resonance imaging (MRI) was also performed.

**Results :** She presented behavioral symptoms including persecutory and jealousy delusions. Additionally, the patient had become cognitive decline with visuo-spatial deficit, psychomotor retardation, and cogwheel rigidity. In neurological examination, she had bradykinesia, bradyphrenia with left hemiparkinsonism and rigidity exaggerated elevated reflexes. In brain MRI findings, it was shown atrophy of insular, frontal and medial temporal lobe. Gut microbiota (GM) and short-chain fatty acids (SCFA), resulting in anti-inflammatory effects, are significantly reduced in the fecal samples of PD patients. However, the genes that synthesize lipopolysaccharide and the type III bacterial secretion system are more in the fecal samples of PD patients than healthy patients. Therefore, the microbiome can be a potential diagnostic and therapeutic target for dementia

**Conclusion :** There are currently various methods for recovering and modulating GM, including the use of antibiotics, probiotics, prebiotics, and FMT. Many studies show that FMT is useful in improving non-GI symptoms in patients with neurological disorders

**Keywords :** Lewy body, dementia, Gut Microbiome

# P95-114: Mucosa-associated Escherichia coli from B2 and D phylogroups colonize gut mucosa of colorectal cancer patients

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**Background and Aim :** Colorectal cancer (CRC) is the third most prevalent malignant tumor in the world. Specific strains of intestinal Escherichia coli (E. coli) can influence the development of CRC. This study aimed to determine the phylogroups of mucosa-associated E. coli isolates from CRC patients and control group.

**Methods :** In a prospective study, a total of 96 patients, 48 with CRC and 48 without were studied, between June 2019 and June 2020, from two referral university-affiliated hospitals in northwest Iran. Fresh biopsy specimens obtained by colonoscopy were used to identify mucosa-associated E. coli isolates after mucolysis. The isolates were then classified into phylogroups using quadruplex PCR method.

**Results :** CRC patients had significantly more mucosa-associated E. coli than the control subjects. Phylogroup D was predominant in CRC patients (41.66%), followed by phylogroups B2 (36.66%), A (15%), and B1 (6.66%). Moreover, control group isolates in this study most frequently belonged to phylogroup A (39.1%), followed by phylogroups B1 (19.51), D (19.51), B2 (12.19), E (4.88) and F (4.88).

**Conclusion :** Gut mucosa of CRC patients more colonized by B2 and D phylogroups of mucosa-associated E. coli; therefore, some strains that belonged to this phylogroups may be involved in the pathogenesis of CRC.

**Keywords :** E. coli, Colorectal cancer, Phylogroups

# P96-115: The role of Escherichia coli in the pathogenesis of colorectal cancer

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**Background and Aim :** Colorectal cancer (CRC) is the third most common cancer in the world. Specific strains of mucosa-associated Escherichia coli (E. coli) can influence the initiation and development of CRC through toxin-mediated DNA damage and by promoting inflammatory pathways. The aim of this study was to review the role of mucosa-associated E.coli in the pathogenicity of CRC

**Methods :** We've searched PubMed, Google scholar, SID and Magiran databases from the year 1990 to 2021 for keywords such as mucosa-associated E. coli, colorectal cancer, colibactin, inflammation and risk factors among published articles.

**Results :** The results of various studies indicated that mucosa-associated E.coli is more frequently isolated from patients with CRC than in healthy subjects. Interestingly, majority E.coli strains from CRC patients carried pks genomic island. This genomic island encodes colibactin toxin that induces DNA damage and chromosomal instability which may play a potential role in CRC carcinogenesis. Moreover, pks+ E.coli induce the cellular senescence and production of growth factors leading to increased tumor growth. Furthermore, E. coli strains from B2 phylogroup can survive and replicate within macrophages and induce chronic inflammation. It is noteworthy that chronic inflammation is an important risk factor for CRC.

**Conclusion :** It seems that some strains of mucosa-associated E.coli especially colibactin-producing E.coli may play a key role in CRC carcinogenesis but more research is needed to confirm the cancer-promoting potential of these strains.

**Keywords :** E. coli, Colorectal cancer, Colibactin, Inflammation

# P97-117: Relationship between Gut Microbiota and Personality: Approach for the future

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**Background and Aim :** A remarkable surge is seen in studies on the relationships between the gut microbiome and personality in humans during the last years. Previous works suggest that intestinal microbiota affects the gut-brain axis in addition to impacts on the digestion, immune system, body metabolism, growth and even behavior. In some recent studies, psychiatric symptoms improved by transplantation of fecal microbiota in patients with intestinal disease. The effects of gut microorganisms on neurons have largely been attributed to various neurotransmitters produced by them

**Methods :** Articles published in the past ten years were searched on PubMed (MEDLINE) using the keywords personality, trait, gut microbial, cognitive, empathy, borderline and neuroticism.

**Results :** Some personality traits are associated with gut microbiota, and some studies have shown that even antibiotic treatment and changes in the microbial flora can affect behaviors and certain mental states. As some studies show the role of dysbiosis, increased levels of oxidative stress and increased inflammatory activity in the pathoetiology of borderline personality disorder. Increase Lactobacillus associated with Self-judgement and decrease of inflammation with cognitive empathy. The prevalence of Lactobacillus spp was directly related to positive self-judgment but was indirectly related to lower cognitive depression and emotional empathy. Some studies have shown that personality traits are significantly associated with the diversity of gut microbiota, and high neuroticism and low conscientiousness groups are associated with high abundance of gammaproteobacteria and proteobacteria, respectively.

**Conclusion :** Regarding the whole spectrum of our current knowledge about the influence of gut microbial diversity on personality, and considering the quite possible reverse situation, that is, the determining role of personal behaviors on foods chosen, travel, individual hygiene, social contacts etc, we think that the following strategies should be followed by the health

policy makers, researchers and academic societies to create a more rational way of life in terms of gaining the most out of microorganisms: • Necessity of development of easy, cheap methods for phenotypic characterization of gut microbiome, to obtain a "microbiome fingerprint" in each individual. • Need for mass genotyping of gut (or even whole organism) microbiota in each person using methods such as 16s rRNA typing or preferably by the metagenomic methods.

**Keywords :** Brain, Gut, Microbiome, Personality, Psychiatry

# P98-123: Gut Microbiome and Limited Systemic Scleroderma

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**Background and Aim :** New recent researches have shown role of inflammation in rheumatologic disease comorbid with depressive states. Therapeutic response is no favorable in these disorders and inside of some medications cause complications, drug-drug interactions. Poor compliance is other major concern about therapeutic alliance and suitable treatment. Also, role of gut microbial is eminent about psychiatric, psychosomatic and organic patients but it is a less known and orphan method for non-pharmacological treatment. Therefore, it suggests assessing gut microbial and various views of symptoms and treatment for these patients.

**Methods :** It is as search in Scopus, PubMed and Google scholar from years of 2000-2021. Also, it is report of a case as clinical data and judgment.

**Results :** Here, we present a 56-year-old, married, right-handed patient who is experienced chronic stage of typical systemic sclerosis with hands involvement. She was referred for the control of pain and redness in all her fingers, nightmare, insomnia and sleep disturbances. She also suffered with uncontrolled hands and feet shaking and restlessness during night. She used Ropixon, Angiopars, Methotrexate, Folicacid, Methylprednisolone, Magnesium and Selenium. There was no history of movement disorder. She also had complaint about recent hyperphagia and obsessed about being obese. No involvement had reported in her lung, heart and skin. The patient had a long history of hypo active sexual desire that recently exacerbated. No past personal psychiatric history and family history had been reported. She was menopaused with no history of hypothyroidism or other medical illnesses.

**Conclusion :** We recommend for caution in prescription of drugs especially, Z drugs and benzodiazepines about these patients. Also, evaluation of psychiatric disorder especially depressive disorders and sleep problems is recommended. Assessment of dietary status, gut microbial is important, too. In some cases with poor response to treatment and GI upset, it suggests assessment of Gut microbial.

**Keywords :** Systemic sclerosis, Gastrointestinal involvement, Gut microbiome, Immune system

# P99-175: Comparison of bacterial diversity in the oral microbiota of multiple sclerosis patients and healthy people by the Denaturing gradient gel electrophoresis (DGGE) method.

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**Background and Aim :** Microorganisms in oral cavity are called oral microbiota, since most bacterial genera are uncultivable, cultural independent methods based on 16SrRNA due to identification of more genera. DGGE is one of these methods that is used for examination of bacterial population variety. Microbiota influence development systemic diseases such as pancreatic cancer, atherosclerosis, diabetes, parkinson, autism, alzheimer's, rheumatoid arthritis and multiple sclerosis (MS) through inflammation, immunomodulatory, metabolism etc. MS is an autoimmune disease and associated with chronic inflammation and demyelination. Bacterial infection is one of environmental factors of MS via their effects on inflammatory process include increase Th17 and inflammatory cytokines. This study carried out for Comparison of oral microbiota in multiple sclerosis patients and healthy people by the DGGE method.

**Methods :** Sampling include 30patients and 30 healthy controls was performed in MS patients center of Kermanshah University of Medical Sciences during october to march 2019. DNA was extracted from 1 ml of saliva, electrophoresis of PCR products were performed on poly acrylamide gel. The desired bands were cut and sequencing was carried out.

**Results :** DGGE images showed that this method can identify a greater number of bacteria genera or species compared with cultural methods. Staphylococcus, Bacteroides, Porphyromonas, Prevotella and Actinomyces genera were higher in the patients group and Micrococcus, Enterococcus and Lactobacillus genera higher in the healthy group, significantly. There was no significant difference among Bifidobacterium, Peptostreptococcus and Streptococcus. Sequencing results showed 28 species were uncultivable and 7 species with Accession number MW880919-25 were submitted in https://www.ncbi.nlm.nih.gov/.

**Conclusion :** Most bacteria that have been identified as inflammatory factors in other research were found to be more prevalent in the patient group in this study, indicating that they have a role in the inflammatory condition of MS patients. Furthermore, Lactobacillus, a beneficial

bacterium, was shown to be less abundant in patients. Finally, the progression of the disease can be slowed by controlling oral infections and using helpful microorganisms with anti-inflammatory properties.

**Keywords :** Microbiome, oral cavity, oral microbiota, Multiple Sclerosis, DGGE.

# P100-311: Gut dysbiosis is associated to multiple sclerosis

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**Background and Aim :** Intestinal microbiota perturbation has been significantly related to several human disorders, including rheumatoid arthritis, obesity, diabetes, and multiple sclerosis (MS). Multiple sclerosis (MS) is an inflammatory autoimmune demyelinating disorder driven by the aberrant infiltration of immune cells into the central nervous system (CNS). MS pathogenesis has been resulting from the interplay of genetic predisposition and environmental factor, although the exact role of environmental factors in the pathophysiology of MS remains unknown. The aim of this study Assessment of the role of gut microbiota in multiple sclerosis pathogenesis.

**Methods :** This study examines the relationship between multiple sclerosis and gut microbiota, using the relevant published articles about microbiota and multiple sclerosis searched in PubMed and Google Scholar databases from 2008 to 2021.

**Results :** Recent research on gut dysbiosis (alteration of commensal bacteria composition) conducted in MS patients and experimental autoimmune encephalomyelitis (EAE), its murine model of encephalitis, has shown that commensal microbiota may play a serious role in the pathogenesis of MS. The gut microbiota regulates the host immune and nervous systems and could have impact role in multiple sclerosis.

**Conclusion :** Given the increase in the prevalence of MS worldwide understanding the interaction in the gut-immune-brain axis relates to the influence of microorganisms in the development of MS and modification of the intestinal microbiome could be a future promising treatment in MS. In this review, the characteristics of gut microbiota, the association between gut microbiota and MS, various factors influenced on intestinal microbiota modification have been discussed.

**Keywords :** Microbiota, Multiple sclerosis, CNS autoimmunity, dysbiosis

# P101-332: A case control study of gut dominant bacterial phylum in people with type-2 diabetes mellitus and nonalcoholic fatty liver disease

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**Background and Aim :** Non-alcoholic fatty liver disease (NAFLD) is the main reason for chronic liver disease, with an incidence that is growing in parallel with the global rise in obesity and type 2 diabetes mellitus (T2DM). The role of the gut microbiome (GM) is gaining interest as a significant factor in NAFLD and T2DM pathogenesis. This study aimed to contrasts the differences of dominant GM phyla among patients with NAFLD as compared to T2DM and control groups.

**Methods :** Group-specific primers were designed to target the 16SrRNA genes of major bacterial phylum present in the gut. After the validation of their specificity, these primers were used in the real-time PCR quantification of phyla in the fecal samples of NAFLD patients with T2DM, NAFLD patients without T2DM, patients only with T2DM, and healthy control subjects.

**Results :** Bacteroidetes and Firmicutes phyla were significantly low in NAFLD patients with T2DM (Firmicutes, 2.55 ± 2.25, Pv 0/0002 and Bacteroidetes, 1.55 ± 2.29, Pv 0/0007). In comparing bacteria phyla between NAFLD and NAFLD with T2DM groups, there were significant differences in Firmicutes and Bacteroidetes (Pv <0.05). Furthermore, in comparison to bacteria phyla between T2DM and NAFLD with T2DM groups, there were significant differences in Firmicutes and Bacteroidetes (Pv <0.05).

**Conclusion :** To conclude, our findings showed that the NAFLD patients with T2DM were characterized by different gut compositions. This study supports the role of GM in the pathogenesis of T2DM and NAFLD.

**Keywords :** Gut microbiota, Non-alcoholic fatty liver disease, Type 2 diabetes mellitus

# P102-160: Expression of the GLFGAIAGF epitope of HA2 protein of Influenza A virus in multiple display on filamentous M13 phage

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**Background and Aim :** Influenza A viruses (IAVs) are one of the primary cause of respiratory diseases. Influenza virus genome fragmentation, antigenic alteration partial and general due to point mutations and genetic rearrangement between the genomes of two influenza viruses that simultaneously infect one cell, modify the sequence of genes that encode HA and NA, creating new strains of the influenza virus. New strains of the virus have become a public health problem around the world by creating epidemics or pandemics. Studies have shown that the GLFGAIAGF epitope (residues 1-9) of HA2 sequence is conserved in all strains of the influenza virus. Using this sequence, we can generate a new generation of vaccines containing protected peptides and eliminate the problem of drifting or shifting influenza A viruses. As this epitope has very low immunogenic potency, so it is not sufficient to protect against serious infections with new IAV strains. Filamentous phage M13 can be used as display carriers and elevate the immunogenicity of foreign peptides. There are 2700 copies of pVIII per M13 phage, so this system is capable of displaying a large number of foreign antigenic peptides to be inserted near the gpVIII N-terminus, followed by a hybrid phage in which the major pVIII protein exhibits the peptide epitope.

**Methods :** In this study, a gene containing N-terminal epitope of HA2 (1-9) which is conserved among all subtypes of IAVs, and gVIII gene of phages M13 (from KM13) was designed, synthesized and joined to each other by Assembly PCR technique. The HA2 (1-9)-gVIII pIT2 vector was transformed into competent E. coli TG1 cells. The biological activities of hybrid phage were accessed after expression and purification.

**Results :** The biological activities of hybrid phage were accessed after expression and purification. The sequencing result revealed that recombinant HA2 (1-9)-gVIII genes have been cloned correctly in pIT2 vector. The expression of GLFGAIAGF on the surface of phages M13 was confirmed in Tricine-SDS-PAG, ELISA and Western blot using anti-HA2 polyclonal antibody.

**Conclusion :** This hybrid bacteriophage could be a good candidate for displaying HA2 antigen and immunization.

**Keywords :** Phage display, Influenza A virus; HA2 (1-9); M13 phage; gVIII.

# P103-194: Safety and immunogenicity study of nanoparticle aluminium hydroxide adjuvanted diphtheria toxoid vaccine

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**Background and Aim :** In recent years, significant advances in nanoadjuvant technology have been made in the field of vaccines formulation. Nanoadjuvant provides a suitable opportunity for the production of a new generation of vaccines with desirable properties. The purpose of this study is to evaluate the safety and immunogenicity of nanoadjuvant aluminium hydroxide using diphtheria toxoid protein as an antigen model administered twice with 2 weeks interval in SPF Balb/c mice.

**Methods :** Briefly, five groups of 10 Balb/c mice free of any pathogens (SPF) were used. Three groups of mice were immunized with diphtheria toxoid vaccine nano adjuvanted aluminium hydroxide, one group as negative control was received normal saline only and the other group was positive control with diphtheria toxoid vaccine formulated with standard microparticle aluminium hydroxide adjuvant. PBMC cells and serum preparation were performed. The cellular immune responses were evaluated by identifying the population of CD4+, CD8+ and CD3+ T-cells using flow cytometer.

**Results :** The results of this study showed that vaccinated mice with diphtheria vaccine adjuvanted with nanoparticle aluminium hydroxide gel induce a high level of specific total IgG antibody compared to groups receiving diphtheria vaccines formulated with microparticle aluminium hydroxide adjuvant and control groups. The results of this study showed that two weeks later, vaccinated groups had a higher expression of T lymphocytes than the control group. The ratio of CD4+ lymphocytes to CD8+ lymphocytes in groups vaccinated by diphtheria toxoid vaccine was significantly higher than the control group. The present study showed that the immune system may be associated with increased cellular immunity, which can be interpreted as T lymphocyte proliferation and increased CD4+ to CD8+ ratio.

**Conclusion :** In conclusion, the present study revealed that the cellular immune response in the toxoid formulated with the nano-adjuvant of aluminium hydroxide precursor is far greater than its macromolecular form, and can enhance both Th1 as well as Th2 immune responses.

**Keywords :** Aluminium hydroxide, Nanoadjuvant, Immunogenicity, diphtheria toxoid

# P104-253: The most common side effects of COVID-19 vaccines

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**Background and Aim :** COVID-19 is a viral disease that has been spreading in Wuhan, China since December 2019. The vaccine for this disease has caused a great change in the natural course and mortality of the disease. The present study was designed to determine the most common side effects of COVID-19 vaccines in the world.

**Methods :** The present study was a brief review study designed in 2021. PubMed / Medline and Scopus databases were used to search for similar studies and extract content. Selected keywords for the search included “COVID-19” and “vaccines”. Summaries of articles published in congresses and conferences were excluded from the study. Initially, 8 articles were finally evaluated.

**Results :** Examining various studies, it was found that the most common side effects of COVID-19 vaccines on humans include pain at the injection site, fatigue, headache, muscle pain, joint pain, nausea, fever, chills, etc. Some studies have also reported diarrhea, edema, vomiting, urticaria, pruritus, and palpitations. A small number of studies have also reported lymph node enlargement, loss of sense of smell, and neurological manifestations.

**Conclusion :** The results of various studies show that the most common side effects of corona vaccines are pain at the injection site, fatigue, headache, fever, chills, muscle and joint pain, etc. These side effects remain between 1 to 3 days. It does not disrupt life, but despite the reluctance of the people to carry out the vaccination plan, governments can encourage people to get vaccinated by providing appropriate information and backgrounds and by granting incentive points.

**Keywords :** COVID-19, vaccines, adverse effects

# P105-313: mRNA vaccines

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**Background and Aim :** Vaccines can save lives of millions people in the world and also they improve the population health. Vaccines are classified into several types and mRNA vaccines are new.

**Methods :** In this systematic review, data were collected by performing searches of key words in search engines like as MEDLINE, ISI Web of Science and Sc. ience Direct. Data were extracted directly from full-length articles.

**Results :** mRNA vaccines are designed in recent years and it is covered by protein layer to protect against cellular enzymes. These molecules translate to proteins which can induce antibody production and these proteins protect the body. over the past decade, mRNA vaccines are examined on CMV, Rabbis, Influenza, Zika. This kind of vaccines are not alive and as a result of fact , they are not dangers for vaccinated people. The molecule of mRNA are not enable to entrance the cell nucleus and it can produce immunity immediately.

**Conclusion :** mRNA vaccines has several advantages in compare with the other kinds of vaccines. Using the specific molecule as a template for vaccine production, inducing the specific antibody, short time for rising the host immunity are the some reasons for using these vaccines.

**Keywords :** mRNA vaccines, Immunity, Protection

# P106-323: The increased Expression of Lipl41 Outer Membrane Protein in Pathogenic Leptospires in combination with Lep Protein: potential application for immunoassay improvement

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**Background and Aim :** Leptospirosis is an important worldwide zoonotic disease that is caused by Leptospira spirochaetes. It is generally found in humid tropical and subtropical regions. Unfortunately, because of the variety of clinical symptoms, its detection has many restrictions. LipL41 is among the most abundant outer membrane proteins in Leptospira and only found in pathogenic species. A small gene called lep is placed very close to lipl41 gene on the bacterial chromosome. Lep is a small chaperone protein which acts as a partner to increase expression of Lipl41. In the present study, the expression and purification of LipL41-Lep combined protein among predominant pathogenic isolates in Iran was accomplished in a prokaryotic system.

**Methods :** All available protein sequences were compared and analyzed using bioinformatics tools from NCBI databases. Recombinant LipL41-Lep protein was produced using the pET32a+ vector and expressed in Escherichia coli BL21 (DE3) competent cells. It was purified by denaturation and confirmed by western blotting.

**Results :** The protein was successfully expressed in BL21 (DE3) and purified. SDS-PAGE results revealed that the full-length 60kD fusion protein was induced by IPTG and present in the insoluble form.

**Conclusion :** The results showed that when Lipl41 is combined with Lep, the level of its expression is increased compared to when it is alone. This recombinant combined protein can be used as a potential application for immunoassay improvement.

**Keywords :** Pathogenic Leptospires, LipL41-Lep recombinant combined protein, Expression, Leptospirosis

# P107-329: Purification of Capsular Polysaccharide Produced by Streptococcus pneumoniae ATCC 49619

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**Background and Aim :** Streptococcus pneumoniae is a major cause of morbidity and mortality worldwide. The capsular polysaccharide (CPS) is the main virulence factor and target antigen in current pneumococcal vaccines. Based on the antigen composition of capsular polysaccharides, Streptococcus pneumoniae is classified into more than 98 serotypes. The purpose of this study was extraction and purification of CPS from Streptococcus pneumoniae ATCC49619.

**Methods :** After cultivation of Streptococcus pneumoniae ATCC49619 on TSB medium at 37 ºC with 5% CO2 for 24 hours, a simplified purification procedure for capsular polysaccharide was carried out after cell lysis with SDS and boiling for 20 minutes at 100ºC. The supernatant pH was adjusted to 4.5 with 5 M acetic acid, and capsular polysaccharides were collected from dialysis of cell lysates after using different concentrations of ethanol and proteinase K treatment (20mg/ml) for 30 minutes at 56ºC. In order to measure the percentage of purity and determine the concentration of capsular polysaccharide, the standard tests were performed including carbazole assay, phenol sulfuric acid test, SDS page, Bradford, agarose gel electrophoresis, and sample absorbance measurement at 260 and 280 nm.

**Results :** This purification procedure rendered purified CPS in a yield of 5mg from 3litre cultivation using the result of phenol sulfuric acid which showed the presence of pentose and hexose compounds in CPS. In all concentrations of ethanol precipitation, we have observed the presence of CPS. The highest and lowest concentrations of purified polysaccharides were found in 80% and 40% ethanol fractions, respectively. The dark purple color in the carbazole assay demonstrated that hyaluronic acid was also present in the CPS component. Nucleic acid and protein contaminations of CPS were successfully eliminated by using fractionation with 30–80% ethanol and proteinase K treatment. The results of Bradford, SDS page, and A280nm proved the removal of protein contamination, and the results of agarose gel electrophoresis and A260nm showed the nucleic acid contamination was eliminated.

**Conclusion :** In this study, we have demonstrated a simple and efficient method for purification of the capsular polysaccharide from Streptococcus pneumoniae ATCC49619 which can be used for conjugation with proteins as a candidate for polysaccharide conjugate vaccine.

**Keywords :** Streptococcus pneumoniae, Capsular Polysaccharide, Ethanol precipitation, Polysaccharide Conjugate Vaccine, Iran.

# P108-420: Evaluation of vaccine candidate antigens in Toxoplasma gondii

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**Background and Aim :** Toxoplasmosis is a parasitic disease caused by Toxoplasma gondii. The parasite has infected almost a third of the world's population, and no suitable vaccine or drug is available. In this study, we examined vaccine candidate antigens in Toxoplasma gondii and reported the best antigens based on scores on the Vaxijen server.

**Methods :** A Vaxquery server was used to find vaccine candidate antigens as well as their protein sequences. Toxicity and allergenicity of these antigens were evaluated with ToxinPred and AllerTOP v.2.0 servers, respectively, and finally, their antigenicity for the immune system was measured by the Vaxijen server.

**Results :** A total of 10 proteins GRA5, hsp70, MIC13, MIC3, OMPDC, P30, Rop2, ROP8, SAG2, and SOD were examined in this study, 3 of which (MIC3, P30, and SAG2) were identified as allergens, and all except GRA5 had toxic sequences for humans. GRA5, MIC13, MIC3, P30, Rop2, SAG2, and SOD antigen scores for the human immune system were more significant than 0.5, which is an acceptable score.

**Conclusion :** According to the results, GRA5 protein with a Vaxijen score of 1.0254 as the highest score and non-toxicity and non-allergenicity for humans is the best option for predicting epitopes and vaccine design.

**Keywords :** Toxoplasmosis; Toxoplasma gondii; Vaccine

# P109-77: In vitro Antibacterial Activity and Phytochemical Screening of Hydroalcohlic Extract of Seeds of Polylophium involucratum (Pall). Boiss. from Ramsar - 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. Polylophium involucratum (Pall). Boiss. is a medicinally essential plant used for the treatment of diverse infectious diseases. The aim of this project was to investigate the antibacterial effect of hydroalcohlic extract of seeds of Polylophium involucratum (Pall). Boiss. (Apiaceae) from Ramsar - Iran, to the three species of common pathogenic bacteria resistant to multiple drugs in vitro such as:, Staphylococcus aureus (PTCC 1113), Bacillus subtilis (PTCC 1156) and Escherichia coli (PTCC 1399).

**Methods :** In this research, hydroalcohlic extract of seeds of Polylophium involucratum (Pall). Boiss. prepared by microwave assisted extraction (MAE) method. The antibacterial activity was determined by (Disk Diffusion Method) against three strains of Gram-positive and Gram-negative bacteria. Also, phytochemical study was performed by using standard phytochemical methods.

**Results :** The hydroalcohlic extract of seeds of Polylophium involucratum (Pall). Boiss. exhibited good antibacterial potential against gram positive and gram negative bacterial strains. Also, our preliminary phytochemical analysis of seeds extract using hydroalcohlic as solvent confirmed the presence of (Flavonoids, Terpenoids, Coumarins, Phenols, Cardiac glycosides, Quinones and Saponins). This indicates that antibacterial activities may be due to presence of secondary metabolites.

**Conclusion :** The findings of the present study demonstrated the potential of phytochemicals from Polylophium involucratum (Pall). Boiss. seeds, a natural source, in the pathway of developing a novel antibacterial agent able of treating bacterial infections.

**Keywords :** Antibacterial drugs, Polylophium involucratum (Pall). Boiss., Bacillus subtilis, Terpenoids.

# P110-109: Evaluation of cold plasma efficiency in reducing the population of bacteria involved in wound infections using argon plasma jet

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**Background and Aim :** Microbial cells in chronic wounds seriously delay wound healing, so inactivating microbial cells is an important step in the healing process. Atmospheric pressure cold plasma can effectively inactivate microbial cells and can be developed as an effective tool for topical antimicrobial therapy. Atmospheric pressure cold plasma produces a wide range of chemically active species including reactive nitrogen and oxygen species (RONS), excited molecules and UV photons. These active species are responsible for inactivating bacterial cells.

**Methods :** In this study, argon plasma jet was applied to two pathogenic bacteria responsible for wound infections, including Staphylococcus aureus and Pseudomonas aeruginosa for different periods of time up to 150s. After plasma exposure, bacterial population was determined using the plate count assay and compared with control.

**Results :** The results showed that argon cold plasma was highly efficient against both strains and plasma exposure for at least 15s caused a significant decrease of bacterial cells by 58 and 61 % for S. aureus and P. aeruginosa. Also, the highest population reduction for S. aureus and P. aeruginosa was recorded by 67 and 76 %, after 150s of plasma exposure.

**Conclusion :** Atmospheric pressure cold plasma is considered a mild disinfection method without undesirable effect on wound heating and without remaining residue on the treated surfaces. Thus, non-thermal technology could be considered a safe, environmental friendly and cost-effective approach compared with alternative disinfection and antisepsis methods.

**Keywords :** cold plasma, antibacterial, antisepsis, wound infection

# P111-122: Anti-Quorum sensing activity of Archangium sp. metabolite extract against Pseudomonas aeruginosa

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**Background and Aim :** Pseudomonas aeruginosa is a common cause of nosocomial and opportunistic infections. Variety of virulence factors present in P. aeruginosa can empower pathogenicity of the bacteria in the host. Most of these pathogenic properties are controlled by a hierarchical system called Quorum Sensing (QS). Myxobacteria are gram-negative rods, producing bioactive secondary metabolites which have antimicrobial activities. In this study, we investigated the effect of Archangium sp. metabolite extract (AME) on biofilm and virulence factors of P. aeruginosa, which are controlled by QS systems.

**Methods :** The minimum inhibitory concentration (MIC) of AME was determined against P. aeruginosa ATCC 27853. AME was tested for its effects on the production of P. aeruginosa virulence factors controlled by QS system (biofilm formation, pyocyanin and rhamnolipid production, swarming and twitching motility).

**Results :** The MIC of AME against P. aeruginosa ATCC 27853 was 2.5 mg/ml. Sub-MIC concentrations demonstrated statistically significant reduction of virulence factors including pyocyanin and rhamnolipid production. Biofilm formation and twitching motility were also reduced after AME treatment.

**Conclusion :** These results indicate that AME inhibited the production of virulence factors and biofilm formation which are under the control of QS systems in P. aeruginosa. Several secondary metabolites produced by Myxobacteria are promising antimicrobial agents. This study shows that Myxobacteria secondary metabolites can have anti-QS activity as well. So, further studies can be focused on the isolation of bioactive molecules with anti-QS activity, to determine their chemical nature and to deduce their mechanisms of anti-QS activities.

**Keywords :** Pseudomonas aeruginosa, QS systems, anti-QS activity, Myxobacteria

# P112-135: Isolation of novel bacteriophage infecting virulent Klebsiella pneumoniae

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**Background and Aim :** Klebsiella pneumoniae is a clinically important pathogen and is isolated from various infections such as respiratory, urinary tract and wound infections. K. pneumoniae has several virulence agents and also due to the emergence of widespread antibiotic resistance, treatment with antibiotics has been challenged. Bacteriophages are viruses that lyse and destroy the host bacterial cell. After attachment to the host cell, they can undergo either lytic or lysogenic cycle. During the lytic cycle, the cell wall of host is lysed and replicated phage is released to invade other bacteria. Phage therapy is an old method and was hindered by the discovery of penicillin. In recent years, by emerging of antibiotic-resistant bacteria, phage therapy has revived. Therefore, present research aimed to isolate a novel bacteriophage against K. pneumoniae and suggest a safe method in the treatment of infections with highly resistant K. pneumoniae.

**Methods :** This study was done during 15 months from March 2020 to June 2021. A Multi-Drug Resistant (MDR) and strong biofilm producer K. pneumoniae was selected as host bacterial cell for isolating bacteriophages. Sewage samples, as sources of bacteriophages, were collected from several hospitals. Then, these samples were filtered and bacterial suspension was added to this sample and then incubated overnight. After incubation, bacteriophages were purified using double-layered agar method. After plating of the phage and performing a spot test, the phage was purified by picking single plaques. A high titer lysate of phage was prepared for further analysis. To determine the host range of the phage, for each strain of K. pneumoniae, double-layered agar and spot test methods were performed. The characterization and morphology of phage was revealed by Transmission Electron Micrograph (TEM).

**Results :** The lytic activity of isolated phage was tested based on clear plaque formation. Our phage had a large clear centered plaque. In vitro bactericidal activity of phage showed that 45.3% of K. pneumoniae isolates were sensitive to phage. Based on the results of electron microscopy, the isolated phage belonged to the siphoviridae family.

**Conclusion :** Bacteriophages have many advantages such as their specificity to host bacteria, single dose applications and low costs. Therefore, more studies are needed on these agents so

that in the future they can be widely used as an alternative in the treatment of antibiotic-resistant bacteria.

**Keywords :** bacteriophage, Klebsiella pneumoniae, MDR, antibiotic-resistant

# P113-140: Antibacterial activity by the peptide microcin J25 in Escherichia coli

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**Background and Aim :** Bacteriocins are generally active antimicrobial peptides against bacteria closely related to the producer. Two types of bacteriocins, colicins and microcins, are developed by Escherichia coli. Microcin J25 (Mcc J25) is an antibacterial peptide inhibits bacterial transcription by binding within, and obstructing, the nucleotide-uptake channel of bacterial RNA polymerase. The objective of this study was to detect and evaluate the wide range of antimicrobial activity of MccJ25 produced by the bacteriocinogenic Escherichia coli.

**Methods :** In this experimental study, 120 clinical specimens were selected from clinical specimens from private diagnostic laboratories at Isfahan during the year 2020. They were cultured on blood agar and EMB media 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 MccJ25 gene. Fidelity of PCR products was confirmed by direct sequencing. Homology analysis was performed by application of BLAST serve. The data were analyzed with Chromasv2.1.1 software.

**Results :** 120 strains 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. of which 25 had positive well test samples and about 5 (20%) of the clinical specimens collected that contaminated with Escherichia coli had MccJ25 gene.

**Conclusion :** This assessment was performed to evaluate its potential as an antimicrobial agent for clinical studies and commercial use to treat bacterial infections. This property can be useful for antibacterial trials.

**Keywords :** Bacteriocins, MccJ25, Escherichia coli

# P114-142: Evaluation of the simultaneous exposure to ibuprofen and ciprofloxacin on some virulence factors of ciprofloxacin resistant Pseudomonas aeruginosa

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**Background and Aim :** Pseudomonas aeruginosa, is considered one of the leading causes of opportunistic and hospital-acquired infections, worldwide. The infections with P. aeruginosa have been linked with difficulties in clinical treatment because of significant resistance of the bacterium to a variety of antibiotics, including ciprofloxacin. Non-steroidal anti-inflammatory drugs (NSAIDs) such as ibuprofen, have displayed antimicrobial activity. Also, in combination with antibiotics, NSAIDs have exhibited significant synergistic antibacterial effects, suggesting that in combination with ciprofloxacin, these drugs could be more efficient for the treatment of drug resistant infections. Thus, in this study, we aimed to evaluate the effect of simultaneous use of ibuprofen and ciprofloxacin on the virulence factors of clinical isolates of P. aeruginosa.

**Methods :** Ciprofloxacin resistant P. aeruginosa strains were isolated from clinical specimens and were identified using biochemical assays. The antibiotic resistance pattern was determined by the disk diffusion method and the Minimum Inhibitory Concentration (MIC) of ibuprofen and ciprofloxacin against P. aeruginosa was determined by broth microdilution assay. The isolated strains were exposed to ibuprofen, ciprofloxacin, and ibuprofen+ciprofloxacin, at sub-MIC concentration. The proteolytic and hemolytic activities were determined using skim milk agar and blood agar assays, respectively. Bacterial swarming, twitching and growth curve were also studied.

**Results :** The isolates were Gram negative rods and, catalase and oxidase positive which grew in cetrimide agar and EMB agar. The MIC of ibuprofen and ciprofloxacin were determined 2048 and 32 µg/mL. Ibuprofen and ciprofloxacin in combination were able to significantly reduce bacterial hemolysis and proteolysis. Also, bacterial swarming and twitching motility was decreased in the presence of both drugs, compared with either agent alone. In addition, the growth curve analysis showed that bacterial growth was reduced by 47.4 % among the bacteria treated with ciprofloxacin and ibuprofen compared with control.

**Conclusion :** According to the study, ibuprofen and ciprofloxacin have a promising synergic activity against P. aeruginosa which could be used for therapeutic approaches. However, further characterization must be performed in this issue.

**Keywords :** Ciprofloxacin, Ibuprofen, Pseudomonas aeruginosa, virulence factors

# P115-145: Antibacterial Activity of Copper Nanoparticles on Streptococcus group A

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**Background and Aim :** Streptococcus group A is one of the most common and important bacteria cause pharyngitis in children and adults. In addition, the bacteria cause diseases of rheumatic fever, scarlet fever, acute glomerulonephritis, necrotizing fasciitis. Resistance of microorganisms to antibiotics is steadily rising, with reports showing that quite a number of the recognized antimicrobial agents in existence have demonstrated resistance by one species of microorganism or another. The aim of this study was to investigate the antimicrobial effect of copper nanoparticles for treatment of streptococcus group A.

**Methods :** In this experimental study, the antibiogram test was performed to obtain the most effective antibiotic. The antibacterial activity of copper nanoparticles and penicillin was determined by Agar Dilution method. MIC and MBC of copper nanoparticles and Penicillin was determined by microdilution method.

**Results :** Minimum bacteriocide concentration in the agar dilution method for copper nanoparticle concentration was 1000 ppm, for penicillin was 6000ppm and for mix of penicillin and copper nanoparticles was 500ppm . Copper nanoparticles compared with penicillin was more effective to kill bacteria. the extent of the impact is less than the synergistic effect of penicillin and copper nanoparticles.

**Conclusion :** copper nanoparticles or mix of copper nanoparticles and penicillincan be used as candidate in the treatment of infections causedby Streotoccus group A.

**Keywords :** Copper nanoparticles, streptococcus groupA ,penicillin, antibiotic resistance

# P116-146: Isolation and characterization of a lytic bacteriophage against xanthomonas campestris pv campestris

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**Background and Aim :** Xanthomonas strains, including Xanthomonas campestris pv. campestris, are responsible for major damage to the agricultural industry and cause infections in more than 400 different plant hosts including citrus, cabbage, wheat, tomatoes, peppers, and more. Conventional methods used to control these bacteria, include the use of copper-based bacteriocines, antibiotics and other solutions which induce and increase environmental damage, accumulation of toxins in the soil and bacterial resistance. finding a new strategy as alternative treatment for plant's pathogenic bacteria seems necessary. Therefore, bacteriophages due to their many advantages and relatively ease of availability, as alternative biological control agents have been proposed. in this study, isolation and characterization of effective lytic phages on Xanthomonas campestris pv. campestris were investigated in order to control these bacteria and prevent contamination of agricultural products and environmental hazards.

**Methods :** A lytic bacteriophage effecting on Xanthomonas campestris pv. Campestris DSM1706 was isolated from Karun river water by double-layer agar method. Host range was determined using the spot test for Xanthomonas pathogenic strains. Its morphology was also investigated by transmission electron microscopy (TEM).

**Results :** The isolated phage, in addition to Xcc DSM1706 strain, had a lytic effect on three other Xanthomonas pathogenic strains isolated from cabbage fields, including: SAM 4209, SAM 4211, SAM 4212. Based on the morphological characteristics, the isolated bacteriophage belonged to Tectiviridae family.

**Conclusion :** Based on the results of this study, lytic bacteriophages can be biological agents with effective antibacterial potential in controlling plant diseases and replace current controlling methods.

**Keywords :** Bacteriophage, Lytic, Xanthomonas campestris pv. campestris, Tectiviridae

# P117-165: Investigation of the phytochemicals and bioactivity potential of essential oil from Nepeta curvidens Boiss. & Balansa

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**Background and Aim :** Nepeta curvidens is a plant of the mint family and an important species of the genus Nepeta. The main habitat of the N. curvidens in the Garin Mountains in Lorestan Province, Iran. Although locals have used N. curvidens as a food flavoring agent for years, few studies have been conducted on its phytochemical and biological properties. The chemical constituents of N. curvidens essential oil and then its biological properties were studied in detail in this investigation.

**Methods :** N. curvidens essential oil was prepared from the aerial parts of the plant using the hydrodistillation method and its chemical composition was analyzed by the GC-MS method. Antimicrobial, antifungal, anti-Leishmania, and cytotoxic activities of the essential oil were investigated in vitro. In addition, antinociceptive and anti-inflammatory effects were evaluated in vivo.

**Results :** Most of N. curvidens essential oil compositions are composed of trans-caryophyllene (17.53%), allo-spathulenol (13.41%), germacrene D (10.12%), bicyclogermacrene (9.36%), α-pinene (9.12%), and β-phellandrene (6.87%). The highest antimicrobial and antifungal effects were observed against L. monocytogenes (MIC=156.25 µg/ml) and K. marxianus (MIC=625 µg/ml), respectively. Concentration-dependent effects were detected in the treatment of L. major, so that the number of macrophages infected with amastigote dropped significantly with higher concentrations. The essential oil showed the highest effect on the lung cancer cell line (A549) with the lowest IC50 (133.2µg/mL). The most resistant cell line to the essential oil was bladder cancer (C450) with an IC50 of 430.69 µg/mL. SI 19.49 index indicated high immunity of the essential oil on macrophage lines. Compared with morphine analgesic, the highest pain control effect of the essential oil was observed in primary and secondary phases at 100 mg/kg concentration in rats. At 100 mg/kg concentration, reduced swelling of the paw and ear was observed in mice compared to the dexamethasone anti-inflammatory drug.

**Conclusion :** The essential oil presents remarkable therapeutic properties such as antifungal, antibacterial, anti-inflammatory properties that probably attributed to the presence of an important trans-caryophyllene compound. Outstandingly, the essential oil has low toxic effects on the normal line and high antitumor properties against cancer cells. Therefore, it is expected to be used in the preparation of less toxic drugs than chemical ones, although more studies are required.

**Keywords :** Nepeta curvidens, antifungal, antibacterial, anti-inflammatory, antitumor

# P118-181: Antibacterial Effects of Essential Oil of Sage and Betony Plants 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 multi drug 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 Salvia officinalis and Stachys lavandulifolia, 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 Salvia officinalis (30 mm), and the minimum of growth inhibition diameter is related to essential oil of Stachys lavandulifolia (10 mm) at the highest concentration (400 mg/ml). In conditions of in vivo, spleen supernatant cultivation, the average number of bacteria for Salvia officinalis and Stachys lavandulifolia 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 Salvia officinalis and Stachys lavandulifolia have the effective antibacterial activity against mentioned bacteria and can be useful to treatment of nosocomial infections.

**Keywords :** Antimicrobial, Essential oil, Salvia officinalis, Stachys lavandulifolia, Staphylococcus aureus

# P119-187: Synergism of ibubrofen with ciprofloxacin against ciprofloxacin resistant Pseudomona aeruginosa through bacterial biofilm inhibition

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**Background and Aim :** Infection with drug-resistant Pseudomonas aeruginosa strains is a major health challenge, worldwide. Biofilm formation by bacterial strains is regarded as a main cause of non-specific resistance to a variety of antimicrobial agents and thus, therapeutic failure. Inhibition of bacterial biofilm is a novel approach to combat the drug resistance phenotype of pathogenic bacteria. Previous studies reported the antibiofilm potential of Non-steroidal anti-inflammatory drugs (NSAIDs) drugs. Therefore, NSAIDs could show synergism with antibiotics against drug-resistant strains through their antibiofilm potential. Therefore, the current work was conducted to evaluate antibiofilm potential and synergism with ciprofloxacin against cirprofloxacin resistant P. aeruginosa strains.

**Methods :** Bacterial strains were isolated from clinical specimens and identified using biochemical assays. Ciprofloxacin resistance was determined using disk diffusion method. Also, the minimum inhibitory concentration (MIC) of ibubrofen and ciprofloxacin was determined in 96-well microtiter plates. The antibiofilm potential of ibubrofen at sub-MIC concentration was determined using the crystal violet staining assay in 96-well plates. Finally, the synergism of the ibubrofen and ciprofloxacin was investigated using the checkerboard titration assay.

**Results :** The isolated strains were Gram-negative, catalase and oxidase positive rods, able to grow in cetrimide agar and also at 42?C. The MICs of ibubrofen and ciprofloxacin were determined 2048 and 32 µg/mL, respectively. At ½ MIC, ibubrofen significantly reduced biofilm formation by 34-56%, compared with the control. Finally, the checkerboard titration assay revealed synergism of the drugs with fractional inhibitory concentration (FIC) of 0.37.

**Conclusion :** This work showed the synergism of Ibubrofen with ciprofloxacin against ciprofloxacin resistant P. aeruginosa strains which could be associated with the antibiofilm activity of ibubrofen. Our results indicated that combined therapy using ibubrofen and ciprofloxacin could be a promising approach against drug-resistant P. aeruginosa infection, after further characterization.

**Keywords :** ibubrofen, biofilm, Pseudomonas aeruginosa, antibiotic

# P120-188: Rare Actinobacteria and Their Biotechnological Potential Applications

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**Background and Aim :** The increasing prevalence of nosocomial infections, due to the arbitrary use of antibiotics, has caused serious health problems. Natural compounds have been used for many years to treat and cure many infections. Rare actinobacteria are one of the main sources for the discovery and isolation of natural compounds with pharmaceutical properties. The main purpose of this review article is to study new metabolites derived from rare actinobacteria, and to evaluate their medicinal and pharmaceutical applications.

**Methods :** This review includes over 183 quality peer-reviewed papers available in the databases of Scopus, PubMed, Web of Science and ScienceDirect from 2015 to 2021.

**Results :** This study presents the chemical structure of 113 new isolated compounds from rare actinobacteria and their biological activity. This study also shows that rare actinobacteria have the ability to produce a variety of biologically active compounds such as alkaloids, flavonoids, terpenes and polyketides with a diverse range of biological activities including antibacterial, antifungal, antiviral and anticancer properties.

**Conclusion :** The results of this study revealed that rare actinobacteria are an excellent source for the production of natural active compounds with high therapeutic and applied potentials in medical, pharmaceutical and agricultural biotechnology. It also highlights the key role of these compounds in the development of drugs needed by humans in the near future.

**Keywords :** : Actinobacteria, chemical composition, chemical properties, anti-bacterial, anti-cancer, anti-fungal

# P121-200: Antibacterial Effects of Extract of Sage and Betony Plants 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 multi drug 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 Salvia officinalis and Stachys lavandulifolia, 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 Salvia officinalis (20 mm), and the minimum of growth inhibition diameter is related to ethanolic extract of Stachys lavandulifolia (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 Salvia officinalis and Stachys lavandulifolia were 1.8×103 CFU/ml and 6.6×103 CFU/ml respectively and for aqueous extract of Salvia officinalis 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 Salvia officinalis and ethanolic extract of Stachys lavandulifolia have the effective antibacterial activity against mentioned bacteria and can be useful to treatment of nosocomial infections.

**Keywords :** Antimicrobial, Salvia officinalis, Stachys lavandulifolia, Staphylococcus aureus

# P122-203: Quorum-sensing inhibitors as anti-pathogenic drugs against Pseudomonas aeruginosa

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**Background and Aim :** Today we are encountering an alarming increase in multi-drug resistant bacteria and as a result, infections that have become non-treatable. This calls for development of alternative treatment strategies. One interesting approach, is to selectively block the control apparatus of pathogenic traits of the bacteria. By doing so, bacteria may fail to adapt to the host environment and establish an infection. Quorum-sensing (QS) signaling systems of pathogens are central regulators for the expression of virulence factors. QS inhibitor (QSI) compounds limit the coordinated expression of virulence factors without interfering with bacterial growth; therefore, they are less likely to be resisted. QS system in P. aeruginosa is composed of four subsets including Las, Rhl, PQS and IQS. Mainly secreted components including elastase, alkaline protease, rhamnolipids, phenazines, cyanide, and lectins are encoded by QS regulon in P. aeruginosa.

**Methods :** Our team are investigating the effect of different medicinal plant extracts and microorganisms' culture supernatants on this bacterium to discover new QSI compounds.

**Results :** Our results have shown that many native medicinal plant extracts have effective inhibitory effect on biofilm formation and virulence factor production of P. aeruginosa. Also, different microorganisms' metabolites used in our studies have anti-QS activity and can interfere with the pathogenic properties of P. aeruginosa in vitro.

**Conclusion :** So, further studies should be focused on the isolation of those bioactive molecules with anti-QS activity, to determine their chemical nature and to deduce their mechanisms of anti-QS activities.

**Keywords :** Pseudomonas aeruginosa, antibiotic resistance, quorum sensing, QS inhibitors

# P123-207: Determination of Host Range of a Specific Pseudomonas aeruginosa Bacteriophage

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**Background and Aim :** Bacteriophages are advanced tools to combat the antimicrobial resistance of human opportunistic strains of Pseudomonas aeruginosa. Phages or bacteriophages have a limited hosting range that accurately identifies which bacteria to target. In this study, the host range of a specific Pseudomonas aeruginosa Bacteriophage on clinical samples of Klebsiella and Acinetobacter has been investigated.

**Methods :** After isolation of specific phages of Pseudomonas aeruginosa from wastewater, purification was done. Then, the phage hosting range was investigated on two bacteria, Klebsiella and Acinetobacter. The plaque formed on the plate was evaluated using point method. First we cultivated bacterial strains in the TSB culture, then added 10 microliters of bacteria in tubes containing 5% Agar Agar Broth. In the next stage, a special phage of Pseudomonas aeruginosa was added in a point form. The plates were incubated for 24 hours at 37 ° C, plaque formation or non-plaque formation was investigated.

**Results :** Pseudomonas aeruginosa hosting renge results showed that this phage does not have a very wide range of influence and did not have a clear plaque on the Klebsiella and Acinetobacter bacteria. With this experiment, we identified the proprietary phage against Pseudomonas aeruginosa strains to treat infections of this bacterium.

**Conclusion :** The results showed that the isolated phage was highly specific and could be used as a smart weapon to replace most of the antibiotics resistant to this gram-negative bacterium to prevent Pseudomonas aeruginosa infections.

**Keywords :** Host range, Bacteriophage, Pseudomonas aeruginosa

# P124-224: An Evaluation of Antimicrobial Activity of Polysaccharides Extracts of Ganoderma lucidum on Growth Inhibition of Pseudomonas aeruginosa Isolated from Urinary Tract Infection

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**Background and Aim :** Pseudomonas aeruginosa is an opportunistic pathogen and also one of the main causes of nosocomial infections. The purpose of this study was to evaluate the antimicrobial effect of polysaccharide extracts from Ganoderma lucidum on Pseudomonas aeruginosa bacterial infection which is resistant to common antibiotics.

**Methods :** In this study, polysaccharide extracts of G. lucidum were initially extracted using seven different methods. Furthermore, antimicrobial tests such as the agar well diffusion test, Minimum Inhibitory Concentration (MIC), and Minimum Bacteriocidal Concentration (MBC) were conducted. In the next step, the drug resistance of microbial strains was determined, and the extract's ability to inhibit free radicals of (DPPH) was evaluated.

**Results :** In this study, by analyzing the yield of extracted polysaccharides indicate that the Soxhlet extractor method with 16% has the highest yield compared to other methods. According to the results of the diameter of the growth zone of inhibition for polysaccharide extract was found as 1.5 cm. Based on the findings, the MIC and MBC for polysaccharide extract were calculated to be 0.859 and 6.875 mg/ml, respectively. The results of urinary drug susceptibility testing indicated resistance to all tested antibiotics. The findings of the DPPH test showed that based on IC50, its value for polysaccharide extract was obtained as 647.76 ?g/ml.

**Conclusion :** The results of this study revealed that G. lucidum has a high antimicrobial ability and can also be suggested as a potential medical treatment for urinary tract infections.

**Keywords :** Antimicrobial, Polysaccharides, G.lucidum, P. aeruginosa

# P125-234: Study of the Combined Effect of *Zataria multiflora* Essential Oil with Tetracycline and Vancomycin against Biofilms of *Enterococcus faecalis* Clinical Isolates

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**Background and Aim :** Introduction: Enterococci are optional gram-positive anaerobic bacteria that are naturally present in the human gastrointestinal flora, known as important pathogens around the world, especially in nosocomial infections. Given the role of biofilms in antibiotic resistance as well as the pathogenicity of new treatment methods to eliminate the appropriate conditions for the formation of biofilms by bacteria, which acts as a protective coating against the host immune system and antibiotics, it is necessary to it seems. One of the proposed methods to combat bacterial biofilm is the use of alternative antibacterial treatments, which include the combined use of herbal essential oils and antibiotics. The aim of this study was to investigate the combined effect of Zataria multiflora essential oil and tetracycline and vancomycin antibiotics against the biofilm of clinical strains of bacterial Enterococcus fecalis.

**Methods :** This study was performed on 30 samples of Enterococcus faecalis isolated from patients with office infections referred to Milad Hospital in 2009. Zataria multiflora essential oil was extracted and its chemical compounds were analyzed by gas chromatography device with mass spectrometry (GC-MS). Antibacterial activity of thyme essential oil and tetracycline and vancomycin antibiotics were investigated by microdermabrasion method against 30 strains of Enterococcus faecalis and the minimum inhibitory concentration (MIC) alone and in combination was determined against the formation of biofilm on polystyrene microtiter plate. The results of antimicrobial interaction were obtained by checkerboard titration method by determining the fraction inhibitory concentration index (FICI).

**Results :** Based on the results of this study, 10 strains of Enterococcus faecalis were able to produce stable biofilm. The results also showed that Zataria multiflora essential oil alone and in combination with tetracycline and vancomycin antibiotics has anti-biofilm activity.

**Conclusion :** Herbal essential oils can be used effectively to control the biofilms of Enterococcus faecalis. This issue highlights the importance of natural compounds as anti-biofilm and potential antimicrobial agents.

**Keywords :** Biofilm, Enterococcus faecalis, Zataria multiflora Essential Oil, Tetracycline, Vancomycin, Synergistic

# P126-237: Study of Aqueous-Alcoholic Extracts of Peganum Harmala Plant on Growth Rate of Escherichia Coli Bacteria Isolated from the Stools of Children with Diarrhea

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1. *The aim of this study is to replace herbal medicines with industrial antibiotics and prevent the increase of bacterial resistance.*

**Background and Aim :** Diarrhea is often induced by infection of digestive system .It is one of the major causes of death in children under 6 years old in developing countries.Among the Bacterial of death in children under 6 years old in developing countries .Among the Bacterial pathogens,E.coli is the most important causative agent of endemic and epidemic diarrhea around the word . Peganum harmala is a perennial plant with abundant green leaves that Belongs to the family Nitrariaceae.Due to the indiscriminate consumption of antibiotics and the increasing resistance of bacteria ,and to seek an appropriate substitute for antibiotics, we proceeded to investigate the effect of hydro alcoholic Peganum harmala extract on the growth rate of E.coli isolated from stool of children with diarrhea.

**Methods :** This descriptive cross-sectional study was carried out on 100 samples isolated from stools of children with diarrhea admitted. Following sample collection and culturing ,E.coli strains causing childrens diarrhea were identified.

**Results :** All of the used antibiotics except ampicillin and tetracycline had a positive effect on E.coli . Of a total of 100 samples collected ,70 samples showed growth ,and of these ,58 samples were related to Shigella.The results of this study showed that Peganum extract shows no effect on E.coli.

**Conclusion :** The Peganum Harmala extract did not show any inhibitory effect on Escherichia coli bacteria. All antibiotics used on Escherichia coli bacteria were effective except for ampicillin and tetracycline that was resistant.

**Keywords :** Peganum Harmala,PCR,Extracts of Peganum

# P127-276: Evaluation of the effect of Mentha piperita essential oils loaded in a chitosan nanogel on clinical isolates of Acinetobacter baumannii in-vitro

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**Background and Aim :** One of the most important problems of health care systems is the increasing prevalence of antibiotic-resistant bacterial infections. The use of natural substances such as plant essential oils with antimicrobial properties as an alternative to antibiotics is increasing. The aim of this study was to evaluate the effect of Mentha piperita essential oils loaded in a chitosan nanogel on clinical isolates of Acinetobacter baumannii in-vitro.

**Methods :** In this cross-sectional study, Acinetobacter baumannii isolates were isolated from selected hospitals in Khorramabad. After preparing Mentha piperita essential oils loaded in a chitosan nanogel, the minimum inhibitory concentration (MIC) of nanogels on Acinetobacter baumannii isolates was determined by micro broth dilution method in plate 96 houses according to CLSI instructions.

**Results :** The lowest and highest concentrations of nanogel MIC against the isolates of Acinetobacter baumannii were 3.12 and> 400 µg/mL, respectively.

**Conclusion :** The results of the present study indicate the ability of Mentha piperita essential oils loaded in a chitosan nanogel on Acinetobacter baumannii isolates

**Keywords :** Nanogel, Essential oil of Mentha piperita, Acinetobacter baumannii

# P128-287: ZnO/GQDs -NPs nanocomposites enhances the Antibacterial Activity of Dermatocarpon miniatum against Methicillin-resistant Staphylococcus aureus isolated from burn wounds

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**Background and Aim :** Over the last few years, the emergence and widespread distribution of microbial resistance to antibiotics is world-wide challenge in the medical science. Consequently, the discovery and characterization of novel methods as new antibacterial agent for the prevention, and treatment of infection bacterial are urgently required .In this regard, Dermatocarpon miniatum is one the most species lichens that have been used in folk medicines and could be replaced by traditional antibiotics. Despite its reported benefits, there are reports associated with D. miniatum adverse effects. The above problems can be solved by encapsulating D. miniatum into nanoformulations. Integrating D. miniatum into nanocarriers may decrease its toxicity and improve the bioavailability, solubility and the antibacterial activity.

**Methods :** In this study, the ZnO/GQDs nanocomposites (NCs) and D. miniatum grafted ZnO/GQDs NCs have been prepared via green method. The prepared products are characterized with XRD analysis, SEM and FTIR.The MICs of D. miniatum, D. miniatum/ZnO/GQDs -NPs were determined using the broth microdilution method as described by the CLSI standards.

**Results :** The result of in-vitro experiments demonstrated that Interestingly, the linking of D. miniatum into ZnO/GQDs NCs demonstrated strong antibacterial activity against Methicillin-resistant Staphylococcus aureus (MRSA) compared to free D. miniatum. The MIC value of D. miniatum /ZnO/GQDs against MRSA was 125 µg/mL, whereas the MIC value against D. miniatum was 625 µg/mL.

**Conclusion :** Finally, results this study reported that the D. miniatum /ZnO/GQDs–NCs formulation could be employed as a novel agent antibacterial to inhibit bacterial growth .

**Keywords :** antibacterial,nanocarriers,Methicillin-resistant Staphylococcus aureus,Dermatocarpon miniatum

# P129-300: Designing as an antiviral approach against Crimean-Congo hemorrhagic fever virus (CCHFV)

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**Background and Aim :** Crimean-Congo hemorrhagic fever (CCHF) is the most widespread tickborne viral infection worldwide: it has been reported in many regions of Africa, the Middle East, and Asia. The geographical distribution of CCHFV corresponds most closely with the distribution of members of the tick genera, and Hyalomma ticks are the principal source of human infection. In contrast to human infection, CCHFV infection is asymptomatic in all species. In recent years, gene therapy has become a powerful strategy against viruses. Therefore, in the present study, the possibility of using and designing shRNA against West Nile virus was investigated.

**Methods :** Oligonucleotides encoded shRNA molecules were designed against nucleocapsid gene of Crimean-Congo hemorrhagic fever virus using the www.invivogen.com/sirna-wizard site 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 submitted, so the most effective shRNAs with desired restriction enzyme sites were designed.

**Results :** Three potentially effective shRNA molecules were designed. Their start target positions included the respectively start positions of 46, 144 and 157 of Crimean-Congo hemorrhagic fever virus nucleocapsid (N) gene.

**Conclusion :** The results showed that there are potentially effective shRNA molecules against nucleocapcid (N) gene of Crimean-Congo hemorrhagic fever virus that can suppress its replication.

**Keywords :** shRNA, Crimean-Congo hemorrhagic fever virus, nucleocapsid (N), gene therapy.

# P130-301: Designing shRNA molecules targeting polymerase gene as a gene therapy tool against West Nile virus (WN)

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**Background and Aim :** West Nile virus (WNV) is the leading cause of mosquito-borne disease. It is most commonly spread to people by the bite of an infected mosquito. Cases of WNV occur during mosquito season, which starts in the summer and continues through fall. There are no vaccines to prevent or medications to treat WNV in people. In recent years, gene therapy has become a powerful strategy against viruses. Therefore, in the present study, the possibility of using and designing shRNA against West Nile virus was investigated.

**Methods :** Oligonucleotides encoded siRNA molecules were designed against RNA polymerase gene of West Nile virus using the www.invivogen.com/sirna-wizard online 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 submitted, so the most effective shRNAs with desired restriction enzyme sites were designed.

**Results :** Four potentially effective shRNA molecules were designed. Their start target positions included with respectively positions of 431, 465, 525 and 693 of West Nile virus RNA polymerase sequence.

**Conclusion :** The results showed that there are potentially effective shRNA molecules against RNA polymerase gene of West Nile virus that can suppress its proliferation.

**Keywords :** shRNA , West Nile virus , RNA polymerase gene, gene therapy.

# P131-302: Designing a RNAi- based treatment for Infectious Pancreatic Necrosis virus (IPN)

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**Background and Aim :** : Infectious Pancreatic Necrosis (IPN) is a fish disease caused by an unenveloped icosahedral birnavirus. The IPN virus is the type species of the genus Aquabirnavirus. It is highly contagious and mainly affects intensively reared salmonid species although it has a wide host range. The virulence of IPNV isolates varies widely; while most are isolated from subclinical cases, some isolates can produce very high fish mortality. This disease is not zoonotic. In recent years, gene therapy has become a powerful strategy against viruses. Therefore, in the present study, the possibility of using and designing shRNA against Infectious Pancreatic Necrosis virus was investigated.

**Methods :** Oligonucleotides encoded shRNA molecules were designed against RNA polymerase (vp) gene of IPN virus using the www.invivogen.com/sirna-wizard site 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 submitted, so the most effective shRNAs with desired restriction enzyme sites were designed.

**Results :** Two potentially effective shRNA molecules were designed. Their start target positions included respectively start positions of 69 and 451 of IPN virus RNA polymerase (vp) gene.

**Conclusion :** The results showed that there are potentially effective shRNA molecules against RNA polymerase gene (vp) of IPN virus that can suppress its proliferation.

**Keywords :** shRNA, IPN virus, polymerase gene (vp), gene therapy.

# P132-324: InvestigatedInhibitory Effect of Aqueous Extract of Pistacia atlantica on Isolates of Pathogenic Escherichia coli

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**Background and Aim :** Today bacterial infections and antibiotic resistance are major challenge for medicines. In this regards, herbal antimicrobial properties due to their availability and low side effects, have been interested for researcher. In this study attempt to investigate the antibactrial effect of aqueous extract of Pistacia atlantica on isolates of Escherichia coli from urine specimens collected from women who suspected to urinary infection tract (UTI) in vitro.

**Methods :** The antibacterial effect of the extract was determined by broth microdilution method on 40 clinical isolates of E. coli and standard strain (ATCC 25922). The difference concentrations of P. atlantica were prepared 0.2-200 mg/ml in96-well plate wells, respectively. Minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) was determined by using colony count on blood agar medium. The collected data were statistically analyzed by SPSS (V. 22) software using Chi-square and t-test.

**Results :** The Mean± SD of MIC and MBC of P. atlantica aqueous extract were determinate 46.8±3.8 and 93.7±77.3 on clinical isolates respectively. The results showed that highest antibacterial effects in 50 mg/ µl concentration on clinical isolates of E. coli. Also, the result did not show significantly difference between MIC and MBC of ATCC (MIC and MBC were 100 and 200 mg/µl respectively) strain with clinical isolates (p= 1.0).

**Conclusion :** Based on the results, the aqueous extract of P. atlantica exhibited antibacterial potency against on the clinical isolates of E. coli and could be affective as natural antimicrobial agent.

**Keywords :** Herbal; Pistacia atlantica; Antibacterial ; E. coli

# P133-331: Antidermatophyte effect of zinc nanoparticle on Epidermophyton floccosum(IBRC-M 30223)

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**Background and Aim :** In the last decades Nanotechnology development in the Science and Technology. Metal nanoparticles (NPs) are used in many industrial applications. Among the different metals, zinc attracts more attention. Zinc nanoparticles are one of the most widely used mineral nanoparticles that are considered by researchers due to their suitable physical and chemical properties that used in the cosmetics industry, especially sunscreens and food industry, their antimicrobial properties have also been proven. In this study, we investigated the antifungal effect of Zinc nanoparticles . Dermatophytosis is one of the most common mycosis that caused by Dermatophytes. Dermatophytes colonized on the keratin tissues and cause infections in skin, hair, and nails. Now a day drug resistance is one of the main problems and researchers are looking for alternatives, one of the effective alternatives is Nanoparticles so in this study, we used zinc nanoparticles and effect of zinc nanoparticles on Epidermophyton floccosum was investigated

**Methods :** Epidermophyton floccosum (IBRC-M 30223) was prepared from Iranian biological Resource Center and cultured in SCC and incubated in 28 ºC for 7-14 day. Zinc oxide nanoparticles was prepared from Nano Nasb Pars Company, the size of them was 20-50 nm. Antifungal effect of them was measured by disc diffusion method, Minimum Inhibitory Concentration (MIC80) by Microdilution method, and Minimum Fungicidal Concentration (MFC)was measured.

**Results :** The results showed that the inhibition zone of the zinc nanoparticles were 21±0.5 mm which is not significantly different from that Griseofulvin ($p \leq 0.05$) and The concentration of MIC80 has been 80±1 µg/ml and the concentration of zinc nanoparticles obtained as an MFC has been 90±1 µg/ml which is not significantly different from that of Griseofulvin, Nystatin and Terbinafine ($p \leq 0.05$).

**Conclusion :** According to the results, the zinc nanoparticles had antifungal effect potential on Epidermophyton floccosum. As a result, the zinc nanoparticles are a very suitable and safe substitute for the treatment of fungal diseases such as dermatophytosis.

**Keywords :** Epidermophyton floccosum, Zinc Nanoparticles, Dermatophyte

# P134-336: An in vitro investigation of effect of chitosan and turmeric (Curcuma longa) extract against the planktonic and biofilm forms of the multiple drug resistant bacteria

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**Background and Aim :** Turmeric belongs to the ginger family, has been traditionally used as a spice and medicine from ancient times and its potential in other fields has been harnessed in recent years. In this study, we aimed to investigate the antibacterial and anti-biofilm effects of turmeric and chitosan against the planktonic and biofilm forms of the multiple drug-resistant (MDR) bacteria.

**Methods :** Forty MDR strains including 10 MRSA strains, 10 strains of CRP, 10 strains of CRE and 10 strains of AmpC-producing Enterobacteriaceae obtained from various clinical specimens. MDR strains were confirmed by the phenotypic and genotypic tests. The broth micro-dilution method was used to investigate the minimum inhibitory concentration of turmeric aqueous extract and chitosan. To investigate the synergistic effect of the combination of these natural compounds, we used the checkerboard assay.

**Results :** The turmeric and chitosan showed inhibitory effects on MDR bacteria, especially on the planktonic form of MRSA as a Gram-positive compared with tested Gram-negative bacteria (carbapenem-resistant Pseudomonas, carbapenem-resistant Enterobacteriaceae, and AmpC-producing Enterobacteriaceae). The antibiofilm effect of turmeric and chitosan were more found in carbapenem-resistant Pseudomonas isolates. There was no significant difference between the tested Gram-negative bacteria because most of the tested strains were inhibited in 512 µg/mL and 1024 µg/mL concentrations of chitosan and turmeric aqueous extract.

**Conclusion :** The results of this study demonstrate that turmeric and chitosan substances have an in vitro inhibitory effect on the planktonic and biofilm form of MDR bacteria. Further examination is needed to completely understand turmeric aqueous and chitosan to improve formulations to make it usable as a drug.

**Keywords :** Biofilm, Chitosan, Multiple drug-resistant, Turmeric

# P135-345: A novel modified peptide derived from DCD-1L can inhibit the biofilm formation of ESKAPE bacteria

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**Background and Aim :** The high ability to develop biofilm as a critical factor in chronic infections along with high rate of drug-resistant ESKAPE bacteria (Enterococcus faecalis, Staphylococcus aureus, Klebsiella pneumonia, Acinetobacter baumannii, Pseudomonas aeruginosa, and Escherichia coli) highlights the need to identify novel antibiotics. The aim of this study was to assess in vitro and in vivo anti-biofilm activities of A novel modified peptide derived from dermcidin-1L (mDCD-1L) against clinical strains.

**Methods :** In vitro antibacterial, anti-adhesive, and anti-biofilm activities of mDCD-1L against standard strains of ESKAPE bacteria (Enterococcus faecalis; ATCC 29212, Staphylococcus aureus; 25923, Klebsiella pneumonia; 700603, Acinetobacter baumannii; 19606, Pseudomonas aeruginosa; 27853, and Escherichia coli; 25922 ) were investigated. Furthermore, a mouse model of catheter-associated biofilm infection was utilized to assess anti-biofilm activity of mDCD-1L against standard strains of mentioned bacteria.

**Results :** Minimum inhibitory concentration (MIC) of mDCD-1L was 4 µg/ml for A. baumannii, P. aeroginosa, E. coli and K. pneumonia and was 8 µg/ml for S. aureus and E. faecalis. mDCD-1L also inhibited biofilm formation by ~ 53% at sub-inhibitory concentration (1/4MIC) and 100% at 1/2 MIC whereas the high value of MBEC (256 µg/ml) indicates ability of mDCD-1L to decrease mass of existing biofilm. Furthermore, in mouse catheter infection model following treatment with mDCD-1L at MIC, the biofilm was significantly reduced as compared to the untreated control.

**Conclusion :** In the present study antibacterial and antibiofilm function of a novel synthetic cationic antimicrobial peptide (AMP) derived from human anionic AMP DCD-1L (mDCD-1L) was demonstrated, suggesting that mDCD-1L could affective as a potential therapeutic agent against chronic, recurrent biofilm infections caused by ESKAPE bacteria.

**Keywords :** Biofilm, Antimicrobial peptide, ESKAPE bacteria, antibacterial, antibiofilm

# P136-346: Identification and Characterization of Novel Antimicrobial Peptide from Hippocampus comes by In Silico and Experimental Studies

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**Background and Aim :** Antimicrobial peptides (AMPs) have attracted attentions as a novel antimicrobial agent because of their unique activity against microbes. In the present study, we described a new, previously unreported AMP, moronecidin-like peptide, from Hippocampus comes and compared its antimicrobial activity with moronecidin from hybrid striped bass.

**Methods :** Antimicrobial activity of moronecidin and moronecidin-like protein was performed against gram negative bacteria and yeasts in physiological pH and salt concentration. Furthermore The time-killing assay, the hemolytic and cytotoxic activities of peptides was done.

**Results :** Antibacterial assay indicated that gram-positive bacteria were more sensitive to moronecidin and moronecidin-like compared with gramnegative bacteria. Furthermore, both AMPs were found to exhibit effective antifungal activity. Comparative analysis of the antimicrobial activity revealed that moronecidin-like peptide has higher activity against Acinetobacter baumannii and Staphylococcus epidermidis relative to moronecidin. Both moronecidin-like and moronecidin peptides retained their antibacterial activity in physiological pH and salt concentration. The time-killing assay showed that the AMPs completely killed A. baumannii and S. epidermidis isolates after 1 and 5 h at five- and tenfold above their corresponding MICs, respectively. Anti-biofilm assay demonstrated that peptides were able to inhibit 50% of biofilm formation at sub-MIC of 1/8 MIC. Furthermore, moronecidin-like significantly inhibited biofilm formation more than moronecidin at 1/16 MIC.

**Conclusion :** Collectively, our results revealed that antimicrobial and anti-biofilm activities of moronecidin-like are comparable to moronecidin. In addition, the hemolytic and cytotoxic activities of moronecidin-like were lower than those of moronecidin, suggesting it as a potential novel therapeutic agent, and a template to design new therapeutic AMPs.

**Keywords :** Biofilm, Antimicrobial peptide, , antibacterial, antibiofilm

# P137-352: Investigation of Antibacterial and Antifungal effect of Hydroalcoholic extract of Ephedra Gerardiana; Compartion with Chlorhexidine 1% on Oral Pathogenesis Microbiome

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**Background and Aim :** Ephedra guardiana is an herbal medicine that has been used in the treatment of asthma, nasal congestion and disorders of the central nervous system.Almost all species of this plant are adapted to the environmental and climatic conditions of Iran and have significant antimicrobial effects.The aim of this study was to investigate the effect of aqueous and alcoholic extracts of Ephedra gerardiana whit chlorhexidine on normal flora of oral bacteria and Candida albicans in vitro.

**Methods :** The antimicrobial effect of the extracts was determined by broth microdilution method on Enterococcus faecalis (ATCC 29212), Streptococcus mutans (ATCC 35668), Lactobacilli casei (ATCC 39392) and Candida albicans (ATCC 10231).Minimum inhibitory concentration (MIC) andminimum bactericidal concentration (MBC) and minimum fungicidal concentration (MFC was determined by using colony count on blood agar medium.

**Results :** Enterococcus faecalis and Streptococcus mutans were resistant to aqueous extractswhile aqueous extract showed inhibitory effect on Lactobacilli casei and Candida albicans.Enterococcus faecalis,was also resistant to alcoholic extracts. However, Streptococcus mutans and Lactobacilli casei and Candida albicans were susceptible toalcoholic extracts.Chlorhexidine 1%showed inhibitory effect on all bacterial strains and Candida albicans.

**Conclusion :** In the present study, regardless ofEnterococcus faecalis, which was resistant to all of aqueous and alcoholic extracts,Ephedra grardiana extract has antibacterial and antifungal properties and therefore can be effective antimicrobial agent.

**Keywords :** Ephedra gerardiana, chlorhexidine 1%, Antimicrobial effect, Enterococcus faecalis, Streptococcus mutans, Lactobacilli casei,Candida albicans

# P138-353: Evaluation of antimicrobial properties of a compound of Nano-Chitosan-Zinc oxide against some bacterial agents of tooth decay

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**Background and Aim :** The activity of bacteria that cause tooth decay is increasing. The use of antimicrobial properties of natural materials based on effective dental compounds is one of the future hopes in the microbiology of oral diseases. Oral & dental pathogenic bacteria such as Lactobacillus and Streptococcus mutans strains can cause dental lesions in both planktonic and biofilm phases. The aim of this study was to investigate a chemically compound of Chitosan-zinc oxide (N-Ch-ZnO) against the Lactobacillus acidophilus (LA) and Streptococcus mutans (SA) which are synthesized in a nanoparticle size.

**Methods :** The Broth Dilution Test (BDT) was used to evaluate the antibacterial properties in Planktonic and the Microtiter Plate Method (MPM) in Biofilm phase .The studied strains were SA (ATCC 35668) and LA (biofilm-producing strain). A chemical compound based on MIC value of Chitosan and ZnO for each tested bacteria (Planktonic) and MBEC value (in Biofilm phase) were used in proportion of 50%. The LA were cultured on MRS medium and SA on BHI medium for 48 hours incubation with 5% Co2. Chlorhexidine was used as a positive and sterile distilled water was used as a negative control. A total of 30 times for Planktonic for each bacteria and 30 times the biofilm phase was tested. The experimental results were analyzed by ANOVA.

**Results :** The results showed that the diameter of the LA growth inhibition zone was 14 mm compared to the 20 mm zone of Chlorhexidine. There was no inhibition zone for SA. In the

biofilm phase, the compound of N-Ch-ZnO could not eradicated the biofilm form each of the bacteria.

**Conclusion :** This study showed that the compound of N-Ch-ZnO was significant relationship in inhibiting LA planktonic phase but not in biofilm phase. There was no significant relationship between SA in either planktonic or biofilm forms. This research indicated that the 50% proportion of Chitosan and ZnO was not proper for biofilm eradication. Therefore is need to more study in other ratios in both form in theses to bacteria is recommended.

**Keywords :** Chitosan-Zinc oxide- nanoparticle -Streptococcus mutans- Lactobacillus acidophilus-MIC-MBEC

# P139-355: Antidermatophytic effect of Stachys schtschegleevii extract on Microsporum canis(IBRC-M 30215)

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**Background and Aim :** Microsporum canis is a zoophilic dermatophyte that causes dermatophytosis. This is a prevalent disease and should be treated properly. There are many reports of resistance to antifungal drugs. On the other hand, these drugs have many side effects so medicinal plants can be appropriate alternatives . Stachys schtschegleevii is a medicinal plant that is used for treatment of respiratory and urinary system infections, Rheumatism and other inflammatory diseases. S. schtschegleevii also has antimicrobial, antioxidant and anti-cancer effects. The aim of this study is to evaluate the effect of Stachys schtschegleevii extract on Microsporum canis.

**Methods :** M. canis (IBRC-M 30215) prepared from microorganisms bank of Iranian Biological Resource Center. Then cultured in SCC and incubated in 28°c for 7-14 days. After preparation of S. schtschegleevii, the extraction carried out using soxhlet method. The antifungal effect of S. schtschegleevii extract was measured by disc diffusion method, MIC80 (Microdilution method) and MFC.

**Results :** According to the results, the inhibitory zone of S. schtschegleevii extract was 19±1 mm which was not significantly different from that of Griseofulvin ( p?0.05). The Minimum Inhibitory Concentration ( MIC80) of S. schtschegleevii extract was 5±0.5 mg/ml. The Minimum Fungicidal Concentration (MFC) of S. schtschegleevii extract was 10±0.85 mg/ml Which was not significantly different from that of Griseofulvin, Nystatin and Terbinafine (p?0.05).

**Conclusion :** Overall, the results of this research showed that S. schtschegleevii extract has a significant antidermatophytic effect on Microsporum canis.

**Keywords :** dermatophytosis, Microsporum canis, Stachys schtschegleevii

# P140-358: Antimicrobial activity of plant essential oils Nano emulsions against Campylobacter jejuni

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**Background and Aim :** This study aimed to examine the antimicrobial potential of three nanoemulsions (NE) of essential oils: Mentha piperita (MPNE), Zingiber officinale (ZONE), and Satureja khuzestanica (SKNE) against Campylobacter jejuni.

**Methods :** Oil-in-water nanoemulsions were prepared using Tween 80 and SDS as surfactant and cosurfactant respectively. The droplet size and size distribution (polydispersity index-PDI) of the nanoemulsion was measured using dynamic light scattering (VASCO2 nanoparticle size analyzer/DLS). The Innate stability of nanoemulsion (the ability of a nanoemulsion to resist changes whiteout phase separation or creaming or flocculation) was assessed. Antibacterial effects of nanoemulsions were determined using Agar well diffusion test and Agar dilution method according to CLSI methods

**Results :** Stable nanoemulsions containing small droplets (d <60 nm) were formed. The MPNE, ZONE, and SKNE inhibition zones were 16 ± 0.0, 17.5 ±0.5, 30 ± 1 mm, respectively. The minimum inhibitory concentration (MIC) results showed that the SKNE (MIC (6.25 µl/ml)) has more antibacterial properties against Campylobacter jejuni than MPNE and ZONE according to the MIC results (MIC (?100µl/ml))

**Conclusion :** The nanoemulsions of these essential oils displayed remarkable activity against C. jejuni, therefore, they could be used as natural anti-Campylobacter in the food industry.

**Keywords :** Nanoemulsions, plant essential oils, Campylobacter jejuni.

# P141-365: Isolation and in vitro evaluation bacteriolytic effect on bacteriophages against reference multi Drug-resistant Gram-negetive and Gram-positive strains from sewage sample

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**Background and Aim :** The spread of multidrug resistance in pathogenic bacteria has become one of the most important discussions among physicians and Multidrug-resistant bacteria account for a high percentage of annual mortality. Multidrug resistance is common in both Gram-positive and Gram-negative bacteria. Meticillin Resistant Staphylococcus aureus is one of the multidrug resistant bacteria. Resistant in Klebsiella pneumonia and Escherichia coli is more due to production of extended resistant beta lactamas. Phagetherapy is a therapeutic Method for drug resistant, which use of viruses that do not have infection for human. The aim of this study was to isolate and evaluation effect bacteriophages against reference multi Drug-resistant Gram-negetive and Gram-positive strains from sewage sample.

**Methods :** After isolation bacteriophage from sewage wastewater, reference strains Meticillin Resistant Staphylococcus aureus, Klebsiella pneumonia and Escherichia coli with Extended Resistant Beta lactamas from Tehran Institute of Pasteur prerared and their specific bacteriophages were identified. For see phage plaque use double layer agar method and then for evaluation bacteriolytic effect use one-layer agar method, the Finally, for study the morphology of bacteriophages was used scanning electron microscopy.

**Results :** Formation clear plaque in the method of double layer agar for Escherichia coli, klebsiella pneumonia and Staphylococcus aureus indicated cell lysis by bacteriophages. In addition, the morphology of this bacteriophage was identified by TEM.

**Conclusion :** The results show that bacteriophages are specific and according increasing resistance Phage therapy can open a new view for multi-drug resistant bacteria as a new treatment.

**Keywords :** phagetherapy, bacteriophage, multidrug resistant

# P142-371: Evaluation of antibacterial and anti-biofilm effect of zinc selenide dual nanoparticles by aqueous extract of mountain tea extract (Stachys lavandulifolia) against pathogenic clinical isolates

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**Background and Aim :** Today, there are various methods for the synthesis of nanoparticles, green nanoparticle center is one of the popular methods, which due to its simplicity and low cost has been considered by many researchers in biology and medicine. Zinc selenide nanoparticles (NPznse) have many applications in biomedicine, but so far its various biological aspects have not been studied in detail.

**Methods :** In this study, dual nanoparticles of zinc selenide were synthesized by aqueous extract of mountain tea extract and confirmed by UV-Vis, FT-IR, EDX and SEM and TEM electron microscopy. The antibacterial and antibiofilm properties of the synthesized nanoparticles were determined quantitatively and qualitatively in Pseudomonas aeruginosa, Escherichia coli, and Staphylococcus aureus using agar well dilution method and 96 microplate method.

**Results :** Zinc selenide dual nanoparticles were synthesized by aqueous extract of mountain tea, the synthesis of which was confirmed by changing its color to light brown. Analysis of this nanoparticle by spectrophotometer showed the absorption peak in the region of 305 nm. These nanoparticles had a spherical structure with dimensions of about 30-60 nm. The diameter of the antibacterial activity halos of zinc dual selenide nanoparticles was between 9.5-17 mm. Also, these nanoparticles at a concentration of 100 ppm had good anti-biofilm activity in the target bacteria.

**Conclusion :** Based on the results obtained in this study, dual nanoparticles of zinc selenide by aqueous extract of mountain tea extract can be used as an effective antimicrobial agent to inhibit the biofilm formation of Pseudomonas aeruginosa, Staphylococcus aureus, and Escherichia coli.

**Keywords :** Biofilm, Antibacterial, Zinc selenide dual nanoparticles

# P143-378: Investigation of antibacterial properties of anthocyanin extracted from purple carrots

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**Background and Aim :** Due to the remarkable ability of different species of bacteria to acquire resistance genes, antibiotic resistance is currently a major challenge for health care in developed and developing countries. With the emergence and spread of drug-resistant pathogens, bacterial infections have become more difficult to treat. Therefore, it is necessary to search for new and cost-effective sources of antimicrobials with the property of inhibiting microbial growth and fewer side effects. Plants contain various bioactive compounds with therapeutic properties that can be a good option for searching for new antimicrobials. The aim of this study was to extract anthocyanin from purple carrots and to investigate its antibacterial effects.

**Methods :** Anthocyanin was extracted using acidic ethanol solvent. Total anthocyanin and monomeric anthocyanin were measured using UV-Vis spectrophotometer at 520 and 700 nm and by pH differential method at pH 1.0 and 4.5. The antibacterial activity also was investigated by broth microdilution assay and spot test.

**Results :** Purple carrots anthocyanin showed significant antibacterial effects against human bacterial pathogens including Staphylococcus aureus, Escherichia coli, and Salmonella typhi. The most antibacterial activity of anthocyanin was observed against Staphylococcus aureus.

**Conclusion :** The results of this study indicate that in addition to being used as a natural colorant in the food industry, anthocyanin extracted from purple carrots can be used as an antibacterial to treat bacterial infections.

**Keywords :** Purple carrot, Anthocyanin, Antibacterial activity

# P144-379: Antibacterial activity of purple cabbage anthocyanin

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**Background and Aim :** Infectious diseases are an important cause of death in developing countries. Today, due to the development of resistance by many microbial pathogens, the use of plant-active compounds is considered as an alternative to current antibiotics to fight microbial infections. Up to now, the antimicrobial properties of some plant-active metabolites against various bacterial strains have been investigated. The aim of this study was to evaluate the antibacterial effects of anthocyanin extracted from purple cabbage.

**Methods :** Anthocyanin was extracted using acidic ethanol solvent. Anthocyanin measurement was carried out using UV-Vis spectrophotometer at 520 and 700 nm and by pH differential method at pH 1.0 and 4.5. The antibacterial activity of the extracted anthocyanin also was examined by broth microdilution assay and spot test.

**Results :** Anthocyanin extracted from purple cabbage showed remarkable antibacterial activity against bacterial strains isolated from human infections, including Staphylococcus aureus, Escherichia coli, and Salmonella typhi.

**Conclusion :** The results of this study showed that purple cabbage anthocyanin can be used as an antibacterial drug to control and treat bacterial infections.

**Keywords :** Purple cabbage, Anthocyanin, Antibacterial

# P145-381: Antibacterial activity of anthocyanins extracted from plum against human pathogenic bacteria

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**Background and Aim :** Infectious diseases are always a serious threat to health. With the discovery of antibiotics, deaths from infectious diseases have been significantly reduced; but with the misuse of antibiotics and resistance to them, these diseases are returning. Due to the increasing resistance to antibiotics, the world is in dire need of changing its consumption pattern and finding new sources of antimicrobials. The development of various alternative drugs is one way to reduce antibiotic resistance. Today, the use of plant-active compounds to treat microbial infections has attracted the attention of many researchers. Anthocyanins are plant-active metabolites that can be tested for antimicrobial properties. Plums contain five different anthocyanins, and the aim of this study was to investigate the antibacterial properties of anthocyanins extracted from plums.

**Methods :** Anthocyanins were extracted from plums using acidic ethanol solvent. Total anthocyanin and monomeric anthocyanin were measured by pH differential method at pH 1.0 and 4.5 and using UV-Vis spectrophotometer at 520 and 700 nm. The antibacterial effects of the extracted anthocyanins were also investigated by broth microdilution assay and spot test.

**Results :** Plum anthocyanins showed significant antimicrobial activity against human pathogenic bacteria including Salmonella typhi, Escherichia coli, and Staphylococcus aureus. Staphylococcus aureus was the most susceptible strain to anthocyanin.

**Conclusion :** The results of this study indicated that, plums can be used as a rich source of anthocyanins with antibacterial activity against bacterial infections.

**Keywords :** Plum, Anthocyanin, Antimicrobial, Resistance.

# P146-400: Benzoic acid and cinnamic acid derivatives in chicory honey may be associated with its specific antimicrobial activity

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**Background and Aim :** Nowadays, human pathogenic bacteria have developed resistance to commonly used antimicrobial drugs. Therefore, new research should be evaluated to find alternative anti-bacterial compounds.

**Methods :** We have previously reported the antimicrobial effects of chicory honey. This study was carried out with an objective to determine the antimicrobial activity of phenolic extract of chicory honey and to characterize these compounds by High Performance Liquid Chromatography coupled to Quadrupole-Time of Flight mass spectrometer (HPLC-ESI-QTOF/MS) in comparison with rose, thyme, chamomile, astragal, locust tree, black cumin, barberry, licorice, alfalfa, and coriander honeys.

**Results :** Using disc diffusion method, at the concentration of 12.5% (w/v), phenolic extract of chicory honey showed the diameter of the inhibitory zone of 13.6 mm and 12.8 mm against reference strains of Escherichia coli and Staphylococcus aureus respectively, while phenolic extract of another honey samples showed weaker activity. Comparison of the phenolic compounds profile of chicory honey with other samples indicated that there are certain derivatives of benzoic acid and cinnamic acid with significant amounts in chicory honey that may be associated with its specific antimicrobial activity. This honey was not significantly different from other samples in terms of amount and type of flavonoids and royal jelly derivatives.

**Conclusion :** These results point out that phenolic extract of chicory honey with distinct benzoic acid and cinnamic acid derivatives had the potential as an antibacterial used for development of medicinal food.

**Keywords :** Chicory honey, phenolic extract, antimicrobial activity

# P147-419: Isolation and characterization of bacteriophage against Klebsiella pneumoniae from Cystic Fibrosis patient

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**Background and Aim :** Today, infections caused by Klebsiella pneumoniae have become a problem in treatment due to the increased proliferation of plasmids carrying antibiotic resistance genes among bacteria of the Enterobacteriaceae family and that is one of the therapeutic problems of Cystic Fibrisis disease. The discovery of novel agents to control Klebsiella pneomoniae infections is urgent due to the broad multidrug-resistance. A phage with the ability to efficiently and specifically lyse bacteria is considered an alternative to control these pathogens. This study aimed to isolate a lytic bacteriophage with the potential to lyse clinical isolates of Klebsiella pneumoniae.

**Methods :** Antimicrobial Susceptibility of clinical Klebsiella pneomoniae Isolates was determined using disk diffusion assays then Water samples were collected from a hospital waste-water in Tehran.The samples were filtered and mixed with an overnight grown culture of Klebsiella pneumoniae in notrient broth . Phage titration, latent period, and burst size measurements were carried out by the double-layer agar method using the Klebsiella pneumoniae. The isolated phage was characterized by Transmission Electron Microscopy (TEM), Spot test was employed to determine the bacterial host range for the isolated phage using eleven multidrug resistant Klebsiella pneumoniae isolates from patients with Cystic Fibrosis and Effectiveness of a phage against Klebsiella pneomoniae biofilms was determined by Minimum Biofilm Eradication Concentration (MBEC) Assay System.

**Results :** The isolated phage belongs to the Myoviridae family and infected seven of eleven tested multidrug-resistant Klebsiella pneumoniae strains.This phage had large burst sizes, efficient rates of adsorption and were stable under different adverse conditions.

**Conclusion :** As the phage was virulent and specific for Klebsiella pneumoniae, and was stable and active at different condition that exhibit a number of properties indicative of potential utility in phage therapy cocktails

**Keywords :** Bacteriophage, Cystic fibrosis, Klebsiella pneumoniae, Phage therapy

# P148-32: SARS-CoV-2 and infection fate

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**Background and Aim :** The novel coronavirus disease 2019 (COVID-19) induced by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a global pandemic, with more than one million death tolls. Immune responses have a prominent role in SARS-CoV-2 pathophysiology. Despite the understanding of the immune response to COVID-19, there are still major gaps in understanding controversial reactions and their impact on infection fate.

**Methods :** In this review, in addition to summarizing the immune responses against SARS-CoV-2, we propose a new perspective on how the virus induces its pathogenicity by hijacking and manipulating NK cells, Dendritic cells, T cells and B cells same as HIV-1.

**Results :** Following HIV-1 entry into the host. The immune cells as well as other cells are infected and act as Trojan horses for spreading the virus.

**Conclusion :** Therefore, based on this evidence, it would be possible antiviral HIV drugs have a positive effect on COVID-19 patients.

**Keywords :** novel coronavirus, COVID-19, SARS-CoV-2, HIV-1, immune response, infection fate.

# P149-52: The impact of a health education intervention program on reducing of head lice infestation among pupils of an elementary school; A subtropical region

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**Background and Aim :** Pediculosis is an important social challenge that can be caused by human head louse, Pediculus humanus capitis. This infestation is cosmopolitan, especially in countries with low hygiene and sanitation. This study aimed to evaluate the impact of a health education intervention program on reducing of head lice among pupils of an elementary school.

**Methods :** In a cross-sectional study, a total of 594 pupils, a girl elementary school, were screened for pediculosis. Interventions were applied in two steps, pediculosis cases eradication and training-oriented prevention program. Visual inspection was applied for initial diagnosis of infection. The suspected cases were confirmed by wood lamp examination. An elementary school in the same area was selected as the control group, with no interference. The prevalence of contamination was obtained in the study group.

**Results :** At the beginning of study, the overall prevalence of pediculosis among pupils was 8.4% (49/594). The mean age in all pupils was 9.86±1.83 years old and the most infestation was showed in fourth-grade students with 10 years old. Analysis of statistics demonstrated a significance difference between having infestation and the number of members in the families. The interventions led to a significant increase of parenting knowledge on prevention program of pediculosis (p-value < 0.001), and a decreased prevalence of pediculosis in pupils to 3% (8/594) (p-value < 0.05).

**Conclusion :** The prevalence of pediculosis was significantly reduced following the interventions in the school. The applied interventions may be implemented in other residual centers to get rid of this important infestation.

**Keywords :** Pediculosis; Training programs; Primary schools; Infestation; Iran

# P150-238: Angiotensin (1-7) levels and disease severity in hospitalized COVID-19 patients with and without cardiovascular diseases

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**Background and Aim :** Angiotensin (1-7) (Ang (1-7)) obtained from the function of angiotensin-converting enzyme 2 (AEC2) improve heart and lung function. Blockade of ACE2 by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in coronavirus disease 2019 (COVID-19) decreases Ang (1-7). In this study, we investigated Ang (1-7) levels and disease severity in hospitalized COVID-19 patients with and without cardiovascular diseases

**Methods :** To do so, the Ang (1-7) levels of hospitalized COVID-19 patients with (136) and without (127) cardiovascular disease in Masih-Daneshvari Hospital, Tehran, Iran were measured by ELIZA kit. , the patients' clinical symptoms, including intensive care unit (ICU) admission, the use of mechanical ventilation, oxygen need, fever, and gastrointestinal disorders were drawing out from the patient's medical record.

**Results :** Results of our investigation showed a significant inverse relationship between the levels of Ang 1-7 and the severity of the disease (P value = 0.000). But there wasn't significant difference between the levels of Ang 1-7 in hospitalized COVID-19 patients with and without cardiovascular diseases.

**Conclusion :** Ang (1-7) reduced the severity of COVID-19 disease, both in patients with and without cardiovascular

**Keywords :** Angiotensin (1-7) ;angiotensin-converting enzyme 2;severe acute respiratory syndrome coronavirus 2

# P151-240: Angiotensin (1-7) levels and disease severity in hospitalized COVID-19 patients with and without diabetes diseases

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**Background and Aim :** Angiotensin (1-7) (Ang (1-7)) obtained from the function of angiotensin-converting enzyme 2 (AEC2) improve heart and lung function. Blockade of ACE2 by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in coronavirus disease 2019 (COVID-19) decreases Ang (1-7). In this study, we investigated Ang (1-7) levels and disease severity in hospitalized COVID-19 patients with and without cardiovascular diseases.

**Methods :** To do so, the Ang (1-7) levels of hospitalized COVID-19 patients with (136) and without (127) cardiovascular disease in Masih-Daneshvari Hospital, Tehran, Iran were measured by ELIZA kit. , the patients' clinical symptoms, including intensive care unit (ICU) admission, the use of mechanical ventilation, oxygen need, fever, and gastrointestinal disorders were drawing out from the patient's medical record.

**Results :** Results of our investigation showed a significant inverse relationship between the levels of Ang 1-7 and the severity of the disease. The severity of the disease in diabetes diseases was significantly more than without diabetes diseases. The levels of Ang 1-7 were significantly lower in diabetic patients than in non-diabetic patients.

**Conclusion :** Ang (1-7) reduced the severity of COVID-19 disease, both in patients with and without diabetes disease and this reduction of Ang (1-7) and increased disease severity is more in diabetic patients.

**Keywords :** Angiotensin (1-7) ;angiotensin-converting enzyme 2;severe acute respiratory syndrome coronavirus 2; diabetes disease

# P152-429: Anti-SARS-CoV-2 Innate Immunity Mediated by Plasmacytoid Dendritic Cell Derived Type I Interferon: A Systematic Review

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**Background and Aim :** Severe Acute Respiratory Syndrome Virus 2, SARS-COV-2 for short, is a pathogenic and immunogenic virus as well as sensitive infectious agent to inhibit through interferon mediated responses. In this context, Plasmacytoid Dendritic Cells (PDCs) which are activated by viral components are known as the most efficient cells in type I interferon (IFN-I) production which are believed to protect cells against virus invasion and infection. this review was written to give a brief description to anti-SARS-CoV-2 innate immunity mediated by PDCs-derived type I interferon.

**Methods :** We systematically searched three online databases including PubMed, google scholar, and ScienceDirect from December 2019 to August 2021. The keywords were “plasmacytoid dendritic cells”, “Interferon”, and “SARS-CoV-2”. By considering certain defined criteria and using the Prisma checklist, a total of 10 studies finally were included for this review.

**Results :** In those who are tested positive for SARS-CoV-2, all subsets of dendritic cells in particular PDCs show a downward trend in their absolute numbers for weeks. This reduction may explain by migration outside the bloodstream or activation of the programed cell death signaling pathway. In addition to numerical reduction, PDCs which are activated by the virus in a non-productively infection, induce a massive and rapid in production of IFN-I secretion. This protein possesses an anti-SARS-CoV-2 activity as inhibits the virus replication in epithelial cells of respiratory tracts. Moreover, the protein is protective as protect infected patients from adverse outcomes such as death. In this context, patients who are severely ill are assumed to experience insufficiency in interferon synthesizing in the absence or low count of PDCs. This may suggest a non-ignorable role for PDCs to provide an innate immunity mediated by interferon. This insufficiency may also result from translational inhibition of interferon messenger ribonucleic acids by certain non-structural proteins. Stimulated PDCs were also

found to be diversified and activated characterizing phenotypically by changes in the expression pattern of cell-associated markers.

**Conclusion :** Considering the highlighting role of host innate immunity to overcome viral infections, PDCs are believed to be critically important to overcome viral infections especially the recent infectious human coronavirus as they are responsible for interferon-mediated viral inhibition.

**Keywords :** Plasmacytoid dendritic cell, Type I interferon, SARS-CoV-2

# P153-432: Brain Tumor Immunotherapy by Oncolytic Zika Virus: A Systematic Review

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**Background and Aim :** Zika is an old and neurotropic mosquito-borne pathogen causing serious brain disorders in newborns and adults and recently being considered by experts in the field of cancer therapy as an emerging immunotherapeutic candidate against intracranial tumors especially Glioblastoma, an aggressive in type and fast in growing brain tumor. In this study, we systematically reviewed the scientific literature to find out whether Zika can be a promising candidate for the treatment of brain tumors.

**Methods :** Three electronic databases (PubMed, Science Direct, and Google Scholar) were systematically searched with the title/abstract filter at a given time interval from January 2020 to July 2021. Using the Prisma checklist, 10 full-text articles were finally selected for review.

**Results :** Targeting treatment-resistant brain tumors by Zika as an oncolytic virus reducing the rate of tumor proliferation and survival in a bed of recruited and activated immune cells. Zika directly infects abnormal but not normal brain cells and leaves no serious clinical side effects in treated models. By modulating the tumor micro-environment, Zika as an immunogenic virus induces a broad and successful anti-tumor immunity in favor of tumor regression and clearance. this induction may result in an increase the count of immune cells and the levels of anti-viral antibodies. Moreover, the virus activates differentiated monocytes and recruits functional leukocytes into the bed of tumors resulting in tumor lysis/clearance by activation of cell-mediated immunity in particular cytotoxic immunity. This type of immunity was found to be greater in induction than the immunity induced by the tumor itself. Additionally, Zika reduces the rate of brain tumor-related deaths by generating durable cytotoxic cell memory aim to overcome tumor remission. These all may support Zika candidacy for virus-based tumor immunotherapy for solid tumors like Glioblastoma.

**Conclusion :** Consequently, using Zika as a powerful oncolytic virus to activate the immune system may serve as a competent platform to fight brain tumors in future. However, being at pre-clinical phase, the efficacy and safety of using such a candidate to treat human brain malignancies is still unclear and needs more time and studies to be well tested and clarified.

**Keywords :** Zika Virus, Brain Tumor, Immunotherapy

# P154-33: Condition of Johne's disease among small ruminants

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**Background and Aim :** Mycobacterium avium subspecies paratuberculosis (MAP) is a major pathogen that is unequivocally the cause of Johne's disease (JD) in domestic livestock, wild ruminants and other animal species, including primates. MAP bacteria multiply in the intestinal mucosa and are frequently excreted in feces, milk, and vaginal secretions from infected animals (atypical animals, sub-clinics and clinics). Newborns are most susceptible to infection and are generally infected in this first lifetime by oral ingestion of contaminated food, water or milk from their infected mothers. The incubation period for JD is long and variable depending on a number of factors such as environmental stress, nutrition, production, concurrent diseases, overcrowding, etc. Clinical cases may be readily detected to diagnose, however, it is difficult to diagnose the preclinical stages of the disease. Sub-clinically infected animals excrete MAP in faecals and milk, thus quietly spreading the infection to other animals in the herd by contaminating the environment. This “silent transmission” occurs over long periods of time before being disposed of from herds. Live MAP bacteria are found in pasteurized milk, milk product, and infant formula made from pasteurized milk. MAP is found in manure of animal origin that can be leached into surface water, cow manure in solid and liquid form that is implemented as fertilizer in agriculture. The existence of bacilli in tap water provides multiple transmission routes for the human population.

**Methods :** JD has been reported to be widespread in different livestock species and in different regions of the world. We standardized and used principal antigen detection tests (microscopy, IS900 PCR, Real-time IS900 PCR, IS1311 PCR_RE) and antibody detection tests (dot ELISA, indirect ELISA, latex agglutination test) for diagnosis of JD.

**Results :** Conventional methods of testing and slaughter have failed to control the propagation of the JD into small ruminant herds, although excretory animals have been eliminated. For sustainable goat and sheep farming, it is essential to monitor JD using the suitable diagnosis test and prevent the disease with an effective vaccine.

**Conclusion :** With a view to preventing human infection, there is an urgent need to conduct comprehensive research to control and eradicate MAP in the domestic livestock population of the country.

**Keywords :** Domestic livestock, Diagnosis, John’s disease, Milk and milk products

# P155-44: Prevalence assessment of Salmonella serovars in apparently healthy pet dogs in Tehran, Iran

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**Background and Aim :** Salmonellosis is considered to be a zoonotic disease. Since pet care has been popular recently, the possibility of transmitting the disease through oral-fecal contact is unavoidable. On the other hand, excessive consumption of human antibiotics to treat livestock has created antibiotic resistance and emerge a new serotype of the bacterium in animals. This study aimed to assess the prevalence of the bacteria and their antibiotic resistance to choose the appropriate antibiotic for controlling the disease.

**Methods :** In this study, the presence of Salmonella serovars in 256 pet dogs' fecal samples was investigated by enrichment and selective culture. Then, the presence of virulence genes and antibiotic resistance genes in addition to phenotypic antimicrobial resistance were evaluated.

**Results :** The total of 256 fecal samples, 8.2% of pet dogs were positive for Salmonella, including S. Typhimurium, S. Enteritidis, S. Infantis, and S. Senftenberg. Based on our findings, all serovars carried virulence genes invA, invF, sitC, fimA and they were sensitive to antibiotics of the Aminoglycoside and Fluoroquinolones groups despite resistance to the Tetracycline group

**Conclusion :** Our findings suggest that pet dogs are potential sources of Salmonella strains that carry a wide spectrum of resistance and virulence genes. Thus, healthy pet dogs play an important role in human Salmonellosis.

**Keywords :** antibiotic resistance gene, pet dog, Salmonella, virulence gene.

# P156-49: Prevalence of contamination of eggs from retail markets by Listeria monocytogenes and Streptococcus spp in Ardabil, Iran

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**Background and Aim :** Bacterial zoonotic diseases are one of the most important health problems in human societies which in this category, food-borne diseases are special importance. Contaminated eggs are increasing the risks of illness in humans. The purpose of this study was to survey the contamination of eggs to Listeria monocytogenes and Streptococcus spp in retail markets Ardabil city of Iran.

**Methods :** A total of 240 eggs (80 local eggs, 80 bulk eggs and 80 labeled industrial eggs) were collected randomly from different retail stores of Ardabil from December 2019 to June 2020. Collected eggs under sterile conditions were transferred to the food microbiology lab to be tested. The shell and contents of the eggs cultured for those bacteria on selective agar and standard microbiological tests performed toidentify the isolated organism.

**Results :** The performed survey showed that there was no contamination by L. monocytogens in all 240 eggs. However, 5 samples (1.66% ) out of 240 samples were contamination by Streptococcus spp. 235 samples were negative for Streptococcus spp (98.34%). The highest contamination to Streptococcus spp was seen in local eggs (80%) and the lowest contamination in bulk eggs (20%).

**Conclusion :** The results of this study indicate that L. monocytogens contamination of eggs does not make up a serious health hazard in this area, While there is contamination with Streptococcus spp. It seems necessary to pay attention to hygienic points in cooking eggs.

**Keywords :** Streptococcus spp, Listeria monocytogenes, Egg

# P157-50: Serological Survey of Avian Influenza Virus H9N2 Subtype in Backyard Chickens of Ardabil, northwestern Iran

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**Background and Aim :** Avian Influenza virus is the most important viral diseases of the poultry which causes economic losses in poultry industry. Backyard poultry are at risk of exposure to various viral contagious diseases such as Avian Influenza. Backyard poultry are considered as a risk factor for the poultry industry. Therefore, the aim of this study was to survey seroprelvance of Avian Influenza Virus H9N2 Subtype in backyard chickens of Ardabil area, Iran.

**Methods :** A descriptive cross-sectional study was conducted in Jane and August 2018 in village chickens of Ardabil area, northwestern Iran. A total of 190 blood samples were collected from unvaccinated backyard chickens in 12 villages. ELISA was used as the screening test and all ELISA-positive samples were examined with the HI test.

**Results :** The performed survey showed that eighty seven out of 190 blood samples were positive on ELISA. In addition to, Eighty five (45 %) were positive and one hundred and five (55 %) were negative on HI test. Five villages out of 12 villages were positive on HI test.

**Conclusion :** According to results of this study seroprevalence of H9N2 influenza virus is high in backyard chickens of villages in Ardabil area.This finding indicates that the virus is endomic. So, vaccination and annual surveillance of backyard poultry seem necessary.

**Keywords :** Influenza virus, HI, Backyard chickens, Ardabil

# P158-73: Inhibitory Effects of Various Concentrations of Tetracycline and Trimethoprim on the Prevention of Congenital listeriosis in Balb/C mice

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**Background and Aim :** Listeriosis is among the diseases occurring to humans, wild and domestic animals. Listeria monocytogenes, the etiologic agent of this disease, is one the most important food-borne pathogens. Given the limited information regarding the effects of various concentrations of different antibiotics on Listeria monocytogenes for in vivo studies, this study is designed. The aim of this study was to evaluate the inhibitory effects of different concentrations of tetracycline and trimethoprim on the prevention of congenital listeriosis in Balb/C mice

**Methods :** In this experimental-analytical study, the effect of various concentrations of tetracycline and trimethoprim on congenital listeriosis was evaluated in 4 groups of modelBalb/C mice, (treated with tetracycline, treated with trimethoprim, positive control and negative control). Minimum inhibitory concentration for Listeria monocytogenes was determinedin Muller-Hinton broth medium.For in vivo study, different dosages of tetracycline and trimethoprim were administered orally. Clinical evidence, sampling and culture methods were used for listeriosis identification

**Results :** The obtained results showed that the percentage of live birth was higher in the treated mice than in the control groups. Using tetracycline and trimethoprim prevented abortion in treated Balb/C mice. For Trimethoprim and Tetracycline were effective for 100% and 74% prevention in abortion, respectively, as observed.

**Conclusion :** Based on the results obtained in this study, it can be concluded thattrimethoprim antibiotic had more inhibitory effects than tetracycline on the abortion prevention in Balb/C mice.

**Keywords :** Listeriosis\ Mice\ Tetracycline\ Trimethoprim

# P159-80: Identification of ESBLs and Colistin Resistance Genes in Escherichia coli Isolated from German cockroaches by Dot – Blot Method

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**Background and Aim :** Recently, multidrug-resistant (MDR) Escherichia coli is one of the main causes of nosocomial infections especially in intensive care units which Prevents the spread of drug resistance. Cockroaches are creatures found in most places. Then, it is not unexpected to find these insects in health care spaces. The presence of these insects in the hospital can carry various infections in addition to their pathogenicity.

**Methods :** This study was performed on hospital cockroaches. First of all, cockroaches were trapped and brought to the laboratory in sterile containers. Samples were taken from their gastrointestinal tract and Escherichia coli was obtained after various tests. Then, their antibiotic resistance pattern was determined by using antibiotic discs.

**Results :** 31 Escherichia coli were isolated from 109 caught cockroaches. By determining the pattern of antibiotic resistance, Ampicillin and Colistin had the highest and lowest resistance frequencies, respectively. DNA Flow Chip kit was identified in order to determine the genes of broad-spectrum beta-lactamase resistance genes, 8 isolates had CTX gene and one isolate had SHV genes.

**Conclusion :** The results indicate that the prevalence of strains with resistance to antibiotics at hospital, the insects such as cockroaches should be taken seriously to prevent the spread of Escherichia coli infections.

**Keywords :** German cockroaches, ESBLs ,Colistin ,Dot -blot, Escherichia coli

# P160-138: Comparison of Cattle Serum Antibody Responses to Five Different Mycobacterial Antigens in An ELISA System

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**Background and Aim :** In view of the fact that the presence of common diseases between humans and livestock caused by Mycobacterium tuberculosis complex (MTBC), and nontuberculous mycobacteria (NTM), Such as Johne's disease in animals and Crohn's disease in humans, early detection of mycobacteria can help Control of health problems and huge economic losses in Iranian livestock. New methods of diagnoIn view of the fact that the presence of common diseases between humans and livestock caused by Mycobacterium tuberculosis complex (MTBC), and nontuberculous mycobacteria (NTM), Such as Johne's disease in animals and Crohn's disease in humans, early detection of mycobacteria can help Control of health problems and huge economic losses in Iranian livestock. New methods of diagnosis are an ELISA method that is easy, fast, and useful. In this research, we attempted to evaluate different crude antigens obtained from mycobacterial species using an indirect ELISA test. The purpose of this assessment is to detect the infection of different mycobacteria in infected livestock.sis are an ELISA method that is easy, fast, and useful. In this research, we attempted to evaluate different crude antigens obtained from mycobacterial species using an indirect ELISA test. The purpose of this assessment is to detect the infection of different mycobacteria in infected livestock.

**Methods :** Five different strains of Mycobacteria (M. tuberculosis, M. phlei, M. bovis, M. avium subsp. Paratuberculosis, and M. bovis AN5) were cultured and precipitated by TCA 4%. The SDS-PAGE of crude antigens of different mycobacteria was accomplished. Protein concentrations determined with Lowry protein assay. After preparing the crude antigens of mycobacteria, the ELISA test was performed, the results of the ELISA test were compared with the PPD skin test and data analysed with SPSS software.

**Results :** Study showed, all five strains had more than 92% detection ability in healthy animals. The highest sensitivity of ELISA tests to M. bovis AN5 antigen is greater than 83% and the highest diagnostic specificity of M. avium subsp. Paratuberculosis is 95.83% and the highest efficiency of diagnostic tests is over 83% concerning this antigen.

**Conclusion :** In conclusion, this study concludes that M. avium subsp. Paratuberculosis and M. bovis AN5 antigens are suitable candidates for the design of diagnostic ELISA due to their sensitivity, specificity, and efficiency.

**Keywords :** Mycobacteria, NTM, PPD, ELISA

# P161-161: Molecular Investigation of Campylobacter spp. infection in Children with Community Acquired Diarrhea

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**Background and Aim :** Acute gastroenteritis is a characteristic disorder that accounts for 8-12% of pediatric outpatient visits. Campylobacter infections account for about 8.4% of global diarrhea cases. Therefore, considering the importance of Campylobacter in diarrheal infections, this study was aimed to determine the rate of infection with different species of this bacterium among children with community-acquired diarrhea. Moreover, minimum limit of diagnosis for this bacterium (LOD) in fecal samples was determined by PCR.

**Methods :** Stool samples of children under 5 years of age with diarrhea were collected. The samples were related children referred to hospitals in Hamadan, Ardabil, Bandar Abbas and two hospitals in Tehran. A questionnaire was filled by physicians and a consent form signed by the participants. DNA was extracted from the samples using a DNA extraction kit from stool. The presence of Campylobacter in the studied samples was detected by polymerase chain reaction using specific primers. A control stool sample was spiked with 10-fold dilution of C. jejuni suspension for LOD measurement.

**Results :** Out of 102 stool samples from children with diarrhea, one sample was positive for Campylobacter jejuni LOD was determined for this test as 100 CFU per gram.

**Conclusion :** According to our results, infection with Campylobacter spp. was not high among the studied symptomatic children with diarrhea during the Covid-19 pandemic in Iran.

**Keywords :** Campylobacter; Children; Diarrhea; Gastroenteritis; PCR

# P162-236: Identification of Loa22 coding gene in the vaccinal Leptospira serovars

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**Background and Aim :** Leptospirosis is one of the most important zoonotic diseases, which is caused by the Leptospira. Some Leptospra membrane lipoproteins perform as bacterial virulence factors. The aim of the present study was to molecular identification and investigation the presence of Loa22 gene encoding a membrane lipoprotein in the vaccinal Leptospira serovars.

**Methods :** In the present study, three vaccinal Leptospira serovars including L. Grippotyphosa, L. Canicola and L. Serjoe hardjo as well as a saprophytic serovar, L. Semanerga, were prepared. After DNA extraction by standard phenol-chloroform method and quantitative and qualitative analysis of the extracted DNA, PCR reaction was performed to amplify the Loa22 gene. PCR products were evaluated by electrophoresis on agarose gel and finally sequenced. The resulting sequences were compared using Megalign software and the serovars genetic similarity was investigated.

**Results :** The results of electrophoresis of PCR products showed 671 bp bands indicating the presence of Loa22 in vaccinal samples, while no band was formed in the saprophytic sample. The percentage of this gene similarity was high in pathogenic serovars so that the minimum similarity was 97.3% and the maximum similarity was 99.6%, which indicates the conservation of Loa22 gene.

**Conclusion :** Loa22 gene is a specific conserved gene of vaccinal Leptospira serovars and can be used as a diagnostic marker to identify these serovars and differentiate them from the saprophytic ones.

**Keywords :** Leptospirosis, Vaccinal Leptospira serovars, Molecular identification, Loa22 gene

# P163-252: Epidemiological status of leishmaniasis: A brief review

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**Background and Aim :** Leishmaniasis is a chronic parasitic disease with a wide clinical spectrum and is a tropical disease that spreads with a wide range of parasitic reservoirs and vectors. The disease is caused by protozoa belonging to the genus Leishmania. The present study was designed to determine the epidemiological status of leishmaniasis.

**Methods :** The present study was a brief review study designed in 2021. PubMed / Medline and Scopus databases were used to search for similar studies and extract content. Selected keywords for the search included “Epidemiology”, “leishmaniasis” and “parasite”. Summaries of articles published in congresses and conferences were excluded from the study. Initially, 14 articles were finally evaluated.

**Results :** More than 20 species of these protozoa can cause disease, and the female genus of sandflies are carriers. Out of about a thousand species of sandflies, 93 species have transmitted leishmaniasis, the most common vectors of which are subfamilies of phlebotomines and luteal mutations. Humans and dogs are known to be the main reservoirs of Leishmania, while wild rodents also play an important role as reservoirs of disease in rural areas, however, there have been limited reports that cats may also be involved in the epidemiology of the disease. The disease is endemic in 100 countries around the world.

**Conclusion :** The incidence of the disease is increasing, so educating people, especially in epidemic and endemic areas can be effective in preventing and controlling the disease.

**Keywords :** Leishmaniasis, Epidemiology, Parasitic Diseases

# P164-262: Epidemiological status of brucellosis in Iran: A brief review

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**Background and Aim :** Introduction & Objective: Brucellosis is a common infectious disease between humans and animals and is caused by aerobic gram-negative bacilli without capsules and spores. The aim of this study was to determine the epidemiological status of Brucellosis in Iran.

**Methods :** The present study was a brief review study designed in 2021. PubMed / Medline and Scopus databases were used to search for similar studies and extract content. Selected keywords for the search included “Coronavirus”, “Epidemiology”, “brucellosis”, “and Iran”. Summaries of articles published in congresses and conferences were excluded from the study. Initially, 17 articles were finally evaluated.

**Results :** Brucella bacteria are the cause of the disease and the most important types of Brucella that can cause disease in humans include Brucella melitensis, Brucella abortus and Brucella suis. Iran is an endemic country in terms of brucellosis. The incidence of brucellosis is higher in rural areas than in cities. The incidence of brucellosis in summer and spring due to livestock and lactation is higher than autumn and winter. In Iran, western and Zagros regions, mountainous areas and areas inhabited by nomads, the rate of brucellosis is high. In the world, Iran ranks fourth in patients with brucellosis and ranks first in the Eastern Mediterranean. Brucellosis is an occupational disease that is more common in herders and people who come into contact with livestock or dairy and meat products.

**Conclusion :** The results of various studies show that Iran is known as an endemic country and due to its geographical area and lifestyle changes, brucellosis has a high potential to increase the prevalence. Therefore, it is suggested that in the beginning of spring, trainings should be given to prevent the disease, as well as vaccination of livestock.

**Keywords :** Brucellosis, Incidence, Iran, Epidemiology

# P165-279: Investigation of the presence of Stn virulence gene in human Salmonella serovars

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**Background and Aim :** Salmonellosis is a common zoonotic disease caused by Salmonella. Because diagnosis methods based on culture and isolation are time-consuming, using methods that can quickly detect the presence of Salmonella in suspected specimens can be effective in preventing disease and outbreaks. Stn is a virulence factor in Salmonella and is known to cause diarrhea because it has been shown to have enterotoxic activity. The present study aimed to investigate the presence of Stn gene in human Salmonella serovars as a molecular diagnostic method.

**Methods :** 43 Salmonella serovars isolated from humans were prepared and samples were cultured on differential media. Serovars were identified using specific antiserum based on the Kauffman-White table. After extraction of genomic DNA, PCR reaction was performed using specific primers for Stn gene and the PCR product was evaluated for the presence of Stn by electrophoresis on agarose gel.

**Results :** In this study, most human serovars included Salmonella paratyphi A, Salmonella paratyphi B and Salmonella enteritidis. All 43 Salmonella samples was positive for the Stn virulence gene.

**Conclusion :** Since the Stn gene plays an important role in the pathogenesis of Salmonella and due to the fact that it is specific to Salmonella, it can be used in the manufacture of diagnostic kits such as ELISA as well as the production of recombinant vaccines.

**Keywords :** Salmonellosis, Salmonella serovars, Molecular identification, Stn gene

# P166-392: Isolation, biochemical and molecular identification of Salmonella isolates from Mazandaran poultry industry submitted to Razi Vaccine and Serum Research Institute

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**Background and Aim :** The genus Salmonella is a group of Gram-negative bacteria belonging to the Enterobacteriaceae family. The importance of research on Salmonella infection in industrial poultry includes irreparable economic losses due to salmonellosis in the poultry industry. Salmonella infection is one of the common major diseases in humans, livestock and poultry. In addition, it is a major cause of humans' food poisoning. From financial and public health prospective, salmonellosis in poultry, its dominant serotypes and antibiotic resistance are interesting topics, which need continuous research. Especially, if new and fast techniques can detect Salmonella serotype.

**Methods :** The isolates were identified by Culture and Biochemical test, then serotyped by Multiplex PCR.

**Results :** In this study, suspicious were 1-10 days old broilers sent from 29 herds in Mazandaran province, which were isolated from a total of 11 herds (37.37%) of Salmonella genus. The most magnificent part of this study was the isolation of two Salmonella enteritidis isolates from broiler brains. The isolates were serotyped by Multiplex PCR. The results showed that, they were Salmonella enterica serovar Enteritidis .The most magnificent part of this study was the isolation of two Salmonella enteritidis isolates from broiler brains.

**Conclusion :** The importance of research on Salmonella infection in industrial poultry includes irreparable economic losses due to salmonellosis in the poultry industry. Salmonella infection is one of the common major diseases in humans, livestock and poultry. In addition, it is a major cause of humans' food poisoning. From financial and public health prospective, salmonellosis in poultry, its dominant serotypes and antibiotic resistance are interesting topics, which need continuous research. Especially, if new and fast techniques can detect Salmonella serotype. In

this study, suspicious were 1-10 days old broilers sent from 29 herds in Mazandaran province, which were isolated from a total of 11 herds (37.37%) of Salmonella genus.

**Keywords :** Salmonella, Poultry, Isolation ,Identification, Molecular, Enteritidis

# P167-403: Report of co-occurrence of sporotrichosis in two DSH cats and their owners

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**Background and Aim :** Sporotrichosis is considered a chronic fungal zoonotic disease caused by the Sporothrix schenckii. Cats inoculated with S. schenckii in the footpads had lymphocutaneous spread similar to localized sporotrichosis in humans. The purpose of this research is to assess sporothrochosis occurrence in 2 cats and their owner simultaneously and investigate the causes and effects of this zoonotic disease.

**Methods :** In September 2020, a referred case to one of the pet hospitals located in Karaj included two male DSH cats in the age of around eight months, developed a draining subcutaneous abscess at the right commissure of the lip (in the first case), and several minor draining puncture wounds over the posterior surface of the left tarsal region (in the second case). After sampling the skin and hair, the samples were sent to the laboratory. Organisms were so numerous that they were easily detected on hematoxylin-and-eosin-stained sections. They were stained with periodic acid-Schiff, Gomori's methenamine silver, and Gram's stains.

**Results :** In both cats there was a pyogranulomatous inflammatory reaction involving the dermis, the panniculus, and the subjacent skeletal muscles. Furthermore, the 56-year-old female owner with a moderate immunodeficiency disease background developed a calf region of her left leg alongside a tender, erythematous pustule over the papular eruption and a localized lymphocutaneous form sporotrichosis on the middle of her right forearm. This lesion was noticed several days after she had cleaned the cat’s lesions.

**Conclusion :** It seems that any contact with the draining lesions of affected cats offers the potential for human infection. In addition, an immunodeficiency background may enhance the risk of sporothrochosis.

**Keywords :** sporothrochosis, cat, immunodeficiency, zoonosis

# P168-409: Frequency of Salmonella Spp in asymptomatic rural dogs from 2020 to 2021

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**Background and Aim :** Different serotypes of Salmonella bacteria with a high host prevalence are the cause of one of the common diseases of humans and animals. Dogs may carry various Salmonella serotypes for a long time without any symptoms. This study aimed to investigate the contamination of fecal samples of rural dogs with Salmonella in Khouzestan provinces.

**Methods :** Rectal swabs obtained from 150 seemingly healthy rural dogs referred to the Veterinary Hospital of Ahvaz University were cultured from 2020 to 2021 and were identified at the genus level by molecular PCR. The division was based on age, sex, breed, region and season.

**Results :** The studied dogs were divided into 3 groups based on age (less than 6 months, 6 months to 3 years and over 3 years) and based on the region into 5 areas (north, east, west, south and centre). The results were analyzed using chi-square test, Fisher's exact test and Z test. 32 of the 150 serum samples (21.33%) had antibodies against Salmonella. The prevalence of infection in over 3-year dogs (41.3%) and at the age of 6 months to 3 years (29.4%) was significantly higher compared to dogs under 6 months (4.3%). The prevalence of infection in male dogs (29.7%) was higher than females (27.6%) in winter (26.2%) and the northern region (31.5%), but the difference between the prevalence of infection in terms of sex, season and region were not significant.

**Conclusion :** Our study showed that the serum prevalence of infection in the serum of rural dogs in Khuzestan province is relatively high.

**Keywords :** Salmonella, dog, Khouzestan, zoonosis

# P169-3: Design and evaluation of nanobiosensor based on Surface Plasmon Resonance (SPR) of gold nanoparticles for rapid detection of V.cholerae genome in water samples

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**Background and Aim :** Vibrio cholerae (cholera) is a curved, motile and gram-negative bacterium that transmits to humans through eating contaminated food and water and is commonly a major health threat to developing and underdeveloped countries worldwide. V.cholerae infection can be confirmed by isolating the organism from the feces on the selected medium, followed by biochemical tests and specific antibodies for serotyping and serogrouping. The aim of this study was to develop a simple, sensitive, and rapid assay for the detection of V.cholerae genome.

**Methods :** ctxA gene was selected as the target then specific probes and primers, targeting this gene were designed. Gold nanorods and fabricated nanoprobes were evaluated and approved by UV-vis (400-900 nm), zeta potential, FT-IR and TEM electron microscopy instruments. Direct detection of bacteria was performed using PCR, Real-Time PCR and biosensor. Limit of Detection (LOD), sensitivity and specificity of all methods were examined using a recombinant plasmid (pJET1.2/ctxA) and finally, the results of all methods were compared with each other.

**Results :** Evaluation of designed primers and probes showed no homology to other bacteria and complete specificity for V.cholerae, then the rod forms of nanoparticles and probe hybridization to GNRs (Nanoprobe production) were confirmed by plasmonic and TEM studies. The specificity of all tests was 100%. Based on the recombinant vector used, LOD for Real-Time PCR, Biosensor and PCR were 10 to the power of 3, 10 to the power of 3, 10 to the power of 4 Copy of target gene respectively.

**Conclusion :** Since methods for practical, rapid, simple and sensitive detection of V.cholerae is in great demands, using surface plasmon resonance (SPR) biosensors which are one of the most sensitive optical biosensors could be reserved as an alternative method of detection.

Although the sensitivity of Real-Time PCR was higher than that of a biosensor, the biosensor was suitable for screening and diagnosis of V.cholerae due to its specificity, acceptable sensitivity (compared to PCR), and its ability to become a useful tool in clinical laboratories.

**Keywords :** Vibrio cholerae, Nanobiosensor, Surface plasmon resonance, ctxA

# P170-54: Validation of the method for evaluating the efficiency of solid lipid formulations containing streptokinase by biochemical method

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**Background and Aim :** In order to confirm the effectiveness of biologically or recombinantly produced drugs by the competent legislative authorities, it is an indicator of the biological activity of those drugs. Recombinant streptokinase is no exception and determining its biological activity is an important factor in controlling the quality of this recombinant product. Previous studies have shown that solid lipid nanoparticles (SLN) as carriers of streptokinase increase the efficiency of this protein. In this dissertation, the efficiency of solid lipid nanoparticles containing streptokinase was studied by biochemical methods

**Methods :** For this purpose, rabbit blood and three different human blood groups were used and the efficiency of solid lipid nanoparticles containing streptokinase on clot lysis was investigated. In this study, di-dimer biochemical method was used and the results were evaluated by determining the biological activity using a chromogenic kit

**Results :** The results of the biological activity of streptokinase containing lipid nanoparticles were measured on the produced samples according to the USP Pharmacopoeia method and then the results were compared with the dimer method.The dimer method was validated against the results of the kit and the results of the two methods were compared. The results showed that the dimer method is a low cost and high speed method that can be effective in screening the effectiveness of anticoagulants.

**Conclusion :** In this study, a combination of D-dimer and WB clot weight was used to validate the WB lyselocyte method in vitro using nanoparticles, streptokinase, streptokinase-nanoparticles on human and rabbit blood. Similarly, no further investigation was possible.

**Keywords :** SLN-Nanoparticle-Recombinant-Streptokinase-in vitro

# P171-76: Selenium Nanoparticles Biosynthesized using Polylophium involucratum (Pall.) Boiss. Seeds Extract and its Antibacterial Activity

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**Background and Aim :** Recently, selenium nanoparticles have emerge as encouraging bactericidal agents, and have been widely applied in various fields of industry such as cosmetic, medical and food industry. In the present project, the biosynthesis of selenium nanoparticles was conducted using the seeds of extract of Polylophium involucratum (Pall). Boiss., and investigation of its antibacterial properties.

**Methods :** In this project the biosynthesis of selenium nanoparticles using hydroalcohlic extract of seeds of Polylophium involucratum (Pall). Boiss. as a reducing agent by microwave irradiation method. The synthesized selenium nanoparticles were characterized using various instrumental techniques. Later, the antibacterial activity of the synthesized selenium nanoparticles was tested by (Disk Diffusion Method) using both gram positive as well as gram negative bacteria i.e. Staphylococcus aureus (PTCC 1113), Bacillus subtilis (PTCC 1156) and Escherichia coli (PTCC 1399) respectively.

**Results :** The phytochemical compounds play a vital role in the nanoparticles synthesis was identified using the UV-Vis, FT-IR, XRD, and TEM. The synthesized selenium nanoparticles hydroalcohlic extract of seeds of Polylophium involucratum (Pall). Boiss. exhibited good antibacterial potential against gram positive and gram negative bacterial strains. Also, our preliminary phytochemical analysis of seeds extract using hydroalcohlic as solvent confirmed the presence of (Flavonoids, Terpenoids, Coumarins, Phenols, Cardiac glycosides, Quinones and Saponins). This indicates that antibacterial activities may be due to presence of secondary metabolites.

**Conclusion :** The synthesized selenium nanoparticles exhibited good antibacterial potential against gram positive and gram negative bacterial strains. Further, efficient antibacterial activity of the synthesized selenium nanoparticles proves the application potential of green synthesis in the area of nano-medicine.

**Keywords :** Selenium nanoparticles, Polylophium involucratum (Pall). Boiss., Staphylococcus aureus, Nano-Medicine.

# P172-113: Antibacterial Activity of Zinc Oxide Nanoparticles Synthesized by Cinnamomum zeylanicum Bark Extract

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**Background and Aim :** Recently, the production of nanoparticles is one of the most successful hopes in the treatment of bacterial infections. The aim of this study was to investigate the antimicrobial effect of Zinc oxide nanoparticles synthesized by Cinnamomum zeylanicum bark extract.

**Methods :** In this study, biosynthesis of zinc oxide nanoparticles from C. zeylanicum was performed using precursor zinc acetate dehydrates and NaOH. The nanoparticles produced were characterized by UV-vis spectroscopy, X-ray diffraction (XRD) spectroscopy, Fourier transform infrared spectroscopy (FTIR), scanning electron microscopy (SEM), and energy-dispersive X-ray spectroscopy (EDX). Then, the antimicrobial activity of synthesized nanoparticles was investigated by broth microdilution method against two strains of gram-positive bacteria Staphylococcus aureus, Bacillus subtilis, and two strains of gram-negative bacteria Pseudomonas aeruginosa, Escherichia coli.

**Results :** The results showed that the zinc oxide nanoparticles were synthesized in a polygonal to round shape with an average size of 37 nm. The determining minimum inhibitory concentration (MIC) of zinc oxide nanoparticles against the studied bacteria was reported between 3.125 - 12.5 µg/ml.

**Conclusion :** According to the results, ZnO nanoparticles synthesized using C. zeylanicum bark extract have antibacterial effects.

**Keywords :** Antimicrobial activity, Green Synthesis, Cinnamomum zeylanicum Extract, Zinc Oxide Nanoparticles.

# P173-162: Synthetic and Biogenic Selenium nanoparticles Boost Macrophage Responses Exposed to Bladder Tumor Cells

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**Background and Aim :** Synthetic and biogenic nanoparticles have shown the lowest deleterious effect in comparison to other common medications. The anti-tumor properties of Selenium nanoparticles (SeNPs) were reported in several types of research. In the present research, the effect of synthetic and biogenic selenium nanoparticles on macrophage responses was assessed and compared to BCG as a common treatment

**Methods :** The biogenesis of selenium nanoparticles were performed synthetically by ascorbic acid and biogenically by intravesical M. Bovis bacillus Calmette-Guérin. Macrophages were cultured and treated with synthetic and biogenic SeNPs, which each of them combined with bladder tumor lysate and BCG. The other experimental groups include SeNPs + tumor lysate + MQs, BCG, BCG+MQs, and MQs. The mRNA levels of IL-27, IFN-γ, IL-12, TNF-α, IL-10, and MHC-I were determined using the real-time PCR method.

**Results :** The gene expression of IL-27, IFN-γ, IL-12, TNF-α, MHC-I were drastically upregulated in the combination treatment of selenium nanoparticles (synthetic or biogenic) with the tumor lysate and macrophages compared to the BCG control group. As such, the expression of IL-10 did not show remarkable differences in all experimental groups among each other. The maximum effect of synthetic and biogenic selenium nanoparticles was observed after 24h treatment.

**Conclusion :** Synthetic selenium nanoparticles showed better activity than Biogenic nanoparticles, and both of them had treatment-dependent-function.

**Keywords :** Synthetic selenium nanoparticles; biogenic selenium nanoparticles; BCG therapy; bladder tumor lysate; Macrophage response

# P174-164: Encapsulation of Satureja khuzistanica jamzad essential oil in chitosan nanoparticles with enhanced antibacterial and anticancer activities

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**Background and Aim :** atureja khuzistanica jamzad (SKJ), which is a member of Lamiaceae, has various proven effects such as antispasmodic and anti-inflammatory, anti-diabetic, antioxidant, and antifungal properties. However, the use of essential oil of plants is limited due to their inherent instability in the environment. Encapsulation with nanoparticles in the nanogel forms is one of their stabilization methods. The aim of this study was to synthesize nano-gel based on chitosan (CS) and extracts of SKJ essential oil, and to evaluate the antibacterial and anticancer activities.

**Methods :** SKJ essential oil was extracted using water distillation method. Then, it was loaded on CS particles using two-step process as following: droplets formation and freezing. The Dynamic Light Scattering (DLS), Fourier transform infrared spectroscopy (FTIR), Scanning electron microscopy (SEM), and Zeta potential determination were used to evaluate the physical and chemical properties of CS-SKJ nanogel, which its result was acceptable. After confirmation of the loaded essential oil rate and releasing amount, the antibacterial effects were evaluated on five Gram-positive bacteria and five Gram-negative bacteria using microbroth dilution method.

**Results :** The encapsulation efficiency, size, polydispersity index, and zeta potential of nanoparticles were characterized were 30.74%, 571.00?nm, 0.451 and ?67.2?mV, respectively. The results were significant not only on Gram-positive bacteria, but also on Gram-negative bacteria. The MIC range was between 7.8 and 500?µg/ml. The CS-SKJ nanogel has acceptable anticancer activities on KB and A549 tumor cell lines. the IC50 range was between 5.6 and 6.71?µg/ml.

**Conclusion :** The results indicate that both CS particles and SKJ alone, and CS-SKJ nanogel could be considered as the outlook to produce new antimicrobial and anticancer drugs.

**Keywords :** Encapsulation, Satureja khuzistanica jamzad, chitosan, antibacterial, anticancer

# P175-172: Phyco-fabrication of bimetallic nanoparticles (zinc–selenium) using aqueous extract of Gracila riacorticata and its biological activity potential otentials

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**Background and Aim :** Zinc selenium nanoparticles (ZnSe NPs) are widely used in many industrial, environmental and biomedical fields. However, the biological potential of ZnSe NPs has not been studied in detail. The present study focused on ZnSe NPs algae-based synthesis using aqueous extract of seaweed, Gracilaria corticata

**Methods :** Successfully synthesized ZnSeNPs were characterized by analytical methods such as UV–Vis, FTIR, XRD, SEM, TEM, DLS, Zeta potential and EDX analyses; additionally, the biological function of ZnSe NPs was performed.

**Results :** The ZnSe NPs exhibited a certain absorbance peak at 350–400 nm in the UV–vis spectrum. The FTIR showed the possible functional groups associated with biomolecules involved the ZnSe NPs synthesis. SEM and TEM demonstrated that ZnSe NPs were spherical in shape with size range of 50–250. XRD and EDX showed NPs crystallite size of 55.5 nm and their elemental composition that constitute selenium and zinc (1:1.5 ratio). These NPs showed antioxidant activity about 67% and antibacterial activity against broad spectrum of bacterial strains. Biofilm inhibition by ZnSe NPs was occurred on P. aeruginosa and B. subtilis at 50 and 40 ?g/ml. Anticancer activity against HTB-9 (ATCC 5637) and KB (ATCC CCL-17) with IC50 of 19.24 and 28.42 ?g/ml.

**Conclusion :** In conclusion, the green synthesis of ZnSe NPs can provide the requisite criteria for therapeutic and preventive applications.

**Keywords :** Zinc selenide nanoparticles (ZnSe) ,Green synthesis, Gracilaria corticata, Biological activity

# P176-173: Bio-inspired silver selenide nano-chalcogens using aqueous extract of Melilotus officinalis with biological activities

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**Background and Aim :** For the first time, an aqueous extract of Melilotus officinalis was used to synthesize bimetallic silver selenide chalcogenide nanostructures (Ag2Se-NCs).

**Methods :** he formation of NCs was confirmed and characterized by UV–visible and FTIR spectroscopy, SEM and TEM imaging, XRD and EDX crystallography, zeta potential (ZP) and size distribution (DLS). The bioactivities of biosynthesized Ag2Se-NCs, such as antibacterial, antibiofilm, antioxidant and cytotoxicity potentials, were then examined.

**Results :** Bio-based Ag2Se-NCs were successfully synthesized with mostly spherical shape in the size range of 20–40 nm. Additionally, the MIC and MBC values of Ag2Se-NCs against β-lactam-resistant Pseudomonas aeruginosa (ATCC 27853) were 3.12 and 50 µg/ml, respectively. The DPPH scavenging potential of Ag2Se-NCs in terms of IC50 was estimated to be 58.52. Green-synthesized Ag2Se-NCs have been shown to have promising benefits and could be used for biomedical applications

**Conclusion :** lthough the findings indicate promising bioactivity of Ag2Se-NCs synthesized by M. officinalis extract (MO), more studies are required to clarify the comprehensive mechanistic biological activities.

**Keywords :** Silver selenide nano-chalcogens (Ag2Se-NCs), Melilotus officinalis, Pseudomonas aeruginosa, Biological activities

# P177-283: A novel bacterial strain isolated from Choghart iron mine as a catalyst for synthesis of silver nanoparticles

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**Background and Aim :** Silver nanoparticles are among the most widely used nanoparticles, and their synthesis has become very common today. Various physical, chemical, and biological methods are used to synthesize these nanoparticles. The biological method is preferable to the other two methods due to its environmental compatibility and low cost. Various studies have shown that different strains of bacteria can regenerate silver ions and convert them into silver nanoparticles. In this study, the reduction of silver ions to silver nanoparticles has been studied by novel strain isolated from the Choghart iron mine.

**Methods :** Biosynthesis of silver nanoparticles was optimized using biomass of bacterial strain isolated from the mine. Finally, ultraviolet-visible spectrophotometer, FTIR, and XRD analysis were used to study the synthesized silver nanoparticles in more detail.

**Results :** Biosynthesis of silver nanoparticles was confirmed by changing the color of silver nitrate solution to dark brown at a concentration of 3 mM, in the presence of light, the existence of a maximum absorption at 437 nm using the spectrophotometer and XRD results.

**Conclusion :** The results showed that the efficiency and rate of silver nanoparticles synthesis would increase with increasing the amount of bacterial biomass and the amount of light emitted into the solution.

**Keywords :** Nanoparticles, Silver nanoparticles, Biosynthesis, Bacteria

# P178-325: Evaluation of the synergistic effects of zinc oxid nanocomposite film and doxycycline nanocomposite film against Staphylococcus aureus and Escherichia coli

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**Background and Aim :** Infectious diseases are a global threat to human health. Excessive and inappropriate use of antibiotics has led to drug-resistant microbes that can neglect clinical treatment. Efforts are being made to develop safe and alternative antimicrobials to overcome such resistant microorganisms, and the birth of nanotechnology is promising to combat these organisms.

**Methods :** In this study, according to the laboratory results obtained through disk diffusion method, determination of MIC (Minimum Inhibitory Concentration) and MBC (Minimum Bactericidal Concentration), Fractional Inhibitory Concentration (FIC) for Confirmation of the synergistic effect of zinc oxide nanocomposites and doxycycline nanocomposites against Staphylococcus aureus, 29213 ATCC and Escherichia coli, 35218 ATCC was determined.

**Results :** Minimum fractional inhibitory concentration to confirm the synergistic effect of zinc oxide nanocomposites and doxycycline nanocomposites against Staphylococcus aureus 0.03 + 0.075 mg /ml and FICI (Fractional Inhibitory Concentration Index) respectively 0.375 ,was observed for Escherichia coli with concentrations of 0.24 + 0.24 mg /ml and FICI 0.5, respectively.

**Conclusion :** During the study and confirmation of the synergistic effect between zinc oxide nanocomposite film and doxycycline nanocomposite film, it can be said that these films had a synergistic effect against the studied bacteria and the greater effect of antibacterial agents on gram-positive bacteria than gram-negative bacteria is clearly known.

**Keywords :** Resistant microorganisms, Nanocomposite films, FIC, Synergistic effect

# P179-326: Evaluation of doxycycline and zinc oxide nanocomposite films effect on some gram positive and gram negative bacteria

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**Background and Aim :** many researches has been done recently on the production and Evaluation of antibacterial effects of medical nanoparticles because of the prevalence of infections caused by bacteria resistance to one or more antibiotics, lack of proper efficacy and recovery from infection, increased treatment costs and widespread side effects due to the use of common antibiotics. Metal nano oxides such as zinc oxide nanoparticles have been considered in recent years, due to stability in various conditions and generally used as safe materials for humans and animals.

**Methods :** In the present study, disk diffusion method, determination of MIC (Minimum Inhibitory Concentration) and MBC (Minimum Bactericidal Concentration) were used.

**Results :** The MIC obtained for zinc oxide nanocomposite film, doxycycline nanocomposites and zinc oxide-doxycycline nanocomposite for Staphylococcus aureus (29213 ATCC) 0.48, 0.03 and 0.00375 mg/ml respectively, for Escherichia coli (35218 ATCC) were 0.96, 0.48 and 0.24 mg/ml, respectively. Concentrations obtained to express the MBC of bacteria for Staphylococcus aureus were 0.96, 0.06, 0.0075 mg/ml, respectively, and for Escherichia coli were 1.92, 0.96 and 0.48 mg/ml respectively. Which was statistically significant during our studies in different groups ($p < 0.05$).

**Conclusion :** The antimicrobial effect of nanocomposite films against bacterial pathogens in all studied methods for Staphylococcus aureus is more significant than Escherichia coli. The increase of these effects against two bacteria for films is also in the form of zinc oxide was determined (Zinc oxide-doxycycline nanocomposite more than doxycycline nanocomposite and more than zinc oxide nanocomposite).

**Keywords :** Antibacterial effect, Metal nano oxides, Nanocomposite films, MIC, MBC.

# P180-434: Antimicrobial Activity of impregnated Chitosan Films with peppermint essential oil and silver nanoparticles

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**Background and Aim :** The resistance of the bacteria to the innumerous antimicrobial agents is a major challenge in the treatment of the infections demands to the necessity for searching and finding new sources of substances with antimicrobial properties. The present study, was done to evaluate the green synthesis of silver nanoparticles and in vitro investigation the antimicrobial activity of chitosan film solution enriched with EOs (CFs+Eos+ Ag NP)against microbial strains .

**Methods :** biosynthesis of silver nanoparticles (AgNPs) by using peppermint essential oil was investigated The silver nanoparticles were characterized by means of UV-Visible spectroscopy, SEM and XRD analyzes. The antibacterial activity of chitosan films containing peppermint essential oil, silver nanoparticles, against gram-negative bacteria (Escherichia coli, Pseudomonas aeruginosa) and gram-positive (Staphylococcus aureus and Staphylococcus epidermidis) was determined by well diffusion Assay.. In three replicates, the minimum inhibitory concentration (MIC) and the minimum bactericidal concentration (MBC) of different treatments including: 1- essential oils (EOs), 2- chitosan film solution (CFs), and 3- chitosan film solution enriched with EOs (CFs+Eos+ Ag NP) were determined using microdilution technique against above mentioned microbes.

**Results :** The silver nanoparticles were effectively synthesized by peppermint essential oils The results indicated that the chitosan films enriched with essential oils (CFs+Eos+AgPN) is capable of inhibiting the bacterial growth even at the lowest concentrations. these compounds had a better inhibitory effect on gram-positive isolates than gram-negative isolates.

**Conclusion :** Chitosan-EOs complexes are the promising candidate for novel contact antimicrobial agents. Gram-positive bacteria were more sensitive to gram-negative bacteria than films prepared from chitosan containing different compounds. Considering the possibility of producing biodegradable films in nature that contain plant essential oils as anti-inflammatory compounds. The films have the potential to be used as active biodegradable films with strong antimicrobial effects

**Keywords :** chitosan films, Antimicrobial Activity, silver nanoparticles

# P181-14: Kermanshahi roghan: Fat quality comparisons between before and after storage

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**Background and Aim :** Kermanshahi roghan is a yogurt by-product which becomes more delicious and aromatic after being kept in storage for a long time. In this study, it was examined whether one-year storage and different ratios of Streptococcus thermophilus to Lactobacillus bulgaricus (3:1, 1:1, 1:3) as the starter culture had an effect on roghan fatty acid profiles and lipid quality indices.

**Methods :** Analyses of samples were performed in a gas chromatograph by a flame-ionization detector.

**Results :** During the storage, the content of saturated unlike unsaturated fatty acids showed a decrease, whereas there were no changes in all roghan samples short-chain fatty acids (except for butyrate). All roghan atherogenic and thrombogenic indices decreased. The omega6 to omega3 and polyunsaturated to saturated fatty acid ratios for all roghan samples were in accordance with the recommendations made by World Health Organization. Monounsaturated to the polyunsaturated ratio in all roghan samples increased which this increased level was related to oleic acid. All bacterial starter cultures (especially 1:1 ratio) had acceptable effects on the roghan samples' lipid quality indices.

**Conclusion :** In conclusion, although Kermanshahi roghan is animal fat, bacterial starter culture and storage have a satisfactory effect on roghan fatty acid profiles and lipid quality indices.

**Keywords :** Kermanshahi roghan; Storage; Fatty acid profiles; Lipid quality indices; Fermentation.

# P182-136: Enzymatic Modification of Milk Proteins for Production of Antimicrobial Peptides

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**Background and Aim :** Modification of food proteins with enzymes is an attractive way for improving the functional and nutritional properties of these proteins. Chemical modification is not desirable for food applications because of the harsh reaction condition, non-specificity, and difficulties of removing residual reagent from the final products, but enzymatic modification has some advantages such as fast reaction rates, mild condition, high specificity, and the possibility of production in large quantities.

**Methods :** Enzymatic modification of milk proteins increases the number of bioactive peptides with biological activity such as antimicrobial properties. These peptides can be released in three ways (a) Enzymatic hydrolysis by digestive enzymes (b) Fermentation of milk with starter cultures (c) Through the action of proteolytic enzymes derived from microorganisms or plants.

**Results :** These bioactive peptides reveal multifunctional properties such as antihypertensive, antioxidative, antimicrobial, immunomodulating, antithrombotic, and opioid or mineral-binding activities. Antimicrobial peptides have been derived from the cleavage of lactoferrin with pepsin. The resulting peptide had better antimicrobial activity than the undigested lactoferrin due to its smaller size which accessed the microbial surface sites. Lactoferricin, a peptide derived from lactoferrin by pepsin digestion, has been shown to display antimicrobial activity against microorganisms including Bacillus, Escherichia coli, Klebsiella, Listeria, Proteus, Pseudomonas, Salmonella, Streptococcus, and Candida. An αS2-casein fragment (165–203), named casocidin-I, containing a high proportion of basic amino acids was also found to be an antibacterial agent which can inhibit the growth of E. coli and Staphylococcus arnosus. αs1-casein f(1-23), isracidin, obtained from chymosin hydrolysis has been shown to protect mice against Staphylococcus aureus and Candida albicans. Whey protein hydrolyzate obtained by pepsin–trypsin treatment inhibited growth of E. coli.

**Conclusion :** The use of enzymes to improve the functional and nutritional properties of milk proteins is developing rapidly, but additional research is necessary for commercially successful application.

**Keywords :** Milk Protein; Bioactive Peptide; Antimicrobial Activity; Enzyme

# P183-174: Antimicrobial properties of sage (Salvia macrosiphon ) seed gum and egg white via Maillard reaction

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**Background and Aim :** Lysozyme could be considered as well-known antibacterial egg white protein, however, its antibacterial activity is mostly limited to gram-positive bacteria. Maillard type covalent conjugation with polysaccharides could be used as suitable method for improvement antibacterial activity of proteins. Sage seeds are traditionally used for antimicrobial and therapeutic effects. So the aim of this study was to investigate the antimicrobial effect of egg white protein (EWP) conjugation with sage seed gum (SSG) via Maillard reaction.

**Methods :** EWP powder and SSG powder were dispersed in deionized water (1:2), magnet stirred freeze dried, ground and sieved to obtain uniform particles. Powder was placed in a desiccator with relative humidity of 79% and incubated at 60 ˚for 0, 3, 5, 7 and 10 days. Antibacterial activity of conjugated powders was checked by disk diffusion method on Mueller Hinton agar against two gram-positive bacteria (Staphylococcus aurous and Bacillus cereus) and two gram-negative pathogens (E. coli and Salmonella).

**Results :** Results showed increase in antimicrobial activity with conjugation days, so 10-days conjugated samples indicated higher antimicrobial activity than other conjugates. Inhibition zone of 10-days EWP-SSG conjugates on gram positive bacteria (12 mm and 20 mm for Bacillus cereus and staphylococcus aurous, respectively) was higher than ceftriaxone disk (7 mm and 15 mm for Bacillus cereus and staphylococcus aurous, respectively).

**Conclusion :** Finally we can conclude Melanoidins could be formed at final stages of Maillard reaction so extending conjugation days improved antibacterial activity of conjugates. EWP-SSG conjugates could be used as suitable antibacterial agents to prolong shelf life of foods.

**Keywords :** Egg white, Sage seed gum, Maillard, Conjugates, Antimicrobial

# P184-222: Effect of Skim milk powder and sugars of terehalose and lactose in combination and single factor on the survival of Saccharomyces cerevisiae during freeze-drying

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**Background and Aim :** Saccharomyces cerevisiae is commonly referred to as bread yeast. This yeast has been used in the bakery industry for many years. Since this yeast suffers from damage during the preparation of yeast and fermentation dough and its efficiency in fermentation and gas production is reduced, it is necessary to prepare stocks from this yeast for storage that provide the initial performance when entering the line Have production. In this study, the effect of carbohydrates (trehalose, lactose) and Skim milk powder on the survival of S. cerevisiae to protect against freezing was investigated using one-factor experiments. Vacuum freeze-drying was used for drying and long-term storage of the sample.

**Methods :** The microorganism used in this study is Saccharomyces cerevisiae, which is environmentally isolated, purified, and finally used. The main ingredients used in this study include Skim milk powder 12%, trehalose 8%, and lactose 8% All protective agents were dissolved in distilled water and prepared in different concentrations, and sterilized at 105 ° C for 15 minutes. YPD agar medium was obtained by combining YPD broth with 20 g of agar and then sterilizing at 121 ° C for 15 minutes. Cells were cultured in a YPD agar medium and cell viability was determined. S. cerevisiae was inoculated with 2% inoculation (v / v) in a 250 ml flask containing 50 ml of YPD broth and then incubated at 30 ° C for 48 h in a sugar incubator at 150 rpm. After culturing, using a refrigerated ultracentrifuge, the product was centrifuged at 10,000 g 100 g for 10 minutes, then the supernatant was discarded and the wet biomass of S. cerevisiae was removed. The cells were then frozen at -20 ° C for 24 hours and then frozen by vacuum freeze-drying.

**Results :** As a result, combining sugars with Skim milk powder has a better protective effect on the desired strain than Skim milk powder alone and without preservatives. Survival rates were 33%, 25%, and 2.3%, respectively, and the number of viable cells was 3.091 ×107,2.3833×107,0.218×107, respectively.

**Conclusion :** The results showed that combined protective agents have a more effective protective effect than single-factor protectors.

**Keywords :** Saccharomyces cerevisiae, freeze-drying, protective agents, sugars, Skim milk powder

# P185-261: Evaluation of the effect of curcumin on the expression of AHA_098 and AHA_3857 genes in Aeromonas hydrophila

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**Background and Aim :** Aeromonas hydrophila is a Gram-negative bacterium able to infect a variety of aquatic and terrestrial animals, including humans. In humans, it can cause bacteremia, gastroenteritis, meningitis and peritonitis. Pathogenesis of A.hydrophila is multifactorial. The involvement of AHA_3857 and AHA_098 genes, the genes responsible for bacterial serineprotease and metalloprotease, respectively, on the pathogenesis of Aeromonas ssp. has been demonstrated. Similar to a variety of virulent factors, the expression of metalloprotease and serineprotease genes is regulated by bacterial quorum sensing (QS) system. QS is a mechanism of cell-to-cell signaling that allow a bacterium to sense its own population. Anti QS potential of curcumin has been described in literature. Curcumin as a potent anti-QS agent, coult interrupt the proper expression of the protease genes and thus reduce bacterial virulence. We aimed to investigate the effect of curcumin on the expression of metalloprotease and serineprotease genes in A. hydrophila using qRT-PCR assay.

**Methods :** The MIC (Minimum Inhibitory Concentration) of curcumin against A. hydrophila ATCC7966 was determined using the broth microdilution method and then, the bacterium was grown in Lauria broth medium containing a sub-MIC concentration of curcumin. After reaching the late exponential phase, the bacterial cells were harvested from the medium and subjected to RNA extraction and cDNA synthesis. The control cells were grown in the media lacking curcumin. Finally, the expression of the AHA_3857 and AHA_098 genes was investigated by quantitative Polymerase Chain Reaction (qPCR) using gene-specific primers. In addition, the 16s rRNA gene was used as an internal reference gene.

**Results :** The MIC of curcumin was determined 1024 µg/mL and bacteria grown in the media containing curcumin with a concentration of 512 µg/mL were selected for further experiments. Our results showed that the expression of AHA_3857 and AHA_098 genes among curcumin-treated cells reduced by 66 and 77% , respectively, compared with the control cells.

**Conclusion :** In this study, we showed that curcumin significantly reduced the expression of AHA_3857 and AHA_098 genes. Attenuation of these genes by curcumin can reduce bacterial infectivity and pathogenicity. Thus, curcumin could be regarded as a promising anti-QS agent to be used against A. hydrophila infections.

**Keywords :** Aeromonas hydrophila, curcumin, Metalloprotease, Serineprotease

# P186-373: Evaluation of the Effect of Curcumin on the expression of hcp and vgrG genes in Aeromonas hydrophila

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**Background and Aim :** Aeromonas hydrophila is an oxidase-positive,gram-negative rod.Curcumin, a polyphenolic compound derived from dietary spice turmeric, possessesdiverse pharmacologic effects including anti-inflammatory, antioxidant, antiproliferative and antian-giogenic activities.The genes hcp and vgrG are expressed in aeromons hydrophila. The type VI secretion system (T6SS) is a recently discovered mechanism in gram-negative bacteria that targets proteins to both prokaryotic and eukaryotic cells.T6SS occur in many pathogenic bacteria and are implicated in virulence in important pathogens. The type VI secretion system (T6SS) functions analogously to a phage tail, allowing injection of virulence factors into host cells via valine glycine repeat G (VrgG) proteins and hemolysincoregulated protein (Hcp), which functions as an antimicrobial pore-forming protein when secreted or as a structural protein. Hcp and Vgr are unable to be secreted which results in decreased biofilm formation.

**Methods :** A. hydrophila strain and cultured in Muller Hinton Agar. Then, antibacterial effect of curcumin was investigated using the well diffusion agar method. The minimum inhibitory concentration (MIC) of Curcumin against A. hydrophila strain was determined using broth microdilution method and sub-mic of curcumin was selected. A. hydrophila grown in Muller Hinton Agar containing sub-mic of curcumin were subjected to RNA extraction and cDNA synthesis.Expression of hcp and vgrG genes will be checked using quantitative polymerase chain reaction (qPCR) with gene specific primers. The relative gene expression will be determined by the expression of 16s rRNA gene and then the results will be compered with control cells.

**Results :** The aim of current study was to Evaluation of the Effect of Curcumin against Aeromonas hydrophila, a bacterial fish pathogen causing hemorrhagic septicemia, by evaluating expression of hcp and vgrG gene. At first, bacterial strains were identified using biochemical and molecular assays. Then, the minimum inhibitory concentration (MIC) of curcumin against bacteria was determined using broth microdilution method. Expression of quorum sensing genes Hcp and VgrG among the bacteria exposed to curcumin at sub-MIC ( ½ MIC) was determined using real-time PCR method and compared to the control.

**Conclusion :** curcumin significantly reduced expression of both Hcp and VgrG among bacterial strain. In conclusion, curcumin showed a promising potential to be used as antiquorum sensing, T6SS and antibiofilm agent against A. hydrophila.

**Keywords :** Aeromonas hydrophila, Curcumin, type VI secretion system, hcp and vgrG genes.

# P187-375: Biochemical and Serological Study of Vibrio Bacteria in Surface Water of Khuzestan Province Before and After the Spring Floodwaters of 2019

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**Background and Aim :** Vibrio genus are gram-negative, motile, oxidase-positive, halophilic bacteria found in seawater, oceans, as well as in surfaces waters and rivers. This genus is a part of Microbial population of environmental waters and has been isolated from sediments, and seafoods . More than a hundred species of this genus have been identified, at least 12 species in this genus are pathogenic to humans .Vibrio cholerae is type species, that causes cholera disease in humans. The aim of this study was biochemical and serological diagnosis of Vibrio species in surface waters of Khuzestan province before and after the 2019 flood.

**Methods :** Water samples were collected from 5 cities of Khuzestan province (Ahvaz, Ramhormoz, Mesjed Soleyman, Izeh and Baghmalek), 70 samples were taken before the spring flood of 2019 and 10 samples after it. Then the samples were to the cultured in Alkaline Peptone Water broth and TCBS agar. The exact species identification was done by performing Biochemical tests. The V.cholerae strains isolated were serotype by specific antisera to V.cholerae O1.

**Results :** In this study, all samples taken before the flood were non-O1 V. cholerae, In these 70 samples, Vibrio cholerae o1 , Vibrio parahaemolyticus and Vibrio mimicus were not identified. In samples taken after floods in Khuzestan province, Nine samples were contaminated with non-O1 Vibrio cholerae and one sample from Ahvaz (Karoon river) was contaminated with Vibrio Cholerae O1. The identified strain was Ogawa.

**Conclusion :** This study showed that non-O1 V. choleara is the predominant species in surface waters of Khuzestan province. The results also show that Vibrio Cholerae O1 exist in the surface water in this province

**Keywords :** Vibrio, Flood, Biochemical, Serological, khuzestan

# P188-388: Evaluation of microbiological quality of Saffron samples produced in Khorasan Razavi province of Iran

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**Background and Aim :** Saffron is globally the most expensive spice and exposed to a wide range of environmental microbial contamination. Several microorganism detected in Saffron. The microbial contaminations of saffron originated from the post harvesting to packaging .The goal of this study was conducted to measure the microbial Contamination of saffron samples from the major origin of saffron production in Khorasan Razavi province in Iran.

**Methods :** In this study, the microbiological quality of 160 samples of Saffron which had been sent to the microbiology department of the Food and Drug Control Laboratory during the years 2018- 2021, determined according to the standard ISIRI#5689 -2018, “Microbiology of saffron – Specifications and test methods” . Preparation of samples and microbial tests performed based on ISO 6887-1:1999 (Preparation of test samples, initial suspension, and tenfold dilutions for microbiological examination) on MRD and ISO 4833:2003 (General guidance for the enumeration of microorganisms Colony-count technique at 30°C) on Plate Count agar, and ISO 21527-3: 2008(Yeasts and mold count) on YGC agar and ISO 7251:2005 (General guidance for detection and enumeration of presumptive E. coli) on L.S.Broth & E.C.Broth and TW medium .

**Results :** In summary, only 12 (7.5%) of 160 samples analyzed were unacceptable according to the ISIRI#5689 specifications for E. coli, , and TAMB (A.P.C) count rate of 8 (5%) of 160 samples were unacceptable according to the ISIRI#5689 Specifications and lowest contamination rate were observed in respect of molds count with rate of 3.1%, 5 from 160 samples , more than 5000cfu/. Eight (5%) surpassed the ISIRI#5689 limits for TAMB, and Five (3.12%) other samples surpassed the limit for molds count contamination

**Conclusion :** The results showed that there was the lowest level of contamination and non-compliance in saffron samples to Molds & TAMB (APC) and highest contamination rate to E.coli . Therefore, microbial contamination of saffron should be regarded as a mild health risk. This finding may be due to the unhygienic harvesting and other defects in good hygienic practices during transport and packaging and storage .

**Keywords :** SAFFERON, MICROBIOLOGY , E.COLI , APC ,mould,TAMB

# P189-401: Antimicrobial effect of Annatto pigment against Bacillus cereus, Salmonella enteritidis and Vibrio parahaemolyticus

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**Background and Aim :** Background: Over the past two decades, the disadvantages of synthetic dyes that are widely used in the food industry have been proven. The most important side effects of using these synthetic dyes are carcinogenicity, weakened immune system, urticaria, allergies, and decreased IQ. Therefore, in recent years, many efforts have been made worldwide to find natural pigments as an alternative to these synthetic dyes. Natural pigments do not have the effects of synthetic dyes, and in addition, various studies have shown their positive effects on public health. Annatto is one of these natural and safe pigment, which is composed of two components, Bixin and Norbixin, and has anti-mutation, anti-cancer and therapeutic properties.

**Methods :** In this study, Norbixin was used (water-soluble component of Annatto). To evaluate the antimicrobial effect, two methods of well diffusion and disk diffusion at different concentrations of Norbixin were used against Bacillus cereus (ATCC 11778), Salmonella enteritidis (PTCC 1291) and Vibrio parahaemolyticus (ATTC 17802).

**Results :** The results of disk diffusion method and well diffusion showed that this pigment has a strong inhibitory effect on both Vibrio parahaemolyticus (220 mm) and Bacillus cereus (223 mm). However, it showed a weak inhibitory effect on Salmonella enteritidis.

**Conclusion :** The results of the present study showed that Annatto pigment has a good inhibitory effect on both gram-positive and gram-negative bacteria. Considering that Annatto is natural and safe and also it's anti-cancer, antioxidant and therapeutic properties have been proven; therefore, this pigment can be used both as a natural pigment and as a natural preservative in various foods.

**Keywords :** Annatto, Antimicrobial, Bacillus cereus, Natural preservative

# P190-411: Assessment of bacterial contamination of the staff of juice shops in Mashhad

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**Background and Aim :** Consumption of handmade juices and traditional ice creams offered in juice shops is popular among the people, especially in the hot seasons. In case of negligence of health issues, juice or ice cream prepared by people contaminated with indicator bacteria. Consumption of contaminated juices is often associated with gastrointestinal disorders such as diarrhea. accordingly, in addition to the preparation process, the personal health of the people involved in the preparation of these juices is also significant.

**Methods :** ♣ In the present study, handmade juices and ice creams prepared in juice shops in Mashhad were collected during 1399. At the same time, people involved in the preparation process were asked to place their hands on a specific culture medium to identify the indicator bacteria involved in the microbial contamination of these products (Finger Test). Microbial tests performed to identify pathogenic bacteria such as Escherichia coli, Staphylococcus aureus, and mold and yeast counts, as well as coliform counts.

**Results :** ♣ Microbial assessment of 100 fruit juices was performed according to the standard provided by the Iran National Standards Organization. In the results, a large volume of samples was not in accordance with the standard, so that 95%, 80%, 53% and 22% of the samples in terms of coliform count, Escherichia coli contamination, mold and yeast count and coagulase-positive staphylococcus aureus contamination were higher than the standard, respectively. In the study of microbial load on the hands of staff, the identification of Staphylococcus aureus, coliform count and identification of Escherichia coli were significantly equal to the results obtained from the examination of juices.

**Conclusion :** ♣ In Iran, various studies have examined the level of contamination of hand-made juices, however, in none of these studies the level of microbial contamination in the hands of individuals. In this study most of the samples and also staff hands are contaminated with coliforms and were related to hands contamination. Same as this study, asadi et al, showed high contamination rate in ice cream (1). ♣ In a study conducted by Razavi et al. in Yazd the rate of microbial contamination in unpasteurized juices was 6% for Escherichia coli and 12% for coliforms. This result was lower than our result (2).

**Keywords :** Microbial contamination rate, juice contamination , food handlers

# P191-412: Safety and application of enterococci in functional foods

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**Background and Aim :** Enterococci as ubiquitous lactic acid bacteria commonly reside in the gastrointestinal tract and humans. They are gram-positive, facultative anaerobic, and non-spore forming lactic acid bacteria. These microorganisms are widely distributed in raw food products and the environment. This review indicate the safety and application of enterococci in functional foods.

**Methods :** The data of this abstract was collected based on ISI papers indexed in Elsevier and Springer publications.

**Results :** For many years, some species of enterococci are considered as opportunistic pathogens in nosocomial settings that cause bacteremia, urinary tract infections, and endocarditis. On the contrary, enterococci represent a promising group of microorganisms as probiotic and starter/adjunct cultures can improve aroma, texture, and flavor of fermented dairy products. They have specific biochemical activities, including lipolysis, proteolysis, and citrate and pyruvate metabolism. Therefore, enterococci provide new opportunities for the development of functional foods and nutraceuticals for human nutrition and immunostimulatory and hypocholesterolaemic impacts. The application of certain enterococcal strains in food has been permitted by Generally Recognized as Safe (GRAS) on the basis of a case-by-case assessment. Accordingly, strains considered for application in food products should not have any virulence determinants and should be susceptible to clinically relevant antibiotics.

**Conclusion :** Implementation of an appropriate risk/benefit analysis, establishment of a strain's innocuity, and consideration for relevant guidelines, legislation, and regulatory aspects surrounding functional food development, can help industry, health-staff and consumers accept enterococci, like other lactic acid bacteria, as important candidates for useful and beneficial applications in food biotechnology.

**Keywords :** Enterococci; Functional foods; Probiotic microorganisms

# P192-413: Application of biosensors for detection of food-borne bacterial pathogens

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**Background and Aim :** Owing to the green revolution in the past years, concerns for food safety and quality has increased importance. Nevertheless, the likelihood of contaminated food has also enhanced by bacterial food-borne pathogens and toxins. Raw food and food products are the potent transmitting agent of more than 250 known diseases. This review indicate the application of biosensors for detection of food-borne bacterial pathogens.

**Methods :** The data of this abstract was collected based on ISI papers indexed in Elsevier and Springer publications.

**Results :** Most important food-borne pathogens includes mycotoxins, exotoxins and enterotoxins from Escherichia coli O157:H7, Staphylococcus aureus, Shigella spp., Bacillus anthracis, Campylobacter jejuni, Clostridium perfringens, Clostridium botulinum, Salmonella spp., Listeria monocytogenes, Vibrio cholera, Yersinia enterocolitica, and Coxiella burnetii. Traditional methods for detection of bacterial pathogens are very sensitive and inexpensive but they are too laborious, time-consuming, and merely depend on the properties of bacteria to form frequent clones. Hence, there is an urgent need for the development of rapid, competent, and reliable approaches for direct detection and identification of food-borne microorganisms. Biosensors act as an indicator of biological molecules with the required features of on spot and multiple analyses systems. The most important microbe-based biosensing methods for detection of microorganisms including optical, surface plasmon resonance, amperometric, potentiometric, whole-cell, electrochemical, impedimetric, piezoelectric approaches.

**Conclusion :** It can be concluded that foreseeable future trends in biosensor research activities for paving the way for fresh and healthy food proposal.

**Keywords :** Biosensors; Food-borne pathogens

# P193-418: Antimicrobial effect of nanocarbons synthesis from glucose and starch on a number of food-borne pathogens

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**Background and Aim :** With increase of microbial resistance to antibiotics, many efforts have been made to find strong, low-resistance, low-cost antimicrobials to replace these compounds. Simultaneously with the advent of nanotechnology in medical science, researchers have tried to produce metal nanoparticles to produce antibiotics that, in addition to solving the problems of chemical antibiotics, have better effects on pathogenic microorganisms. However, due to the high cytotoxicity of metal nanoparticles, the production of green nanoparticles became one of the important issues in this field. Nanocarbons synthesized from organic compounds such as glucose and starch can be considered as a suitable alternative in this field due to their bactericidal and bacteriostatic properties and lack of cytotoxicity.

**Methods :** In this study, organic compounds such as glucose and starch were used to produce nanocarbons. Nanocarbon synthesis was performed by hydrothermal method (140 ° C for 6 hours). Also, to evaluate the antimicrobial effect of synthesized nanocarbons, by Well diffusion method from concentration of 0.2 molar glucose and starch against L. monocytogenes (ATCC 19115), Salmonella typhimurium (ATCC 14028) and Staphylococcus aureus (ATCC 25923) used.

**Results :** The results showed that nanoparticles synthesized from glucose and starch had a good antimicrobial effect on all pathogenic bacteria. So that the highest mean diameter of inhibitory at 0.2 M glucose was on Listeria monocytogenes, Staphylococcus aureus and Salmonella typhimurium with mean diameters of 14.36, 14 and 11.73 mm, respectively. Also, the inhibitory effect of glucose-synthesized nanocarbons were greater than starch-synthesized nanocarbons and the lowest level of inhibition was observed on Salmonella typhimurium.

**Conclusion :** The results of the present study showed that synthetic nanocarbons from organic compounds have strong antibacterial effects against all pathogenic bacteria. Therefore, due to the increasing antibiotic resistance of some pathogens as well as problems caused by metal nanoparticles such as cytotoxicity, so these synthesized nanocarbons can be a suitable alternative for different uses in medicine and the food industry.

**Keywords :** Nanocarbon, Glucose, Starch, Cytotoxicity, Antimicrobial

# P194-423: The possibility of enhancing the Conjugated linoleic acid (CLA) in ripened cheese containing sunflower oil using Lactobacillus plantarum spp. isolated from traditional fermented products

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**Background and Aim :** Conjugated linoleic acid (CLA) is an isomer of linoleic acid (LA) that is produced by the activity of some bacteria such as Lactobacillus plantarum and is considered due to its health properties today. Sunflower oil with about 30 to 70% linoleic acid can be a suitable and affordable for microbial CLA production. Therefore, increasing the amount of CLA in cheese as a high-consumption pragmatic product can be one of the best ways to deliver this beneficial fatty acid to people.

**Methods :** At the first step, the potential of CLA production by 17 strains of L. plantarum isolated from traditional fermented products (including 6 strains from traditional jug cheese, 3 strains from Iranian Lighvan cheese, 5 strains from fermented olives, 2 strains from salted olives, 1 strain from sourdough) and 1 strain of L. plantarum, was purchased from Persian type culture calcination were studied in MRS broth containing extra pure linoleic acid by spectrophotometric method. Then the strain with the highest production of CLA was applied as a co-culture in cheese production. Sunflower oil levels and co-culture were evaluated as experimental treatments. CLA content of the samples was analyzed by using the gas chromatography (GC).

**Results :** Lactobacillus plantarm strain isolated from sourdough was selected as the most CLA-producing strain from the screening step and used as a co-culture in cheese preparation. The results of GC showed that increasing the oil elevated the amount of CLA and the highest amount of CLA was in the control sample of cheese. Sensory evaluation showed, that the samples of cheeses containing sunflower oil had better sensory properties than cheese samples without oil.

**Conclusion :** So that, the manufacture of products higher in CLA content may be have a significant impact on human nutrition. ripened cheeses showed high nutritional quality, being a viable source of CLA for human consumption.

**Keywords :** Conjugated linoleic acid, Lactobacillus plantarum, ripened cheese, Sunflower

# P195-426: Bio-pigments as antibacterial, anti-tumor, antioxidant and pharmaceutical substances

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**Background and Aim :** Synthetic colors have been widely used in various industries including food, pharmaceutical and cosmetic. Accordingly many synthetic colorants have been banned or being banned due to their carcinogenicity and other toxicological problems. However toxicity problems caused by synthetic pigments have triggered intense researches in natural colors and dyes.

**Methods :** in this study, we searched for articles in google scholar, science direct databases using keywords such as: Bio- pigments, natural colorants, pharmacological, antibacterial and antioxidant.

**Results :** Among the natural sources, pigment produced by microorganisms hold a promising potential to meet current challenges. Natural colorants or dyes derived from microorganisms, flora and fauna are believed to be safe because of being non-toxic, non-carcinogenic and biodegradable in nature. On the other hand, currently, people interpret the content of synthetic products as contaminants and the tendency has been to products and natural pigment to cause pharmacological properties, antibacterial, antifungal, anti-tumor, antiviral and antioxidant activity reinforced. The number of advantages of using natural pigments over synthetic colorants has further boosted.

**Conclusion :** Natural pigments not only have the capacity to increase the marketability of products, but also display advantageous biological activities as antioxidants and anticancer attributes. Therefore, it is essential to explore further natural sources of colorants and their applications.

**Keywords :** Bio- pigments, Natural colorants, Pharmacological, Antibacterial, Antioxidant

# P196-430: Investigation of the possibility of increasing Conjugated linoleic acid in ripened cheese in salt water containing sunflower oil using yogurt starter as a co-culture in cheese

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**Background and Aim :** Conjugated linoleic acid (CLA) are the geometric and spatial isomers of linoleic acid (LA) in which the double bonds are in the conjugated state. Its anti-cancer properties, reduction of body fat and improvement of immune function are its health effects. As a high-consumption dairy product, cheese can provide public access to this micronutrient. In several studies, the strains in yogurt starter have been identified as producing CLA. Sunflower oil with a high percentage of LA is an affordable source of CLA precursor; Therefore, it can be used to increase the CLA content in cheese.

**Methods :** At the first step, a pre-test based on the potential of CLA production by yogurt starter was performed in MRS broth containing extrapur LA by spectrophotometry method and after confirming the production of CLA in MRS broth by GC, it was used as a co-culture in cheese production. CLA production was measured at two oil levels (1and2 %), with or without yogurt starter (as co-culture) and ripening length by using the gas chromatography (GC).

**Results :** The results showed that the highest amount of CLA production was related to cheese containing 2% sunflower oil before reaching the end of the ripening period. Examination of GC data showed that increasing the arrival time reduced the CLA. On the other hand, increasing the oil in cheese has increased the amount of CLA produced.

**Conclusion :** Using food as a pragmatic product to deliver CLA to the body is better than its medicinal form. Therefore, increasing the amount of CLA in cheese by adding oil in its formulation as a high-consumption dairy product can be one of the best ways to deliver this beneficial fatty acid to people.

**Keywords :** CLA, Sunflower, yogurt starter, co-culture, cheese

# P197-440: The antimicrobial efficacy of Mentha oil nanoemulsion on some of the food-borne pathogens

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**Background and Aim :** Concerns about the use of some chemical preservatives and the negative reaction of consumers to the use of these substances have led to increased attention to natural preservatives, including plant essential oils as alternatives to chemical preservatives. Nanoparticles of essential oils have been proposed to eliminate the shortcomings related to the use of essential oils in food and strengthen its antimicrobial properties. This study aimed to determine the effect of nanoemulsion of peppermint essential oil on its antimicrobial properties against some pathogenic microbes of food origin.

**Methods :** For this purpose, the essential oil of the mint plant, which was prepared by Najian Tabriz Company, was used. Thirteen samples of nanoemulsions were prepared from the purchased essential oil. Bacillus Cereus, Escherichia Coli, Salmonella Enterica and Staphylococcus Aureus were used in this study.

**Results :** The minimum inhibitory concentration and the minimum bactericidal concentration of free and nano emulsified essential oil were evaluated by the microdilution method. Particle size and zeta potential were also evaluated by a dynamic light scattering device. Antioxidant inhibition was also measured by diphenyl hydroxy picryl-hydrazine. The minimum growth inhibitory concentrations of free essential oil against Staphylococcus Aureus, Bacillus Cereus, Escherichia Coli and Salmonella Enterica were 31.25, 62.5, 250, and 250 µg / ml, respectively, while in the case of nanoemulsion against all of the above bacteria it was 50 micrograms per milliliter. The minimum bactericidal concentrations of free essential oil were 31.25, 62.5, 250, and 250, respectively, and in the case of nanoemulsion against all the above bacteria was 50 µg / ml. Regarding the antioxidant inhibition of essential oil containing peppermint nanoparticles, it had poor antioxidant properties unlike essential oil without peppermint nanoparticles. In the case of the zeta potential, the particle size of the prepared compound is

260 nm, and the single peak indicates that the particles are monodispersed. In addition, the zeta potential is -5.67 mV, which indicates the surface charge of the nanoparticles, which can be a parameter of nanoparticle stability.

**Conclusion :** In general, it can be said that nanoparticles of peppermint essential oil by nanoemulsion method strengthens its antimicrobial properties, especially against gram-negative bacteria.

**Keywords :** Mentha, Food-borne pathogens, Nano, Antimicrobial efficacy

# P198-67: An overview of the modulatory effects of probiotics in infectious diseases by regulating the immune system

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**Background and Aim :** Extensive use of antibiotics has been used for many years to inhibit and eliminate microbial agents and enhance the growth of livestock and poultry. In the long term could cause antibiotic resistance. Probiotics can be considered as an ideal alternative to antibiotics that have attracted attention during pathogenic infections in humans and animals, with an emphasis on regulating the immune system.

**Methods :** This study is a review that by searching the electronic sources of PubMed, Science Direct, and Embase, by using the keywords probiotics, infectious diseases, antibiotics, antibiotic resistance from 2015 to 2021 and 63 articles related were found and then analyzed.

**Results :** The results indicate that if probiotics are taken in sufficient quantities, they have good health effects on the host body and also play an important role in regulating the immune system response in the host body during infectious diseases.

**Conclusion :** Probiotics are live microorganisms that are non-pathogenic beneficial by modifying the gut microbiota and immune system modulators have a positive impact.

**Keywords :** Probiotics, Infectious diseases, Antibiotics, Antibiotic resistance.

# P199-68: Investigation of the structure and mechanism of action of COVID-19 and The effect of microbiome and probiotics in its treatment and prevention

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**Background and Aim :** COVID-19, a novel infectious disease, caused by SARS-CoV-2, affected millions of people around the world with a high mortality rate.,The present review emphasizes the latest research related to COVID-19, it caused an excessive inflammatory cytokine storm and could be the main cause of increased vulnerability in the frail population. In patients with diabetes and/or heart disease, and elder. Coronavirus Disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a Public Health Emergency of International concern and has been associated with rapidly progressive pneumonia. in this study, we discuss the possible biological, physiopathological, and clinical implications of gut microbiota in COVID-19 and probiotics effect in coronavirus.

**Methods :** در این بررسی اجمالی در سایتهای Elsevier-Pup med- ncbi- nature-researchergate- با کلمات کلیدی Mechanism of action-virous covid-19-probiotic- microbiom به بررسی و مطالعه پرداختیم

**Results :** People with good natural immunity overcome the burden of the virus. like the We know that the gold standard for healthy and strong safety lies In bowel functions and diet. Nutritional probiotics and immune boosters that work in intestinal homeostasis The research focused on the special role of probiotics in natural enhancement Killer cell function, stimulation of IgA antibodies and mucosa Barrier, inflammation control increases the interest of the new generation, Probiotics boost immunity to treat COVID-19 viruses. And maybe if the bacteria are manipulated, we can produce probiotic bacteria that can produce antibodies against covid-19 in our intestine

**Conclusion :** As per the literature review of COVID-19 cases, it is evident that people with good natural immunity overcomes the virus load. As we know, the gold standard for healthy and robust immunity lies in the gut and diet functions. The nutritional and immunity-enhancing probiotics operating homeostasis in the gut must be paid research attention to. Regular physical exercise, a healthy lifestyle, and probiotics supplementation can be prominent players inducing immunity. The specific role of probiotics to enhance natural killer cells' function, stimulation of IgA antibodies, and mucosal barrier inflammation control promoted an interest in new generation probiotics to strengthen immunity to treat COVID-19 viruses.

**Keywords :** Researchergate googlscholar Scincedirect-ncbi pupmed با کلمات کلیدی covid-19-probiotic- microbiota Mechanism of action-virous microbiom به بررسی و مطالعه پرداختیم.

# P200-103: Evaluation of E. coli Nissle 1917 as a novel probiotic in growth inhibitory of clinical Pseudomonas aeruginosa strains

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**Background and Aim :** Escherichia coli Nissle 1917 (EcN; O6: K5: H1) as a probiotic is attributed to a non-pathogenic and commensal E. coli. Special characteristics of this strain are the production of several antimicrobial substances such as microcins and β-defensin-2. Gut-microbiota, by producing metabolites and conveying them to the host, plays a crucial role in the management of homeostatic and health conditions in the host.

**Methods :** E. coli Nissle 1917 (EcN; Ardeypharm GmbH, Herdecke, Germany) strain was grown in Lauria-Bertani (LB) broth overnight at 37°C with shaking (150 rpm). The cell-free supernatant was prepared according to the method proposed by Ogunbanwo. Fresh overnight pathogenic bacterial cultures were inoculated into Mueller Hinton Broth in 96-well plates. The cell-free supernatant of E. coli Nissle1917 was prepared in different concentrations. Next, 100 µl of each clinical pathogenic bacterial culture along with standard strain and 100 µl of cell-free supernatant at various concentrations were mixed in each well in a final volume of 200 µl. The lowest percentage of supernatant that can affect inhibition of growth bacteria was considered as the minimum inhibitory percentage (MIP).

**Results :** RThe antimicrobial effect of E. coli Nissle1917 metabolites against 10 clinical Pseudomonas aeruginosa and reference strain was characterized by the agar well diffusion assay. Zones of inhibition against all clinical samples and the standard strain showed that some clinical strains had significantly better inhibition zones compared to the other clinical strains. This result can reflect the different properties of each strain.

**Conclusion :** Numerous studies have confirmed the inhibitory effect of different probiotics on various pathogenic strains. As well as our studies have shown E. coli Nissle1917 as a probiotic can have an inhibitory effect on clinical Pseudomonas aeruginosa strains. The supernatant of our probiotic evaluated in different concentration and our data demonstrated that they can result in growth inhibition in Pseudomonas aeruginosa strains.

**Keywords :** Probiotic, E.coli, Pseudomonas aeruginosa, MIC

# P201-104: Isolation and identification of potential probiotic Lactobacillus species from feces of infants in southwest Iran

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**Background and Aim :** To evaluate the potential probiotic properties of Lactobacillus strains isolated from feces of infants and also to determine their antimicrobial activity against some enteropathogenic bacteria.

**Methods :** The Fecal samples were prepared from 120 infants aged less than 24 months. In total, 105 Lactobacillus strains were identified by phenotypic tests. Thirty isolates were randomly selected to study their potential probiotic properties. These isolates were examined for resistance to acid (pH: 2.5, 2 h) and bile (oxgall 0.3%, 8 h), adhesion to HT-29 cells, antibiotic susceptibility, and antimicrobial activities.

**Results :** On the basis of 16S rRNA sequencing, 30 isolates identified as Lactobacillus fermentum (n = 11; 36.7%), Lactobacillus plantarum (n = 9; 30%), Lactobacillus rhamnosus (n = 6; 20%), and Lactobacillus paracasei (n = 4; 13.3%). All tested strains survived at acid and bile conditions. Six Lactobacillus strains revealed high adherence to HT-29 cells. Three strains including the L. fermentum (N2, N7), and the L. plantarum (N20) showed good probiotic potential and inhibited the growth of Yersinia enterocolitica ATCC 23715, Shigella flexneri ATCC 12022, Salmonella enterica ATCC 9270, and enteropathogenic Escherichia coli (EPEC) ATCC 43887. The antibiotic resistance test showed that all the isolates were susceptible to tetracycline, and chloramphenicol.

**Conclusion :** Lactobacillus strains like L. fermentum (N2, N7), and the L. plantarum (N20), could be potential probiotic, but further in vitro and in vivo studies on these probiotic strains are still required.

**Keywords :** Lactobacillus; Adhesion; Probiotic; Enteropathogens

# P202-134: Isolation of probiotic Lactobacilli from local dairy products in Tehran province

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**Background and Aim :** Probiotics are live bacteria with valuable properties on genital and gastrointestinal health. The growth in the consumption of industrial dairy products instead of the traditional ones may enhance the possibility of missing the probiotic bacteria. The aim of this investigation is to isolate lactobacilli from local cheeses and yogurts produced in rural areas of Tehran province and also to assessment their antibacterial profile against common pathogenic bacteria.

**Methods :** In current study, 25 samples of local yogurts and cheeses from three separated rural areas were collected. Probiotic lactobacilli were isolated using MRS medium, selective screening methods, catalase test. Additionally resistance to bile and acidity and some relevant biochemical tests were carried out. Bactericidal effects of the isolated probiotics against Staphylococcus aureus, Escherichia coli, Pseudomonas aeruginosa, and Salmonella typhimurium were assessed by using disk diffusion and well diffusion agar methods.

**Results :** Out of the 25 cheese and yogurt samples, 12 isolates of acid-stable lactobacilli were selected at the first stage. At the next stages, 5 isolates of acid-stable and bile-stable lactobacilli were isolated including: L. rhamnosus (in two places) L. casei, L. plantarum, and L. acidophilus. While the growth of the pathogenic bacteria was suppressed by all 5 lactobacilli, L. casei and L. plantarum showed the strongest bactericidal effects.

**Conclusion :** Local products may have probiotic bacteria with beneficial properties. These bacteria can be used for mass production of industrial dairy products.

**Keywords :** Probiotic Bacteria, Antimicrobial, Local dairy products.

# P203-291: Biochemical and molecular identification of lactobacillus isolated from traditional Maragheh yogurt

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**Background and Aim :** Probiotics are known as beneficial microorganisms that their consumption in adequate amounts provide health effects for the host. Lactic acid bacteria (LAB) are the most common type of probiotics. Probiotics have demonstrated significant potential as therapeutic options for a variety of diseases, but the mechanisms responsible for these effects have not been fully elucidated yet. The aim of this study was to identify and evaluate the probiotic properties of isolated bacteria from traditional Maragheh yogurt via phenotypic and genotypic characteristics.

**Methods :** After collecting, the traditional yogurt samples were isolated by culturing on MRS broth and agar media contained. The isolate was evaluated through microbial and biochemical tests including gram staining, catalase and oxidase activity, fermentation of carbohydrates, and acid and bile salts resistance. Moreover, the isolated bacteria was evaluated by 16s rRNA gene amplification of lactobacilli. The asparaginase and glutaminase production was evaluated by qualitative method.

**Results :** The isolated bacteria showed the characteristics of gram-positive, catalase- and oxidase-negative. Furthermore, it could be able to grow at bile salts and acidic pH and showed no hemolysis. Based on 16S rRNA gene amplification, it was identified as Lactobacillus. Moreover, the production of asparaginase and glutaminase was confirmed.

**Conclusion :** : Lactic acid bacteria isolated from traditional Maragheh yogurt showed probiotic potentials. It could be a good candidate to use in in food and pharmaceutical industries.

**Keywords :** Probiotics, Lactic Acid Bacteria, Traditional yogurt

# P204-292: Isolation and Characterization of Effective Probiotics against Drug-Resistant Acinetobacter Strains

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**Background and Aim :** Today, with the increase of nosocomial infections caused by opportunistic gram-negative pathogens such as Acinetobacter and the indiscriminate use of antibiotics, multidrug resistance has increased, following the increase in antibiotic resistance and side effects. From the use of chemical drugs, the use of alternative therapies seems necessary. Therefore, probiotics and their metabolites, including organic acids and bacteriocins, can be widely used in therapeutic applications. The emergence of antibiotic-resistant and foodspoilage microorganisms has renewed efforts to identify safe and natural alternative agents of antibiotics such as probiotics. The aim of this study was to Isolation and Characterization of Effective Probiotics against Drug-Resistant Acinetobacter Strains.

**Methods :** First, over a period of six months, 100 samples of Acinetobacter were collected from four main hospitals in Isfahan, and after determining the antibiotic susceptibility test in them, 53 strains of Acinetobacter were resistant to carbapenem and 6 strains of Acinetobacter were resistant to colistin. The antimicrobial effect of 20 different probiotic bacteria isolated from dairy products against Acinetobacter was investigated by diffusion method in plate well and biofilm formation was investigated by three different methods.

**Results :** The results showed that one probiotic strain isolated from local yogurt in Isfahan province was resistant to all strains of Acinetobacter and by hot staining it was determined that the bacterium Lactobacillus and the colony form is a non-diphtheria bacillus. The lethal and inhibitory effects of this probiotic on the killing of resistant strains were confirmed. The results showed that this probiotic killed pathogenic bacteria only after 1 hour and its inhibitory mechanism was due to organic acids such as lactic acid and acetic acid.It was resistant to bile acid and low pH tolerance. Various pathogenicity tests, including catalase, hemolysis, CAMP, Dnase, and antibiotic susceptibility to the probiotic strain indicate lack of pathogenicity and lack of antibiotic resistance.

**Conclusion :** The results were demonstrated by high performance liquid chromatography (HPLC) analysis Its inhibitory effect was due to the production of two main organic acids

including lactic acid and acetic acid. Due to the widespread activity of this strain, it can be potentially used in the biological control of drug-resistant Acinetobacter strains.

**Keywords :** Antibiotic resistance, Acinetobacter, Gram negative bacteria, Drug, probiotic

# P205-312: Biochemical and molecular identification of probiotic bacteria isolated from traditional Maragheh buttermilk

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**Background and Aim :** : Probiotics are defined as living microorganisms, when ingested in sufficient amounts provide health benefits for the host. The two main types of probiotics are Lactobacillus and Bifidobacterium. Probiotics can be used in the form of powders, syrups, tablets and fortified foods. Application of probiotics and prebiotics as biotherapeutics is the new field in developing dietary strategies.

**Methods :** To identify the isolated bacteria, microbial and biochemical tests including gram staining, catalase and oxidase activity, sugar fermentation of carbohydrates, antibacterial tests and acid and bile salts resistance were performed. The asparaginase and glutaminase production was evaluated by raid plate assay. Also, bacterial DNA was extracted and 16S rRNA gene was amplified through PCR using universal primers.

**Results :** The results confirmed the isolated bacteria as a probiotic including; gram-positive, catalase- and oxidase-negative, grow at bile salts and acidic pH and no hemolysis. Based on 16S rRNA gene amplification, it was identified as Lactobacillus. Furthermore, the production of therapeutic enzymes asparaginase and glutaminase was verified.

**Conclusion :** The isolated bacteria from traditional buttermilk confirmed as lactobacillus and further experiments about asparaginase and glutaminase production are running.

**Keywords :** Buttermilk, Lactobacillus, Probiotic, 16s rRNA

# P206-318: Assessment of the anti-biofilm capacity of Lactobacillus plantarum strains isolated from kefir dough against streptococcus mutans

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**Background and Aim :** The Streptococci are the pioneer strains in plaque formation and Streptococcus mutans is the main etiological agent of dental plaque and caries. Probiotics can release bioactive substances that can inhibit the growth and biofilm formation of pathogenic microorganisms. Among of those probiotic bacteria Lactobacillus plantarum has been proposed that boost oral health. The present study focus on determination of the L. plantarum supernatants on biofilm formation of S. mutans (ATCC35668).

**Methods :** In this experimental study, we isolated 5 strains of L. plantarum from local kefir dough of Isfahan region were used as probiotic which were cultured at 37°C in anaerobic condition, then identified using morphological characteristics, biochemical tests and PCR technique. Biofilm formation was detected by crystal violet assay using 96 well microtiter plate.

**Results :** All 5 Lactobacillus strains showed anti-biofilm activity on S. mutans. L. plantarum which isolated from five different sources demonstrated variable effect on biofilm from five times reduction to nine times. They demonstrated significantly reduction on biofilm.

**Conclusion :** It seems that supernatant of the probiotics isolated from kefir dough can be used as an antibiotic alternative to decrease the chance of dental caries.

**Keywords :** Supernatant, Streptococcus mutans, Kefir dough, Probiotics, Lactobacillus plantarum, Anti-biofilm

# P207-333: The effect of probiotics on immune system function: Focus on studies in Iran

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**Background and Aim :** Probiotics are living microorganisms with many benefits for the health if consumed in sufficient and appropriate amounts; One of the main and important mechanisms of action of these bacteria is host immune system regulation. In this article, the effects of probiotics on immune system functions would be presented with focus on studies have been conducted in IRAN.

**Methods :** The search in reputable scientific sites and journals with suitable key words.

**Results :** There are many findings with relatively extensive diversity about the effects of probiotics on immune system functions, but could be summarizes as the following: 1. Extensive effects of probiotics on different parts of immune system: The functional ability of probiotics on immune system include: initiation of mucosal / systemic immune responses, modulation of the innate / adaptive immune system, stimulation of cytokine secretion etc. 2. Probiotics can increase protection against the pathogens and improve the effectiveness of the vaccine. 3.Beneficial effects of probiotics on some important disorders such as cancer, allergy and autoimmune diseases via modulation of immune functions. Studies have confirmed the effect of probiotics in the potential prevention of cancer or as adjunctive therapy during chemotherapy. In addition, probiotics improve allergy symptoms by modulating the Th1 / Th2 balance. 4.There are some publications about molecular mechanisms for elucidation of probiotic effects. A review of recent studies in Iran and other studies suggests that probiotics may reduce NF-κβ activation and the production of proinflammatory cytokines. Probiotics have also been shown to increase intestinal barrier function by stimulating B cells and stimulating the production of immunoglobulin A. Some species of probiotic bacteria, such as Lactobacillus, play an important role in innate immunity by increasing the activity of natural killer cells and macrophages, and by interacting with dendritic cells and enterocytes. 5.The effects of probiotics on immune system are partially species-specific and dose-dependent.

**Conclusion :** The beneficial effects of probiotics on immune system functions have been verified, but more studies are needed to get the optimal use of probiotics.

**Keywords :** Probiotics, Microbiota, Allergy, cancer, immunomodulation

# P208-349: The probiotic safety assessment for incidence of virulence in lactic acid bacteria isolated from different regions of Iran

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**Background and Aim :** A large variety of bacteria are intentionally added to the food supply. These include starter cultures for the production of fermented foods and probiotics in food and dietary supplements. Since these bacteria are typically viable when consumed, considerable characterization is required to ensure the absence of undesirable properties

**Methods :** In this study, 244 strains from different sources of traditional dairy products such as, yogurt, yogurt drink, milk, and butter were collected from different regions of Iran. 20 out of 244 LAB isolates were selected due to their primary probiotic properties (resistance to low pH, bile tolerance, and tolerance to pepsin and trypsin) and identified by phenotypic and 16S rRNA gene sequence analysis. The 20 isolated species were assessed for the incidence of virulence determinant genes (gelE, efaAfm, efaAfs, ace, espfs, cylM, cylA and cylB), and phenotypic action of gelatinase

**Results :** The incidence of virulence genes was determined by polymerase chain reaction and Enterococcus faecalis ATCC 11700 was used as positive control. The dominant bacterial genera isolated were Lactobacillus, Lacticaseibacillus, and Bifidobacterium. Also, the results of this study showed no virulence genes for all 20 isolated species. Also, the phenotypic study of gelatinase proved the deficiency of gelE gene in all strains.

**Conclusion :** The results of this study showed that candidate isolates as probiotics are safe in terms of pathogenic potential. However, for further assessment, it is recommended that whole-genome sequencing of each strain be performed.

**Keywords :** Probiotic, Virulence, Lactic Acid Bacteria, fermented food, 16S rRNA

# P209-350: Characterization and screening of the potential probiotic lactic acid bacteria strains isolated from traditional dairy products

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**Background and Aim :** Probiotics are living microorganisms that provide beneficial properties to the host. Due to their health properties, they are widely used in the pharmaceutical and food industries. Traditional dairy products are the natural habitats of microbes, especially lactic acid bacteria (LABs). Lactic acid bacteria are the largest group of probiotics. These bacteria must tolerate to harsh gastrointestinal conditions until they reach the target point, and then they can offer their physiological activities and beneficial capabilities.

**Methods :** The aim of this study was to screen and select potent probiotic LAB strains isolated from different traditional dairy products and to evaluate the feasibility of their use in the production of probiotic products. From 120 samples collected from different dairy products, 180 bacterial isolates were isolated in four different media. Probiotic characteristics of isolated bacteria were determined based on acid tolerance, bile tolerance, and tolerance to digestive enzymes pepsin and trypsin tests.

**Results :** Of the 180 isolates studied, 23 microorganisms were resistant to bile, 5 isolates were resistant to acid, pepsin, and trypsin. These five resistant isolates were identified by 16S rRNA gene sequence analysis as Lactobacillus delbrueckii (n=2), Lactobacillus acidophilus (n=1), Lactobacillus gasseri (n=1), and Lacticaseibacillus rhamnosus (n=1).

**Conclusion :** In the present study, the isolated lactic acid strains had good probiotic potential and high resistance at low pH and digestive enzymes. Further studies such as the safety assessment of these strains are needed to introduce these samples as probiotic strains.

**Keywords :** Probiotics, Lactic acid bacteria, traditional dairy productsi, Lactobacillus.

# P210-405: Antibiotic resistance in Lactobacillus sp. isolated from probiotic yogurts

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**Background and Aim :** Recently The use of probiotic products has increased, due to their beneficial effect on human health. The overuse of antibiotics has led to increasing resistant bacteria. Lactobacillus(L.b) may act as reservoirs of antibiotic resistance genes and transfer to pathogen bacteria or microflora. This study aimed to assess the antibiotic resistance among Iranian commercially available probiotic yogurts.

**Methods :** Thirty Iranian probiotic yogurt samples were selected, then de Man Rogosa and Sharpe (MRS) media were used for isolating Lactobacillus Sp. After purification of colonies by Streak plate method, L.b colonies were identified for morphology, gram staining, and biochemical tests (catalase, oxidase, fermentation of various sugars, methyl red, motility test, indole test). The disk diffusion method was used to detect the resistance of strains to erythromycin, tetracycline, chloramphenicol, vancomycin, gentamycin, ciprofloxacin, streptomycin, ceftriaxone according to the CLSI method.

**Results :** Resistant bacteria were determined based on the inhibition zone diameter, using flowing breakpoints: for vancomycin and tetracycline less than 14 mm, for ceftriaxone, chloramphenicol, streptomycin, and erythromycin less than 13 mm, for gentamycin less than 12 mm and streptomycin less than 11 mm inhibition zone diameter was categorized as a resistant. The isolates showed a high level of resistance toward vancomycin (26/30), gentamycin (27/30), ciprofloxacin (27/30), and streptomycin (29/30). None of the strains showed resistance to erythromycin, tetracycline (4/30 intermediate), chloramphenicol, ceftriaxone (9/30 intermediate).

**Conclusion :** Due to the observed antibiotic resistance, it is highly recommended to evaluated antibiotic resistance Lactobacillus strains before using in yogurt preparation.

**Keywords :** probiotic, Lactobacillus, antibiotic resistance

# P211-435: Effects of probiotics on lipid profile in patients with type-2 diabetes mellitus: A narrative review

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**Background and Aim :** Probiotic supplementation seems to be an effective approach in treatment and management of type-2 diabetes mellitus (T2DM). Dyslipidemia is a major concern in T2DM, affecting the cardiometabolic status in these patients. A growing number of studies suggest that modification of the gut microbiome through probiotics may improve the lipid profile in T2DM. The effectiveness of probiotic interventions and the underlying mechanisms are still unclear. Therefore, in this review, we aimed to evaluate the effects of probiotics on lipid profile among patients with T2DM.

**Methods :** A search was conducted on PubMed, Cochrane Library, and Web of Science databases from 2011 to 2021 using the terms "probiotics", "lipid profile", "type-2 diabetes", and " gastrointestinal microbiome".

**Results :** Probiotics supplementation significantly decreased total cholesterol, LDL-c, VLDL, LDL/HDL ratio, and triglycerides and increased HDL-c in patients with T2DM, although there is still some recent evidence showing no effects of probiotics on the lipid profile of these patients. Furthermore, the most common probiotics strains were lactobacilli acidophilus and Bifidobacterium. These probiotics also significantly reduced the levels of systemic endotoxin through modifying the gut microbiome composition and strengthening the intestinal epithelial barrier function, which is regarded as a potential underlying mechanism of probiotics effect on lipid profile. Longer trials and multi-strain probiotics were more efficient and modified a higher number of lipid and cardiometabolic factors.

**Conclusion :** Finally, our findings suggest that probiotic supplementation is a potential candidate for adjuvant therapy in managing dyslipidemia of patients with T2DM. Lack of microbial and gene expression data assessments, different probiotic doses, small sample sizes, and combination with drug therapy were among the most important challenges leading to discrepancies between different studies. Therefore, further human studies are required to overcome these challenges, confirm these findings, and provide optimized protocols to manage lipid profile in T2DM patients.

**Keywords :** Probiotics- Type 2 Diabetes Mellitus- Dyslipidemia- Gastrointestinal Microbiome

# P212-436: The effect of probiotics in improving viral infections: focusing on COVID-19

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**Background and Aim :** Respiratory tract infections (RTIs) are one of the most common infectious diseases of viral or bacterial origin. Coronavirus disease 2019 (COVID-19) is an emerging epidemic. The lack of effective classical treatment for COVID-19 has led to a focus on other strategies for achieving prevention and treatment of infection. One of these cases is the use of beneficial microbes. Due to the beneficial effect of intestinal microbiome in creating immune responses in distant mucosal areas; Including the lungs, the use of probiotics in the prevention and treatment of infections has been considered, and in this article, their effect on respiratory infections has been considered.

**Methods :** The search in reputable scientific sites and journals with suitable key words.

**Results :** Evidence supports the role of probiotics in regulating the immune system, both intrinsic and acquired. Probiotics have shown a positive response in the clinical treatment of several diseases; Reduce the severity of infection in the upper respiratory tract. Reduction of viral load in vivo has been well established using Lactobacillus. Studies have shown the antiviral activity of probiotic species against common respiratory viruses such as rhinovirus, influenza and respiratory syncytial virus. The effects of probiotics on several species of coronavirus have been reported in various studies. Probiotics can be an effective strategy for treating patients with COVID-19 to reduce secondary infection and modulate immunity. They can also prevent COVID-19 by preserving the human gastrointestinal tract or lung microbiota because dysbiosis plays an important role in susceptibility to infectious diseases. Probiotics can also reduce the spread of Coronavirus through the gut. Some probiotic components can bind to virus-receptor proteins: spike proteins and ACE2 and prevent the virus from entering the host body; however, these probiotic species have not yet been administered to the respiratory tract.

**Conclusion :** Despite reports of the effects of probiotics on several coronavirus species, these mechanisms have not yet been seriously investigated for the new SARS-CoV-2. Further studies are needed to evaluate the ability of probiotics to fight COVID-19.

**Keywords :** Probiotics , Microbiota, , COVID-19, Respiratory

# P213-39: Creating an Efficient Strain for Purity of TEV-Labeled Recombinant Proteins

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**Background and Aim :** Peptide tags are protein sequences that are used in recombinant proteins mainly in order to increase the solubility or facilitate the purification of the proteins.. Generally, the used tags need to be removed accurately and appropriately after the production and purification of the recombinant proteins. Using the some proteases such as TEV protease is a common method to remove the fusion tags. This protease is a highly sequence-specific cysteine protease, produced by Tobacco etch virus (TEV) and considered as one of the best endpeptidases for removing of the tags. Accordingly, in the present study, a plasmid was constructed that exclusively encoded TEV protease using arabinose as the inducer. This vector was independent of the vector used to express the recombinant protein. In this plasmid, TEV encoding sequence was located under the BAD promoter, and p15A Ori, which is compatible with pBR322 Ori in pET expression vectors was used. We also used Neo-Kna resistance gene in the plasmid that allows the selection of transformed bacteria that already had pET vector with Amp resistance gene.

**Methods :** First, the specific primers that contained suitable restriction enzymes at the 5' ends were designed for amplification of GST tagged TEV coding fragment (GST.TEV) form pGEX-4T1 vector. Amplified GST.TEV was cloned into a T vector and subsequently sub-cloned into the expression vector pBAD-GIIIA, called pBAD/GST.TEV. The transcription terminator (TT) sequence was then amplified from pBAD-GIIIA vector by proper primers and sub-cloned downstream of GST.TEV fragment in the pBAD/GST.TEV. The resulted vector was named pBAD/GST.TEV/TT. Moreover, the coding sequence of neomycin-kanamycin phosphotransferase (Neo-Kan) was amplified from pEGFPC1 vector by the suitable primers and was sub-cloned in pBAD/GST.TEV/TT, downstream of transcription terminator that resulted pBAD/GST.TEV/TT/Neo-Kan. At the end, the p15A Ori segment was amplified from the pG.TF2 vector by designed primers and sub-cloned into pBAD/GST.TEV/TT/Neo-Kan downstream of Neo-Kan fragment. The constructed final vector was pBAD/GST.TEV/TT/Neo-Kan/p15AOri, which was briefly called pBAD/GST

**Results :** In this study, a new subspecies of Shuffle T7 Express E. coli was obtained by transformation of an expression plasmid, which could produce the soluble and active TEV protease

**Conclusion :** This protease could cleave its specific site between TRX and IGF-1 in the host bacterial cells and separate TRX tag from the recombinant IGF-1, which was expressed by an independent pET vector

**Keywords :** E. coli, Expression vector, Fusion protein, Protein tag Recombinant protein, TEV protease.

# P214-56: The Utilization of modern biotechnology methods for the protection of Persepolis World Heritage Site

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**Background and Aim :** In the last few decades, the development of biotechnology has led to the development of revolutionary techniques useful for diagnosing the deterioration of cultural heritage caused by microorganisms and developing successful conservation/restoration methods. Certainly, biotechnology is a great resource for setting up effective strategies that are safe for works of art. the main purpose of this study was to investigate the microorganisms involved in biodegradation. This study is based on genomic DNA analysis and metabolic byproducts.

**Methods :** DNA was extracted using the FAVORGEN kit. PCR was performed utilizing specialized primers 27 F and 338R. Then, All samples were sequenced by the NGS method. Some samples were prepared for studies related to the substrate and the effect of microbial secondary metabolites on them and studies for mineral bio colonization, were analyzed using XRD, ICP, and FTIR/ATR methods.

**Results :** Results of this study suggest that the range of factors involved in Persepolis biodeterioration is not confined to macro-level factors. The results indicated that a variety of heterotrophic bacteria, microscopic algae, meristematic fungi, and cyanobacteria are present in Persepolis. The chemical analysis results confirmed the presence of carbonic acid due to the presence and activity of microorganisms in this calcareous environment, which in turn causes corrosion in the substrate.

**Conclusion :** Our studies showed that the hidden life of microorganisms on the surface of Persepolis rocks is a serious threat to this monument. furthermore, the Secondary metabolites provide further evidence for colonization and biodeterioration.

**Keywords :** Biodeterioration, Microorganisms, Biotechnology

# P215-60: Growth assessment of Auricularia auricula in two diffrent substrates containing sawdust and wheat straw

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**Background and Aim :** Auricularia auricula, the Jelly Ear Fungus, is mainly seen in winter and spring. It grows mainly on dead elder trees and on fallen branches, but occasionally you may also find it growing on other kinds of hardwood. The so-called Jelly Fungi are not really a taxonomic group but more a rag-tag of basidiomycetes with jelly-like textures, although few are a soft as the jelly we eat with custard. Many are capable of reconstituting and continuing to produce spores when wetted after desiccation

**Methods :** This process consists of solid culture substrates, such as wheat straw and sawdust with a certain percentage of rice bran. The spawn of A.auricula was prepared on sorghum grain+wheat bran (3:1) substrate. 250 gram of the substrate with 60 percent of moisture was filled in poly propylene bags of size 12”×12” (80 gauge thickness) and autoclaved at 121atm pressure for 20 min. After sterilization, the bags were inoculated with 100g of spawn each and incubated at 25-28°C

**Results :** According to the results, solid culture bed containing 90 percent of sawdust and 10 percent rice bran has the high amount of biomass production in the Auricularia fungus.

**Conclusion :** All the results presented here suggest that Auricularia auricula can grow in sawdust solid substrate better than the wheat straw substrate because this fungus has a lignin peroxidase, so it can degradate the lignin in this solid state

**Keywords :** Auricularia auricula - sawdust - solid substrate

# P216-81: Evaluation of Rapeseed Meal, Soybean Meal, and Fertilizer (NPK) Amendment on Improving Enzymatic Activities of Diesel-Contaminated Soil

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**Background and Aim :** Introduction: Soil contamination with recalcitrant organic compounds like diesel created widespread environmental complications. So, clean-up strategies are required to remediate the contaminated site. Biostimulation, adding nutrients to a contaminated site to stimulate the growth of the indigenous soil microbial community, is known as effective bioremediation strategy to accelerate bioremediation process

**Methods :** Material and Method: Soil sample was collected from an arable land of Pistachio farm, Damghan. The pristine soil was manually contaminated with the diesel. The effect of amending rapeseed meal (BS1), soybean meal (BS2), and fertilizer (NPK-BS3) as biostimulants was studied on pH, catalase and dehydrogenase activities of diesel-contaminated soil. Uncontaminated soil and diesel-contaminated soil without amendment were used as controls.

**Results :** Results: The pH of uncontaminated soil at first week was 8.3 and diesel contamination reduced pH to 7.8. The final pH value of BS1 (6.4) and BS2 (6.77) groups was near neutral. pH values of treatment groups were 8-6.3 in BS1, 8.4-6.4 in BS2, and 9.15-7 in BS3 groups. The results showed that amending BS1, BS2, and BS3 was resulted in 9.96, 7.7, and 6.75-fold increase in dehydrogenase and 2.52, 2.4 and 2.52-fold enhancement in catalase activity of diesel-contaminated soil in comparison with natural attenuation group.

**Conclusion :** Conclusion: it is obvious that amending organic compounds to the contaminated soil is an effective, cost effective and environmentally friendly approach to improve bioremediation rate of diesel contaminated sites.

**Keywords :** Biostimulation; Bioremediation, organic and inorganic amendment

# P217-90: Immobilization of a microbial lipase on celite for enzymatic improvement of n6/n3 ratio in polyunsaturated fatty acids from plant oil

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**Background and Aim :** Polyunsaturated fatty acids (PUFA) are essential in human nutrition since they play an important role in the prevention of several diseases. The enzymatic esterification using solvent tolerant lipase has become an attractive approach for polyunsaturated acylglyserols production. The aim of this study is immobilization of a solvent tolerant lipase for enzymatic improvement of n6/n3 ratio in PUFAs from flaxseed oil.

**Methods :** Solvent tolerant lipase obtained from Actinomadura sediminis UTMC 2870 was immobilized by incubating 150 U of the enzyme per gram of the carrier in phosphate buffer (50 mM, pH 7.4) and stirring at 25 °C for 45 min. Enzymatic synthesis of AGs rich in n-3 PUFAs was divided into four main stages: (i) the extraction of FFAs from flaxseed oil, (ii) PUFA concentration, (iii) enzymatic esterification, and (iv) GC analysis. The reusability of the immobilized lipase was evaluated by measuring the recycling efficiency in sequential reaction cycles until the enzyme activity was markedly reduced.

**Results :** GC analysis of fatty acid composition revealed that the product contain 50 % w/w of PUFA including 42 % w/w α-linolenic (ALA, 18:3, n-3) and 9.7 % w/w linoleic acid (LA, 18:2, n-6). Value of n-6/n-3 ratio of the product with 0.24 was comparable to cod liver, Herring, Salmon, and Sardine oils with n-6/n-3 ratio of 0.04, 1.01, 0.03, and 0.07 respectively and it showed remarkably different with seed oils showing high value of n-6/n-3 ratio.

**Conclusion :** Due to the high efficiency of the enzyme to n-3 PUFA, specifically in present organic solvent, lipase from A. sediminis can be suggested as an ideal alternative in the production of omega-3 concentrates in their natural form.

**Keywords :** Immobilization, Polyunsaturated fatty acids, Solvent tolerant lipase

# P218-91: Simultaneous immobilization-purification of a microbial lipase for biodiesel production

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**Background and Aim :** Serious reduction of fossil fuels resources together with the world increase of greenhouse gas emissions and ecological pollution have led to the quest for alternative renewable and clean fuels. Up to now, almost 100% of transportation energy and 86% of the global energy consumption are provided by fossil fuels. Fatty acid alkyl esters (FAAEs) are introduced as a promising alternative of diesel that named biodiesel. The aim of this study, is to introduce a heterogeneous biocatalyst of SBA-15@oleate@lipase for biodiesel production.

**Methods :** In the present study, a mesoporous silica of SBA-15 modified with oleic acid and a solvent tolerant lipase from Actinomadura sediminis (SBA-15@oleate@lipase) was designed as the heterogeneous biocatalyst with maximum activity by a protein loading of 32.0 mg per gram of the support. The enzymatic trans-esterification reaction was catalyzed for converting oil of the cyanobacterium Synechococcus elongatus into biodiesel. The physico-chemical characteristics of the cyanobacterial oil and biodiesel were estimated using biodiesel analyzer software and compared with the standards of ASTM D6751.

**Results :** The maximum immobilization efficiency (68%) and yield (80%) were also obtained at 200 µg ml−1 of the protein with reaction time of 60 min. The enzymatic trans-esterification reaction was performed with an 85%±3.2 yield under optimized conditions. The designed heterogeneous biocatalyst revealed a high efficiency towards palmitoleic acid (C16:1) in the microalgal oil that is one of the best fatty acids to produce a high-quality biodiesel. The produced biodiesel demonstrated suitable cetane number and oxidative stability compared with the standards of ASTM D6751.

**Conclusion :** This work also highlights the simultaneous combination of purification and immobilization of the bacterial lipase by interfacial activation mechanism, to the synthesis of a solid biocatalyst for production of a cyanobacterium-based biodiesel.

**Keywords :** Biodiesel, Immobilization , SBA-15@oleate@lipase

# P219-92: Evaluation of Probiotic Properties of Anti-Microbial Exopolysaccharide Producing Lacticaseibacillus sp. AS20(1)

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**Background and Aim :** Lactic acid bacteria are the most common microorganisms applied as probiotics. Probiotic microorganisms should possess properties to confer their beneficial effects. Acid resistance, attachment to epithelial cells, and prevention of pathogen colonization on the intestinal surface are some of these properties. Also, they should have no hemolysis and transmissible antibiotic resistance to be recognized as safe.

**Methods :** Lacticaseibacillus sp. AS20(1) was isolated from a screening study as an anti-microbial EPS-producing isolate. In the current study, we aimed to evaluate its probiotic properties. For this purpose, its resistance to acidic pH (2 and 3), cell surface hydrophobicity, autoaggregation, and coaggregation abilities with Listeria monocytogenes, Yersinia eterocolitica, Bacillus cereus, and Salmonella enterica subsp. enterica were evaluated. Finally, the safety of this strain was assessed via studying its hemolysis activity and antibiotic susceptibility.

**Results :** Lacticaseibacillus sp. AS20(1) showed excellent survival at pH 2.0 and 3.0. It showed more than 71% survival rate after incubation at pH 2.0 and 3.0 for 2 h. It showed a hydrophobicity value of 47.5%. and indicated 65.6%, 71.2% and 92.6% autoaggregation after 2, 3, and 24 h incubation, respectively. Also, it exhibited more than 35% and 45% coaggregation ability after 3 and 24 hr incubation with all tested bacterial pathogens, respectively. It was susceptible to all tested antibiotics (diameter of growth inhibition zones> 21 mm). Lacticaseibacillus sp. AS20(1) whit no hemolytic activity can be generally accepted as safe.

**Conclusion :** Lacticaseibacillus sp. AS20(1) can be considered a promising probiotic strain with potential application in food industries.

**Keywords :** Lacticaseibacillus sp. AS20(1); Probiotic properties; Lactic acid bacteria

# P220-167: The genomic analysis of Brucella melitensis field isolates based on OMP31 gene

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**Background and Aim :** Brucella melitensis is the global pathogenic species of Brucella that contributed to ovine, caprine and, human brucellosis.The gene of omp31encodes the major 31-kDa Brucella Outer Membrane Proteins of B. melitensis and play important roles indirectly interacting with host cells but littleinformation is available on genomic analysisof these proteins in different serovars of B. melitensisand different hosts of human, goat, sheep cattle and camel in Iran. The purpose of the project is to know the genomic characterization of the omp31 based PCRfrom Iranian isolates of B. melitensis in this study.

**Methods :** 146 samples were selected from human blood samples, bovine and camel lymph nodes as well assheep and goat aborted fetuses including fetal kidney, abomasum, liver, lung, spleen, andheart for bacteriological investigation. The molecular detection of omp31 and IS711 gene were performed using theisolated B. melitensis (n=14). Sequencing of omp31 gene of B. melitensisin Iranian field isolates was performedfor whole gene sequencing. The omp31 gene of 14Iranianhuman and animal field isolatesof B. melitensis were analyzed for the presence of nucleotidevariations by PCR amplification and sequence analysis and the results confirmed with AMOS- PCR assay.

**Results :** Our results showed thatB. misolates were recovered from 14 examined cases and confirmed by the IS711 based-PCR with a PCR product of 731 bp.The 14 Iranian B.melitensis sequences clustered together as a monophyletic grouping with abootstrap support of 63, and they are most closely related to the B. melitensis references isolates.

**Conclusion :** This omp31 based phylogenetic placement powerfullyindicates a monophyletic origin of Iranian B. melitensis in different animals and human hosts. Our data may help to develop improved diagnostic tools and a subunit vaccine candidatefor the control of brucellosis.

**Keywords :** Brucella melitensis, omp31gene, PCR, Genomics

# P221-215: Statistical optimization of the lipase production from Lactobacillus plantarum strain C26 isolated from dairy products

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**Background and Aim :** Lactic acid bacteria (LAB) as an important source of biocatalysts help shape the desired sensory attributes in various food products and provide health benefits for the gastrointestinal tract when consumed in the diet. Lactobacillus plantarum is a good source of lipase and esterase enzymes and lipolytic activity have been described in various reports. The main purpose of this study was to optimization of the lipase production from L. plantarum isolated from dairy products.

**Methods :** In this study, L. plantarum was isolated from dairy products during screening of 92 isolates using MRS agar. The optimal cultural conditions for lipase production obtained with Response Surface Methodology experimental design (Central Composite Design; CCD). 20 experimental combinations were designed to investigate three independent factors including Oil content (x1), Peptone concentration (x2), and MgSo4 concentration (x3) at five various levels with six repetitions at the central point.

**Results :** The results of optimization of the lipase production showed the lipase yield ranged from 0.6 U/ml to 3.4 U/ml, and the experiments of 6 and 12 gave the minimum and maximum yields, respectively. The quadratic model was summarized after removing the insignificant coefficients. According to the predicted model, the maximal lipase production was achieved at 4.6 % of peptone, 7.2% of oil and 0.5% of MgSo4 concentration.

**Conclusion :** The lipase of L. plantarum is expected to consider an appropriate candidate can be applied to overcome malabsorption, to reduce cholesterol levels, and to improve fat digestion in the diet.

**Keywords :** Lipase enzyme, Probiotic, Optimization

# P222-221: Optimization of ammonium sulfate precipitation of a chimeric peptidoglycan hidrolysing Enzme

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**Background and Aim :** Endolysins are essential bacteriophage encoded enzymes in the lytic phage life cycle, which hydrolyze the host cell wall and are a good antibiotic substituent against Antibacterial resistance. The endolysins of Gram-positive bacteria infecting bacteriophages contain catalytic domain(s) and binding domain. Histidine-dependent Amidohydrolase Peptidase (CHAP) domain is one of the most active domains, which has Anti-Staphylococcus aureus activity.

**Methods :** The chimeric protein that contains the CHAP domain and binding domain was expressed in BL21(Gold). Bacterial cells were sonicated and the chimeric protein ammonium sulfate precipitation was optimized.

**Results :** We confirmed the level of precipitated chimeric protein using SDS-PAGE. The highest level of chimeric protein precipitate was observed in 10% ammonium sulfate concentration.

**Conclusion :** In this study, ammonium sulfate precipitation of a new chimeric peptidoglycan hydrolase was done to prepare crude lysate for the next step of purification. Ammonium sulfate precipitation is a useful technique as the first step in protein purification because you can have quick, bulk precipitation of cellular proteins.

**Keywords :** Histidine dependent Amidohydrolase Peptidase (CHAP), Chimeric protein, Ammonium sulfate precipitation, Endolysin

# P223-274: Evaluation of yeast biodiversity in Iranian traditional Kefir samples

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**Background and Aim :** Kefir is a fermented product with numerous attributed health benefits due to the presence of a mixture of bacteria and yeasts in an exopolysaccharide matrix. Although the bacterial population is dominant in kefir, the presence of yeast plays an important role to develop the flavor and the chemical composition of the kefir product. Moreover, the yeast strains are important for the microbial balance by providing the essential nutrients for a probiotic bacteria population such as vitamins and amino acids and produce some compounds that contribute to the kefir drink taste.

**Methods :** Ten traditional kefir grain samples were acquired from 3 different cities of Iran (Mashhad, Tehran and Zanjan). Dilutions of the sample were directly plated on Rose Bengal agar and incubated at 25 °C for 72 h. Fungal colonies were subcultured and purified on yeast peptone glucose agar (YPG agar) at the same condition. The morphological and biochemical characteristics of the isolates were determined according to the standard methods. Different morphotypes were identified based on the sequencing of their large subunit rDNA D1/D2 domain.

**Results :** 41 yeast strains were isolated from ten different kefir samples and 17 morphotypes were chosen for identification by molecular sequencing. All the selected morphotypes lacked urease activity and showed negative Diazonium Blue B reaction approving them as members of ascomycetes. Molecular identification revealed the morphotypes belongs to Pichia fermentans (7 strains), Kluyveromyces marxianus (6 strains), Saccharomyces cerevisiae (3 strains), and Pichia kudriavzevii (1 strain).

**Conclusion :** Pichia and Kluyveromyces were found to be the most abundant population in the traditional kefir samples.

**Keywords :** Kefir grains; Microbial biodiversity; Molecular identification; Yeast

# P224-282: Statistical optimization of the biosurfactant production from Lactobacillus brevis isolated from dairy products

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**Background and Aim :** Biosurfactants are well known as one of the adhesion inhibitors to prevent pathogens from attaching to the adhesion on epithelial cells of urogenital and intestinal tracts and can be used by humans despite being a probiotic source. The main purpose of this study was to optimization of the biosurfactant production from Lactobacillus brevis isolated from dairy products.

**Methods :** In this study, L. brevis was isolated from dairy products during screening of 70 isolates using MRS agar. The optimal cultural conditions for biosurfactant production obtained with Response Surface Methodology experimental design (Central Composite Design; CCD). 20 experimental combinations were designed to investigate three independent factors including Oil content, Yeast concentration, and Glucose concentration at five various levels with six repetitions at the central point.

**Results :** The results of optimization of the biosurfactant production showed the biosurfactant Oil Spreading ranged from 28 mm to 99 mm, and the experiments of 9 and 7 gave the minimum and maximum Spreading, respectively. The quadratic model was summarized after removing the insignificant coefficients. According to the predicted model, the maximal biosurfactant production was achieved at 2.75% of glucose, 3.625% of oil and 4.25% of yeast concentration.

**Conclusion :** The biosurfactant of Lactobacillus brevis is expected to consider an appropriate candidate can be applied to adhesion inhibitors, to inhibit human pathogenic biofilm producers.

**Keywords :** biosurfactant, Lactobacillus, probiotic, optimization

# P225-284: First detection of mobilized colistin resistance mcr-1 gene in Escherichia coli isolated from livestock and sewage in Iran

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**Background and Aim :** The increasing prevalence of antibiotic resistance is one of the global health threats in the 21st century.Polymyxins are the latest agents for the treatment of infections related to multidrug resistant gram negative bacteria (MDR-GNB) .plasmid-mediated colistin resistance genes have been reported in the Enterobacteriaceae family.Escherichia coli studies have particularly demonstrated that poultry and livestock can potentially carry isolates containing mcr genes;therefore, they can transfer drugresistant bacteria to humans.This study aimed to determine the prevalence of colistin-resistant isolates as well as the prevalence of mcr genes in E.coli in Iran

**Methods :** The 65 isolates of E.coli were collected such as rectal stool swab samples from cows (n = 38), chickens (n = 47) and urban sewage samples (n = 30) from two veterinary between February and August 2019 in Iran (Qazvin and Karaj). Colistin resistance was determined using the broth microdilution method by colistin Minimum inhibitory concentration (MICs) to characterize their antimicrobial susceptibility based on Clinical Laboratory Standards Institute guidelines2019,and PCR and ERIC-PCR were used to detect the mcr-1,6 genes

**Results :** The antimicrobial susceptibility tests (MIC) showed that only 3 (4.6%) isolates were resistant to colistin. All of the colistin-resistant isolates had MICs of 4 µg/mL. According to the PCR results,only one(33.3%)colistin-resistant isolate from cows harboured the mcr1 gene ,It was mcr-1 positive. The nucleotide sequences of the mcr-1 gene from E. coli were submitted to the GenBank database under accession number MN539105.

**Conclusion :** In conclusion, to this study is first report the mcr-1 gene in a colistin-resistant E. coli animal isolate in Iran. According to the present results, the spread of this gene in domestic animals and its possible transmission to humans raise public health concerns. To prevent the transmission of this gene to humans, it is necessary to the colistin-resistant strains. Proper administration of colistin and subsequently decreasing the selective pressure caused prevent the spread of antibiotic resistance

**Keywords :** Colistin resistance, Escherichia coli, livestock, mcr-1

# P226-286: 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. 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 β-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 discrimi natory power for detecting AmpC β-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-Lactamase, Escherichia coli, Klebsiella pneumoniae

# P227-296: Groundwater Bioremediation through Application of Calcium Peroxide Nanoparticles and Small Bioreactor Chambers

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**Background and Aim :** Groundwater is one of the most important water resources that is widely used in washing and irrigation processes for about 40 % of the world's agricultural products. Pollution of groundwater with various contaminants such as phenols is a crucial environmental concern and threatens the health of human society. This study evaluated the effects of calcium peroxide and small bioreactor chambers on phenol removal from groundwater.

**Methods :** Design the experiments and analysis of results were performed by a statistical package Design-Expert version 11 and analysis of variance (ANOVA), respectively. Powdered and encapsulated synthesized-calcium peroxide (CaO2) nanoparticles were applied to investigate the effect of biostimulation in groundwater contaminated by phenol. Bioaugmentation was also performed by using innovative Small Bioreactor Chambers (SBCs) containing a phenol-degrading consortium which was successfully isolated from a water well located in Iran.

**Results :** Designed experiments revealed that the highest growth rate and phenol degradation of the ph100-consortium were observed at 15 °C and pH 7.5 in the presence of 500 mg·L-1 of powdered CaO2 and 100 mg·L-1 of phenol as a sole source of carbon. According to the next-generation sequencing (NGS) analysis of the consortium, Proteobacteria and Bacteroidetes with 75.3% and 16.2% relative abundance were the dominant phyla in the ph100-consortium, respectively. At the class level, the predominant taxa were Gammaproteobacteria, followed by Bacteroidia, Alphaproteobacteria and Actinobacteria. Batch experiments results indicated that the addition of 500 mg·L-1 of encapsulated CaO2 was the optimum concentration for phenol (100 mg·L-1) bioremediation in 60 days with the negligible negative impacts on the microbial population. In addition, the highest biodegradation percentage were achieved during incubation of SBCs in a medium supplemented with 500 mg·L-1 CaO2 powder in 25th days of experiment.

**Conclusion :** These results provide evidence for a successful application of calcium peroxide nanoparticles and SBCs containing the selected microbial cultures in water treatment processes.

**Keywords :** Bioremediation, Bioaugmentation, Biostimulation, Groundwater, Phenol

# P228-297: Kinetics of desulfurization by Rhodococcus erythropolis SHT87

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**Background and Aim :** Biodesulfurization is using living systems to reduce sulfur content in fossil fuels at moderate pressure and temperature conditions. Here, the pattern of dibenzothiophene (DBT) reduction by using Rhodococcus erythropolis SHT87, was studied.

**Methods :** Solutions, containing 0.1 to 6.5 mM DBT in n-Tetradecane, were used to study the biodesulfurization process by this bacterium. The resting cells of Rhodococcus erythropolis SHT87, were added to the reaction mixture up to 10 gDCW/L. Then, the specific desulfurization activities in the first two hours were determined by HPLC (with a C18 column). The mobile phase was a 4:1 mix of acetonitrile: water at 1.8 ml/min). All statistical analyses were performed by using GraphPad Prism software.

**Results :** The results show the hyperbolic relationship between the specific desulfurization activity and the initial concentrations of DBT. It shows that the biodesulfurization process by this bacterium follows the Michaelis–Menten kinetics in these conditions. Vmax and Michaelis constant (Km) were estimated 0.51 micromol/gDCW/min and 0.34 mM.

**Conclusion :** Such a relationship between the specific desulfurization activity of the resting cells and the initial concentration of DBT has been reported many times in different desulfurizing microorganisms. In previous reports for other cells, different values from 0.04 to 3 micromol/gDCW/min have been shown for Vm. So, it can be said that the maximum velocity of biodesulfurization by SHT87 is appropriate and acceptable. Km in this research is less than the same parameter in many other experiments, which have been done by the other members of Rhodococcus and by Pseudomonas strains.

**Keywords :** Biodesulfurization; Rhodococcus erythropolis SHT87; Kinetics

# P229-298: Dibenzothiophene desulfurization by Rhodococcus erythropolis SHT87 in stirred tank bioreactor

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**Background and Aim :** The world is moving towards zero-sulfur fossil fuels. Among the different technologies to remove sulfur from petroleum, biodesulfurization (BDS) is an effective approach. It's based on the sulfur metabolism in some of the living systems including archaeal, bacterial, and fungal members. BDS occurs at ambient temperature and pressure with high selectivity, without undesirable side-products. It significantly reduces sulfur content in a cost-effective manner. In recent years, Rhodococcus erythropolis SHT87 has been identified and introduced as a bacterium capable of desulfurizing resistant sulfur-containing compounds including dibenzothiophene (DBT) in fossil fuels.

**Methods :** Rhodococcus erythropolis SHT87 was cultivated in a minimal culture medium (BMV) including the phosphate buffer solution, the metals solution, and the vitamins solution. BMV medium had glycerol (5 g/L) and DBT as the only source of carbon and the only source of sulfur. In the middle of the logarithmic phase, the SHT87 cells were precipitated by centrifuge and were eluted by the phosphate buffer solution. Then, according to the determined relation between optical absorbance in 660 nm and dry cell weight, the prepared resting cells of SHT87 were added to the biphasic system (mixture of 2:1 n-tetradecane/water) up to 10 gDCW/L. DBT concentration was 3 mM and the process was run in a 3L bioreactor (30 oC, pH 6, 400 rpm, and 1 vvm).

**Results :** The specific desulfurization activity in the first two hours was measured by HPLC based on 2-HBP production. It was 1.2 micromole 2-HBP/gDCW.min.

**Conclusion :** This study demonstrates that R. erythropolis SHT87 has desired specific activity of DBT desulfurization in the stirred tank bioreactor. Therefore SHT87 can be used for improving fossil fuels.

**Keywords :** Rhodococcus erythropolis SHT87; stirred tank bioreactor; fossil fuels.

# P230-342: Nanomaterial augmented formulation of disinfectants and antiseptics in controlling SARS CoV-2

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**Background and Aim :** The worldwide COVID-19 pandemic has brought significant consideration toward innovative strategies for overcoming the viral spread. Since the long-term usage of disinfectants and antiseptics at high concentrations has deleterious impacts on well-being and the environment, the use of nanomaterials (NMs) provides an exciting possibility to promote new antiviral treatments with a low possibility of increasing drug resistance in contrast with typical chemical-based antiviral treatments. Depending on the dimension, form, and surface charge, NMs can possess various formations and antiviral characteristics. The primary NMs reported for their inactivation effect on respiratory viruses can be subdivided into Polymeric, Self-assembling proteins, Inorganic (Copper, Silver, Zinc, and TiO2), and peptide-based NMs. The Mechanism of action of NMs outside the host cell includes inhibiting the viral entry inside the cell, solvation of the lipid bilayer envelope of it, and production of ROS. Mechanisms of action inside of the cell are polyprotein processing, transcription of the viral genome, translation of the viral protein, and the most common mechanisms are activation of transcription agents through receptor signaling as a response of viral RNA, and the production of pro-inflammatory cytokines (IL-1B), and activation of the Th2 route, which leads to the production of neutralizing antibodies (IL-4, IL-5, and IL-13), or Th1 route, leading to the production of opsonizing antibodies (IgE, C4b, C3b, and IgG).

**Methods :** -

**Results :** Although NMs have molecular targets and remarkable antiviral activity to inactivate several viral pathogens, these compounds have toxic effects on social health and the ecosystem due to the accumulation of their wastes in the environment and the inability to eliminate or detoxify them from the ecological cycles. Also, according to toxicological studies of NMs so far, the entry of NMs through inhalation, ingestion, and skin is of utmost importance,

respectively. As a result, before any toxicological trial, a comprehensive characterization of the contents of the nano-based antiseptics/disinfectants is essential.

**Conclusion :** In this report, the latest advancement in studying NMs and disinfectants are discussed from three perspectives: positive impacts, toxicity, and their mechanisms of action. As a result, the prevalent commercialization and usage of NM-based disinfectants during this pandemic can have long-lasting detrimental effects on human health and other animals, environmental microorganisms, and plants in the ecosystem.

**Keywords :** Nanoparticles, Antiseptics, Disinfection Ecological safety, Biosafety, COVID-19, Toxic nanomaterials

# P231-364: Investigation of increased production of Citric acid by Aspergillus Niger mutant isolates

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**Background and Aim :** Citric acid is one of the most important organic acids that its consumption is very important in the world and its demand is increasing every year. The aim of this study was to induce mutations in normal isolates and compare the ability to produce citric acid between normal isolates and mutant isolates.

**Methods :** Isolation of fungi used in this study from different environments (air, soil, water) was used. After successive cultures on PDA medium, the isolates were identified and purified. The main isolates as well as mutant isolates were cultured in the center of CZapek Dax Agar specific medium by inoculation in the center Acid production was observed every 24 hours by measuring the diameter of the halo. Aspergillus Niger (PTCC 5010) was used as a control. Finally, the isolates were inoculated into liquid culture medium and the amount of citric acid production was investigated.

**Results :** 5 different isolates obtained 5 new mutant isolates by inducing mutation in each. The highest amount of citric acid production was related to mutant isolate No. 5 called AMR and the lowest amount was related to isolate without mutant No. 1.

**Conclusion :** In isolates without mutation, the maximum production of citric acid was 15 g / l and in isolates after induction of mutation, a maximum of 21 g / l was observed.

**Keywords :** Aspergillus Niger, CZapek Dax Agar, Citric acid, Mutant isolates

# P232-369: Isolation and Identification of Electron Transfering Bacteria from Soil of Gold Mines (Case Study: Sistan and Baluchestan Province, Iran)

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**Background and Aim :** Exoelectrogen bacteria (bacteria with the ability to transfer electrons through their outer membranes) that play a key role in MET (Microbial electrochemical technologies) are found in natural environments such as soil and water, but there are many other diverse bacteria in These environments disrupt the purification process of these bacteria in the culture medium in the laboratory. The aim of this study was to isolate isoelectrogen bacteria from soil to use in microbial electrolysis cells as a catalyst and to introduce a method to facilitate its purification process.

**Methods :** At first, the gold mine soil of Sistan and Baluchestan province of Iran was sampled. Samples were incubated in an anaerobic reactor consisting of two electrodes and a mixture of CO2 / N2 gas at a ratio of 80/20 and with geobacter synthetic culture medium for two days. Moreover, a 0.4 V constant current source was connected to the electrodes. Then, for purification, the obtained bacteria were cultured on geobacter medium with 1.5% agar and incubated at 28 °C for 48 h. DNA was extracted from purified samples by phenol-chloroform method. Also, PCR test was performed with 16S rRNA primer.Finally, Sequences were sent to Gen Fan Avaran Company for sequencing.

**Results :** By using Sanger sequencing for 16s rRNA gene and blast, the results were identified in the two-way gene database of Bacillus circulans and Pseudomonas stutzeri.

**Conclusion :** The presence of an external electrode into the culture medium facilitates the purification and separation of exoelectrogen bacteria from the medium. The two bacteria, Bacillus circulans and Pseudomonas stutzeri, are exoelectrogenic that can be used in many applications, including wastewater treatment or electricity generation.

**Keywords :** Exoelectrogen bacteria, gold mine soil, Microbial electrochemical technologies, purification, separation.

# P233-382: Evaluation of different methods for isolation of Bacillus thuringiensis from soil samples

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**Background and Aim :** Bacillus thuringiensis is the most known environment-friendly biopesticide. Various methods were performed for the isolation of Bt from different types of samples. High-performance methods with different principles are needed because a single method is not suitable for isolating organisms from various environments. Currently, obtaining an effective isolation method is a challenge.

**Methods :** In this study, 60 soil samples from the south of Iran were collected. The efficiency of four methods in isolation of Bt was evaluated. The number of samples in which Bt colonies were found was used to determine each method's efficiency. Four methods were the dry heat pretreatment method, heat shock method, sodium acetate selection method, and the isolation of Bt using the M9 medium supplemented with L-serine.

**Results :** Bt was isolated from 23, 18, 12, and 35 samples using the dry heat pretreatment method, heat shock method, sodium acetate selection method, and M9 medium supplemented with L-serine method, respectively.

**Conclusion :** In this research, the efficiency of standard methods in isolation of Bt was examined. The results reveal that the M9 medium supplemented with L-serine has minor errors and a higher rate of Bt isolation. This method showed 34%, 49%, and 69% more efficiency than the dry heat pretreatment method, heat shock method, and sodium acetate selection method isolation of Bt colonies, respectively. Despite its limitations, the finding has important results for future practices to optimize and devise methods to improve the isolation of Bt from various samples.

**Keywords :** Bacillus thuringiensis, Soil, Isolation, Biopesticide, Biocontrol

# P234-383: Development of a Plasmid Selection System for E. coli Host Based on Bacterial fab Genes

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**Background and Aim :** Over the past few years, plasmid DNA (pDNA) vectors have played a crucial role in preventing infectious diseases and meeting the needs of researchers by facilitating gene transfer to prokaryotic and eukaryotic cells, whether bacterial or animals. Furthermore, progress towards all form of non-viral gene therapy has led exponential growth in the demand for safe plasmid vectors. As the goals for preparation of intact plasmid DNA have been increased over time, the attention of the health organizations and biotechnology research scientists is focused on antibiotic resistance genes in pDNA backbones as selectable markers which cause several issues including arising in multidrug-resistance (MDR) bacteria, probable responses of the host's immune system, and epigenetic changes. In order to proper handling of these problems, developing antibiotic-free selection systems such as overexpression of fabI gene can be convenient.

**Methods :** To test the method in E. coli, fabI and fabV genes were used as the plasmid selectable markers in pcDNA3.1(+) vector which lacked the resistance related genes to Kanamycin and ampicillin. The recombinant strains were grown in adverse conditions with biocide Triclosan as the selective agent

**Results :** The recomibant vector with fabI as a selective marker gene, enabled selection by Triclosan at 6 µg/ml and the one with fabV selectable marker, was grown in selective media containing 500 µg/ml Triclosan. However, plasmid stability and plasmid yield decreased for both recombinant vectors through plasmid extraction.

**Conclusion :** While a variety of non-antibiotic selectable markers have been designated, the fabV-triclosan selection system provides a suitable plasmid choosing without using antibiotics resistance selectable markers.

**Keywords :** plasmid DNA (pDNA) vectors, antibiotic-free selection systems, The overexpression of fabI gene, fabV gene

# P235-391: the study of optimal drying method of Keratinase Enzyme With the aim of maintaining its efficiency

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**Background and Aim :** Keratinase is an extracellular endopeptidase moreover maximal activity in its particular keratin substrate has the capacity to degrade a wide range of substrates such as casein, collagen, elastin, globulin, and hemoglobin and in numerous industries including pharmaceuticals, Leather industry, livestock, insecticides, prion decomposition, cosmetics, and organic agricultural fertilizers, it also functions in a diversity of temperature and PH ranges. The aim of this study is to investigate the optimal method of drying the enzyme to maintain its activity by oven, vacuum oven, and freeze dryer.

**Methods :** In the first instance, after cultivating bacteria for four days in an alkaline medium containing feathers and salt, complete decomposition of the feathers Took place.Afterwards, with the intention of separating the feathers and bacteria from the medium, centrifugation was performed and the enzyme in the supernatant was precipitated by ammonium sulfate salt.Eventually, after the final centrifugation, the precipitate containing the enzyme was dried in freeze dryer, oven, and vacuum oven, and the keratinase and protease activity of the samples were measured.

**Results :** The keratins activity of dried samples in an oven, vacuum oven and freeze dryer by feather substrate, respectively; 6.5 (U /ml), 6.8 (U / ml) and 25.5 (U / ml) were measured. Also,protease activity of the same samples by casein substrate, respectively; 12.7 (U / ml), 13 (U / ml) and 97 (U / ml) were measured.

**Conclusion :** Considering the numbers obtained from the activity of the enzyme after drying per all three methods, it is concluded that drying the enzyme by a freeze dryer clearly preserves the keratinase and protease activity of the enzyme compared to the other methods.

**Keywords :** Protease, keratinase, freeze dryer, oven, vacuum oven

# P236-404: Photoeradication of exopolysaccharide-producing Leuconostoc mesenteroides as a harmful microorganism in the sugarcane processing industry

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**Background and Aim :** The production of exopolysaccharides (EPS) by Leuconostoc mesenteroides causes some critical problems in the cane sugar refining process. So, it is necessary to eliminate L. mesenteroides as an undesirable microorganism in the cane sugar refinery. Photodynamic inactivation (PDI) is a novel and attractive strategy to eradicate undesirable microorganisms. In this study, we aimed to evaluate PDI of L. mesenteroides using methylene blue (MB).

**Methods :** Cells suspensions of L. mesenteroides (PTCC 1591) were treated by different concentration of methylene blue (6.25-100 µM) and subsequently subjected to laser light (650 nm). Effect of sub-lethal photodynamic inactivation on the production of EPS by L. mesenteroides was also assessed. Meanwhile, the effects of PDI (at lethal and sub-lethal levels) on L. mesenteroides cells were visualized using scanning electron microscopy (SEM).

**Results :** PDI mediated by MB (25-100 µM) caused a significant reduction in the number of viable L. mesenteroides cells (>3 log10 CFU reduction). L. mesenteroides exposed to sub-lethal photodynamic inactivation produced significantly less EPS than untreated cells. Scanning electron microscopy analysis clearly confirmed the potent ability of PDI to kill L. mesenteroides cells.

**Conclusion :** PDI mediated by methylene blue offer a new modality for fast and efficient elimination of L. mesenteroides cells, suggesting its potential use in sugar industry.

**Keywords :** Photodynamic inactivation, Undesirable microorganism, Exopolysaccharide, Sugar industry

# P237-421: Immunoprotectivity of Loop 3 from Omp34 against A.baumannii in murine model

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**Background and Aim :** Acinetobacter baumannii is one of the most important species of nosocomial infections and its clinical importance is due to its special ability to acquire and regulate virulence factors, making it one of the most successful multidrug resistant organisms (MDRs). Several different resistance mechanisms are involved in the development of multidrug-resistant phenotypes in A.baumannii, one of which is to reduce the permeability of the outer membrane protein (OMP). The aim of this study was to investigate the partial protection of loop 3 of Omp34 protein against A.baumannii in a mouse model.In this study, we targeted Omp34 protein by selecting immunologically active loops from A.baumannii. The surface epitopes were displayed and a hybrid antigen from the loopless C lobe of the Omp34 protein of Neisseria meningitides referred to as LCL was constructed. The nucleotide sequences of the immunogenic loops of Omp34 were amplified and implanted in the LCL.

**Methods :** The recombinant genes were expressed and purified. The purified proteins were administered to BALB/c mice. Both active and passive immunizations were carried out. The mice were then challenged with a clinical isolate of A.baumannii. Indirect ELISA confirmed significant antibody rise to the antigens.

**Results :** In the active immunization, the survival rates of 66.8%, 83%, and 50% were achieved with the loops derived from Omp34, and combination of both loops respectively. Significant decrease in the bacterial loads were noted in the spleen, liver and lungs of the immunized mice groups

**Conclusion :** In conclusion, Loop 3 of Omp34 plays an effective role in immunoprotectivity against A.baumannii infections

**Keywords :** Acinetobacter baumannii - Omp34 - Immunogenicity- Vaccine.

# P238-431: Biosynthesis of iron nanoparticles and evaluation of its antimicrobial activity by Bacillus cereus

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**Background and Aim :** The chemical methods used to synthesize nanoparticles mainly lead to environmental pollution, instead of leaving some toxic reagents and not using the resulting nanoparticles in biological applications. Due to the environmental pollution caused by the synthesis of nanoparticles by chemical and physical methods and also the incompatibility of their use in medicine, the purpose of this study is to synthesize iron nanoparticles and investigate its antibacterial activity.

**Methods :** In this study, Bacillus cereus was cultured in broth nutrient medium. Then active bacterial suspension in a ratio of 1: 1 with a solution of 0.1 M Iron nitrate synthesis and biosynthesis of iron nanoparticles were performed after 22 minutes at room temperature. Nanoparticle synthesis was confirmed by spectrophotometer, electron microscopy and X-ray diffraction. Then, the antimicrobial effects of nanoparticles made using disk diffusion and tubular dilution methods on standard strains of Staphylococcus aureus, Bacillus cereus, Pseudomonas aeruginosa were evaluated.

**Results :** The absorption peak of iron nanoparticles was observed at wavelengths of 220 nm. The synthesized iron nanoparticles were multifaceted. The average size of iron nanoparticles was in the range of 50-70 nm. For Staphylococcus aureus, Bacillus cereus, Pseudomonas aeruginosa were measured as 0.012, 0.0069, 0.017, ml / mg, respectively.

**Conclusion :** The results showed that the synthesized nanoparticles have antibacterial properties against pathogenic strains. The highest diameter of growth inhibition halo was observed by iron nitrate bioparticles for Pseudomonas aerosinosa and the lowest diameter of growth inhibition zone was observed for Bacillus cereus.

**Keywords :** Bacillus cereus, Antibacterial activity, Iron nanoparticles

# P239-445: Investigation of applications of extremophilic bacteria isolated from hot springs in advanced biotechnology

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**Background and Aim :** In recent years, a lot of research has been done on hot spring microbes and their identification and isolation has become important. Despite having difficult conditions for life, such as high temperature, high salt concentration, alkaline or acidic pH, it has conditions. They live and a variety of microbes live inside them. They produce enzymes that have countless uses.

**Methods :** Isolated from hot springs and after Westernization, the applications of these metabolites are investigated.

**Results :** Extremophiles are microorganisms that grow in very harsh conditions, become microbial enzymes such as alkaline proteases are of great importance in modern biotechnology. Used for respiratory problems, rheumatism, circulatory problems and skin diseases

**Conclusion :** Study on the research and development of enzymatic products of extramophilic bacteria in hot springs is very important and also due to their important role in Therapeutic properties, anticancer, antimicrobial, petrochemical industry, pharmaceutical, petroleum and metal purification The heaviness of the environment is very important

**Keywords :** Hot springs, extremophiles, alkaline proteases, modern biotechnology

# P240-86: Meconium microbial toxins and microbiota; a novel and non-invasive proposed diagnostic sample to anticipate severity of neonates COVID-19

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**Background and Aim :** After entrance of COVID-19 into the body it could affect the balance of microbiota combination which can result in microbiota dysbiosis and eventually leads to immune imbalance. It is possible to observe simultaneous penetration of microbial toxic metabolites like bacterial lipopolysaccharide (LPS), into intrauterine space. This potent cytokine storm inducer then might lead to immune imbalances in neonates, which are predictable. It is demonstrated that COVID-19 Spike protein attaches to bacterial LPS and increases inflammatory activations. N proteins of SARS-CoV and Middle East respiratory syndrome coronavirus (MERS-CoV) exasperate LPS causing pneumonia through triggering MASP-2 activity. The presence and transmission of LPS to the fetus and pregnancy fluids and their potency to induce lung inflammatory diseases has also been demonstrated in previous studies. Based on these findings, we consider that it may be possible to measure the amount of LPS in the body as a prognostic marker of COVID-19 in pregnant mother or newborn baby.

**Methods :** narrative review

**Results :** narrative review

**Conclusion :** there has been no study conducted to test physiological relation of maternal microbiota toxic metabolites like bacterial LPS in COVID-19 positive mothers and neonate's meconium. We suggest to analyze meconium's LPS levels and Gram-negative microbiota and detection of Corona virus itself as a noninvasive, reliable and potential test beside other virus detection methods of COVID-19 in infants with COVID-19 positive mothers. It could equip us with better strategies to keep newborns safe. Because levels of mentioned microbiome and their products like LPS, might act as a clock bomb during probable cytokine storm formation.

**Keywords :** Meconium , LPS , COVID19 , SARS-CoV-2 , Microbiota

# P241-98: Incidence, Characteristics, and Outcome of COVID-19 in Patient on Liver Transplant Program: A Retrospective Study in North of Iran

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**Background and Aim :** The risk of severe COVID-19 disease seems to be higher in individuals with solid organ transplantation. Therefore, the purpose of the present study is to describe the laboratory data and epidemiologic factors of liver transplant recipients with diagnosed COVID in comparison with the patients waiting for liver transplantation.

**Methods :** In this study, we evaluated the records of patients on the waiting list for liver transplantation and recipients of a liver transplant. Demographic data, underlying disease, history of drug use, and participants' outcomes were collected. The diagnosis of SARS-CoV-2 infection for all patients was confirmed using a nasopharyngeal swab specimen with real-time RT-PCR. During the study period, 172 patients were enrolled, among whom 85 patients (49.4%) were on the waiting list for liver transplantation and 87 patients (50.6%) were recipients of a liver transplant.

**Results :** Out of them, 10 (5.8%) had a positive result for SARS-CoV-2. Of these patients, 6.9% (6/87) and 4.7% (4/85) of patients on the waiting list and recipients of liver transplant were positive for SARS-CoV-2, respectively. Patients on the waiting list with COVID-19 infection had a higher median of albumin, ALT, AST, TBIL, DBIL, HDL, and LDL values compared to recipients of a liver transplant. In summary, the incidence of COVID-19 in liver transplant patients was slightly high.

**Conclusion :** The existence of underlying liver diseases should be well known as one of the poor predictive factors for worse outcomes in patients with COVID-19. So, comparative studies are recommended to identify risk factors for COVID-19 in patients with liver injury.

**Keywords :** SARS-CoV-2, COVID-19, Liver transplant patients, Iran

# P242-118: Ibuprofen and SARS-CoV-2 infection are synergistic on cell death

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**Background and Aim :** coronavirus disease 2019 (COVID-19) has created a growing alarm due to lack of chemotherapy and global strategy for eradication. Many speculations have been put forth about strategies, prevention, and therapy of this new coronavirus infection. One was from the University Clinic of Vienna on the possibility of synergism between RNA replication of severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) and consumption of ibuprofen in patients with high frequency of death (data not published to date). It means ibuprofen would have parallel effects with SARS-CoV-2 on the death of patients. What are the scientific reasons?

**Methods :** Let's look at the brief description in the field of interaction between ibuprofen and antiviral cell system. We know that ibuprofen, as a nonsteroidal anti-inflammatory drug (NSAID), inhibits activity of Cox1 and Cox2 enzymes . Cox1 and Cox2 enzymes can catalyze arachidonic acid to prostaglandin after some intermediate substrates . Prostaglandins such as PGE2 and PGI2 play a role within the immune system toward protection against infection

**Results :** So consumption of NSAIDs such as ibuprofen in patients with COVID-19 can lead to intervention in cell defense mechanisms . In addition, ibuprofen is a scavenger of nitrogen radicals

**Conclusion :** A previous study has indicated an antagonistic effect of ibuprofen on nitric oxide synthetase isoforms . More studies are needed, but it seems that a decrease of nitrogen radicals in infected cells with SARS-CoV-2 can lead to an increase of viral RNA load in cells.

**Keywords :** Ibuprofen, SARS-CoV-2, COVID-19, nitrogen radicals, immune system, anti-inflammatory

# P243-127: Comparison COVID 19 manifestations between kidney and liver transplantation

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**Background and Aim :** Although transplant recipients are at high risk for severe Coronavirus disease-2019 (COVID-19), there is a dearth of research on the presentations and outcomes of the disease in these patients. This study aimed to compare the presentations and outcomes of liver and kidney transplant recipients who were infected with COVID-19 in the Iranian population.

**Methods :** This cross-sectional study was conducted at Imam Reza and Montaserieh Hospitals affiliated with Mashhad University of Medical Sciences, Mashhad, Iran, between 2020 and 2021. In general, 52 patients were selected and divided into two groups of the kidney (n=28) and liver (n=24) transplantation. Demographic characteristics of the patients, including age, gender, medical history, time interval since the transplantation, common symptoms of COVID-19, clinical presentation, laboratory tests, COVID-19 medications, immunosuppressive agents, chest symptoms, severity of infection based on chest computed tomography scan, and outcome were recorded in a checklist. Data were compared between the two groups, and the relationship among various variables was assessed in this study

**Results :** In general, severe COVID-19 infection was reported in 61% of the patients. Except for one case, other recipients were in the late phase of post-transplantation. There was no significant difference between the two groups in terms of symptoms, except for cough ($\chi2$=8.09; P=0.004), clinical condition, and laboratory symptoms, except for creatinine (Z=14; P<0.005), alkaline phosphatase (Z=4.55; P=0.03), total bilirubin (Z=8.93; P=0.03), and partial thromboplastin time (Z=5.97; P=0.01). Higher D-dimer (t=-2.13; P=0.04), lymphocyte count (t=-3.98; P=0.001), and total lymphocyte count (t=2.62; P=0.01) were correlated with the severity of COVID-19 in the liver transplant recipients. The most common medications for the treatment of COVID-19 included Hydroxychloroquine (63.5%), Azithromycin (48.1%), and Remdesivir (23.1%) in descending order. There was no relationship between the outcome and the use of immunosuppressive medications (P>0.05). All patients with kidney transplantation survived, while two cases in the liver transplantation group failed to survive ($\chi2$=2.42; P=0.11).

**Conclusion :** In summary, severe acute respiratory syndrome coronavirus 2 infections were reported in almost all liver and kidney transplant recipients. Furthermore, the mortality rate was higher in the liver transplant recipients, compared to the patients who underwent kidney transplantation. No relationship was reported between the severity or mortality and immunosuppressive agents.

**Keywords :** COVID-19, Immunosuppressive, Mortality, Transplantation

# P244-128: Immunosuppressant agents and liver transplantion at COVID19 pandemic

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**Background and Aim :** It seems that transplant recipients are at high risk for severe COVID-19, especially in the presence of comorbidities and immunosuppression. This study aimed to determine the effects of previous treatment with immunosuppressants and received dosage and the risk of COVID-19 severity and mortality in liver transplant recipients in various post-transplantation phases in the Iranian population

**Methods :** This was a cross-sectional study conducted among 24 patients undergone liver transplantation, who were referred to two transplant centers (Imam Reza and Montaseriyeh hospitals) affiliated to Mashhad University of Medical silences, Mashhad, Iran, during 2020-2021. The demographic and clinical characteristics of the patients were recorded in a checklist and the relationships between various variables were analyzed

**Results :** The majority of the patients (96%) were in the late phase of post-transplantation, and 8.3% of the cases expired. COVID-19 severity and mortality did not show a significant relationship with previous treatment with immunosuppressants and received dosage ($P>0.05$). In addition, there was no relationship between the symptoms of COVID-19 and immunosuppressant dosages, except for headache. No significant correlation was found between immunosuppressants dosage and laboratory findings, and only prednisolone dosage was found to be correlated with heart rate ($r=-0.62$, $P=0.03$), BUN ($r=-0.84$, $P=0.002$), and D-dimer ($r=-0.72$, $P=0.01$)

**Conclusion :** Severe SARS-CoV-2 infection was reported in the majority of liver transplant recipients. The severity of COVID-19 was not related to previous treatment with immunosuppressants and received dosage

**Keywords :** COVID-19, Immunosuppressive, Mortality, Transplantation

# P245-129: Prevalence of COVID 19 in the Brain-Dead Candidates for organ transplantation

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**Background and Aim :** This study aimed to evaluate the prevalence of Coronavirus Disease 2019 (COVID-19) positive cases meeting clinical brain death criteria; moreover, it was attempted to assess the uncommon manifestations of the infection in this study

**Methods :** This retrospective observational study was conducted on all brain-dead patients who were referred to the emergency department of hospitals in Mashhad, Iran, from February to October 2020. The demographic characteristics, clinical information, and laboratory data were collected and recorded in a researcher-made checklist

**Results :** The PCR test result was positive for COVID-19 in 54% of the patients, and syncope was reported in 16.1% of the cases (n=10). Furthermore, the majority of the patients (52.9%) showed central nervous system (CNS) hemorrhagic manifestations. A comparison was made between the patients with positive and negative PCR test result in terms of syncope; accordingly, there was a significant difference between them in this regard ($\chi 2$=4.5; P=0.03). The CNS hemorrhagic manifestations were significantly higher in patients with positive PCR, compared to those with negative PCR ($\chi 2$=4.57, P=0.03). Moreover, the grand glass opacity and pleural effusion were the most common findings of the chest computed tomography in brain-dead patients with COVID-19

**Conclusion :** Due to the high prevalence of COVID-19 among brain-dead patients, it seems that syncope attack should be regarded as one of the possible symptoms of COVID-19. Moreover, syncope as a result of COVID-19 may itself cause traumatic events. It is worth mentioning that CNS hemorrhagic manifestations have been reported in more than half of the patients with brain death.

**Keywords :** Brain death, COVID-19, Prevalence, Transplantation

# P246-156: Evaluation of Blood culture and antimicrobial susceptibility pattern of bacteria isolated via VITEK2 from Hospitalized Patients with severe COVID-19

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**Background and Aim :** Antibiotic-resistant bacterial infections are one of the leading causes of morbidity and mortality in hospitalized patients with viral respiratory infections. In this regard, the coincidence of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic with the global crisis of antibiotic resistance has complicated the problem.

**Methods :** This retrospective descriptive study was conducted on patients with acute COVID-19 who were hospitalized in the intensive care unit (ICU) of Imam Reza Hospital in Mashhad, Iran, during the three COVID-19 peaks (between 2019 to 2020). The participants were chosen based on information found in the medical records of patients who were diagnosed with COVID-19 by laboratory diagnostic tests and PCR tests between March 2019 and March 2020.

**Results :** In general, the information of 25 patients (21 male and 4 female) were gathered. Source of culture was blood 100 % of patient (25 patients). All patients suffered from severe COVID-19. The identified agents isolated from patients were Gram-negative bacteria and (n=12, 46%) and Gram-positive bacteria (n=13 54%). . Non-Fermenting Gram-Negative Bacterium (Pseudomonas aeruginosa, Acinetobacter baumannii complex, and Stenotrophomonas maltophilia) was observed in five cases. Based on the obtained results, three strains of Acinetobacter baumannii complex was extreme drug resistant (XDR) ,that was sensitive to Tigecycline and Colistin (MIC≤0.5). Pseudomonas aeruginosa was Carbapenemase-producing Enterobacteriaceae (CPE) , that was resistance to Meropenem and Imipenem at the concentration of ≥16. Stenotrophomonas maltophilia was sensitive to Tigecycline amd Trimethoprim Sulfamethoxazole (MIC≤2.37). Among, gram- positive bacteria, two strains isolated from S. aureus was Methicillin-resistant S. aureus (MRSA) at the concentration of >2 (Oxacillin), while Cefoxitin was sensitive to S. aureus. Enterococcus was Vancomycin-resistant Enterococcus (VRE) at the concentration of higher than 4 (MIC≥32).

**Conclusion :** The serious and dangerous organisems including MRSA, VRE, VRSA, XDR acinetobacter baumannii, CPE have been isolated from clinical specimens of critical COVID-19 patients. There are some evidences on the remarkable increase of various antibiotics MIC

during COVID-19 pandemic due to antibiotic-induced pressure towards mutations, which highlight the impact the use of steroids on the risk to develop during COVID-19.

**Keywords :** COVID-19, Blood culture, antimicrobial

# P247-168: SARS-CoV-2 as a betacoronavirus comprises five structural proteins?

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1. *MiladZandi*
2. *Letter*

**Background and Aim :** Dear editor, We read with interest a review article by Bakhshandeh et al. (Bakhshandeh et al., 2021). The authors considered hemagglutinin esterase (HE) as one of the structural proteins of SARS-CoV-2 (Bakh- shandeh et al., 2021). Although, scientific evidences show that the genome of SARS-CoV-2 lacks the HE gene and it has no hemagglutinin- esterase glycoprotein (Kumar et al., 2020; Anastasopoulou and Mouzaki, 2020; Crawford et al., 2020; Zhang et al., 2020). Thus, HE cannot be considered as an antigenic component in SARS-CoV-2 and it has no role in SARS-CoV-2 infection.

**Methods :** SARS-CoV-2 as a betacoronavirus contains a non-segmented posi- tive-sense, single-stranded RNA (Pal et al., 2020). The genome of SARS- CoV-2 has been sequenced, and based on the genomic sequence, SARS- CoV-2 shared 79.6% sequence identity to SARS-CoV and 96% identity similar to bat coronavirus (Zhou et al., 2020). The genome organization of SARS-CoV-2 is 5'UTR-Rep-S-3a-3b-E-M-6-7a-7b-8-N-10-3'UTR (Abdel-Moneim and Abdelwhab, 2020).

**Results :** Coronaviruses comprise four structural proteins spike (S), envelope (E), membrane protein (M), and nucleoprotein (N) (Fani et al., 2021), however, some betacoronaviruses such as OC43-CoV, Bovine-CoV and HKU1-CoV and, murine hepatitis virus encode hemagglutinin esterase (Lang et al., 2020). Therefore SARS-CoV-2 lacks HE and comprises four structural proteins S, E, M and N.

**Conclusion :** Declaration of competing interest The authors declare that there is no conflict of interest for this manuscript entitle "SARS-CoV-2 as a betacoronavirus comprises five structural proteins?"

**Keywords :** SARS-CoV-2 , betacoronavirus , hemagglutinin esterase

# P248-191: Seroepidemiological Investigation of SARS-CoV-2 Infection among Asymptomatic Children in Tehran

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**Background and Aim :** COVID-19 is an emerging infectious disease; however, there is little data about the infection, disease severity and its relationship to demographic characteristics in children. In current study, a seroepidemiological survey was done to show infection rate among asymptomatic children in Tehran.

**Methods :** In this investigation, children younger than 14 years old who had referred to laboratories during invitation through Snapp urban transportation system, public health centers, and outpatients' admission units of private and governmental clinics during autumn, winter, spring and summer entered to the study. Blood samples were collected in gel clotted tubes, and related sera were preserved for measurement of IgG antibody ratio against SARS-CoV-2 using EUROIMMUN ELISA kit. Demographic information and infection status in participants were reported by completing questionnaires and the relationship between variables were examined by statistical analysis.

**Results :** Out of 1142 blood samples collected from children with no common COVID-19 symptoms, history of SARS-CoV-2 infection was detected in 33.3% of them (381/1142). Borderline status was characterized among 3.5% (40/1142) of the samples. The infection rate was higher among children lower than six years old in compare to other age groups.

**Conclusion :** Results of this study showed that SARS-CoV-2 infection can occur in children, which could be without common symptoms. Restriction of children from contact with family members who are at increasing risk of the infection is recommended during the pandemic to reduce its secondary transmission.

**Keywords :** ELISA, COVID-19, Immunoglobulin G, SARS-CoV-2, Antibody ratio

# P249-204: Ocular manifestations of COVID-19: a narrative review

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**Background and Aim :** Until now, seven types of CoVs are known to infect humans. Mostly lead to infections in the respiratory system. Many other viruses, such as adenovirus, enterovirus 70, and H1N1, can cause ocular complaints besides systematic symptoms. According to recent reports, conjunctival congestion, conjunctivitis, epiphora, or chemosis are common ocular symptoms in COVID-19 patients.

**Methods :** A comprehensive search was done using the electronic databases of PubMed, Scopus, and Google Scholar. The keywords coronavirus infection, COVID-19, SARS-CoV-2, Ocular, conjunctivitis were used to identify Ocular diseases and Ocular manifestations articles of COVID-19 for identifying and managing infected patients.

**Results :** Based on this review study, in addition to lung, COVID-19 can cause diseases in other organs, including the eyes, which subsequently leads to ocular diseases and manifestations like conjunctivitis, episcleritis, keratoconjunctivitis, etcetera. As the eyes are one of the possible routes for entrancing the virus to the host, ocular manifestations caused by virus entrance may be evidence of infection in the host. As a result, detecting and treating these ocular manifestations can prevent virus transmission.

**Conclusion :** Although there is no documented evidence for possible SARS-CoV-2 transmission via ocular secretion, it is probable to be infected by COVID-19 from a confirmed COVID-19 patient with conjunctivitis. Therefore, the use of Personal protective equipment (including Slit Lamps) and avoid touching the eyes before washing or disinfecting the hands with Alcohol-based hand sanitizers to prevent infection is recommended.

**Keywords :** COVID-19, SARS-CoV-2, Ocular, conjunctivitis

# P250-219: Is it reasonable or irrational to take selenium and vitamin D supplements in the COVID 19 epidemic?

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**Background and Aim :** Vitamin D and selenium seem to be important factors in COVID-19 disease and these two factors can be supplemented for these patients because selenium has a positive effect on the function of vitamin D.In this study, we are trying to find a significant association between the rate of symptoms and coronary mortality with selenium and vitamin D levels in previous studies.

**Methods :** ((((covid 19) OR (sars cov 2)) AND (vitamin d)) OR (selenium)) AND (("2019"[Date - MeSH] : "3000"[Date - MeSH]))

**Results :** Vitamin D and selenium seem to be important factors in COVID-19 disease. However, vitamin D has not yet been fully confirmed as an effective ingredient in the treatment

**Conclusion :** Previous studies on selenium have shown that there is a significant relationship between blood selenium levels and the severity of COVID-19 symptoms. However, its consumption should be closely monitored because excessive use can be toxic to the body. Vitamin D should be considered. Almost all the articles have considered it's used to be effective in preventing and increasing resistance to COVID-19, but there is still controversy about its use for a positive effect on the treatment process of COVID-19

**Keywords :** covid 19 selenium vitamin D

# P251-231: Candidemia in COVID-19 patients; Novel cases in the northeast of Iran

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**Background and Aim :** Blood infections caused by Candida species (candidemia) can be very serious. They can cause death in hospitalized patients, especially in COVID-19 patients. Accurate identification of pathogens plays an important role in the targeted treatment and the epidemiological status of this infection.

**Methods :** Twenty patients with candidemia showed positive Candida cultures through the BACTECH system and subculture on mycological media. The Candida isolates were purified using CHROMagar Candida, and the species were correctly identified by the 21-plex PCR method.

**Results :** Of the 20 patients, 4 (20%) had COVID-19 that all of them died in the one-year study. Two of the patients had two Candida species as C. albicans/ C. parapsilosis. The frequencies of the Candida isolates among the patients were C. albicans (n = 3, 50%), C. parapsilosis (n = 2, 33%), and, C. tropicalis (n = 1, 17%).

**Conclusion :** The mortality rate among COVID-19 patients affected by candidemia is high. C. albicans was the main cause of yeast-derived candidemia among the COVID-19 patients with candidemia.

**Keywords :** Candidemia, Blood, Candida, COVID-19

# P252-233: Skin manifestations associated with COVID-19: A meta-analysis from Case Reports/Case Series

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**Background and Aim :** Since the onset of the 2019-nCoV disease (COVID-19), many skin manifestations have been reported in COVID-19 patients. This study aims to provide a systematic review and meta-analysis of various skin manifestations among patients with COVID-19 through case reports/case series and prevalence studies.

**Methods :** A systematic literature search strategy was conducted by reviewing original research articles published in Medline, Web of Science, and Embase databases in 2020. Statistical analysis was performed using STATA software, version 14.0 (Stata Corporation, College Station, Texas, USA) to report the global prevalence of skin manifestations among patients with COVID-19.

**Results :** Forty-three studies (35 articles were case reports/case series, and 8 articles were prevalence studies) were included in our study. A meta-analysis of prevalence studies showed that skin manifestations among patients with COVID-19 were reported in four countries (China, Thailand, France, and Italy), with an overall prevalence of 1.0% [(95% CI) 0.1–1.9] among 2,621 patients. Evaluation of the results of the case reports/case series revealed that, out of 54 patients with COVID-19, 48 patients (88.8%) showed skin manifestations. Erythematous rash (59.1%) and urticaria (14.8%) were the most common skin manifestation reported in studied patients.

**Conclusion :** Infection with 2019-nCoV may lead to skin manifestations with various clinical symptoms. These clinical features combined with clinical symptoms of COVID-19 may aid in the timely diagnosis of patients with COVID-19.

**Keywords :** coronavirus, 2019-nCoV, COVID-19, skin manifestations, meta-analysis

# P253-239: A bioinformatic analysis of Staphylococcal enterotoxin B structure alteration in COVID-19 variants

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**Background and Aim :** Since the global outbreak of COVID-19, amounts of papers pointed to the superantigen (SAg) activity of SARS-COV 2. By molecular analysis, a superantigen-like motif, similar to Staphylococcal enterotoxin B (SEB), near the S1/S2 cleavage site of SARS-CoV-2 Spike protein was discovered.it seems that mutations in SARS-COV 2 Spike protein may cause different SAg activities. Here, based on bioinformatics data, SEB-like Motifs were compared in each variant.

**Methods :** Based on CDC data, the SARS-COV 2 variants from April 2019 to June 2021 were recognized and Variants of Concern were extracted (4 mutations). the spike sequences and 3-D structures especially the superantigen motif were investigated from "Uniport" and "viralzone.expasy" databases, then the sequences were compared by NICBI blast. finally, the Obtained data were evaluated.

**Results :** the variants extracted were included: ALPHA, BETA, DELTA, and GAMMA. The original (Wuhan) SARS-COV 2 SEB-like SAg sequences were: TNSPRRARSV. ALPHA, BETA, DELTA and GAMMA SEB like superantigens sequences were: TNSHRRARSV, TNSPRRARSV, TNSRRRARSV, TNSRRRARSV. In the ALPHA variant, Histidine replaced proline, BETA no change was observed, In DELTA, Arginine replaced proline and in gamma, Arginine replaced proline also.

**Conclusion :** The SEB-like SAg sequence variation was observed in ALPHA, DELTA and GAMMA and interestingly the level of superantigen activity of these variants has been changed. Also, Despite the similarities between Wuhan and BETA SAg sequences, other factors may have effect on superantigen activity and lethality of BETA variant. More researches required to realize of SAg alteration impacts on virus properties.

**Keywords :** SARS-CoV-2, super antigen , Staphylococcal enterotoxin B , Bioinformatic, spike

# P254-250: Coronavirus disease 2019 (COVID-19) among HIV-positive patients: A systematic review and meta-analysis

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**Background and Aim :** Whether human immunodeficiency virus (HIV) infection is associated with a higher risk of morbidity and mortality due to corona virus disease 2019 (COVID-19) is unclear. In the present study, we aimed to provide a systematic review and meta-analysis of HIV among patients with COVID-19 through case reports/case series and prevalence studies.

**Methods :** A systematic literature search strategy was conducted via reviewing original research articles published in Medline, Web of Science, and Embase databases in 2019 and 2020. Statistical analysis was performed using STATA software, version 14.0 (Stata Corporation, College Station, Texas, USA) to report the prevalence of HIV among patients with COVID-19. Case reports/case series were also evaluated as a systematic review.

**Results :** Sixty-three studies (53 case reports/case series and 10 prevalence studies) were included in our study. A meta-analysis of prevalence studies showed that HIV infection among patients with COVID-19 were reported in 6 countries (Uganda, China, Iran, USA, Italy and Spain) with an overall frequency of 1.2 % [(95% CI) 0.8-1.7] among 14424 COVID-19 patients. Conforming to the results of the case reports/case series, 111 patients with HIV have been reported among 113 patients with COVID-19 from 19 countries. Most of the cases were in the USA, China, Italy, and Spain.

**Conclusion :** People with HIVare more likely to develop more severe complications from COVID-19. . Targeted policies should be considered to address this raised risk in the current pandemic. Our findings highlight the importance of identifying underlying diseases, co-infections, co-morbidities, laboratory findings, and beneficial treatment strategies for HIV patients during the COVID-19 pandemic.

**Keywords :** Prevalence, 2019 novel coronavirus, COVID-19, HIV, Meta-analysis

# P255-251: The first case of fatal mucormycosis in a patient with Covid 19 in Ghaem Hospital of Mashhad

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**Background and Aim :** Fungal infections are one of the most common infections, especially in susceptible and immunocompromised patients. In some cases, the concurrence of fungal infections such as mucormycosis with other infections such as COVID-19 can disrupt the treatment and control of the infection.

**Methods :** The patient was a 70-year-old woman with underlying diabetes who was admitted to Ghaem Hospital in Mashhad due to COVID-19. He had sinusitis at the beginning of hospitalization and the maxillary sinuses were rapidly expanding necrotic. The sinus tissue specimen was examined for routine mycological procedures.

**Results :** The results of direct experiments are reported by observing broad mycelium without septate (non-septate hyphae), with a Rhizopus spp. colony. Despite timely treatment with amphotericin B and other supportive therapies during COVID-19, the patient died after 10 days due to disease progression.

**Conclusion :** Mucormycosis is one of the deadly and acute infections that timely diagnosis and treatment with new antifungals can be effective in reducing mortality, especially among COVID-19 patients.

**Keywords :** Fungal infection, Mucormycosis, COVID-19, Mashhad

# P256-255: Comparison of coronavirus epidemics: SARS, MERS, COVID-19

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**Background and Aim :** From 2002 to 2019, three deadly human viruses broke out, all three coronaviruses of the family (Coronaviridae) belonging to the beta-coronavirus class, and their genetic material is positive in the form of a single-stranded ribonucleotide chain. The aim of this study was to compare the coronavirus epidemics of SARS, MERS, and COVID-19.

**Methods :** The present study was a brief review study designed in 2021. PubMed / Medline and Scopus databases were used to search for similar studies and extract content. Selected keywords for the search included “Coronavirus”, “COVID-19”, “SARS”, “and MERS”. Summaries of articles published in congresses and conferences were excluded from the study. Initially, 5 articles were finally evaluated.

**Results :** Various studies have shown that SARS, MERS and COVID-19 coronaviruses became prevalent in 2002, 2012 and 2019, respectively, and their mortality rates are estimated at 10, 34 and 4%, respectively. The incubation period of coronavirus is 5-6 days in MERS, while SARS is 2 to 7 days and Covid-19 is 2 to 14 days. COVID-19 is more contagious than SARS and MERS and has a high rate of spread, but the mortality rate in MERS is higher than that of SARS and COVID-19.

**Conclusion :** The results of various studies showed that all three types of coronavirus have the same symptoms as fever, chills, fatigue, headache, cough, and shortness of breath. The viral composition of Covid-19 is 79% and 50% similar to that of SARS and MERS, respectively, so studying the SARS and MERS viruses can greatly enhance human immunity to COVID-19.

**Keywords :** COVID-19, SARS, MERS

# P257-280: Coronary Artery Diseases in Patients with COVID-19: A Systematic Review and Meta-analysis

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**Background and Aim :** Comorbidities affect a high percentage of COVID-19 patients. Several studies conducted in China reveal that 15–40% of patients with COVID-19 had a history of cardiac disease. Laboratory indicators of cardiac injury and cardiovascular involvement are found in 2–5% and 10–30% of patients, respectively. COVID-19 and cardiovascular disease are directly related in clinical studies. Preexisting cardiovascular diseases in patients with COVID-19 lead to more severe complications and a higher mortality rate.

**Methods :** A comprehensive systematic literature review was conducted by searching original papers published in Medline, Web of Science, and Embase databases in 2021. The following phrases were used in the search strategy: COVID OR COVID-19 OR novel coronavirus OR new coronavirus OR coronavirus 2019 OR 2019-nCoV OR nCoV OR CoV-2 OR SARS-2 OR SARS-CoV-2 OR severe acute respiratory syndrome coronavirus 2, CAD OR coronary artery disease.

**Results :** The meta-analysis of prevalence studies indicated that the frequency of CAD was 10.8% (95% CI 8.2-13.3) among 10889 patients with COVID-19 in America, 12.4% (95% CI 9.6-15.2) among 5799 patients in Europe, and 11.7% (95% CI 9.6-13.8) among 3400 patients in Asia. No data were available on the prevalence of CAD infection among patients with COVID-19 in Africa and Oceania. The highest incidence of CAD was reported among patients with COVID-19 in the USA.

**Conclusion :** The results of the present meta-analysis reveal that minor symptoms such as cough, shortness of breath, or abnormal laboratory findings should be considered in people with a history of coronary artery disease, especially the elderly and men. Timely referral to medical centers prevents infection and worsening of the clinical condition in patients.

**Keywords :** CAD, Coronary Artery, COVID-19, SARS-CoV-2

# P258-281: COVID-19 infection and diabetes : A Narrative Review

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**Background and Aim :** The pandemic of the novel human coronavirus disease (COVID-19) has become an evolving global health issues due to high morbidity and mortality rate. Patients who have comorbidities including diabetes, hypertension, obesity, cancer and cardiovascular disease significantly increases the risk for administration into the ICU and this situation also could affect the survival of infected patients. Among the various comorbidities in this review we emphasis in diabetic patients who are highly affected because of increased viral entry into the cell via angiotensin-converting enzyme 2 (ACE2) in the respiratory system and therefore decrease immunity.

**Methods :** A comprehensive study was conducted using the electronic databases of PubMed, Scopus, and Google Scholar. The keywords coronavirus, COVID-19, SARS-CoV-2, Diabetes, Comorbidity and underlying diseases were used to identify prevalence of diabetes in patients with COVID-19.

**Results :** Diabetes causes damage to the respiratory system due to lung damage caused by microangiopathy. In diabetic people compared with healthy individuals, the lung capacity is decreased, possibly due to increased collagen and elastin accumulation in the connective tissue of the chest wall and lung parenchyma compared to healthy individuals. COVID-19's infection is affected by diabetes, creates a more stressful condition that accompanies hyperglycemia. Secretion of indicator hormones like catecholamines and glucocorticoids can increase blood sugar. Based on researches, hypoglycemia regulates pre-inflammatory monocytes and increases the platelet numbers. These conditions are related to cardiovascular mortality in diabetic patients. Also, it has been shown that diabetic people affected by COVID-19 have a severe condition, and higher mortality rate than non-diabetic patients.

**Conclusion :** Due to the rapid global prevalence of COVID-19 and its huge mortality rate, the importance of virus pathogenesis and different clinical aspects can be a great help to have an accurate and rapid diagnosis for patients. Also, examine some disease severity predisposing factors in patients with COVID-19 is substantial. Research conducted on comorbidity and COVID-19 shows that people with high age, diabetes, hypertension, and suppressed immune

system have a higher risk of being affected by the virus and also a higher mortality rate. Thus, clinicians should diagnose and cure COVID-19 patients with underlying diseases.

**Keywords :** COVID-19, Diabetes, Comorbidities, Manifestations

# P259-310: Evaluation of clinical trials for affected people with COVID-19 in Qorveh city

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**Background and Aim :** COVID-19 is an infectious disease caused by Corona virus. Many studies have shown that Corona virus can cause significant changes in clinical trials and hematology of patients. Symptoms of COVID-19 vary from person to person, but often include fever, cough, headache, fatigue, respiratory problems, and loss of smell and taste. At least one-third of infected people do not have significant symptoms. Accordingly, the present study aimed to access the effects of COVID-19 on the experiments of a number of patients.

**Methods :** In this descriptive-analytical study, among patients affected by Corona virus, they admitted to Shahid Beheshti Hospital in Qorveh, 60 patients were randomly selected and the results of their biochemistry and hematology tests were analyzed by SPSS 20.0 software. Pearson correlation were used to compare the means and the relationships.

**Results :** Results showed that most of the patients were in the age range of 61 to 70 years old. Cr level in 60% of patients was less than one and had a significant difference compared to other groups ($P<0.01$). Also, the frequency of Na indicates that 60% of patients showed less than 35 mEq/l, which is less than the normal range (135-135). About 84% of people had a K level of 4.1 to 5 (normal range =3.6-5.2). More than 70% of people have WBC less than 5,000 per µl. RBC in 50% of patients was 4.1 to 5. About 17% of patients had higher than normal RBC. The results showed that PLT in 45% of people was 200.1-300 (×109 per liter). The level of MCV in 40% of patients was higher than normal. Most patients (80%) had MCH from 35 to 31.5 (g/dL). Results showed a positive linear relationship between increasing the age and WBC ($R^2 = 0.077$). Also, with increasing age, PLT showed a high decreasing ($R^2 = 0.257$).

**Conclusion :** In this city, most of the people affected by Corona virus and were hospitalized,(that most of them was women) was old people (60-71 years old) and with increasing age of patients, the amount of PLT decreased and the rate of MCV and MCH increased.

**Keywords :** Corona virus, Clinical traits, Qorveh

# P260-315: A review of the therapeutic effects of Althaea officinalis L as involved in the treatment of secondary bacterial and fungal infections COVID_19

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**Background and Aim :** One of the leading causes of death in patients with Covid_19 is secondary bacterial and fungal infections caused by a weakened immune system. Therefore, due to antibiotic resistance against bacterial and fungal infections, the use of herbs with fewer side effects and more effect can be of great help in the treatment of patients with Covid_19. The aim of this study was to review the therapeutic effects of Althaea officinalis as a possible candidate in the treatment of secondary bacterial and fungal infections in patients with Covid_19.

**Methods :** The present study is a review study that by searching in reputable scientific databases such as PubMed, Google scholar, Scopus, from 2015 to 2021 using the keywords SARS-Covid_19, , Althaea officinalis, antibacterial, antifungal , treatment, The latest information has been obtained.

**Results :** In this study, 62 articles were reviewed, so Althaea officinalis with effective compounds such as mucilage, malvin, anthocyanin, flavonoids such as camiferol, quercetin, has antibacterial activity and is antifungal that the results of these studies in vitro, in vitro and clinical trial confirm the therapeutic effects of Althaea officinalis

**Conclusion :** Due to the pandemic nature of Covid_19 disease and its complications such as decreased immune system and pathogenicity, bacterial and fungal infections Such as Staphylococcus aureus, Streptococcus pneumoniae, Pseudomonas aeruginosa, Candida albicans, Aspergillus fumigatus that lead to sepsis, blood clots and shock, diffuse infections, and mortality require effective medication. which according to the study of Althaea officinalis plant due to their effectiveness in case of failure in the treatment of drugs with Covid_19 is experienced in clinical trials

**Keywords :** Althaea officinalis L, Covid_19, Therapeutic effects, treatment

# P261-316: A review of the Anti-inflammatory effects of Mentha pulegium as a possible candidate in the treatment of patients with COVID_19

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**Background and Aim :** One of the major complications in patients with Covid-19 disease is cytokine storm, which is an abnormal immune response that leads to severe pneumonia. TNF-α, IFN-α are important secretory cytokines in this disease, both of which have a synergistic effect in inflammation, lung damage and mortality. Due to the lack of a suitable drug in the treatment of Covid-19 disease, many studies have shown that plant extracts have a variety of biological effects such as immunomodulatory properties. the aim of this study was to review the Anti-inflammatory effects of Mentha pulegium as a possible candidate in the treatment of patients with COVID_19.

**Methods :** The present study is a review study by searching reputable scientific databases such as Pubmed Google scholar, Scopus from 2015 to 2021 using the keywords SARS-COV-2, Covid-19, TNF-α, IFN-γ, cytokine storm , Treatment, Anti-inflammatory Latest information obtained.

**Results :** In this study, 30 articles were reviewed, Therefore, Mentha pulegium plant has anti-inflammatory activity with effective compounds such as alkaloids, flavonoids, thymol and carvacrol. The results of these studies as invitro-invivo confirm the therapeutic effects of Mentha pulegium.

**Conclusion :** Due to the widespread prevalence of Covid_19 disease and secretion of TNF-α, IFN-γ, which can cause shock due to further spread of lung damage and subsequent pneumonia, acute respiratory distress syndrome, loss of respiratory control and other organs, and death. Therefore, a drug is needed to block and inhibit these cytokines. Due to having the mentioned active ingredients, oregano Mentha pulegium plant can be evaluated as a possible drug candidate in the treatment of patients with covid_19 clinical trial.

**Keywords :** Mentha pulegium, covid-19, Anti-inflammatory,Treatment

# P262-367: The Opportunistic Infections Related to Recent SARS-Cov-2 Infection Outbreak

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**Background and Aim :** The role of opportunistic infections in the morbidity and mortality rates of the coronavirus disease 2019 (COVID-19) patients remains challenging in resource-poor settings. Recent studies based on co-infections and superinfections of hospitalized patients with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection discovered some opportunistic infection in dead individuals including fungal, bacterial and viral infections.

**Methods :** Patients with acute respiratory distress syndrome are more susceptible to influence by opportunistic infections. And also, whom received broad-spectrum antibiotics, immunosuppressants or corticosteroid, and supported by invasive or noninvasive ventilation are the other high-risk groups. Unnecessary antimicrobial utility for SARS-CoV-2 infected patients following admission, potentially promoting the selection of drug resistant infections. The respiratory bacterial infections including Streptococcus pneumoniae and Staphylococcus aureus were the most common types. Coagulase-negative Staphylococci are more frequent organisms causing bloodstream infection. Fungal co-infection was more diagnosed by Aspergillus fumigatus tracheobronchitis and Candida albicans in bloodstream.

**Results :** Although recent reports announced the frequency of opportunistic infections are uncommon and it is not comparable to the other viral pandemics, but empirical antimicrobial therapy is one of the critical factors that increase opportunistic infections in COVID-19 patients.

**Conclusion :** In conclusion, the reliable risk factors determination is difficult for evaluation, because some factors like genetic variation, chronic disease, etc raised the potential of co-infections and superinfections. In this manner based on WHO recommendation, in mild to moderate COVID-19 patients the antimicrobials treatment should not prescribed without clear indexes of infection.

**Keywords :** COVID-19, SARS-CoV-2, opportunistic infections, drug resistance

# P263-368: The Correlations Between Epidemiological and Clinical Characteristics, laboratory tests and CT Scan reports in the diagnosis of cases 2019 novel coronavirus pneumonia. A Diagnostic Accuracy Study

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**Background and Aim :** The role of laboratory parameters and the relationship of them with radiology reports, CT scan and clinical outcomes in screening of COVID-19 patients not been definitely established, but this disease presented a major challenge in the field of clinical tests, radiology reports, clinical outcomes that help to monitoring and treatment COVID-19 disease.

**Methods :** This study was performed on 340 suspected COVID-19 patients, who presented to Chamran Hospital, Shiraz University of Medical Sciences Shiraz, Iran from 20 February to 31 August, 2020. Information each patient's will be completed using a data collection forms based on records. The evaluation of lungs involvement in CT scan and their relationship with laboratory indicator including biochemical and hematological factors, is the best scale for the severity and prognosis of Covid 19 patients.

**Results :** The findings of this study indicated ALT, AST, CRP, NEU, LDH, and Urea have very good accuracy in predicting cases with positive RT-PCR for COVID-19. Considering the significant difference in CT scoring and laboratory parameters, can hope to model or predict the results of coronavirus testing based on routine laboratory tests. We realized CT scan findings may be predictive of patients ‘outcome and had a correct correlate with laboratory findings and disease severity.

**Conclusion :** In conclusion, finding of this study shown the correlation of clinical and laboratory findings with CT-based quantitative score of pulmonary involvement in COVID-19 pneumonia and our findings could be usable to development future clinical research associated with COVID-19 infection and show relationship of CT scan reports and clinical outcomes in the diagnosis and severity of patients with COVID-19.Thus, expected future studies can indicated better clarify impact on clinical decision-making and larger clinical trials.

**Keywords :** Clinical Outcomes, laboratory findings, coronaviruses, COVID- 19 infection, CT scan reports.

# P264-386: Molecular characterization of airway yeast colonization in tracheal aspirates of patients with SARS-CoV2 infection admitted to the intensive care unit in Isfahan, Iran

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**Background and Aim :** The coronavirus disease 2019 (COVID-19) have been related with significant morbidity and mortality even when appropriately diagnosed and treated. Recent studies have indicated that SARS CoV-2 might increase the risk of bacterial and fungal co-infections. There is currently increasing concern about the relation between fungal infections or colonization with SARS-COV2 infection. This study aimed to investigate the prevalence of yeast colonization in tracheal aspirates in patients with SARS-CoV2 infection admitted to the intensive care (ICU) unit by conventional and molecular identifications.

**Methods :** This study was conducted on tracheal aspirates of patients with SARS-CoV2 infection in intensive care unit (ICU) referring to the Alzahra hospital in Isfahan, Iran. Demographic profile, predisposing factors, presenting complaints and clinical findings of clinically diagnosed patients were evaluated and analyzed. Tracheal aspirates samples were collected, transported and examined by direct examination and then cultured on Sabouraud dextrose agar and CHROM agar Candida medium. Genomic DNA was extracted by boiling method and identified based on different molecular method with PCR-RFLP technique, amplification of the hyphal wall protein (HWP) gene and sequencing of the internal transcribed spacer (ITS) region.

**Results :** A total of 94 samples were obtained from men (n=55, 58.51%) and female (n=39, 41.49%) patients with SARS-CoV2 infections. Molecular identification showed that 51 species C. albicans (54.26%), 20 species C. tropicalis (21.28 %), 18 species C. glabrata (19.15%), 1

species C. krusei (1.06%),1 species C. lusitaniae (1.06%), 2 species C. kefyr (2.13%) and unusual yeast-like species, Wickerhamomyces anomalus (1.06%). Candida albicans (n = 50, 98.04 %), C. africana (n = 1, 1.96%) were isolated from 51 C. albicans complex species. The prevalence of Candida species demonstrated no statistically significant relationship with age, gender and patients with SARS-CoV2 infection in intensive care unit (ICU) (P > 0.05).

**Conclusion :** To conclude, it is necessary to adopt a consistent method for the implementation of primary detection of yeast colonization in patients with SARS-CoV2 infections. However, further studies are still needed to better define the epidemiology of fungal colonization in COVID-19 patients from the world and the clinical significance of their isolation.

**Keywords :** Molecular characterization, yeast colonization, SARS-Co2 infection, intensive care unit

# P265-415: Investigation the effect of probiotics in the treatment of SARS-CoV-2 (Systematic review)

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**Background and Aim :** The coronavirus disease 19 (COVID-19) is a highly transmittable and pathogenic viral infection and real health challenge of the 21st century for all human life worldwide. Probiotics can contribute to defense against potential pathogens by promoting effective immune interactions. So the aim of this study is investigating the effect of probiotics in the treatment of SARS-CoV-2.

**Methods :** This review article was performed within articles published at PubMed, Science direct, Google Scholar, SID and Cochrane until August 2021. The keywords were SARS-CoV-2, probiotics and treatment. By searching this database; 152 articles were found, 74 of them by reading titles and abstracts were removed. 78 articles were selected under the inclusion criteria. All articles chosen from English and Persian articles.

**Results :** Finally, 78 articles were included in the study. Probiotic actions such as IgA secretion stimulation to improve mucosal immunity, influence on cytokines production by intestinal epithelial cells, modulation of levels and function of regulatory cells, activation of phagocytosis and macrophage production, and induction of dendritic cells maturation, probably affected systemic inflammation. Adjunctive therapies based on the modulation of the gut-lung axis and re-establishment of eubiosis could be a significant therapeutic procedure for diminishing the harmful ramifications of COVID-19. Lactobacillus contained a HSP27-inducible polyphosphate fraction. Thus, probiotic-derived polyphosphates, escalated the epithelial barrier function and kept intestinal homeostasis through the integrin-p38 MAPK pathway. Therefore, the role of probiotics-based therapy became substantial in the management of viral infections. Probiotics could modulate host immune responses and warded off the cytokine storm produced during COVID-19 infection.

**Conclusion :** It seems that probiotics have abundant benefits such as balancing the composition of human gut microflora, strengthening gut barrier function, and protective immune responses in COVID-19 management. However, need to be more research done at this topic.

**Keywords :** Probiotics, SARS-Cov-2, COVID-19, Treatment

# P266-427: Frequency and Antimicrobial Resistance Pattern of Bacterial Isolates Involved COVID-19 Hospitalized Patients in Two Main Zanjan Educational Hospitals in 2019-2020

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**Background and Aim :** The outbreak of COVID-19 has been challenging the global health systems. As one of the major associated concerns, microbial coinfections and antimicrobial resistance (AMR) play critical roles in the prognosis of the disease. This study aims to evaluate coinfections in COVID-19 patients and the regarding AMR.

**Methods :** A number of 5530 Real Time PCR-confirmed COVID-19 cases, who were admitted to two major educational Hospitals in Zanjan, Iran, from February 2019 to February 2020 were investigated. Specimens were cultured on selective media. Isolate identification, disc diffusion susceptibility tests and data analysis were carried out.

**Results :** Bacterial and fungal coinfections were confirmed in 423 patients (8.1%). Coinfections were more prevalent among females (53.2%) than males (46.8%). Conifected patients had a mortality rate of 54.8%, which was significantly higher than that of those without coinfections (12.2%). Acinetobacter baumannii was the most prevalent bacteria isolated from respiratory tract (15.4%) and blood (2.1%). Escherichia coli (12.5%) was the most frequent bacteria in urine. Fungal coinfection was confirmed in 174 (3.36%) patients. Gram-negative bacteria were highly sensitive to colistin (95.2%) and widely resistant to ampicillin and trimethoprim-sulfamethoxazole (100%). Gram-positive bacteria were majorly sensitive to cefezolin, cloxacillin and vancomycin (75%). Tetracycline and ampicillin and were the least effective antibiotics for gram-positive bacteria with respective resistance rates of 100% and 91.3%.

**Conclusion :** Given the high incidence of bacterial coinfections is COVID-19 patients, it is important to develop rapid and efficient diagnostic, therapeutic and disinfection strategies to control these infections in the hospitals.

**Keywords :** Bacterial isolates, Covid-19, Drug resistant, Mortality and morbidity. Susceptibility patterns

# P267-1: Prevalence of ESBL Genes in Clinical Isolates of Pseudomonas aeruginosa from Burn Patients in Isfahan, Iran

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**Background and Aim :** Pseudomonas aeruginosa is very common in burn wound infections. The biofilm formation and the production of beta-lactamase enzymes have made this bacterium resistant to many antibiotics. This study aimed to evaluate antibiotic resistance, biofilm formation, and the frequency of strains that carry blaTEM and blaVEB.

**Methods :** A cross-sectional study was carried out from March 2017 to March 2018 on 103 clinical isolates of P. aeruginosa, identified from 420 burn wound infection samples by phenotypic tests. Antibiotic resistance and biofilm formation were evaluated by the Kirby-Bauer disk diffusion method and microtiter plate assay, respectively. Double disk synergy test (DDST) was used for phenotypical detection of Extended-spectrum beta-lactamases (ESBL) producing isolates. ESBL genes were detected by polymerase chain reaction (PCR).

**Results :** Of 103 strains isolated from burn wound infection, 91.3% were multiple drug resistance (MDR). The resistance to levofloxacin was the highest (93.2%). The ability of biofilm formation was observed in three groups: 47.6% of isolates had no biofilm formation, 38.8% were weak, and 13.6% showed moderate biofilm formation. The prevalence of DDST-confirmed ESBL was 54 (43.9%). The isolates had 28.15% and 21.35% of blaVEB and blaTEM genes, respectively.

**Conclusion :** This study showed that MDR strains are common in burn infections. Biofilm formation and produce beta-lactamase enzymes also showed a growing trend.

**Keywords :** Pseudomonas aeruginosa, Biofilm formation, Antibiotic-resistant, blaTEM, blaVEB

# P268-2: Bacterial Infections and Antimicrobial Resistance Patterns of Burn Wound Infections: A One Year Study from Burn Hospital, Isfahan, Iran

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**Background and Aim :** The development of infections in burn wound is serious because of their effects on the course of the disease and the patient outcomes. The rate of infection in burn cases is extremely high in developing country. The aims of this study were to identify the common bacterial agents responsible for burn wound infection and determine antimicrobial susceptibility patterns in burn Hospital, Isfahan, Iran.

**Methods :** This cross sectional study was conducted at one year period for all patient with burn wound infection. Burn wounds suspected of infection were collected aseptically and conventional bacteriological methods were followed for identification of the bacteria. Antimicrobial susceptibility tests were performed by using the disk diffusion method in accordance with CLSI recommendations.

**Results :** from the total of 1500 wound culture, 957(63.8%) samples were detectd positive. The highest rate of infection was in the ICU ward and the lowest was in the restoration ward. The most common gram negative bacterias were Acinetobacter baumannii (34.9%) with the highest and the lowest antibiotic resistance to Ceftazidime and Tobramycin. Among recovered Gram positive isolates, Staphylococcus aureus (10.2%) were the predominant isolates with the highest and the lowest antibiotic resistance to Penicillin and Vancomycin.

**Conclusion :** : Due to the variable nature of antibiotic susceptibility patterns and pathogens causing burn wound infection, continuous evaluation and detection of dominant bacterial infections and sensitivity patterns to locally available antibiotics in burn wound patients in order to modify the drug regimen for Proper antibiotic treatment is important and seems reasonable.

**Keywords :** bacterial infection, burn patients, antimicrobial resistance pattern

# P269-22: Prevalence and Population Structure of Helicobacter pylori Isolates from Patients with Dyspepsia in Isfahan, Iran

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**Background and Aim :** Helicobacter pylori (H. pylori), a spiral-shaped bacterium colonizing the human stomach, is generally acquired in childhood. This pathogen is highly diverse and can be used as genetic markers for predict the history of human migrations. This study was aimed to determine the genetic diversity of H. pylori isolates from patients with dyspepsia by the multilocus sequence typing (MLST), and update data on the prevalence of H. pylori among Iranian dyspeptic patients.

**Methods :** In this descriptive cross-sectional study, 165 gastric biopsy specimens were obtained from patients with dyspepsia referred to Dr. Shariati Hospital of Isfahan, Iran from April to July 2018. The status of H. pylori infection was determined by FISH in paraffin-embedded biopsy specimens. MLST of seven housekeeping genes was performed for 20 H. pylori isolates. The phylogenetic tree was plotted using CLC v8 and iTol software.

**Results :** The overall prevalence of H. pylori infection was 53.3%. In the results of the analysis of MLST, a total of 14 new STs were recorded. The results of the global analysis showed that all the isolates, with a wide diversity, have a genetic affinity with members of the European population, such as Italy and Russia, and are in the hpEurope haplotype.

**Conclusion :** Given the high prevalence of Helicobacter pylori infection in this region, early and accurate identification of patients seems necessary. Sequence analysis and determination of the origin of the phylogeny of strains can be effective in clinical management and monitoring of risk factors for chronic and recurrence of infection.

**Keywords :** Helicobacter pylori, MLST, prevalence

# P270-28: Polio virus inactivation using silver nanoparticles

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**Background and Aim :** Antiviral drug resistance these days becomes an important issue which led us to antiviral agents that can be effective against resistant strains of viruses. Silver nanoparticles count as one of these unresistable agents and many researches has done about their antiviral activity. There are different kinds of silver nanoparticles due to their synthesis methods and their components. In this study, biosynthesized silver nanoparticle with aqueous extract of dried Juglans regia green husk antiviral activity estimated against polio virus. This virus belongs to Picornaviridae family and is a sample for viruses without envelope and/or whit RNA genome.

**Methods :** Silever nanoparticle cytotoxicity examined through MTT assay and the nanoparticles was so toxic to be exposured Vero cell line in high stable concentrations that can show antiviral activity so gathering them after affecting on viruses becomes a solution. Viruses treated with the highest 24 hours stable concentration of silver nanoparticle which is 300 µg/ml and then added to magnetic Fe nanoparticles therefore they could be gathered using magnet. Treated virus exposure to cell without any cytotoxicity.

**Results :** Polio virus titration reduced after being treated with both silver nanoparticle and magnetic Fe nanoparticle that showed both of nanoparticles had antiviral activity and they enhanced each others through synergism mechanism and they resulted in at least 4 log inactivation.

**Conclusion :** Silver nanoparticle and magnetic Fe nanoparticle could use as an antiviral agents but using high stable concentrations of silver nanoparticle is possible when it used with magnetic Fe nanoparticle because of its cytotoxicity. Using both of nanoparticles could decrease polio virus titration without existing in the medium after treating the virus.

**Keywords :** Antiviral, Disinfectant, Polio virus, Silver nanoparticles

# P271-29: Herpes simplex type 1 virus inactivation using silver nanoparticles

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**Background and Aim :** Silver nanoparticles have been used against wide range of viruses and they have shown low possibility to be resisted by viruses, comparing to other common antiviral agents. Silver nanoparticles consist of two main parts which are silver salts and capping agents which make them different from each other and showing different features. herpes simplex type 1 virus belongs to herpes viridae family which is enveloped and has double stranded DNA genome. These two features can make the virus, a model for viruses which has common properties with it. So silver nanoparticles probable antiviral activity against the virus can be used for a range of viruses with those two common properties.

**Methods :** In this study, AgNO3 and aqueous extract of dried Juglans regia green husk play the role of two main components to make silver nanoparticles. Silver nanoparticle cytotoxicity examined on Vero cell line and the maximum non toxic dose was 10 µg/ml that shows this nanoparticle is so toxic. Silver nanoparticle prepared in that low concentration and tested on the virus but it didn't have any antiviral effect and Cytopathic effect was seen. For using highest stable concentration of silver nanoparticle which is 300 µg/ml , magnetic Fe nanoparticles get involved so silver nanoparticle in that toxic dose could be gathered before being exposure to cells and cause their death.

**Results :** In this method, treated viruses exposure to cells and virus titre decreased without any nanoparticles toxicity. Both magnetic Fe nanoparticle and silver nanoparticle showed antiviral activity by their own but their result on virus titre reduction enhanced when they used together and they showed synergism effect. Both nanoparticles caused at least 4.5 log inactivation.

**Conclusion :** Silver nanoparticle reduced herpes simplex type 1 virus titration before getting exposure to cells and this give the possibility of effecting on virus attachment stage. Due to silver nanoparticles variable synthesis methods and sizes, the exact mechanism of them is not clear.

**Keywords :** Antiviral, Disinfectant, Herpes simplex type 1 virus, Silver nanoparticles

# P272-30: Alterations of gene expression levels in uropathogenic Escherichia coli by antibiotics at subinhibitory concentrations

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**Background and Aim :** Urinary tract infection (UTI) caused by Escherichia coli remains an important health problem. Bacteria in the urinary tract may be exposed to sub-minimum inhibitory concentrations (sub-MICs) of antibiotics. Our aim was to investigate the possible changes in presence of virulence genes within the presence of antibiotics in UTI-associated E. coli.

**Methods :** A total of 99 E. coli isolated from UTI in Sanandaj, Iran were examined for susceptibility to antibiotics using the disk diffusion method and possession of virulence genes by PCR. Expression changes were measured in sub-MICs of antibiotic. Total RNA were isolated from 0.25 sub-MICs and gene expression levels were determined by quantitative PCR. P value was set at 0.05.

**Results :** Out of the 99 isolates, 36.4% carried pap adhesin, 23.2% carried hlyA hemolysin, 21.2% carried cnf toxin, and 9.1% carried afa adhesin. The prevalence of hly in the ceftriaxone-susceptible isolates was significantly higher than in the -resistant isolates ($P< 0.05$). Therefore, the alteration of hly expression level at 0.25 sub-MICs of ceftriaxone in seven hly-positive strains was investigated. The MIC values of ceftriaxone were from 0.03 to 0.125 µg/ml depending on the isolate. For all strains, ceftriaxone dramatically reduced mRNA levels of HlyA compared to that of the untreated control (from 90% to 5%, depending on the strain).

**Conclusion :** The results showed that antibiotics may play a role in determination of the pathogenicity of E. coli and therefore the outcome of infection.

**Keywords :** Escherichia coli, gene expression, antibiotic resistance, hemolysin

# P273-40: Global concerns about trachoma

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**Background and Aim :** Trachoma is probably the third most common cause of blindness worldwide, after cataract and glaucoma.. In 1996, WHO launched the alliance for the global elimination of Trachoma by the year 2020, based on the 'SAFE' strategy (surgery, antibiotics, facial cleanliness, and environmental improvement) Although tremendous progress towards the 2020 goal of global elimination of trachoma as a public health problem has been made, it will not be achieved. Future targets are now being considered. One option is changing the goal to eradication. The World Health Organization is leading a global effort to eliminate Blinding Trachoma, through the implementation of the SAFE strategy. This involves surgery for trichiasis, antibiotics for infection, facial cleanliness (hygiene promotion) and environmental improvements to reduce transmission of the organism. To assess the evidence supporting the antibiotic arm of the SAFE strategy by assessing the effects of antibiotics on both active trachoma (primary objective), Chlamydia trachomatis infection of the conjunctiva, antibiotic resistance, and adverse effects (secondary objectives). A number of different antibiotics have anti-chlamydial activity and have been used for treatment of trachoma. Currently, the most commonly used options are tetracycline eye ointment applied twice a day for 6 weeks or a single oral dose of azithromycin (20 mg/kg up to a maximum dose of 1 g). This is a particular problem for control programmes in determining who should be offered antibiotic treatment; if only those with signs of trachoma are given antibiotic, many infected individuals with significant loads of infection would be left untreated.The WHO currently recommends that mass community-wide treatment should be used

**Methods :** This review was a summary of several related articles

**Results :** Development of alternative indicators for trachoma surveillance and continued investment in trachoma programmes, particularly focused support in the most heavily affected populations, might increase enthusiasm for the feasibility of eradication.

**Conclusion :** Development of alternative indicators for trachoma surveillance and continued investment in trachoma programmes, particularly focused support in the most heavily affected populations, might increase enthusiasm for the feasibility of eradication.

**Keywords :** trachoma, Chlamydia trachomatis, antibiotics

# P274-51: Evaluation of antimicrobial activity of dihydropyrimidines and imidazo [1, 2-a] pyridine derivatives against pathogenic bacteria from urinary tract infection

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**Background and Aim :** In addition to the problems of antibiotic resistance, resistance to antiseptic compounds has encouraged chemists to find new chemical compounds as antimicrobials. since Urinary tract infection (UTI) is one of the most common bacterial infections. In this study, the susceptibility of isolates of some bacteria was investigated by performing various microbiological methods to the chemicals dihydro-pyrimidines and Imidazo [1, 2-a] pyridines derivatives.

**Methods :** In this cross-sectional study, 30 isolates were collected from patients with Urinary tract infections referring to the medical diagnostic laboratory in Mashhad, Iran. Clinical samples were determined by biochemical and microbiology tests. Minimum inhibitory concentration test was used to optimize the best concentration of chemical derivatives, the dihydro-pyrimidine and Imidazo [1, 2-a] pyridines, for four strains standard such as Enterococcus faecalis, Staphylococcus aureus, Escherichia coli, and Pseudomonas aeruginosa by the using microdilution method. The susceptibility of these strains of bacteria was evaluated and the best combination was selected to examining the clinical samples by agar well diffusion method.

**Results :** In this research, the relative frequency of bacteria isolated from the urine samples in bacterial culture were 40% Escherichia coli, 23.3% Staphylococcus aureus, 16.6% Klebsiella pneumonia, 16.6% Enterobacter spp., and 3.3% Pseudomonas aeruginosa. According to the results of MIC, the best compound and concentration was derivative of Imidazo [1, 2-a] pyridines and 15 ?g /ml respectively for 4 standard strains of bacteria, but the effective concentration in the agar well diffusion was 200 ?g /ml almost for all UTI bacteria.

**Conclusion :** The results of this study show that derivatives of Imidazo [ 1,2-a] pyridines can be used as antibacterial products in Urinary tract infections.

**Keywords :** Dihydro-pyrimidines, Imidazo [1, 2-a] pyridines, Urinary tract infection, MIC

# P275-61: Transcriptional Profile of Helicobacter pylori virulence genes in patients with gastritis and gastric cancer

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**Background and Aim :** Numerous molecular epidemiology studies have been done about the frequency of Helicobacter pylori virulence genes in patients with H. pylori infection so far. This study was conducted to detect transcriptional profile by cDNA of H. pylori virulence genes in gastric biopsy samples of gastritis and gastric carcinoma patients.

**Methods :** In a case-control study, based on the prevalence of gastritis and gastric cancer in Sanandaj city during 2018 and 2019, 23 and 11 gastric antral biopsy samples with H. pylori infection were collected from gastritis and gastric carcinoma patients by consecutive and available sampling method. Pathological characters, including tumor grades and tumor areas for gastric carcinoma biopsy samples prepared from gastric cancer areas, were determined by the pathologist. Total RNA of gastric antral biopsy samples was extracted, and their cDNA was synthesized by TaKaRa kit. Detection of H. pylori virulence genes' cDNA using specific primers and PCR. This study's results were analyzed by SPSS version 25 and statics chi-square tests for determination of relationship and correlation between cDNAs of H. pylori transcriptional profile and clinical outcomes of H. pylori infection, including gastritis, gastric carcinoma, tumor grades, and tumor area.

**Results :** The positive statistical correlations were observed between transcripts of cagA, cagA-EPIYAC, cagE, and cagY genes and H. pylori infection clinical outcomes ($P<0.05$).

**Conclusion :** Detection of the H. pylori virulence genes' cDNA in gastric biopsy samples can help provide the prognosis of clinical outcomes.

**Keywords :** Helicobacter pylori, Gene Expression Profiling, Virulence Factors, cDNA, Gastric Cancer, Gastritis

# P276-64: sirt3, 6, and 7 genes´expression in gastric antral epithelial cells of patients with Helicobacter pylori infection

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**Background and Aim :** As the intracellular acylation enzymes, Sirtuins play a crucial role in regulating the cell's physiological activities. Previous studies have shown a different sirtuin genés expression in types of cancer. This study has surveyed transcription of sirt3, 6, and 7 genes in gastric antral epithelial cells of gastritis and gastric adenocarcinoma patients with and without H. pylori infection.

**Methods :** A case-control study was conducted, including 50 and 53 gastric antral biopsy samples collected from gastritis and gastric adenocarcinoma patients with and without H. pylori infection referred to hospitals of Sanandaj city during 2018-2019. Total RNAs were extracted from biopsy samples, then cDNAs were synthesized by using Takara kits. Quality essay of H. pylori virulence genés expression and relative quantitative essay of sirt3, 6, and 7 genés expressions in gastric antral biopsy samples were performed using the Real-Time RT PCR method.

**Results :** The statistical correlations were observed between H. pylori vacA s1m2 and sabA cDNA with gastric antral epithelial cells sirt3 genes´expression [p=0.05, 0.023 respectively]. sirt6 genes´ expression decreased with age increasing in gastric adenocarcinoma patients [p=0.03]. The cDNA of H. pylori hopQII, oipA, and sabB were companied with gastric antral epithelial cells sirt7 genes´ expression of gastritis patients [p=0.031, 0.048, and 0.042 respectively].

**Conclusion :** In conclusion, the expression of H. pylori virulence genes and age increasing of patients have correlations with gastric antral cells sirt3, 6, and 7 genes´expressions of patients.

**Keywords :** Helicobacter pylori, sirt3, sirt6, sirt7, Gastric Cancer, Gastritis

# P277-65: ptk2 and mt2a genes´expression in patients with Helicobacter pylori infection

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**Background and Aim :** Many studies show that the Helicobacter pylori virulence factors determine the direction of the infection's clinical fate. Previous studies indicate ptk2 and mt2a gene products are located at both ends of the spectrum of cell destiny including proliferation and apoptosis, respectively.

**Methods :** In this study by designing a case-control study involved gastric adenocarcinoma and gastritis patients with and without H. pylori infection, the correlations between ptk2 and mt2a genes´expression in gastric antral epithelial cells were surveyed.

**Results :** The results showed the negative correlations between age and type of disease with ptk2 gene ΔCt value ($p<0.05$). The presence of H. pylori iceA1/2 and cagE genes cDNA in gastric biopsy samples had positive and negative correlations with the ptk2 gene ΔCt value ($p<0.05$).

**Conclusion :** There was a weak correlation between the presence of H. pylori babA2/B, oipA, and cagY genes cDNA in gastric biopsy samples and mt2a gene ΔCt value ($p<0.1$).

**Keywords :** Helicobacter pylori, ptk2 gene, mt2a gene, Virulence genes, Gastric adenocarcinoma, Gastritis

# P278-78: Comparison of Helicobacter pylori by polymerase chain reactions and surface cultivation methods for presenting consumed water tap of selected hospitals in Tehran in 2020

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**Background and Aim :** Helicobacter pylori is the most common gastrointestinal pathogen that more than half of the world's population is infected with this bacterium. Helicobacter pylori is a bacterium that causes gastrointestinal ulcer (chronic gastritis), stomach cancer, lymphoma, and adenocarcinoma. This pathogenic bacterium is associated with an increased risk of gastrointestinal cancer among sludge workers. Epidemiological studies propound person-to-person transmission and environmental transmission through water and food. The aim of this study was to compare polymerase chain reaction (PCR) and surface culture methods for the presence of Helicobacter pylori in consumed water of selected hospitals in Tehran in 2020.

**Methods :** In this study, sample analysis was randomly selected. Samples of consumed water taps of the drinking water distribution system 22 samples and well water 6 samples were prepared from selected hospitals in different areas of Tehran from September 5 to November 20, 2020. The samples were collected in sterile bottle according to procedure detailed in national standard methods. In this study, Helicobacter pylori was evaluated using polymerase chain reaction (PCR) and surface culture.

**Results :** This study showed the prevalence of Helicobacter pylori by PCR in two cases. The mean of Helicobacter pylori in consumed water tap and well water samples was 0.18 ± 0.85 and 0.67±1.63, respectively. The mean of Heterotroph Plate Count in consumed water tap and well water samples was 0.00 ±0.00 and 7.83±2.10, respectively. The mean of Escherichia coli, Pseudomonas aeruginosa, Clostridium perfringens, Streptococcus faecalis in consumed water tap samples was 0.00±0.00 and well water samples was 0.00 ±0.00 (as a negative control), 5.20±0.22 (as a positive control), and 2.2±0.22, 2.2± and 7.83±2.10, respectively.

**Conclusion :** So according to our results, Infection control and preventive strategies planning in order to reducing the exposure risk to Helicobacter pylori due to producing a safe water supply is purposed to public health authorities. Evaluation of biological quality (Heterotrophic bacteria, Coliforms, Escherichia coli, Pseudomonas aeruginosa, Clostridium perfringens, Streptococcus faecalis), physicochemical quality of water and Helicobacter pylori are among the strengths and innovations of this research.

**Keywords :** Drinking water distribution system, Helicobacter pylori, Heterotroph Plate Count, Surface culture, Polymerase Chain Reaction (PCR) method, Water well.

# P279-89: Correlation between DNMT1 genes expression and Helicobacter pylori virulence genes

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**Background and Aim :** DNMT1 contributes to the cell-critical gene expression by methylation of DNA cytosine-rich sequences. Environmental factors, including Helicobacter pylori infection, change host cells' epigenetics by affecting DNMT1 gene expression. This study investigates the correlation between H. pylori virulence genes and DNMT1 gene expression in gastric epithelial cells of gastric adenocarcinoma and gastritis patients.

**Methods :** In a case-control study, 50 and 53 gastric antral biopsy specimens from patients with gastritis and gastric adenocarcinoma were evaluated, respectively. The urea breath test results showed that 23 and 21 patients with gastritis and gastric adenocarcinoma had H. pylori infection, respectively. After RNA extraction from gastric biopsy samples and cDNA synthesis, virulence genes and EBER of H. pylori and Epstein-Barr virus were detected by PCR. Relative Real-Time RT PCR used to detect the DNMT1 gene expression and fold changes in groups of patients were surveyed by ΔΔCt.

**Results :** The results showed that with increasing age and the H. pylori cagA, cagY, and cagE genotypes, the DNMT1 gene expression increases in patients' gastric epithelial cells gastric cancer ($p < 0.05$).

**Conclusion :** Increased expression of DNMT1 induced by H. pylori with epigenetic effect on host cells is involved in the increased risk of gastric cancer in people with H. pylori .

**Keywords :** Helicobacter pylori ,DNMT1 gene , epigenetics, gastric adenocarcinoma,

# P280-102: Association of antibiotic resistance patterns in clinical isolates of A. baumannii and frequency of biofilm formation

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**Background and Aim :** Background: Acinetobacter baumannii due to high propensity of biofilms formation and high frequency of multi-drug resistant (MDR) is an important microorganism that causes nosocomial infections. Aim: The aim of this study was investigation of antibiotic resistance patterns in clinical isolates of A. baumannii and frequency of biofilm formation, and correlation between MDR and propensity of biofilms formation.

**Methods :** Methods: One hundred A. baumannii isolates were collected from three University affiliated hospitals in Tabriz, Iran during 2015-2016. The antibiotic resistance patterns and in vitro biofilm-forming ability were evaluated by the disk diffusion and microtiter plate methods, respectively

**Results :** Results: Eighty-eight A. baumannii isolates were MDR and have high resistant to cefepime, third generation cephalosporins, imipenem, ciprofloxacin, cotrimoxazole, amikacin, meropenem and gentamicin. Resistance to colistin was observed in 4 isolates. Assessment of biofilm formation introduced 75% of the isolates biofilm producer. A significant correlation was observed between the ability of biofilms formation and MDR strains.

**Conclusion :** Conclusion: The results of this study indicate that high levels of drug resistance of clinical isolates of A. baumannii. The ability of biofilm formation in MDR isolates causing infection ability and stability of the organisms in the hospital environment. The results of this study highlight the importance of developing detailed programs to control infections caused by Acinetobacter baumannii in our hospitals.

**Keywords :** Acinetobacter baumannii, biofilms, Drug Resistance

# P281-121: Tuberculosis and Social acceptance

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**Background and Aim :** Social acceptance in patients that suffering from tuberculosis is defined as the support which is offered by social network around them includes family, friends and colleagues that often cause the better management and prognosis. Lack of social acceptance is a barrier which proscribes the patients to receive their medications, compliance, resilience and supports. If the social acceptance is significantly low in patients with tuberculosis, an appropriate plan can raise the level of knowledge and the culture bound issue of the community to enhance the level of patient and community acceptance.

**Methods :** In this descriptive-cross sectional study, 29 pulmonary TB patients who had referred to Rafsanjan health center were selected. The Marlou-Crown questionnaire was completed by patients and the scores were calculated based on the questionnaire key by using SPSS 16. T-test, Fisher and chi-square tests were used for evaluation and the significance level was P-value <0.05.

**Results :** The results showed that the frequency of moderate to high and low social acceptance among patients was 62% and 38% respectively. Fifteen (52%) patients were male and 14 (48%) were female. The age range of patients was 8 to 90 years. Among the variables age, sex, education, place of residence, nationality and family history of TB which were inspected, the relationship between age ،nationality, family history of TB and social acceptance was significant (P-value <0.05).

**Conclusion :** This study concludes that older patients, those with a family history of TB and Afghan patients have higher social acceptance.

**Keywords :** Tuberculosis; Social acceptance; Marlou-Crown questionnaire; Pulmonary Tuberculosis

# P282-124: The Investigation of Frequency of sea,sec and tst genes in Staphylcoccus aureus isolated from Clinical sources in Karaj

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**Background and Aim :** Staphylococcus aureus is a common nosocomial and community-acquired pathogen. This bacterium has different virulence factors and provides conditions for invading the host by secreting various toxins, including superantogenic enterotoxins. Among them, various types of enterotoxins and toxins of toxic shock syndrome have a high role in pathogenesis. The aim of this study was to investigate the frequency of sea, sec and tst genes in Staphylococcus aureus isolates isolated from clinical sources in Karaj.

**Methods :** This descriptive-analytical study was performed on 100 Staphylococcus aureus isolates, which were identified and confirmed by biochemical methods. Then, antibiogram test was performed by disk diffusion agar method according to CLSI 2019 instructions and PCR method was used to identify sea, sec and tst genes.

**Results :** The results showed that the highest resistance to antibiotics penicillin, ceftazidime, tetracycline, erythromycin, cefoxitin, ciprofloxacin, oxacillin, clindamycin, respectively 92%, 82%, 47%, 43%, 38%, 36%, 34%, 33% and also the lowest resistance were related to gentamicin, trimethoprim, sulfamethoxazole, chloramphenicol with 23%, 16%, 4%, respectively, and no vancomycin-resistant isolates were observed. PCR results also showed that86% of the isolates contained at least one of the sea, sec and tst genes, of which 79% contained the sea gene, 5% contained the sec gene and 43% of the isolates had the tst gene.

**Conclusion :** The spread of antibiotic resistance in patients and patients referred to clinical sources which has increased due to improper use of antibiotics and inappropriate prescription of such drugs and Also, the high prevalence of sea, sec and tst gene expression in Staphylococcus aureus strains in hospitals can be a serious warning and danger to public health. Given the clinical importance of these isolates and their threatening role in public health, it is necessary to pay more attention to them.

**Keywords :** Staphylococcus aureus, Antibiotic resistance, Staphylococcal enterotoxins, Toxic shock syndrome syndrome

# P283-141: Evaluation of bioaerosol populations in Zanjan Zinc Industrial Park

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**Background and Aim :** Bioaerosols (such as fungi and bacteria) are a group of biological air pollutants that environmental factors and concentration of chemical pollutants effect on their type and populations.

**Methods :** In the present study, three-stations in the Zanjan Zinc Industrial Park are selected and air samples prepared using sampling pump (SKC-Flite 3) for a period of 5 min and the flow rate of 14.3 L/min. The first station at the entrance, the second near the depot site, and the third was selected adjacent to one of the major companies in the zinc industrial park.

**Results :** The lowest and highest concentration of acid and particulate matter was determined in the 1 and 3 stations, respectively. Bacteria and fungi in the collected samples grown on nutrient agar and Sabaroud dextrose agar, then isolate populations determined using colony-forming units (CFU/m3). Subsequently, the microbe types determined using microscopic examination and biochemical methods.The microbial population in the second and third stations were > 4×103 CFU/m3. The highest number of bacteria in the second station was gram positive coccus. The population of gram positive bacillus was the highest at No. 3 and No. 1 stations. At station 3, the variety and population of fungi species were considerably high compare to the others. The isolates of Penicillium and Aspergillus sp were dominant in the stations 1 and 2.

**Conclusion :** The high level of metal particles from the waste depot presented by various microbes is a serious environmental challenge. An appropriate location for waste depot, attention to climate change, and using bioremediation technologies are essential steps to reduce environmental pollutions.

**Keywords :** Bacteria, Fungi, Air pollution, Metal

# P284-144: Characterization of bacteriophages from wastewater sources on Streptococcus spp. isolated from biological samples

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**Background and Aim :** In recent decades, inappropriate and excessive use of antibiotics have resulted in frequent antimicrobial resistance in bacteria. This phenomenon has created several problems in treatment of bacterial infections, leading to increased case mortalities and treatment expenses. A good solution to solve the problem is use of bacteriophages in bacterial treatment as these bacterial viruses include zero or minimum side-effects. The aims of this study were to isolate and identify bacteriophages from biological samples.

**Methods :** In this study, wastewater samples were used to characterize bacteriophages on streptococcal isolates from clinically isolated biological samples in Tehran, 2019–2020. Then, bacteriophages were comprehensively characterized using phenotypic and molecular methods.

**Results :** Of all samples collected from the hospital, 20 isolates belonged to viridans group and Group B streptococci. Overall, five bacteriophages were isolated from Streptococcus agalactiae strains with no host specificity since these bacteriophages lysed Enterococcus spp. as well.

**Conclusion :** Since emergence of antibiotic-resistant bacteria has created numerous medical problems, characterization of bacteriophage to use in infection treatment seems a promising solution.

**Keywords :** Bacteriophage, Streptococcus spp., Biological samples

# P285-147: Biofilm-forming ability of mucosa-associated Escherichia coli isolates from colorectal cancer patients and control subjects

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**Background and Aim :** Colorectal cancer (CRC) is the third most common incident cancer and the second most common cause of cancer death in the world. The results of recent studies have shown that bacterial biofilms are associated with CRC. The aim of this study was to compare the biofilm-forming ability of mucosa-associated Escherichia coli (E. coli) strains from CRC patients and non-cancerous patients.

**Methods :** Between June 2019 and June 2020, a total of 80 colonic mucosa-associated E.coli isolates, 40 from CRC patients and 40 from control subjects were collected from two Educational-Health Care Centers of Tabriz University of Medical Sciences in Northwest Iran. In vitro biofilm formation by these isolates was determined using a microtiter plate assay.

**Results :** Around 37.5% of E. coli isolates from CRC patients were able to form biofilms, compared to 15% of the isolates from the control group ($p < 0.05$). Among the biofilm producing isolates from the control subjects, all isolates were weak biofilm producers. Amongst CRC isolates 40% were strong and moderate biofilm producers, and 60% were weak biofilm producers.

**Conclusion :** Biofilm-producing mucosa-associated E. coli isolates may play a role in the pathogenesis of CRC.

**Keywords :** E. coli, Colorectal cancer, Biofilm

# P286-148: Vitamin D Receptor genes polymorphisms (BsmI and TaqI ) and susceptibility to pulmonary tuberculosis in world population (2010-2020): a meta-analysis and systematic review

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**Background and Aim :** Tuberculosis still remains an important cause of morbidity and mortality worldwide. A polymorphism in the vitamin D receptor gene may contribute to susceptibility to tuberculosis. Proper activity of vitamin D receptor on macrophage nuclei as one of the main components of innate host immunity against Mycobacterium tuberculosis. In this study, in the form of a systematic review and meta-analysis, we investigated the frequency of vitamin D, TaqI, and BsmI receptor genes in people with tuberculosis in the world population.

**Methods :** The full texts of English and Persian articles related with these subjects from 2010 to 2020 were included. Review articles, abstracts, articles in languages other than English and Persian, articles with unknown sample locations were excluded. Data were analyzed using meta-analysis and random effects models with the software package Meta R, Version 2.13 ($p < 0.0001$) (confidence interval: 95%).

**Results :** The frequency of BB, Bb and bb genotypes in patients with tuberculosis were 29%, 39%, 38% and the frequency of TT, Tt and tt genotypes in patients with tuberculosis were 62%, 30% and 8%, respectively.

**Conclusion :** In this study, a significant relationship was observed between the genotypic frequency of TaqI and BsmI in VDRL gene in patients with tuberculosis.

**Keywords :** Vitamin D Receptor gene, polymorphisms, pulmonary tuberculosis

# P287-149: Prevalence and determination of antibiotic pattern of Enterobacteriaceae causing urinary tract infection in Valiasr Clininc in Mashhad

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**Background and Aim :** Urinary tract infection is one of the most common bacterial infections affecting the human body and the most common type of nosocomial infections. On the other hand, this infection is one of the most common sources of increased antibiotic resistance, which has highlighted the need to evaluate the pattern of antibiotic resistance to improve experimental treatment. The aim of this study was to determine the frequency and pattern of antibiotic resistance of Enterobacteriaceae isolates in patients with urinary tract infections.

**Methods :** In this cross-sectional descriptive study which was performed in the clients of Valiasr Clinic of Mashhad during a quarterly period in 2021, the detection of the desired bacteria was performed using conventional microbiological methods and standard biochemical tests. Disk diffusion method was investigated for determination of antibiotic pattern.

**Results :** Out of 438 positive urine cultures for Enterobacteriaceae, Escherichia coli (75.4%), Klebsiella (14.6%), Enterobacter (4%), Proteus (3.2%) And other bacterial species were observed in (2.8%) cases. Clinical isolates were most sensitive to piperacillin-tazobactam (89%) and amikacin (87%) also had the highest resistance to Cefazolin (81%).

**Conclusion :** Considering the frequency of urinary tract infections and in order to prevent its serious complications, the study of the regional resistance pattern of medical centers for effective treatment should be done in a timely manner. Amikacin and piperacillin-tazobactam antibiotics are recommended for the experimental treatment of urinary tract infections. Finally, more comprehensive clinical statistical research is needed to confirm the findings and results of this clinical study.

**Keywords :** Urinary tract infection, Antibiotic pattern, Enterobacteriaceae, Antibiogram

# P288-150: The role of nutrition in multiple sclerosis

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**Background and Aim :** The role of nutritional interventions with a significant effect on the prognosis of multiple sclerosis (MS), especially in the relapsing-remitting type, if used at the beginning of the disease and with minimal disability has been discussed.

**Methods :** While reviewing in scientific databases (Pub Med, Google Scholar, Science Direct) by applying keywords and also applying free full text filter in the period 2017 onwards, 57 approved articles in these databases and completely related to the topic ahead of us were obtained.

**Results :** Required diet includes reducing fat intake, getting enough essential omega-6 and omega-3 fatty acids, antioxidants, vitamins D and 12B and increasing consumption of foods containing fiber, biotin with carboxylase dependent function In the tricarboxylic acid (TCA) cycle, while increasing the expression of the ATP molecule, it is contrary to the hypoxic consequences of MS and also curcumin reduces nerve damage and inflammation by reducing inflammatory mediators such as IL-1? and TNF-? and is effective in mitochondrial dynamics. And causes oxidative damage by creating aerobic metabolism.

**Conclusion :** These are promising topics to study in the management of MS. However, these patients are at risk of malnutrition with anorexia due to inactivity and side effects of medications. But, a strategic nutritional model has not yet been developed for patients to take these supplements. Therefore, more clinical trials are needed to fully evaluate its effect on the recovery of MS.

**Keywords :** Multiple sclerosis, Nutrition, Diet.

# P289-159: Frequency of cagA, vacA and oipA genes in Helicobacter pylori samples isolated from patients with gastrointestinal disorders in Mashhad

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**Background and Aim :** Helicobacter pylori, with its great diversity in pathogenic genes, is directly and indirectly involved in many disorders of the gastrointestinal tract and even outside the gastrointestinal tract. The aim of this study was to evaluate the frequency of this infection in patients referred to endoscopic centers in Mashhad and the presence of some important virulence genes such as cagA, vacA and oipA.

**Methods :** In this study, from 89 patients who referred to an endoscopy center, two pieces of tissue were prepared from the antrum or duodenum by a physician. One of the two pieces of tissue isolated from the patient's stomach was allocated for urease test and the other piece was used for DNA-extraction by phenol-chloroform method. First, the frequency of Helicobacter pylori was examined in all samples by PCR and glmM primer, and then for glmM positive samples, multiplex-PCR test was performed with primer of cagA, vacA and oipA genes. PCR results were read on gel electrophoresis.

**Results :** 54% of biopsies (48/89) were urea-positive. Bacterial frequency with glmM gene was 48% (43/89). The frequency of cagA, vacA and oipA pathogenic genes among positive H.pylori samples was 77%, 65% and 51% by PCR, respectively.

**Conclusion :** The importance of pathogenic genes and its high frequency in patient samples indicate the need to use rapid and accurate identification methods such as PCR in clinical diagnoses. Also, due to the fact that in Multiplex-PCR test, several genes are examined simultaneously, this method is preferred to better identify the dominant strains in each region, by examining the number of more pathogenic genes to provide more effective treatments.

**Keywords :** pathogenic genes, glmM, endoscopy, Helicobacter pylori

# P290-169: Assessment of Demodex folliculorum density in psoriasis

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**Background and Aim :** The two Demodex species Demodex folliculorum and Demodex brevis are common obligatory parasites of the pilosebaceous units in human beings. Demodex folliculorum is usually found in the infundibulum of hair follicle and Demodex brevis in the sebaceous glands and ducts. Psoriasis is an autoimmune diseases. Immunocompromised patients with acquired immunodeficiency syndrome developed facial lesions of demodicidosis. Since immunosuppressive are also frequently used for inflammatory or autoimmune skin diseases, we aimed to determine the number of Demodex mites.

**Methods :** This study included 50 patients (10 male, 40 female; mean age 61_20 years) who were admitted to the Dermatology Clinic and were treated with immunosuppressive therapies for psoriasis. The control group consisted of 50 healthy subjects (17 male, 33 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 35 patients (70%) and 12 controls (12%). The average of Demodex mite density in patients with psoriasis was 23.66 Demodex test was positive in 6 men (60%) and 29 women (72.5%) in psoriasis.

**Conclusion :** Although Demodex mites might be seen in healthy people, density remains low. They become pathogenic when they multiply and reach to the density in skin. However factors affecting the density of Demodex mites are still not known exactly. Some local or systemic factors may induce the proliferation of mites. Immune deficiency was suggested to be the possible cause of overgrowth of mites.

**Keywords :** Demodex mite, psoriasis, autoimmune

# P291-170: Relationship between Demodex mite concentration and some lifestyle features

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**Background and Aim :** Aims: Demodex mites is located in human hair follicles and sebaceous glands. They feed on epithelial cells, dead cells and sebum. Immune system control microorganism population. Our aim in this study is assessment of relationship between Demodex counts and some lifestyles and skin features.

**Methods :** Methods: This study tested on 126 females and 29 males with average of age 31.25 years old. Demodex test did on facial skin and scalp by an acne tool to taken standard amount of sebum then putted samples on glass microscope slides with clear mineral oil. Patients filled the questionnaires that contained skin types, average time of sleep on day, average of number shower on week, etc.

**Results :** Results: Positivity Demodex test means five or more mites per cm2. Results of test in 60 (47.61%) females and 15 (51.7%) males was positive. At all positives, average of sleep a day, count of shower a week was 7.1 hour and 3.95 times per week. Most type skin of high density of Demodex were seen oily (42 person) then mixed skin (9 person).

**Conclusion :** Discussion: High density of Demodex can be related to abnormality in immunity. Due to it expected that some factors in personal life style affected on Demodex concentration. Daily sleep time, number of showers in a week and skin type checked. In some studies showed that Demodex feed sebum and proliferation easily in oily skin. The results of this study showed Demodex concentration increased in oily skin. There was no significant statistic difference between time of sleep and shower number on a week with Demodex concentration.

**Keywords :** Key words: Demodex mite, Skin, lifestyle

# P292-195: Prevalence of latent tuberculosis infection among people in house hold contact with pulmonary tuberculosis in Iran

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**Background and Aim :** Latent tuberculosis infection (LTBI) is present in one-quarter of the world's people and is more likely spread to tuberculosis, especially at a young, diagnosis and treatment and prevention are an important part of the World Health Organization's(WHO) TB control program. We aimed to evaluate the prevalence of LTBI among Family member of TB cases in two high-burden provinces in Iran.

**Methods :** 668 house hold contacts of 149 pulmonary tuberculosis cases were followed up retrospectively and prospectively in Gorgan and Zabol cities at 0, 3, 12 and 18 months after the start of the study. For LTBI diagnosis, tuberculin skin test (TST) and QuantiFERON®-TB Gold Plus (QFT-Plus) were performed.

**Results :** A total of 668 people, who had contact with an index TB case. The number of LTBI cases based on QFT or TST positive test was 52.9%. In children under 5 years of age, the number of LTBI cases was 33.3%. LTBI cases in the age group over 18 years with 5 to 18 years and less than 5 years were significantly different, while there was no significant difference between the age group of less than 5 years and 5 to 18 years.

**Conclusion :** This study showed that most cases of infection occur before the diagnosis of the index or in the first step of the study. Therefore, we emphasize that the people living in close contact with an infectious TB case should be screened effectively and receive prophylactic therapy.

**Keywords :** Pulmonary tuberculosis, Latent Tuberculosis, Tuberculin skin test

# P293-198: Exploring students' learning experiences in a flipped classroom instructional model: A study on Master's students of Medical Microbiology

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**Background and Aim :** Background: Recently, flipped classroom (FC) instructional model has received more attention. However, application of this method at a Master's level has less been studied. The aim was to investigate the effectiveness of the FC model on Master's students of Medical Microbiology for education of Systematic Bacteriology (SB).

**Methods :** Method: The FC study was conducted during 2018-2019 at Kurdistan University of Medical Sciences. We examined students' learning experiences and self-perceived knowledge. We also compared examination scores of the FC students to those of students who were taught with a traditional lecture-based classroom (TC) model. A Mann-Whitney U test was used to compare the two groups. A P value < 0.05 was considered significant.

**Results :** Results: FC students reported positive learning experiences and an increase in self-perceived knowledge. Students agreed that the FC helped to promote their learning motivation and to enhance communication ability and problem solving skill; however, they reported pressure in the FC activity. Students from the FC performed better on the test when compared to those from the TC group (P<0.05).

**Conclusion :** Conclusion: The results showed that the FC had a positive effect on learning and self-perceived knowledge and it was helpful for examination; however, this approach warrants further consideration and research.

**Keywords :** Keywords: Flipped learning, Medical microbiology, Systematic bacteriology, Lecture-based classroom

# P294-227: Effect of endophytic fungi isolated from saffron (Crocus sativus) on human pathogenic fungi in libratory conditions

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**Background and Aim :** Saffron (Crocus sativus) is a perennial plant that belongs to Liliaceae family. The three main secondary metabolites of saffron, namely crocin and its derivatives, are responsible for the color of saffron, picrocrocin is responsible for the bitter taste of saffron, and safranal is responsible for the aroma of saffron. According to some researches, it has anti-cancer and antimicrobial properties. The antioxidants and active ingredients of saffron block the effect of free radicals in the body and inhibit DNA mutations that lead to overgrowth of cells. Endophytes are microorganisms that live at least one stage of their life cycle inside plants without causing any symptoms. These microorganisms have been found in many species and are recognized as a potential source of effective natural compounds for use in medicine, agriculture and industry. This information led us to the conclusion that saffron can be another source of endophytic fungi with biological activity. Also, studies on the antagonistic and biocontrol activities of plant endophytes from this plant have shown the positive effect of these microorganisms in preventing the growth of pathogenic pathogens. Therefore, the inhibitory effect of endophytic fungi from saffron on human pathogenic fungi was considered

**Methods :** To investigate the effect of endophytic fungi isolated from saffron plant on human pathogenic fungi, a randomized complete block design with 6 treatments (5 endophytic fungi +Control) and three replications was performed. Cross-culture on PDA against human pathogenic fungi such as Aspergillus flavous, Cryptococcus neoformans and Candida albicans was carried out. Means comparing was performed by SPSS 20.0 software based on Duncan test.

**Results :** The analysis of variance showed that the effect of endophytic fungi on these human pathogens was significant ($p<0.01$). Cadophora malorum FT19 showed no inhibitory effect on C. albicans and other endophytic fungi had similar effect (ns), except Alternaria chlamydosporigena FB21 that had the lest effect. A. niger FT16 showed the maximum effect on C. neoformans (51.28%) and A. flavus (87.50%). Other endophytic fungi had similar effect on C. neoformans and A. flavus (NS).

**Conclusion :** A. niger FT16 (an endophytic fungi) could be a promising microorganism for future as a biocontrol and antagonist on studied human pathogenic fungi.

**Keywords :** Saffron, Endophytic fungi, Aspergillus flavous, Cryptococcus neoformans, Candida albicans

# P295-228: Complementary therapies and Bacterial vaginosis in Iran: a review of clinical trials

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**Background and Aim :** Bacterial vaginosis (BV) is prevalent in women. BV is characterized by the overgrowth of anaerobic bacteria. Discharge, fishy odor, and irritation are common features of BV. Complementary remedies like medical planets and natural substances can be designed for better vaginal health. This study aims to review clinical trials on the effectiveness of Complementary therapies in BV in Iran.

**Methods :** In this study, electronic databases such as PubMed, Scopus, Google Scholar, and Cochrane library were searched with the keywords “Bacterial vaginosis” in the title/abstract and “plant/ / herb” and "complementary therapies" in the whole text for clinical trials on Complementary therapies for BV in Iran. Data were collected from inception until April 2021. Only papers with English and Persian full-texts were included in our study.

**Results :** Herbs and supplementary remedies in the form of oral and/or topical (cream or suppository vaginal) were assessed in BV via clinical and laboratory tests. Nigella sativa, Oak Gall, Zataria multiflora, Hypericum perforatum, Garlic, Calendula officinalis, and Myrtuscomunis have a large body of evidence supporting their effectiveness in BV. supplementary remedies as honey and probiotics and vitamin D were evaluated in BV. These supplementary remedies have evidence of effectiveness in BV.

**Conclusion :** The current study supports the efficacy and safety of several plants and natural substances for BV; however, some herbs and substances do not have enough evidence to support the use of complementary therapies. Thus, future studies are needed to assess the efficacy and adverse effects of these treatments.

**Keywords :** Complementary medicine, Bacterial vaginosis, clinical trials

# P296-243: Detection of hybrid uropathogenic/diarrheagenic Escherichia coli strains among uropathogenic E. coli isolates

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**Background and Aim :** Urinary tract infection) UTI) is one of the most common bacterial infections that caused by Escherichia coli at least in 80% of cases. There is evidence that some uropathogenic E. coli (UPEC) isolates have diarrheagenic source; therefore, in the present study we investigated the presence of diarrheagenic markers among UPEC isolates.

**Methods :** A total of 200 UPEC isolates were screened by multiplex¬-PCR for the presence of main diarrheagenic marker genes including aggR and pCVD for enteroaggregative E. coli, invF gene for the enteroinvasive E. coli, stx1, stx2, eaeA and hlyA for enterohemorrhagic E. coli, stla, stlb and lt for enterotoxigenic E. coli and escV for enteropathogenic E. coli.

**Results :** aggR, pCVD, eaeA genes were found in 20, 18, and 1 isolates, respectively, while the other genes were not found. Therefore, 2% of UPEC strains were hybrid EAEC/UPEC.

**Conclusion :** Results indicated that some diarrhea-causing E. coli isolates may also have the potential to cause urinary tract infections. Among these, the EAEC pathotype is more important than the other diarrheagenic E. coli pathotypes.

**Keywords :** Urinary tract infection, Escherichia coli, diarrheagenic marker, uropathogenic E. coli

# P297-244: Synthesis of new antibacterial dental monomer by 5-hydroxy-3-phenyl-1H-pyrazole-1-carbothioamide and Investigation of its compressive strength

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**Background and Aim :** Secondary caries is the most important reason for replacement and removal of restorative materials contains composite resins because caries is an infectious complication and many bacteria, including Streptococcus mutans and lactobacilli, have been isolated from cariogenic plaques, and given that composites base resins increase the growth of Streptococcus Therefore, the use of composite resins that have antimicrobial properties in the prevention of secondary decay will be very useful in this study, we synthesized 5-hydroxy-3-phenyl-1H-pyrazole-1-carbothioamide as a new antibacterial compound and used it in dental composite and Investigated of its compressive strength.

**Methods :** In this experimental study, 5-hydroxy-3-phenyl-1H-pyrazole-1-carbothioamide was synthesized by reaction between Thiosemicarbazid and Ethyl benzoylacetate and the antibacterial activity of flowable dental composites containing 0–5 wt% 5-hydroxy-3-phenyl-1H-pyrazole-1-carbothioamide and also of their compressive strength on flowable dental composites were investigated. Statistical analysis was performed using one-way ANOVA test ($P < 0.001$).

**Results :** The direct contact test demonstrates that by increasing the 5-hydroxy-3-phenyl-1H-pyrazole-1-carbothioamide content, the bacterial growth is significantly diminished ($p<0.001$). the mean of compressive strength results show no significant difference between 0-3% of groups ($p>0.001$).

**Conclusion :** Incorporation of 5-hydroxy-3-phenyl-1H-pyrazole-1-carbothioamide into flowable dental resin composites in 4% wt can reduce the activity of Streptococcus mutans

**Keywords :** 5-hydroxy-3-phenyl-1H-pyrazole-1-carbothioamide; Streptococcus mutans; flowable dental resin composites; secondary caries .

# P298-245: Synthesis of new antibacterial dental monomer by 6-bromo-2-oxo-2H-chromene-3-carboxylic acid and Investigation of its compressive strength

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**Background and Aim :** Secondary caries is the most important reason for replacement and removal of restorative materials contains composite resins because caries is an infectious complication and many bacteria, including Streptococcus mutans and lactobacilli, have been isolated from cariogenic plaques, and given that composites base resins increase the growth of Streptococcus Therefore, the use of composite resins that have antimicrobial properties in the prevention of secondary decay will be very useful in this study, we synthesized 6-bromo-2-oxo-2H-chromene-3-carboxylic acid as a new antibacterial compound and used it in dental composite and Investigated of its compressive strength.

**Methods :** In this experimental study, 6-bromo-2-oxo-2H-chromene-3-carboxylic acid was synthesized by reaction between 5-Bromo-2-hydroxybenzaldehyde and Malonic acid and the antibacterial activity of flowable dental composites containing 0–5 wt% 6-bromo-2-oxo-2H-chromene-3-carboxylic acid and also of their compressive strength on flowable dental composites were investigated. Statistical analysis was performed using one-way ANOVA test ($P < 0.001$).

**Results :** The direct contact test demonstrates that by increasing the 6-bromo-2-oxo-2H-chromene-3-carboxylic acid content, the bacterial growth is significantly diminished ($p<0.001$). the mean of compressive strength results show no significant difference between 0-4% of groups ($p>0.001$).

**Conclusion :** Incorporation of 6-bromo-2-oxo-2H-chromene-3-carboxylic acid into flowable dental resin composites in 4% wt can reduce the activity of Streptococcus mutans

**Keywords :** 6-bromo-2-oxo-2H-chromene-3-carboxylic acid; Streptococcus mutans; flowable dental resin composites; secondary caries .

# P299-247: Genome analysis of an enterococcal prophage Entfac.MY

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**Background and Aim :** Bacteriophages (phages) are bacterial intracellular parasites. They are the most abundant organisms in the world and are present in any environment that contains bacteria, including sewage. Lysogenic phages, unlike lytic phages, do not begin to multiply immediately after entering the host and may integrate their genome into a bacterial gene called a prophage. Prophages can have a wide range of phenotypic effects on host bacteria. They can also regulate bacterial populations by altering bacterial gene expression. Enterococcus are gram-positive bacteria whose species cause infections in humans. Recently, Enterococcus has become resistant to a variety of antimicrobials, so that today we see high resistance of Enterococcus to a variety of antibiotics, including vancomycin.

**Methods :** In this study, Enterococcus faecium EntfacMY was isolated from biological samples and its genome was examined.

**Results :** After analyzing the genome of these bacteria, 254 prophage genes were identified. The prophage included 39 housekeeping genes, 41 genes related to replication and regulation, 80 genes in the group of structural and packaging genes and 48 genes in the group of lysis. 46 genes with unknown function were also identified.

**Conclusion :** As a result, identification and analysis of prophage genomes can be effective in better understanding their role in the development of bacterial resistance to antibiotics. Identifying and studying prophages can also help develop genetic engineering tools and therapeutic use of bacteriophages. The identified genes were annotated in the DNA Data Bank of Japan.

**Keywords :** Prophage, Enterococcus faecium, Genomic sequencing

# P300-254: A prion-derived peptide can reduce Aβ42 oligomer cytotoxicity on SH-SY5Y neuroblastoma cells without changing the structure or oligomerization state of oligomer

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**Background and Aim :** Alzheimer's disease is an aging-related and devastating neurodegenerative disease that is caused by cerebral accumulation of amyloid beta (Aβ) peptide. Cellular prion protein is a toxic receptor with high binding affinity for Aβ42 oligomers. The level of viability of neuroblastoma cells after treatment with Aβ42 oligomers (ADDLs) in presence and absence of a prion- derived peptide was assessed. Aggregation state of ADDLs in present of peptide was also investigated.

**Methods :** The viability of SH-SY5Y neuroblastoma cells after treatment with Aβ42 oligomers (ADDLs) in present and absence of a short peptide (PrP107-120) was analyzed using the MTT assay. To determine the effect of the peptide on ADDLs aggregation state, the ADDLs structure in presence of PrP107-120 prion-derived peptide was investigated using ANS fluorescence, dot blot assay, Thioflavin T fluorescence and circular dichroism spectroscopy.

**Results :** We found that addition of the synthetic peptide PrP107-120 to Aβ42 oligomer significantly increased cell viability compared with the cells treatment with ADDLs alone. Moreover, other results indicated that prion-derived peptide was not able to change the Aβ42 ADDLs structure.

**Conclusion :** The present study suggests that PrP107-120 can significantly protect neuroblastoma cells against the toxicity induced by Aβ42 oligomers, although it cannot change the oligomerization state of ADDLs.

**Keywords :** Alzheimer, Aβ42 oligomer, prion peptide, ADDLs

# P301-268: Epidemiological evaluation of meningitis in hospitalized patients in shahid madani hospital of khorramabad

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**Background and Aim :** Familiarity with the epidemiological, clinical and laboratory features of meningitis is important for rapid diagnosis and initiation of therapy. This study aimed at evaluating patients with meningitis based on their epidemiological, clinical and laboratory findings and comparing these variables between patients with septic and aseptic meningitis.

**Methods :** This retrospective study included all the patients hospitalized in 2014 and 2015 and suspected for meningitis. The cases were compared for their epidemiological, clinical and cerebrospinal fluid (CSF) laboratory aspects.

**Results :** Among 63 patients with meningitis, 30 (47.6%) had septic meningitis and 33 (52.4%) had aseptic meningitis. Of the 30 patients with septic meningitis, 4 patients (13.3%) had positive microbial culture. Most of the bacteria (50%) isolated from the samples were pneumococcus. The means for CSF-WBC, CSF- glucose and CSF-protein in the septic meningitis compared with the aseptic meningitis patients were 64.81 ± 6.27 vs. 28.26± 8.90 cell/mm3 of CSF, 40.95± 9.70 vs. 72.10± 5 mg/dl and 115.23 ± 13.28 vs. 61.94±9.49 mg/dl, respectively (P<0.001). There was a difference between season (autumn and winter) and the risk of meningitis, and more septic meningitis was found in males.

**Conclusion :** The prevalence of septic meningitis was higher than that of aseptic meningitis. Similarly, WBC, glucose and protein in CSF were helpful in differential diagnosis of septic meningitis vs. aseptic meningitis. Headache and fever are very important signs in diagnosis of meningitis.

**Keywords :** septic meningitis, aseptic meningitis, microbial culture

# P302-270: Comparison of Reasoner'2 Agar and Muller Hinton Agar Media for Microbiological Monitoring of Dialysis Water

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**Background and Aim :** Microbiological culture of dialysis water is a routine safety measure. In, Khorramabad laboratories perform these cultures on Muller Hinton Agar (MHA) at 35–378C for 48 h, not on the Reasoner's 2A agar (R2A) at 17–238C for 7 days recommended by international standards, the objective of the present study was the comparison of the efficiency of R2A and MHA media in the counting of heterotrophic bacteria in the samples of water collected in dialysis centers from 2 hospitals in Khorramabad, from September to November 2019.

**Methods :** A total of 165 samples of treated water in dialysis centers were collected aseptically and then transported in ice packs to the Department of Medical Microbiology of the Lorestan University of Medical Sciences and the pour plate technique was carried out for the enumerating of heterotrophic bacteria. Finally, bacterial colonies were counted after incubation at 34 ± 2ºC for 48 hours on MHA and 25 ºC for 1 week on R2A.

**Results :** Results showed heterotrophic bacterial counts in R2A were greater than those in MHA in 89% of the samples, so enumeration of heterotrophic bacteria should be carried out in R2A agar associated with longer incubation times, because of the greater sensitivity. The proportion of water samples yielding colony counts ≥200 CFU/mL by R2A -7d was significantly different from the proportion by MHA -48h ($P<0.001$)

**Conclusion :** The results proposed using R2A agar combined with relative low culture temperature (20-25 °C), and an extended incubation time (7-10 days) is more efficient. However, as the spectrum of bacterial contamination is not the similar for dialysis centers and countries, many of studies using different media and culture parameters are required in order to confirm this.

**Keywords :** Dialysis water, Heterotrophic bacteria, Pour plate, Reasoner'2 Agar

# P303-273: Frequency of Helicobacter pylori infection in patients with peptic ulcer referred to the endoscopy department in Khorramabad city hospitals, Iran during 2013-2016

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**Background and Aim :** In this study, the prevalence of Helicobacter pylori infection was investigated in peptic ulcer patients referred to the endoscopy department in Khorramabad hospitals during 2013-2016

**Methods :** All patients were studied who had been referred to the endoscopy department and also their endoscopic and pathology reports were available and complete. After recording endoscopic reports, 1224 peptic ulcer (gastric or duodenal ulcer) cases were selected, which biopsy assay was performed for them to examine the type of wound and the presence of Helicobacter pylori bacteria. Pathology reports were collected by referring to the pathology departments. The information in the pathology report, including demographic information, was included in a pre-designed questionnaire to match the endoscopic reports, the location of the pathology sample, and other details, including the presence or absence of Helicobacter pylori bacteria. Finally, the data were analyzed using SPSS version 21

**Results :** Of the 1224 patients studied, the mean age of patients was 15.5 ± 17.5 years old. 664 (54.2%)cases had gastric ulcers, 445 (36.4%) cases had duodenal ulcers, and 115 (9.4%) cases had both gastric and duodenal ulcers. In gastric ulcer patients, 512 (65.7%) patients have gastric in the antrum area and 74.3% (579 persons) of the gastric ulcers were clear.

**Conclusion :** The prevalence of infection was statistically significant based on the peptic ulcer and duodenal ulcer location, between different stomach areas, between different types of gastric ulcer and duodenal ulcer and between the number of gastric ulcers, and duodenal ulcers.

**Keywords :** Peptic ulcer, Gastric ulcer, Deodorant ulcer, Helicobacter pylori

# P304-339: Biodegradation of crude oil through fungi isolated from southern parts of Iran

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**Background and Aim :** Extensive consumption of crude oil and its derivatives (Petroleum) leads to an enormous increase in contaminating the natural environment. Crude oil is a complex mixture containing thousands of hydrocarbon molecules with immunotoxic and carcinogenic impacts.

**Methods :** Here, we isolated the fungal populations associated with the soils contaminated by crude oil from southern regions of Iran to discover promising candidates with a high ability to biodegrade crude oil. Soil samples from surface soil were collected, and fungi were isolated on Potato Dextrose Agar (PDA), Water agar (W), and Malt Extract Agar (MEA) media. Fungal genera were identified based on the morphological characters and classified according to available taxonomic keys. Additionally, the molecular assay is currently ongoing to determine the fungal species. Bushnell-Haas broth medium was applied to corroborate the ability of the isolated fungi to biodegrade the crude oil. To this accomplish, the addressed medium was amended by tween 80 (0.1%), redox reagent (2% 2, 6-dichlorophenol indophenols), and crude oil (1%).

**Results :** Among the 270 identified isolates, the main group was Alternaria, representing 81% of isolates and, to a lesser extent, Fusarium, Cladosporium, Rhizoctonia, Trichoderma, Penicillium, Aspergillus, Geotrichum, Epicoccum, and Zygomycetes. Based on the colorimetric assay through redox reagent, isolates possessing the enormously high capacity to degrade the crude oil belonged to Alternaria (13 isolates) and Cladosporium (5 isolates), which significantly degraded crude oil compared to the control.

**Conclusion :** Our results demonstrated the biodegradation efficiency of some fungal isolates that can be employed as biological agents to eliminate hazardous molecules from the environment.

**Keywords :** Biodegradation, Crude oil, Colorimetric test, Fungi

# P305-341: Isolation and Identification of Staphylococcus saprophyticus Lytic bacteriophages from Urban and Hospital Wastewaters in Gorgan city

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**Background and Aim :** Staphylococcus saprophyticus is the ability to cause urinary tract infections. The introduction of the first lytic phage of S.saprophyticus by researchers at Golestan University of Medical Sciences raised the possibility of identifying its variants for complementary therapies in urinary tract infections. This study aimed to isolate and identify S.saprophyticus lytic bacteriophages from the hospital and municipal effluent samples in Gorgan.

**Methods :** S.saprophyticus were collected from medical diagnostic laboratories in Gorgan diagnosis of bacteria can be performed with microbiological tests as well as PCR of the 16SrRNA gene. Antibiotic resistance of isolates was performed according to CLSI s.saprophyticus bacteriophages were isolated using spot test and Double-Layer Agar (DLA) method. After purification, the host domain and morphological characteristics of bacteriophages were examined by electron microscopy.

**Results :** 35 isolates with an initial diagnosis of S.saprophyticus were collected in Golestan province, all of which were confirmed as S.saprophyticus after resuscitation and purification by biochemical tests and 16 SrRNA confirmation tests. The results of the antibiogram test showed that all isolates were sensitive to nitrofurantoin, linezolid, gentamicin antibiotic discs. Out of 64 effluent samples, 5 bacteriophages were isolated from municipal effluents. bacteriophages were named VB_SsapS-101, VB_Ssaps105-, VB_SsapS-46, VB_SsapS-111, VB_SsapM-190 according to the Kropinsky method. VB_SsapS 111(60%) and VB_SsapS105 (51.4%) showed the highest host range. None of the 5 bacteriophages had an inhibitory effect on other bacteria.

**Conclusion :** S.saprophyticus showed good sensitivity to existing antibiotics, for the treatment of urinary tract infections Due to the wide host range of the two bacteriophages VB_SsapS111- and -VB_SsapS105, they can be a good candidate for adjuvant therapy.

**Keywords :** Staphylococcus saprophyticus, bacteriophage, urinary tract infection, antibiotic susceptibility, sewage

# P306-343: Investigation of Helicobacter pylori infections and lifestyle factors in patients in Mashhad

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**Background and Aim :** Although Helicobacter pylori (H. pylori) infection has been demonstrated to be associated with several gastrointestinal disorders, it is still not clear which patients' lifestyle factors are associated with H. pylori infection in the Iranian population. This study aimed to investigate the relationship between H. pylori infection and patient with different lifestyle factors such as stress level and diet.

**Methods :** In this study, two gastric biopsies were taken from 134 patients with gastrointestinal symptoms who were referred to two endoscopy centers. The patients answered a questionnaire, including four items as follows: stress level, tea consumption, tobacco, fruits and raw vegetables. For confirming the presence of H. pylori DNA in a biopsy, the glmM gene was identified by PCR. A Chi-Squared test was used to evaluate the relationship between each factor and the prevalence of infection.

**Results :** Among the 134 samples, H. pylori was isolated from 57 (43%) patients including 26 men and 31 women. According to the statistical testing the P-value for stress level, tea consumption, tobacco and fruit and raw vegetable was detected <0.5, <0.75, <0.5and <0.5, respectively.

**Conclusion :** There was no association between stress level, consumption of tea, tobacco and fruit and raw vegetable and H. pylori-positive status. The small population analysis of this study can affect the results.

**Keywords :** Helicobacter pylori, Chi-squared, stress, endoscopy, glmM

# P307-348: A review article: bacterial strain and antibiotic resistant pattern in burn wound

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**Background and Aim :** Microbial infection is the most common and serious complication of burn injury, which is a major cause of morbidity and mortality. Burn infections are one of the most common serious illnesses caused by pathogens, mainly by both gram-negative and gram-positive bacteria. The aim of this study was to determine the bacteriological stains and the antibiotic resistance patterns in Burn wound

**Methods :** We carried out a systematic search on the bacterial stain and antibiotic resistant pattern of burn wound infections in the world using different electronic databases including Embase, Scopus, Web of Sciences, PubMed/Medline, during 2005 to 2020. These databases were explored to find out potentially relevant pieces of literature. Keywords were used was the prevalence, bacterial isolates, burn wound antibiotic resistance.

**Results :** Our study included 31 data report of comprising 15855 patients sample (female and male), with about 5500 total positive cultures from different countries. Various Gram negative bacteria Pseudomonas aeruginosa, Klebsiella pneumoniae, Proteus spp, Escherichia coli and Gram positive bacteria including Staphylococcus spp especially S.aureus (MSSA, MRSA), S. epidermidis, Coagulase-Negative Staphylococci (CoNS), Streptococcus spp. The obtained results showed that P. aeruginosa demonstrated resistance to ciprofloxacin 94%, Amikacin 88%, gentamicin 82%, imipenem 70% and ceftazidime 64%. Also, S.aureus demonstrated similar trends with resistance to ciprofloxacin 80%, Amikacin 60% , gentamicin 60%.

**Conclusion :** Due to various reasons, including the indiscriminate use of antibiotics, especially in recent years, the resistance of bacteria to antibiotics is increasing. As shown in different

studies, bacteria, especially gram-negative ones, are MDR and resistant to different antibiotics, which is one of the serious challenges in treating wound infections.

**Keywords :** bacterial strain, wound infection, antibiotics resistance, world

# P308-356: 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 Kashan textile factory in the presence of carbon sources of fructose, glucose, xylose, lactose, and sucrose.

**Results :** This strain decolorized Acid Red 14 dye at 50 ppm with pH 7 and temperature of 37 ° C in the incubator and the presence of fructose, after 24 h and 48 h, 16%, and 92%, respectively. The analysis of the visible-ultraviolet spectrophotometer showed that the discoloration is due to a microbial analysis by the bacterial strain.

**Conclusion :** The bacteria strain isolated from the effluent of Kashan textile factory decolorized Acid Red 14 dye at the especial condition.

**Keywords :** Decolorization, Azo dyes, Bacteria, Optimization, Waste water

# P309-372: High prevalent bacterial contamination of ATM keyboards in Sari city- north Iran

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**Background and Aim :** Today, one of the most significant factors increasing the risk of hand contamination by antibiotic resistant microorganisms is the use of automated teller machines (ATMs). This study aimed to investigate the prevalence of contaminating bacteria and the antibiotic resistance pattern of the bacterial strains isolated from the keyboard of the ATMs.

**Methods :** In this study, 200 samples were collected from ATM keyboards in Sari city by sterile swab before and after disinfection with 70% ethanol. The samples were transferred to the laboratory and different bacteria were identified using standard diagnostic methods. The antibiotic resistance pattern of the bacteria was evaluated by disk agar diffusion method.

**Results :** Bacterial contamination was observed in 97% of the samples. The most isolated bacterium was Klebsiella pneumoniae (36.08%), however lowest frequency (1.55%) was observed about Bacillus cereus. Also, we funded significantly decreased rate of contamination after disinfection with ethanol. In the case of Klebsiella pneumoniae, 91.42% and 82.85% of the isolates were resistant against tetracycline and ampicillin, respectively. Besides, among the Escherichia coli isolates, the highest resistance rate was detected about ampicillin (90.24%) and tetracycline (78.04%), while none of the E. coli isolates were resistant against imipenem. Also, 95.08% of the Staphylococcus epidermidis isolated from ATMs were resistant to ampicillin.

**Conclusion :** The ATMs are one of the most important sources of the spreading communicated associated resistant bacteria. So, it is important to monitor the sale of over-the-counter antibiotics in pharmacies and to avoid the arbitrary use of antibiotics by people to combat this problem.

**Keywords :** automated teller machines, keyboards, antimicrobial resistance

# P310-385: Discovery of Potential Inhibitors for Trihydroxynaphthalene Reductase (3HNR) by virtual screening

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**Background and Aim :** Curvularia lunata is a dark pigmented fungus that is the causative agent of several diseases in plants and humans like that immunodeficient, eyes infection and allergic disease.1,8-Dihydroxynaphthalene-melanin (DHN) was produced by Trihydroxynaphthalene Reductase (3HNR) enzyme during the biosynthetic pathway in the cell wall of C. lunata which cause disease. The aim of this study is to discover novel inhibitors for the 3HNR enzyme to prevent the production of DHN by using in silico virtual screening method.

**Methods :** All molecular modeling was carried out using the small-Molecular Drug Discovery Suite 2015-2 (Schrodinger, LLC, New York, NY, 2016). proteins were obtained from a protein data bank (PDB: 1DOH). The protein preparation and prime application were performed to minimize the protein strains state. The High Throughput Virtual Screening (HTVS) protocol was used as a method for discovering novel 3HNR inhibitors. The molecular modeling was subjected to using the Glide application using extra precision (XP) protocol. Over 6000 natural products downloaded from ZINC15 were prepared with Ligprep application; The ADME properties of all compounds were analyzed and a final selection was made based on the Lipinski rule of five.

**Results :** The results of molecular docking showed that ZINC9590342, ZINC14814612 (isochromen-1-one) and ZINC31166 (epilupinine) with docking scores -9.656, -9.487 and -9.324 kcal/mol, respectively are good candidates. These compounds formed a hydrogen bond with SER164 and TYR178, had high affinity to receptor with the highest inhibitory activity on 1-DOH receptor.

**Conclusion :** Our finding shows that these compounds on inhibitory potential 3HNR enzyme and controlling C. lunata fungi in humans and plants. The isochromen-1-one is coumarin derivatives, previously reported to have activity against Candida albicans species and inhibited sterol 14-alpha demethylase enzyme.

**Keywords :** Curvularia lunata, trihydroxynaphthalene reductase, Molecular Docking, Natural product

# P311-389: Evaluation of antibiotic resistance pattern of Acinetobacter strains isolated from patients admitted to four hospitals in Isfahan province

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**Background and Aim :** Nosocomial infections are common causes of mortality, disability, increased length of hospital stay, increased hospital costs, and health problems. . Although efforts to control nosocomial infections have been successful, recent advances in medical science and repeated medical interventions, including the widespread use of immunosuppressive and anti-inflammatory drugs, have been successful. Antibiotics have increased the number of vulnerable people, which has been exacerbated by the development of transmissible resistance to pathogens against antibiotics. . Multidrug resistance to gram-negative bacteria such as Acinetobacter is a growing global problem. The aim of this study was to evaluate the pattern of antibiotic resistance of Acinetobacter strains isolated from patients admitted to four main hospitals in Isfahan province.

**Methods :** In this study, during six months, 53 strains of Acinetobacter were collected from four main hospitals in Isfahan province. Biochemical tests were performed to identify the isolated bacteria. Antibiotic susceptibility testing was performed by disk diffusion method.

**Results :** The results of antibiotic susceptibility test showed that the highest susceptibility of 46 strains (87%) was to colistin antibiotic and 53 strains (100%) were resistant to meropenem, ciprofloxacin and piperacillin tazobactam. Other antibiotics include: 52 strains of ceftazidime (98.1%) resistant and 1 strain (1.9%) semi-sensitive, gentamicin 50 strains (94.3%) resistant and 1 strain (1.9%) semi-sensitive and 2 Sensitive strain (3.7%), cefipime 47 strains (88.68%) resistant and 6 strains (11.32%) semi-susceptible, trimenoprim sulfamethoxazole 47 strains (88.68%) resistant and 3 strains (5.6%) semi-sensitive and 3 strains (5.6%) sensitive, ampicillin sulbactam 46 strains (86.80%) resistant and 6 strains (11.32%) semi-sensitive and 1 strain (1.9%) sensitive, amikacin 45 strains (84.90%) resistant And 3 strains (5.6%) are semi-sensitive and 5 strains are sensitive (9.43%).

**Conclusion :** Antibiotic susceptibility testing of Acinetobacter strains showed that 6 strains of MDR (Multidrug resistant), 43 strains of XDR (Extensively drug resistant) and 4 strains of

PDR (Pandrug resistant) were detected. Since Acinetobacter is one of the most important causes of nosocomial infections, it is necessary to study the patterns of drug resistance in it.

**Keywords :** Antibiotic resistance, Acinetobacter, Gram negative bacteria

# P312-390: The prevalence of Symptomatic and Asymptomatic Bacterial Vaginosis in Women with Unexplained Infertility Problems

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**Background and Aim :** Bacterial vaginosis (BV) is a polymicrobial syndrome described by vaginal itching, vaginal discharge, odorous, and/or burning. BV can occur when vaginal lactobacilli are replaced by different anaerobic bacteria. This study was aimed to determine the prevalence of bacterial vaginosis among women with unexplained infertility problems

**Methods :** A total of 100 infertile women, who referred to obstetrics and gynecology clinics in Tabriz City for suspected vaginal infections, were tested for possible BV. Interviews were performed to collect data on socio-demographic characteristics, history and characteristics of vaginal discharge. BV was diagnosed by laboratory methods according to the Amsel criteria. The presence of Gardnerella vaginalis, Atopobium vaginae, Neisseria gonorrhoeae, Mycoplasma genitalium, and Ureaplasma urealyticum was verified by polymerase chain reaction (PCR) using specific primers on the DNA extracted from the vaginal specimens.

**Results :** : Among women tested for suspected vaginal infections, 36 cases of BV (23 symptomatic and 13 Asymptomatic) were confirmed using defined criteria. In 58% (21/36) and 41% (15/36) of these BV cases, the presence of G. vaginalis and A. vaginae was confirmed by PCR, respectively. The prevalence of U. urealyticum, M. genitalium, and N. gonorrhea were as 21%, 10%, and 4%, respectively.

**Conclusion :** The prevalence of BV was high among patients with unexplained infertility. The cultural and socio-economic factors contribute to the risk of the condition.

**Keywords :** Bacterial vaginosis; Infertility; Gardnerella vaginalis; Atopobium vaginae

# P313-396: Co-infection of Gardnella vaginalis and human papillomavirus in cervical samples: A multicenter study in Iran

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**Background and Aim :** HPV infection is unlikely to be sufficient to cause cervical cancer, and the contribution of other sexually transmitted infections (STIs) could be the determining factor for cervical lesion-progression. STIs have an influence on women's health, related with cervicitis, urethritis, pelvic inflammation, complications of reproductive health. The aim of this study was to estimate the prevalence of Gardnerella vaginalis associated with HPV-positive cervical samples patients in Iran.

**Methods :** Three hundred and fourteen women between 18 and 63 years and living at 14 different city in Iran Nucleic acid was extracted from vaginal swab suspensions (Add bio, Korea) and G. vaginalis was detected by single 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 34.33 years (age range: 18-63years). A total of 124 (mean range of 33.6 years) patients were found positive for HPV with 11.46% (n=36) infected with high-risk type, 14.64% (n=46) infected with low-risk type and 13.37% (n=42) infected with multiple types. Among the 314 women, there were 14.33% (n=45) G. vaginalis infection. Among 124 women with HPV infection 17.74% (n=22) suffered from G. vaginalis. The most common HPV genotypes in low-risk type's co-infection with G. vaginalis was HPV6 (22.22%) and in high –risk type was HPV31 (8.88%).

**Conclusion :** In current study, G. vaginalis rate was 14.33%. In HPV high-risk type and low risk-type, HPV31 and HPV6 showed the highest prevalence, respectively. HPV infection is associated with a number of factors, including age, pregnancy, and impaired immune function. Recent studies have shown that, in addition to the aforementioned factors, vaginal infection may be associated with increased odds for HPV infection.

**Keywords :** Molecular characterization, co-infection, Human papillomaviruses, Gardnerella vaginalis

# P314-410: Diagnosis of Helicobacter pylori by serological and invasive pathology in Shahr e kord patients

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**Background and Aim :** Helicobacter pylori is a gram-negative, helical-negative bacterium found in the gastric mucosa and is the leading cause of gastric ulcer and chronic gastritis and is usually asymptomatic. The bacterium is more prevalent in developing countries. The aim of this study was to evaluate and compare invasive and serological methods in the diagnosis of Helicobacter pylori

**Methods :** This cross-sectional laboratory study was performed on 233 patients in which biopsy specimens were randomly collected from hospitals in Shahr e kord in 2019. Gastric and duodenal antrum biopsy was performed by pathology and staining (H&E) and stabilization, and serological antibody (IgG) was measured by ELISA to detect Helicobacter pylori. The data were analyzed using SPSS statistical software.

**Results :** prevalence of infection in the age group (27-35 years) 38% shows the importance of biopsy sampling and tissue staining among young people. This study also showed that antibody titration alone is not sufficient and invasive pathology sampling is required for final diagnosis. In this study, no significant relationship was observed between polymorphisms in the control group and patients with HBV infection.

**Conclusion :** According to the present study, the age range of 27 to 35 years was shown as the most infected group with this bacterium. This difference may be due to differences in diet and geographical sampling range. Finally, considering the importance and consequences of Helicobacter pylori infection, the obtained epidemiological information and data analysis, and considering the increasing prevalence in the young age group, it is better to consider this issue in clinical evaluations.

**Keywords :** Helicobacter pylori, Biopsy, Serology,Shahr e kord

# P315-422: Phosphinic amides and oxadiazole 2-oxides potential drug candidates for schistosomiasis

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**Background and Aim :** Schistosomiasis is a chronic parasitic disease that affects the health of millions of people around the world. Due to the increased drug resistance to praziquantel (PZQ), which is the main drug for schistosomiasis, new drugs for the treatment of schistosomiasis are significant. Phosphinic amides and oxadiazole 2-oxides have been identified as potential anti-schistosomiasis agents that target thiodoxine glutathione reductase (TGR).

**Methods :** For collecting the related published paper, we searched PubMed with the keywords of Schistosomiasis, "Phosphinic amides", and "Oxadiazole 2-oxides" from 2005 till now.

**Results :** The activities of phosphinic amides and oxadiazole 2-oxides were examined against both the GR and the TrxR activities of recombinant schistosome TGR. The compounds inhibited both TGR activities, with most showing greater inhibition of the TrxR activity.

**Conclusion :** Given the importance of the TGR system for the survival of Schistosoma in vertebrate hosts, inhibition of this system can limit and inhibit schistosomiasis. Phosphinic amides and oxadiazole 2-oxides derivatives can well inhibit this system and prevent the survival of Schistosoma and disease. Therefore, these compounds could be potential drug candidates for schistosomiasis and a viable alternative to praziquantel.

**Keywords :** Schistosomiasis, Phosphinic amides, Oxadiazole 2-oxides, Drug

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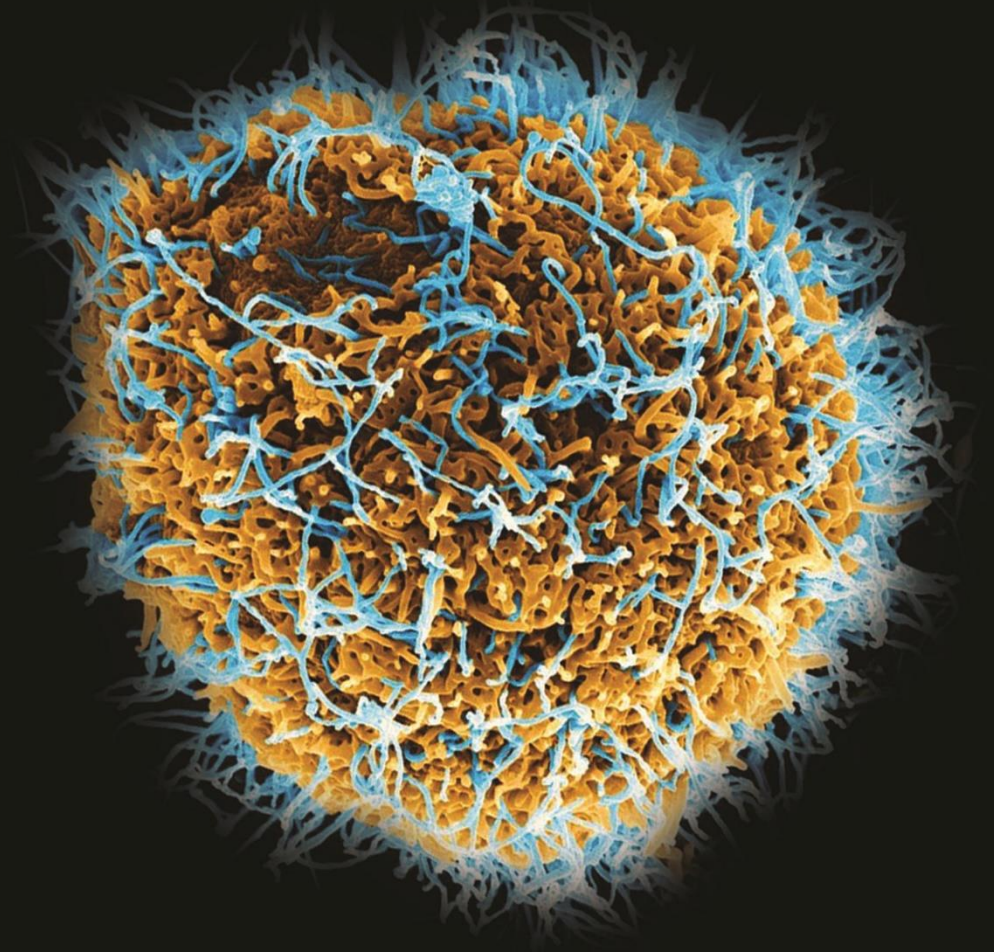

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