Abstract Book

18th Professor Alborzi

International Congress of Clinical Microbiology

October 21-23, 2025

Shiraz- Iran

Secretariat:

Prof. Alborzi Clinical Microbiology Research Center, Shiraz University of Medical sciences, Namazi Teaching Hospital, Shiraz, Iran

President:

Abdolvahab Alborzi, MD

Professor of Pediatric Infectious Diseases

Co-chair:

Gholamreza Pouladfar

Associate Professor of Pediatric Infectious Diseases

Scientific Secretary:

Ali Amanati, MD

Associate Professor of Pediatric Infectious Diseases

Executive Secretary:

Marzieh Jamalidoust, PhD

Assistant Professor of Virology

PAICCM2025

18th Professor Alborzi International Congress of Clinical Microbiology

Congress Financial Supporters

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Foreword

Guidelines and Innovations in the Clinical Microbiology and Infectious disease

Dear Colleagues

The 18th Professor Alborzi International Congress of Clinical Microbiology (PAICCM) was successfully held from 21 to 23 October 2025 (29 Mehr to 1 Aban 1404) in the beautiful and historic city of Shiraz, Iran. As one of the most distinguished scientific gatherings in the field of clinical microbiology and infectious diseases in Iran and the region, this year's congress once again served as a dynamic platform for the exchange of ideas, presentation of novel research, and promotion of collaboration among experts, researchers, and healthcare professionals from around the world.

The congress program featured a wide range of topics, including advances in immunization and infection prevention and control, innovations in clinical microbiology across bacteriology, virology, mycology, parasitology, and immunology, and implementation of clinical guidelines and antimicrobial stewardship programs. Participants benefited from keynote lectures, symposia, panel discussions, workshops, oral and poster presentations, and the opportunity to interact with prominent scientists and clinicians from Iran and abroad, including experts from Switzerland, Belgium, the United States, and Australia.

Organized by the Professor Alborzi Clinical Microbiology Research Center—recognized as the Center of excellence in Clinical Microbiology in Iran—in collaboration with domestic scientific societies, the Communicable Diseases Control Directorate of the Ministry of Health and Medical Education, and the National Vaccination Committee, the congress reflected a shared commitment to advancing the understanding, diagnosis, prevention, and management of infectious diseases.

The 18th PAICCM also honored excellence in the field through the presentation of the Professor Alborzi Clinical Microbiology Award and the Professor Abdulwahab Alborzi Award in Infectious Diseases, recognizing outstanding contributions to research and clinical practice.

Building on the achievements of previous years, this congress continued to uphold the mission of the PAICCM: to foster scientific excellence, encourage innovation, and strengthen collaboration in clinical microbiology and infectious diseases for the benefit of patients and public health in Iran, the Eastern Mediterranean region, and the world.

We express our deepest gratitude to all participants, speakers, sponsors, and organizers who contributed to the success of this event. Their dedication and enthusiasm made the 18th PAICCM a memorable and impactful scientific gathering.

Introduction by the Scientific Secretary

Today, the rapid growth of medical knowledge has heightened the importance of specialized scientific congresses in advancing education, research, and the scientific development of the country. The 18th International Congress of Clinical Microbiology, Professor Alborzi, has become a venue for researchers, professors, and students from across the country and the world to share the latest findings, experiences, and innovative approaches in health, diagnosis, and treatment of common infectious diseases. Addressing current themes and challenges, including vaccination, pharmaceutical innovations, and antimicrobial resistance, clearly signals the new horizons of this scientific event.

The Congress Scientific Committee, considering criteria of innovation, research originality, scientific ethics, and an interdisciplinary approach, welcomes abstract submissions and, through rigorous peer review, provides a platform for presenting prominent researchers and impactful projects. These selections will play a decisive role in promoting community-based research.

Our scientific community, backed by talented youth, committed professors, and robust academic infrastructure, has today attained a special role in the region and the world—a role that should be reinforced through continuous research, higher standards, and support for innovative currents.

It is hoped that the current collection of articles will inspire future scientific movements and pave the way for advancing knowledge and public health. The Congress Secretariat expresses gratitude to all researchers, reviewers, and administrative collaborators who, with diligence and responsibility, made this event possible. Undoubtedly, this path will continue and remain dynamic only with the participation of all members of the scientific community and the effort to apply the achievements to solving the country's current and real issues.

Dr. Ali Amanati

The Scientific Secretary of the 18th PAICCM

The Professor Alborzi Clinical Microbiology Award (PACMA)

As part of the 18th "Professor Alborzi International Congress of Clinical Microbiology (PAICCM)", the "Professor Alborzi Clinical Microbiology Award" was presented to recognize outstanding scientific contributions in the field of clinical microbiology and infectious diseases.

During the congress, submitted research papers were carefully reviewed by the "Scientific Committee" based on originality, scientific quality, relevance to the congress themes, and potential impact on clinical practice and public health.

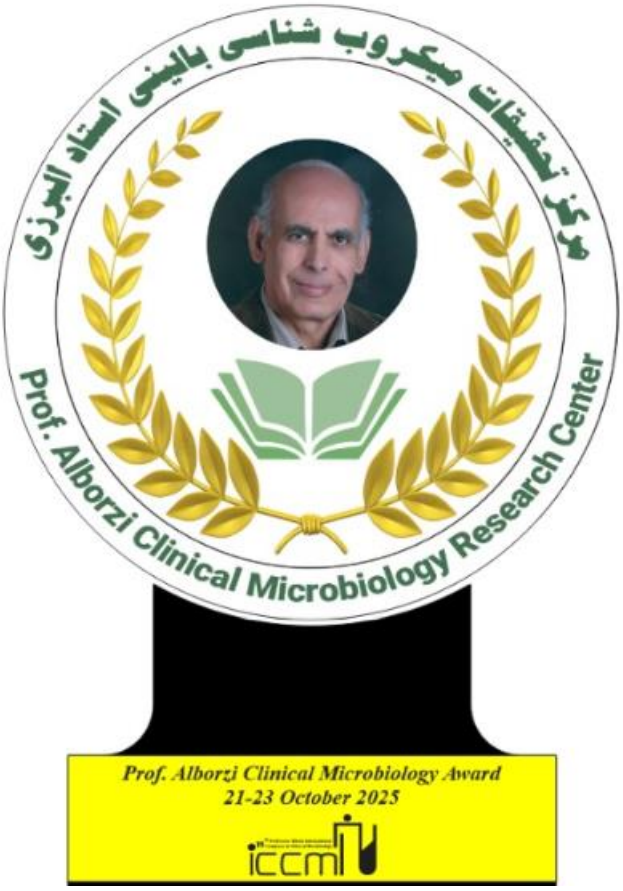
Following a rigorous evaluation process, "three outstanding papers" were selected to receive this prestigious award. The winners of the 18th PAICCM "Professor Alborzi Clinical Microbiology Award" are as follows:

1- Hadi Feizi – Bacterial and Metabolic Signatures in Colorectal Cancer Development
2- Samira Saedi – Comparison of gut microbiota and short-chain fatty acids in patients with inflammatory bowel disease and healthy individuals
3- Fatemeh Mosaffa Jahromi – Some virulence genes are associated with antibiotic susceptibility in Enterobacter cloacae complex

This award reflects the congress's commitment to promoting excellence in research, encouraging innovation, and supporting the next generation of scientists and clinicians dedicated to the prevention, diagnosis, and treatment of infectious diseases.

We extend our sincere congratulations to the winners and express our appreciation to all researchers who contributed their valuable work to this year's scientific program.

The Statuette of the Professor Alborzi Clinical Microbiology Award



Professor Abdulwahab Alborzi Award in Infectious Diseases

The second Professor Abdulwahab Alborzi Scientific Award in the field of Infectious Diseases was proudly presented during the 18th Professor Alborzi International Congress of Clinical Microbiology (PAICCM), held in Shiraz from October 21 to 23, 2025 (29 Mehr to 1 Aban 1404).

This distinguished award was first introduced in 2023 (1402) by the Fars Elite-Developing Benefactors' Association, in collaboration with the Fars Elite Foundation, and was initially presented at the 17th Professor Alborzi International Congress of Clinical Microbiology to recognize the most outstanding residency thesis.

Funded by generous donors, this annual award honors resident and sub-specialty physicians from various medical disciplines who have directly participated in research projects related to infectious diseases. Eligible candidates must present the results of their research, which should (1) have been completed during their residency period and (2) resulted in an article published or accepted for publication in a reputable scientific journal within the past five years.

Each year, a specialized review committee—comprising professors from Shiraz University of Medical Sciences, representatives of the Fars Elite Charitable Association, and the Fars Elite Foundation—evaluates the submitted research projects. The award is presented to the study that demonstrates the most practical impact in addressing challenges related to infectious diseases.

In this year’s congress, the Professor Abdulwahab Alborzi Award in Infectious Diseases was granted to Dr. Fatemeh Zia for the research entitled “Survival and prognostic factors in rhino-orbito-cerebral mucormycosis: A 3-year cohort study.”

This award reflects the enduring legacy of Professor Abdulwahab Alborzi in inspiring scientific excellence and innovation in infectious disease research and serves as a tribute to those who continue his mission to improve patient care and public health.

Scientific Committee

(Alphabetic order)

Alighayoumi Seyedmohammad
Alison Kasson
Abotalebi Narjes
Abdoli-Oskouei Shahram
Aelami Mohammadhassan
Alborzi Abdolvahab
Aghighi Yahya
Aliabadi Nasrin
Alp Mese Emine
Asadi Nasrin
Amanati Ali
Ataei Behrooz
Alavi Mehrosadat
Alimohammad ghelichkhan Zahra
Mahmoodi Soosan
Badeei Parisa
Bagheri Lankarani Kamran
Abdollah Bazargani
Bonyadi Behrouz
Bordbar Mohammadreza
Boven Annelies
Davarpanah Mohammad Ali
Kadivar Mohammadrahim
Mehrabi Zeinab
Molavi Hossein
Mardani Masoud
Moradi Ghobad
Mansour Ghanaei Roxana
Mirhendiesfahani Seyed hossein
Masoumi Asl Hossein
Mehrabi Zeinab
Volige Erica
Moattari Afagh
Mansoorghenaei Roxana
Mostafavi Sayed Nasser
Motamedifar Mohammad
Oboodi Barat
Pakshir Keyvan
Pittet Didier
Pouladfar Gholamreza
Pourabbas Bahman
Pourmoghaddas Zahra
Rafei Tabatabaei Seyeded sedigheh
Razelansari Ali Akbar
Rezaianzadeh Abbas

Fahimzad Ali Reza

Fallahi Mohammad Javad

Farokhnia Mehrdad

Fata Abdolmajid

Farhadi Ali

Foroghi Mehdi

Ghaderian Mehdi

Ghadimi Moghadam Abdolkarim

Ghayumi Seiyed Mohammad Ali

Ghatei Mohammad Amin

Shiravani Fariba

Hamedi Abdol Karim

Hamzavi Seyedeh Sedigheh

Hatam Masoumeh

Hemati Fariba

Hosseini Vahid

Hossininasab Ali

Jaafarian Hadis

Jafari Maedeh

Shafeikhani Mojtaba

Jamalidoust Marzieh

Kalani Mehdi

Karimi Abdollah

Kamali Kiyanoush

Sabri Mohammad Reza

Sadjjadi Seyed Mahmoud

Saebi Esmaeel

Sanaei Anahita

Ilami Owrang

Shorafa Islam

Sarvari Jamal

Sasan Mohamad Saeid

Sedighi Iraj

Sadeghi Esmaeil

Soltani jaffar

Shahriarirad Bahador

Shamsizadeh Ahmad

Sherkatolabbasieh Hamid Reza

Salehi Mohammad reza

Shorafa Eslam

Tabarsi Payam

Yaghoobi Ramin

Zand Farid

Zarei Najmeh

Roshanzamir Zahra

Zingg Walter

Yavarian Jila

Versporten Ann

Executive Committee

(Alphabetic order)

Abbasi Pejman

Abbasian Amin

Aliabadi Nasrin

Asaei Sadaf

Abbasi Ali reza

Abdi pour Reza

Abbasi Amin Reza

Bamia Fatemeh

Choopanizadeh Maral

Dehyadegari Mohammad Ali

Dorostkar Sara

Farokhmanesh Shahdad

Farhadi Mohammad

Farkariyan Armina

Ghasemi Fatemeh

Habibi seyed Amir Hossein

Heydari Marandi Nahid

Hosseini Marzieh

Homayoun far Fatemh

Jafarpour Zahra

Maddahi Arman

Malek pour Mehdi

Mokhtari nasab Saeeid

Namayandeh Mandana

Heydari Marandi Nahid

Rafatpoor Nooredin

Reisi Pedram

Sabzehzar Maryam

Sepehrpoor Shima

Rafei Mehdi

Veisi Maral

Congress Program, October 21th, 2025	
8:00- 9:30	**Opening Ceremony**
8:00-8:10	Quran Recitation
8:10- 8:15	Anthem of Islamic Republic of Iran
8:15- 8:25	Music Performance
8:25- 8:35	**Welcome:** Dr. Seyed Basir Hashemi (the president of Shiraz UMS)
8:35- 8:45	**Opening**: Prof. Abdolvahab Alborzi (the president of the congress)
8:45- 8:50	**Aims of congress**: Dr. Ali Amanati (the congress manager)
9:30-10:00	**Break & visiting posters**
Panel I	
10:00- 10:30	**Comprehensive lecture**: Title: Responsibilities of university administrators towards medical students **Yahya Aghighi** MD, Senior Professor of Pediatric Rheumatology
10:30- 12:15	**Panel I Subject:** **Global Vaccination Updates and Outlook**
Coordinator: **Dr. Abdolvahab Alborzi** (Professor of Pediatric Infectious Disease, Shiraz UMS) **Panel staff**: **Dr. Jafar Soltani** (Associate Professor of Pediatric Infectious Disease, Tehran UMS) **Dr. Zhila Yavariyan** (Professor of Medical Virology,) **Dr. Shahram Abdoli-Oskouei** (Associate Professor of Pediatric Infectious Disease, Tabriz UMS) **Dr. Ali Hossininasab** (Professor of Pediatric Infectious Disease, Kerman UMS) **Dr. Roxana Mansour Ghanaei** (Professor of Pediatric Infectious Disease, Shahid Beheshti UMS)	
12:15-12:30	**Discussion, Q&A**
12:30- 13:30	**Lunch and break**

Congress Program, October 21th, 2025	
Panel II	
13:30- 13:45 Iran Time,	**Comprehensive lecture:** Title: **Clinical and paraclinical differentiation between Acanthamoeba and fungal keratitis** **Dr. Fata Abdolmajid (PhD in Medical Parasitology)**
13:45- 15:15	**Panel II Subject:** Guidelines for Diagnosis and Treatment of Common Infectious Diseases in Cancer and Bone Marrow Transplant Patients

Coordinator:
Dr. Masoud Mardani (Professor of Infectious Diseases, Shahid Beheshti UMS)

Panel staff:
Dr. Payam Tabarsi (Professor of Infectious Diseases, Shahid Beheshti UMS)
Dr. Sayed Nassereddin Mostafavi (Associate Professor of Pediatric Infectious Disease, Isfahan UMS)
Dr. Seyed Hossein Mirhendi Esfahani, (Assistant Professor of Medical micology,)
Dr. Mehralsadat Alav(Nuclear medicine specialist)

Dr. Seyedeh Sedigheh Hamzavi (Assistant Professor of Pediatric Infectious Disease, Shiraz UMS)

Discussion, Q&A (15:15- 15:30)

15:30- 16:00	**Break and visiting posters**

Congress Program, October 21th, 2025	
Panel III	
16:00- 16:۲۰ Iran Time,	**Comprehensive lecture**: Klebsiella pneumoniae: high resistance and hospital Threats **Dr. Bahman Pourabbas** (Assistant Professor of Medical Microbiology, Shiraz UMS)
16:20- 17:45	**Panel III Subject:** **Updates in Pharmacotherapy of Infectious Diseases**

Coordinator:
Dr. Ali Amanati (Associate Professor of Pediatric Infectious Disease, Shiraz UMS)

Panel staff:

Dr. Mojtaba Shafiekhani (Assistant Professor of Clinical Pharmacy, Shiraz UMS)

Dr. Shahnaz Armin (Associate Professor of Pediatric Infectious Disease, Tehran UMS)
Dr Hadis Jaafarian (PhD of medical mycology, Shiraz UMS)
Dr. Zahra Ali Mohammad Ghelich Khan (Assistant Professor of Clinical Pharmacy)
Dr. Mehdi Kalani (Assistant Professor of Clinical Immunology, Shiraz UMS)

Discussion, Q&A (17:45- 18:00)

Congress Program, October 22th, 2025	
8:00-8:15	Quran Recitation
Panel IV	
8:15- 10:00	**Panel IV Subject**: **Development of Vaccine Programs in Iran's Health System**
Coordinator: **Dr. Abdollah Karimi** (Professor of Pediatric Infectious Disease, Shahid Beheshti UMS) **Panel staff**: **Dr. Abdolvahab Alborzi** (Professor of Pediatric Infectious Disease, Shiraz UMS) **Dr. Ali Reza Fahimzad** (Professor of Pediatric Infectious Disease, Shahid Beheshti UMS) **Dr. Iraj Sedighi** (Professor of Pediatric Infectious Disease, Hamadan UMS) **Dr. Fariba Ravaneshi** (Professor of Pediatric Infectious Disease) **Dr. Sosan Mahmoudi**(Pediatrician and neonatologist) **Dr. Seyedeh Sedigheh Rafei Tabatabaei** (Professor of Pediatric Infectious Disease) **Dr. Eslam Shorafa** (Assistant Professor of Pediatric Intensive Care, Shiraz UMS)	
Discussion, Q&A (10:0- 10:15)	
10:15- 10:45	**Comprehensive lecture**: **Title: Epidemiological trends and the impact of communicable diseases in the region** **Dr. Ghobad Moradi(Head of the Ministry's Communicable Diseases Department)**
10:45-11:15	**Break and visiting posters**

Congress Program, October 22th, 2025	
Panel V	
11:15- 13:00	**Panel V Subject:** **Updates in Respiratory Viral Infections and Future Perspectives**
Coordinator: **Dr. Mohammad Rahim Kadivar** (Professor of Pediatric Infectious Disease, Shiraz UMS) **Panel staff:** **Dr. Mohammad Ali Davarpanah** (Professor of Infectious Disease, Shiraz UMS) **Dr. Marzieh Jamalidoust** (Assistant Professor of Medical Virology, Shiraz UMS) **Dr. Narjes Abotalebi** (Assistant Professor of Pediatric Intensive CareDepartment of Pediatrics, School of Medicine) **Dr. Seyed Mohammad Ali Ghyoumi**) Professor of Pulmonary DiseasesDepartment of Internal Medicine, School of Medicine) **Discussion, Q&A** (13:00- 13:15)	
13:15- 14:15	**Lunch and break**

Congress Program, October 22th, 2025	
Panel VI	
14:15- 14:30 Iran Time	**Comprehensive lecture**: Title: **How to recognize a reliable clinical guideline**? **Dr. Hossein Molavi** (**PhD in Epidemiology**)
14:30- 16:15	**Panel VI Subject:** Clinical guidelines for the diagnosis and treatment of acquired pneumonia in children and adults.
Coordinator: **Dr. Gholamreza Pouladfar** (Associate Professor of Pediatric Infectious Disease, Shiraz UMS) **Panel staff**: **Dr. Zeinab Mehrabi**, (Associate Professor of Pediatric Infectious Disease, Shiraz UMS) **Dr. Zahra Roshan-Zamir** (Specialist in pediatric lung diseases) **Dr. Ramin Yaghoubi (**Professor of Medical Virology) **Dr. Sedigheh Hamzavi** (Associate Professor of Pediatric Infectious Disease, Shiraz UMS) **Dr. Mohammad Motamedifar** (Professor of Medical Microbiology, Shiraz UMS) **Dr. Mohammad Javad Fallahi** (associate Professor of Pulmonary Diseases) **Discussion, Q&A** (16:15- 16:30)	
16:30- 17:00	**Break and visiting posters**
17.00- 17:20	**Comprehensive lecture** Title: **Hand Hygiene** **Dr. Didier Pittet (University of Geneva)** **MD Infectious diseases specialist,** **University of Geneva Hospitals** **and Faculty of Medicine,** **Switzerland**
17:20- 17:40	**Comprehensive lecture**: **Title: Interpret yourGlobal-PPS feedback and antibiotic prescribing practices in your hospital latest fetures** **Dr. Ann Versporten (University of Antwerp)**
17:40-18:00	**Comprehensive lecture** **Title: Global-PPS feedback results and evaluate antibiotic prescribing practices in outpatients setting** **Dr. Erica Velige**

Congress Program, October 23th, 2025	
8:00-8:15	**Quran Recitation**
8:15- 8:35	**Comprehensive lecture** **Title: Kingella kingae infections** **Dr. Alison Casson (Australia)**
8:35-8:55	**Comprehensive lecture** **Title: Febrile Child – Antibiotic: Yes or No?** **Prof. Esmaeil Sadeghi (Professor of Pediatric Infectious Disease, Shiraz UMS)**
8:55- 9:15	**Comprehensive lecture** **Title: AMR control programs in Iran and the world** **Dr. Kianoosh Kamali**
9:15- 9:45	**Comprehensive lecture** **Title: Arboviral infections – Zika, Dengue, Chikungunya** **Dr. Esmaeel Saebi, MD** **Infectious diseases specialist, Tehran, Iran**
9:45- 10:15	**Break and visiting posters**

Congress Program, October 23th, 2025	
Panel VII	
10:15- 11:45	**Panel VII Subject:** **Advances in TORCH Infections**

Coordinator:

Dr. Anahita Sanai Dashti (Associate Professor of Pediatric Infectious Disease, Shiraz UMS)

Panel staff:

Dr. Ali Farhadi (Associated Professor of Medical Virology, Shiraz UMS)

Dr. Fariba Hemmati(Professor of Neonatal-Perinatal MedicineDepartment of Pediatrics, School of Medicin)

Dr. Nasrin Asadi) Professor of PerinatologyDepartment of Obstetrics and Gynecology, School of Medicine)

Dr. Ahmad Shamsizadeh (Professor of Pediatric Infectious Disease, Ahvaz UMS)

Dr. Maedeh Jafari (Assistant Professor of Pediatric Infectious Disease, Kerman UMS)

Dr. Mohammad Amin Ghatei (Professor of Medical Parasitology, Shiraz UMS)

Discussion, Q&A (11:45 – 12:00)

12:00- 13:00	**Lunch and break**

Congress Program, October 23th, 2025	
Panel VIII **Comprehensive lecture** **Title: Global antimicrobial resistance: challenges, impacts and strategies for a sustainable future** **Dr. Walter Zing**	
13:20- 15:00	**Panel VIII Subject:** **Guidelines for Healthcare-Associated Infections (HAIs)**
Coordinator: **Dr. Mohammadhassan Aelami** (Associate Professor of Pediatric Infectious Disease, Mashhad UMS) **Panel staff:** **Dr. Bahman Pour Abbas** (Assistant Professor of Medical Microbiology, Shiraz UMS) **Dr. Hossein Masoumi Asl(** Professor of Pediatric Infectious DiseaseDepartment of Pediatrics, School of Medicine) **Dr. Mahdi Foroughi(** Assistant Professor of Pediatric SurgeryDepartment of Surgery, School of Medicine) **Dr. Owrang Ilami(** Associate Professor of Infectious DiseaseDepartment of Family Medicine, School of Medicine) **Dr. Eslam Shorafa(** Assistant Professor of Pediatric Intensive CareDepartment of Pediatrics, School of Medicine) **Discussion, Q&A** (15:00- 15:15)	
15:15- 15:45	**Break and visiting posters**

Congress Program, October 23th, 2025		
15:45- 16:00	Hadi Feizi	Bacterial and Metabolic Signatures in Colorectal Cancer Development
16:00- 16:15	Fatemeh Mosaffa Jahromi	Some virulence genes are associated with antibiotic susceptibility in Enterobacter cloacae complex
6:15-16:30	Samira Saedi	Comparison of gut microbiota and short-chain fatty acids in patients with inflammatory bowel disease and healthy individuals
16:30- 16:45	Bahman Pourabbas	Synergistic effects of colistin-based combinations against colistin and carbapenem-resistant Klebsiella pneumoniae isolated from nosocomial bloodstream infections
16:45-17:00	**Comprehensive lecture**	**Top Research presentation**
17:00- 18:00	**Closing Ceremony And Award ceremony**	

Oral Presentations

October 21th

Time	Speaker	Title	
10:00- 10:30	Prof. Yahya Aghighi	physician's responsibility toward medical student's university	Comprehensive lecture
13:00-13:45	Dr. Fata Abdolmajid	Clinical and paraclinical differentiation between Acanthamoeba and fungal keratitis	Comprehensive lecture

Oral Presentations

October 22th

Time	Speaker	Title	
10:15- 10:45	Dr. GHobad Moradi	Epidemiological trends and the impact of communicable diseases in the region	Comprehensive lecture
14:15- 14:30	Dr. Hossein Molavi	How to recognize a reliable clinical guideline?	Comprehensive lecture
17.00- 17:20	Dr. Didier Pittet	Hand Hygiene	Comprehensive lecture
17:20- 17:40	Dr. Ann Versporten	:Interpret yourGlobal-PPS feedback and antibiotic prescribing practices in your hospital latest fetures	Comprehensive lecture
17:40- 18:00	Dr. Olga Kaye	Global-PPS feedback results and evaluate antibiotic prescribing practices in outpatients setting	Comprehensive lecture

Oral Presentations

October 23th

Time	Speaker	Title	
8:15- 8:35	Dr. Alison Casson (Australia)	Kingella kingae infections	Comprehensive lecture
8:35-8:55	Prof. Esmaeil Sadeghi	Febrile Child – Antibiotic: Yes or No?	Comprehensive lecture
8:55- 9:15	Dr. Kianoosh Kamali	AMR control programs in Iran and the world	Comprehensive lecture
9:15- 9:45	Dr. Esmaeel Saebi	Arboviral infections – Zika, Dengue, Chikungunya	Comprehensive lecture
12:20- 13:00	Dr. Walter zing	Global antimicrobial resistance: challenges, impacts and strategies for a sustainable future	Comprehensive lecture

Keynote lectures

Clinical Practice Guidelines for Community-Acquired Pneumonia in Children and Adults: Updates and Comparative Review

Gholamreza Pouladfar

Professor Alborzi Clinical Microbiology Research Center, Pediatric Department, Faculty of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran

Effective management of community-acquired pneumonia (CAP) in both children and adults requires adherence to the most recent international and local clinical practice guidelines. This session reviewed the major updates from the 2019 IDSA/ATS guidelines for adults and children, the updated 2025 ATS guidelines for adults, the 2025 NICE pneumonia management guidelines, and the 2024 WHO guidelines on pneumonia and diarrhea in children under 10 years of age.

Key aspects of CAP management include accurate diagnosis, classification into community-acquired versus health care–associated pneumonia, and appropriate decisions regarding outpatient or inpatient treatment. CAP should also be stratified into mild and moderate-to-severe categories. Routine testing of biomarkers such as C-reactive protein (CRP), erythrocyte sedimentation rate (ESR), procalcitonin, and complete blood count with differential, as well as microbiological testing for respiratory viruses (e.g., RSV, SARS-CoV-2, influenza) and bacterial pathogens (including *Mycoplasma*, *Legionella*, and common bacteria), is generally not recommended for outpatients with mild disease. In contrast, laboratory investigations for hospitalized patients should be tailored according to disease severity and underlying comorbidities.

Empiric antibiotic selection depends on patient age, underlying conditions, and recent antibiotic exposure. High-dose amoxicillin or amoxicillin-clavulanate, with or without a macrolide, remains the preferred regimen for outpatients. Chest imaging is not routinely advised for mild outpatient cases without risk factors, especially in children. For hospitalized patients, third-generation cephalosporins with or without macrolides are recommended to cover *Streptococcus pneumoniae*, *Mycoplasma pneumoniae*, and *Chlamydia pneumoniae*. Risk factors for *Staphylococcus aureus* and *Pseudomonas aeruginosa* should also be considered. The emerging role of lung ultrasound was discussed, though it has not yet replaced chest radiography. Finally, corticosteroid use was supported only in adults with severe pneumonia.

Vaccination: Current recommendations and Prospects Adult

Pediatrics Department, Faculty of Medicine, Tehran University of Medical Sciences

Jafar Soltani

Adult vaccination is a critical public health intervention aimed at reducing morbidity and mortality from vaccine-preventable diseases in the growing adult and elderly populations. Current recommendations categorise vaccines into two groups: those for the general adult population and those targeted at individuals with specific risk factors, such as chronic illnesses, immunocompromising conditions, occupational exposures, or travel needs. Routine annual influenza vaccination is advised for all adults, accompanied by tetanus, diphtheria, and pertussis boosters every 10 years. Pneumococcal vaccination has evolved with the introduction of conjugate vaccines (e.g., PCV21), which offer improved immune responses, particularly for adults aged 50 years and older. This addresses the limitations of polysaccharide vaccines (PPV23), which provide only moderate protection and limited duration. The herpes zoster vaccine is recommended for older adults to prevent shingles and its complications.

Other vaccines, including those for COVID-19, HPV, meningococcal disease, hepatitis A and B, and varicella, have age-specific or risk-based indications, highlighting the complexity of adult immunization schedules.

Despite the availability of effective vaccines, adult vaccine uptake remains suboptimal globally due to factors such as passive risk-based recommendations, lack of awareness, and fragmented health systems. However, the future of adult vaccination is promising. Innovations in vaccine development are targeting emerging bacterial threats like Staphylococcus aureus and Clostridium difficile, which are increasingly problematic due to antibiotic resistance and ageing immune systems. Multivalent vaccines against these pathogens are in clinical trials, offering hope for future protection.

Prospects include expanding adult vaccination coverage through unified, well-funded national programs, enhanced public and provider education, and annual monitoring of vaccine uptake and effectiveness. The importance of these initiatives cannot be overstated. Advances in vaccine formulations with more potent adjuvants and tailored immunization schedules to overcome immunosenescence are key areas of research. Leveraging the success of pediatric vaccination programs, a coordinated effort among manufacturers, healthcare providers, and policymakers is essential to improve adult immunization rates and reduce the infectious disease burden in the aging population, ultimately improving health outcomes and quality of life.

This presentation aims to inform healthcare professionals, policymakers, and public health stakeholders about the critical role of adult vaccination. It encourages multidisciplinary collaboration, highlighting the unique contributions of each stakeholder group, to enhance vaccination coverage and protect adult populations worldwide from preventable infectious diseases.

Overview of Bacterial Etiology and Diagnostic Microbiology in patients with Community-Acquired Pneumonia (CAP)

Mohammad Motamedifar

Department of Bacteriology & Virology- HIV/ AIDS Research Center, Institute of Health, Shiraz University of Medical Sciences, Shiraz, Iran

The management of adults with Community-Acquired Pneumonia (CAP) relies on a precise understanding of its bacterial etiology and the strategic use of microbiological diagnostics, as emphasized by contemporary international guidelines (IDSA/ATS 2019, ERS/ESICM/ESCMID/ALAT 2023)

Streptococcus pneumoniae remains the predominant cause of typical CAP. *Haemophilus influenzae*, *Staphylococcus aureus* (including MRSA), and enteric Gram-negative rods (e.g., *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*) are also significant, particularly in patients with specific risk factors like recent antibiotic use, comorbidities (e.g., COPD), or severe illness requiring ICU admission. Atypical bacteria, such as *Legionella pneumophila* and *Mycoplasma pneumoniae*, are crucial targets in severe CAP or cases with epidemiological clues.

Modern guidelines advocate for a targeted, non-routine diagnostic approach to promote antimicrobial stewardship. For most non-ICU inpatients, routine blood and sputum cultures are not recommended. However, testing is strongly indicated in severe CAP (all ICU patients) and in those with risk factors for drug-resistant pathogens (e.g., prior MRSA, recent hospitalization/antibiotics). The diagnostic paradigm is shifting from reliance on slow cultures alone to integrating **rapid microbiological techniques**. The 2023 ERS/ESICM guidelines strongly recommend using multiplex PCR panels on respiratory samples and *Legionella* urinary antigen testing. These tools provide results within hours, enabling early de-escalation from broad-spectrum empiric therapy or targeted escalation for resistant pathogens, thereby improving outcomes. Blood cultures retain their critical role in detecting bacteremia and providing isolates for comprehensive susceptibility testing.

In conclusion, a strategic, evidence-based diagnostic approach—combining rapid molecular methods for immediate guidance with traditional cultures for confirmation—is essential for optimizing antibiotic therapy and improving care for hospitalized CAP patients.

Virus Related Community Acquired Pneumonia: From Clinical Features to Advanced Diagnostics

Ramin Yghoubi

Shiraz transplant research center stem cells research institute Shiraz university of medical sciences

Abstract

One of the most significant clinical and health issues of the twenty-first century is community acquired pneumonia, which is caused by various respiratory viruses, such as coronaviruses, influenza viruses, and respiratory syncytial viruses (RSV). Efficient differentiation between bacterial and viral induced community acquired pneumonia poses a significant obstacle to therapeutic decision-making and the prudent prescription of antibiotics. Molecular diagnostic methods have impacted the treatment of this disease. Clinicians can start antiviral or supportive medication based on real-time data thanks to techniques like RT-PCR, simultaneous multi-assay panels, next-generation sequencing, and CRISPR-based systems, which enable quick and reliable pathogen identification in a matter of hours. Studies of inflammatory biomarkers and genomic analysis have also shed light on the severity of the disease and the immune response. Widespread use of these technologies is, however, limited by challenges including high cost, the requirement for advanced technology, and a lack of collaboration between laboratories. Precision medicine, a method that allows for the identification of the viral agent, prediction of treatment response, and avoidance of needless antibiotic usage, can be made possible by the intelligent integration of molecular and clinical data with machine learning algorithms. The future of virus induced community acquired pneumonia management is dependent on the convergence of rapid diagnosis, conceptual data analysis, and focused treatment selection.

Key words; Virus, Community acquired pneumonia, Multiplex RT-PCR, CRISPR, Artificial Intelligence.

Infection Prevention in Healthcare Systems

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Infection prevention in healthcare systems is essential to safeguard patients, healthcare workers, and the community from healthcare-associated infections (HAIs). Effective prevention relies on a multifaceted approach including strict hand hygiene, proper use of personal protective equipment (PPE), sterilization and disinfection of medical instruments and environments, and adherence to isolation protocols. Additional measures such as safe injection practices, antimicrobial stewardship, and continuous staff education play critical roles. Surveillance and timely reporting enable early detection and management of outbreaks. Implementing comprehensive infection control strategies not only reduces morbidity and mortality but also minimizes healthcare costs and improves overall patient safety.

Key Words: Healthcare-associated Infections, Infection Control, Hand Hygien.

Management of Pediatric Community-Acquired Pneumonia (CAP): Key Recommendations from IDSA/ATS 2019, WHO 2024, and NICE 2025 Guidelines

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Community-acquired pneumonia (CAP) in children is clinically defined by cough, fever, and tachypnea, with age-specific respiratory rate thresholds: ≥50/min for infants 2-11 months, ≥40/min for children 1-5 years, and >20/min for those over 5 years. The first critical step is severity assessment using major criteria (mechanical ventilation, shock, SpO_2 <90%, or need for NIV) and minor criteria (tachypnea, PaO_2/FiO_2 <250, multilobar infiltrates, altered mental status, hypotension, effusion, comorbidities, or unexplained metabolic acidosis). Mild CAP presents with SpO_2 90-92% without meeting any severity criteria, while severe CAP requires ≥1 major or ≥2 minor criteria. For mild CAP managed outpatient, chest X-ray and laboratory tests are not routinely recommended.

First-line treatment is oral amoxicillin for 5 days in fully immunized children (amoxicillin-clavulanate in high-resistance areas per IDSA/ATS), with azithromycin added if atypical pathogens are suspected. Moderate -Severe CAP requires hospitalization with oxygen therapy (target SpO_2 ≥92%), IV fluids (cautious hydration per WHO), and diagnostic workup including chest X-ray (PA/LAT views), CBC, CRP, blood culture, and RT-PCR for influenza/RSV/COVID-19 (NICE 2025). Empirical IV antibiotics should include ceftriaxone/cefotaxime (ceftriaxone preferred for incompletely immunized children), with clindamycin or vancomycin added for complicated cases (empyema, abscess). Follow-up within 48 hours is advised for non-responsive cases (NICE 2025).

Prevention emphasizes PCV13, Hib, and influenza vaccination (IDSA/ATS). These evidence-based guidelines integrate severity stratification, targeted diagnostics, and context-appropriate therapy to optimize outcomes in pediatric CAP.

Oral Presentation

Oral 1

Systems-Biology Approaches to Identify Potential Gene Targets and Pathways in Hepatocellular Carcinoma through Microbiota–Metabolite Interactions

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Introduction: Hepatocellular carcinoma (HCC) is the third-leading cause of cancer mortality worldwide. Growing evidence links gut dysbiosis and the metabolites it produces to chronic liver inflammation, oncogenic signalling and variable therapy response. We therefore set out to integrate real-world transcriptomic, microbiome and metabolomic layers to pinpoint modifiable genes and pathways in HCC.

Methods: We combined RNA-seq profiles from the TCGA-LIHC project covering 374 tumour and 50 matched non-tumour samples (portal.gdc.cancer.gov), then shotgun faecal metagenomes from 51 patients across Barcelona Clinic Liver Cancer stages A–D deposited under BioProject PRJNA1111312 (pmc.ncbi.nlm.nih.gov) and untargeted serum lipidomics from Metabolomics Workbench study ST001640 (31 HCC, 24 chronic-liver-disease, 13 healthy controls) (metabolomicsworkbench.org). Differential expression was computed with DESeq2 (FDR 0.01). Microbial abundances were profiled with MetaPhlAn 4, centred-log-ratio normalised and linked to genes via MaAsLin2. All three matrices were harmonised in DIABLO (mixOmics); module detection used WGCNA. Pathway enrichment relied on KEGG/Reactome, and drug–gene matches on DGIdb.

Results: The cross-omic network retained 1842 differentially expressed genes, 68 bacterial taxa and 112 lipids at Q 0.05. Bacteroides stercoris recently reported as depleted in late-stage HCC clustered inversely (ρ = –0.45, p 0.001) with a Wnt/β-catenin sub-module centred on CTNNB1 and ceramide species (Cer d18:1/16:0). Bile-acid chenodeoxycholic acid correlated positively with FXR (NR1H4) and negatively with pro-inflammatory IL1B (adj. p = 0.004), supporting bile-acid–microbe crosstalk in tumour immunity. Network centrality highlighted CTNNB1, TP53, SLC1A5 and FXR as high-betweenness nodes; DGIdb flagged available FXR agonists and Porcupine (Wnt) inhibitors as tractable therapeutics.

Conclusion: A multi-omic systems-biology framework uncovered a triad linking bile-acid metabolites, Bacteroides stercoris depletion and Wnt/β-catenin activation as a potential driver of HCC progression. The data nominate FXR modulation and Wnt pathway blockade as gene–metabolite targets amenable to microbiome-informed intervention in HCC.

Keywords: Hepatocellular carcinoma; Gut microbiome; Metabolomics; Wnt/β-catenin signalling.

Oral 2

The CRISPR–Cas9 system for genome editing of the ASS1 gene in human cells to predict its effect on HSV-1 replication

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Introduction: Herpes simplex virus type 1 (HSV-1) is a highly contagious pathogen that establishes lifelong latent infections. The replication of HSV-1 is potentially influenced by the arginine succinate synthase (ASS1) gene, a key regulator of cellular metabolism. This study utilized the CRISPR–Cas9 genome editing platform to specifically target and disrupt the ASS1 gene to examine its effect on viral propagation.

Methods: A guide RNA (gRNA) was designed to complement a sequence within the ASS1 gene. A donor plasmid and the pCas-guide plasmid were cloned and cotransfected into the human embryonic kidney (HEK) cells with sheared adenovirus (Ad)5 DNA (HEK293-AD) cells. Potential ASS1-knockout clones were identified and validated via polymerase chain reaction (PCR) and DNA sequencing analysis. The impact on HSV-1 replication was quantified via a plaque assay to determine the viral titer.

Results: Sequencing data from ASS1-gRNA/Cas9-treated cells did not confirm successful gene knockout, as the intended ASS1 disruption was not achieved. The viral titer did not significantly differ between the HSV-1 infection group (MOI=0.01) and the control group. These findings indicate that the single gRNA designed for this study lacked sufficient specificity to elicit a CRISPR-Cas9-mediated gene knockout.

Conclusion: Therefore, employing a set of more specific gRNAs is recommended to increase targeting efficiency. Further investigations are needed to elucidate the desired genetic modification and observe its subsequent effects on HSV-1.

Keywords: Genome editing, HSV-1, CRISPR-Cas9, ASS1 gene

Oral 3

Decoding the Omicron Lineage in Southern Iran: Functional Impacts of RBD and ORF9b Mutations

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Introduction: The emergence of the Omicron variant in November 2021 marked a significant turning point in the COVID-19 pandemic due to its unprecedented number of mutations compared to previous variants. To better understand its clinical impact and evolutionary trajectory, we conducted a comprehensive genomic epidemiology study analyzing 528 SARS-CoV-2 samples collected in Iran between March 2021 and March 2023.

Methods: Between March 2021 and March 2023, a total of 3,700 nasopharyngeal swab specimens were collected from patients presenting with symptoms of COVID-19 at hospitals in Hormozgan Province. Whole-genome sequencing was performed using Oxford Nanopore Technology (ONT). Using nanopore sequencing, which achieved ≥96% genome coverage, along with advanced bioinformatics tools such as the Nextclade platform, we systematically characterized the phylogenetic tree and mutational profiles of circulating variants. Molecular docking simulations using ClusPro 2.0 were performed to evaluate the effects of mutations in the RBD and ORF9b proteins on their interactions with the ACE2 and TOM70 receptors, respectively. We also employed molecular dynamics simulations to characterize the structural dynamics of both the wild-type ORF9b and its variant forms, using the OPLS-AA force field in GROMACS 2022. Parallel simulations were conducted for the wild-type RBD and its Iranian variants, with each system simulated for 100 ns.

Results: Our analysis revealed BA.5.2 as the dominant strain (32.4% prevalence), followed by XBB.1.9.1 (14.2%); only 17.6% of cases occurred in vaccinated individuals. Through molecular docking and dynamics simulations, we demonstrated that key variants—including BA.5.2, XBB.1.5, and XBB.1.9—exhibit enhanced binding affinity to host receptors. Specifically, the RBD showed stronger interactions with ACE2, while ORF9b variants displayed improved binding to TOM70.

Conclusion: Notably, our findings suggest similar pathogenic potential between the XBB.1.5/XBB.1.9 and BA.5 lineages, while highlighting the utility of whole genome entropy analysis for predicting viral evolution patterns. These results provide valuable insights for guiding vaccine development, therapeutic design, and public health strategies against evolving SARS-CoV-2 variants.

Keywords: SARS-CoV-2, whole genome sequencing, mutation

Oral 4

Anti-Leishmanial Effects of Tobacco Extract on Leishmania infantum In Vitro/Ex Vivo Abstract

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Introduction: Visceral leishmaniasis (VL) caused by Leishmania infantum is a global health challenge with limited treatment options due to toxicity and drug resistance. This study evaluates the anti-leishmanial effects of hydroalcoholic tobacco (Nicotiana tabacum) extract on L. infantum promastigotes and intracellular amastigotes.

Methods: Hydroalcoholic tobacco extract (12.5–200 µg/mL) was tested against L. infantum (strain MCAN/IR/96/LON-49) promastigotes using mortality rate and MTT assays to determine IC50 values at 24, 48, and 72 hours. The extract's effect on intracellular amastigotes was assessed by infection rate in murine macrophages. Cytotoxicity on macrophages was evaluated using the MTT assay to determine CC50 and selectivity index (SI). A solvent control (70% ethanol) was included. Statistical analyses used one-way ANOVA and Tukey's post-hoc test.

Results: The extract reduced promastigote viability with IC50 values of 338, 63, and 27 µg/mL at 24, 48, and 72 hours, respectively, showing a time- and dose-dependent effect. At 50–200 µg/mL, mortality rates were comparable to Glucantime (50, 100 µg/mL). The infection rate of amastigotes decreased significantly at 50–200 µg/mL. The extract showed low cytotoxicity on macrophages (CC50=500 µg/mL at 72 hours, SI=18.5). The solvent control showed no significant effects.

Conclusion: Hydroalcoholic tobacco extract exhibits potent anti-leishmanial activity and low host cell toxicity, suggesting its potential as a natural alternative for VL treatment. Further in vivo studies are needed.

Keywords: Leishmania infantum, hydroalcoholic tobacco extract, anti-leishmanial activity, infection rate, mortality rate, cytotoxicity

Oral 5

16-Year Trends of Antimicrobial Resistance in Staphylococcus aureus Bloodstream Isolates: A Linear Regression Analysis from a Tertiary Teaching Hospital in Southern Iran (2008–2024)

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Introduction: The emergence and spread of antimicrobial resistance (AMR) among bacterial pathogens causing bloodstream infections (BSIs) represent one of the most critical threats to global public health, undermining our ability to effectively treat these potentially life-threatening infections. This study aimed to investigate 16-year trends in antimicrobial resistance among Staphylococcus aureus isolates causing BSIs in a tertiary teaching hospital in Shiraz, Iran.

Methods: We conducted a retrospective observational study at the Professor Alborzi Clinical Microbiology Research Centre, affiliated with Shiraz University of Medical Sciences, Shiraz, Iran, over a 16-year period (2008–2024). Bloodstream isolates were obtained from patients with suspected sepsis. Bacterial identification was performed using the API and Microgen systems. Antimicrobial susceptibility testing was conducted through minimum inhibitory concentration (MIC) determination and/or disk diffusion methods. Data were analysed using WHONET 5.6 software, and temporal trends were assessed using linear regression models.

Results: A total of 929 Staphylococcus aureus BSI isolates were analysed. A significant decreasing trend in resistance was observed for gentamicin (β = –6.136, p = 0.007), while a significant increasing trend was detected for erythromycin (β = 2.194, p = 0.042). Resistance trends for vancomycin (β = –0.139, p = 0.833), rifampin (β = –2.892, p = 0.145), trimethoprim-sulfamethoxazole (β = –1.823, p = 0.336), and penicillin G (β = –0.945, p = 0.080) showed non-significant decreases over the 16-year period. Conversely, resistance to doxycycline (β = 0.296, p = 0.831), ciprofloxacin (β = 1.219, p = 0.364), clindamycin (β = 1.611, p = 0.115), cefoxitin (β = 0.090, p = 0.974), and oxacillin (β = 0.825, p = 0.750) exhibited non-significant increases.

Conclusion: Over the 16-year period, Staphylococcus aureus isolates causing bloodstream infections showed variable resistance trends. The significant decline in gentamicin resistance may reflect improved antimicrobial stewardship and reduced selective pressure. Conversely, the significant rise in erythromycin resistance highlights persistent challenges related to macrolide overuse. Although resistance to vancomycin, rifampin, trimethoprim-sulfamethoxazole, and penicillin G decreased non-significantly, these downward trends are encouraging, particularly for vancomycin, which remains a key agent against MRSA. Non-significant increases in resistance to doxycycline, ciprofloxacin, clindamycin, cefoxitin, and oxacillin indicate relative stability but underline the ongoing presence of MRSA and the need for continued vigilance. Overall, these findings emphasize the dynamic nature of S. aureus resistance patterns and the necessity of sustained surveillance, rational antibiotic use, and infection control measures to prevent further spread of resistant strains in hospital settings

.**Keywords**: Antimicrobial resistance, Staphylococcus aureus, Bloodstream infections, linear regression analysis, Tertiary teaching hospital, Iran

Oral 6

Evaluation of the efficacy of an attenuated Toxoplasma gondii vaccine in inducing an immune response and protecting against lethal challenge in a mouse model

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Introduction: Toxoplasmosis, a disease caused by the obligate intracellular parasite *Toxoplasma gondii*, is a widespread infection with severe consequences in immunocompromised individuals and pregnant women. The development of an effective vaccine is considered an essential preventive strategy. This study was designed to evaluate the efficacy of a live attenuated vaccine in inducing humoral and cellular immune responses and providing protection against a lethal challenge with wild-type strain *T. gondii* in a mouse model.

Methods: In this experimental study, 40 adult mice were randomly divided into four groups of 10: * **Group 1:** Vaccinated with a high dose of the attenuated vaccine. * **Group 2:** Vaccinated with a low dose of the same vaccine. * **Group 3:** Vaccinated with a high dose, but not challenged (positive control group for immunogenicity assessment). * **Group 4:** Recipient of sterile saline solution as negative control group. After the immunization period, all mice in groups 1, 2, and 4 were challenged with an acute and lethal strain of *T. gondii*. Immune responses, including measurement of specific antibody titers (presumably IgG type) and levels of the cytokine gamma interferon (IFN-γ), as the main indicator of cellular immune response, were assessed before challenge. The survival rate of mice was monitored for a specified period after challenge.

Results: Pre-challenge immunological assessments showed that both vaccine groups (high dose and low dose) had significantly higher antibody titers and gamma interferon levels compared to the negative control group. These results indicated successful induction of both humoral and cellular immunity by the vaccine. After lethal challenge, survival results showed significant differences between groups: in the **high dose group, all 10 mice (100%) survived**. In the **low dose group, 6 mice (60%) survived and 4 mice (40%) died**. In contrast, the **negative control group suffered heavy losses, with only 2 mice (20%) surviving and 8 mice (80%) dying**. The third group (high dose without challenge) also showed no signs of disease, emphasizing the safety of the vaccine in the absence of challenge.

Conclusion: The findings of this study clearly demonstrate that the attenuated vaccine studied is capable of inducing a strong humoral and cellular immune response and providing significant protection against a lethal challenge with *T. gondii*. A direct and significant relationship was observed between the vaccine dose and the level of protection, with the high dose providing complete protection (100%) and the low dose providing partial protection (60%). These results indicate the high potential of this vaccine as a promising candidate for the prevention of toxoplasmosis. Future studies should focus on dose optimization, evaluation of the duration of protection, and testing of this vaccine in other species.

Keywords: Vaccine, Toxo plasma gondei

Oral 7

Seroprevalence of Anti-HBs Antibodies among Female Sex Workers in Fars province, Iran, 2023-2024

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Introduction: Hepatitis B virus (HBV) is a long-recognised occupational hazard for female sex workers (FSWs) because of frequent exposure to body fluids and the absence of mandatory adult boosters. We therefore quantified anti-HBs antibody (anti-HBsAb) titres in FSWs across Fars Province and analysed sociodemographic and behavioural correlates of protective immunity.

Methods: In this cross-sectional study, 206 FSWs presenting to outreach clinics in Shiraz and Marvdasht (2023 – 2024) were recruited by convenience sampling. Five millilitres of venous blood were collected, centrifuged, and the separated sera stored at –20 °C until analysis. Anti-HBsAb titres were measured with a commercial ELISA kit (DiaPro, Italy); titres ≥ 10 mIU mL^{-1} were deemed protective. Demographic, social and behavioural variables—including age, education, income, condom use, partner/client numbers, substance use and sexually transmitted infection (STI) history—were captured by structured interview. Associations were tested with χ^2 or linear-by-linear trend in SPSS v26; p 0.05 signified significance.

Results: Valid serology was obtained from 202 women (mean ± SD age 42.3 ± 9.7 years, range 17–68). The Mean Anti-HBsAb titre was 45.3 ± 84.1 mIU mL^{-1} (median 0 mIU mL^{-1}). Only 70/202 participants (34.7 %) had protective titres (10–100 mIU mL^{-1}: n = 38; 100 mIU mL^{-1}: n = 32), whereas 132/202 (65.3 %) were unprotected, including 46 who were completely seronegative. A significant positive linear trend was observed for condom use: women reporting more consistent use were more likely to be immune (trend $\chi^2 = 7.59$, p = 0.006), although the overall five-level χ^2 narrowly missed conventional significance ($\chi^2 = 20.17$, df = 12, p = 0.064). No significant association emerged between antibody status and age group, marital status, literacy level, income, partner/client numbers, STI history, drug use, syringe sharing, imprisonment, alcohol consumption or tattooing (all p 0.15).

Conclusion: Nearly two-thirds of FSWs in Fars Province lacked serological protection against HBV, despite three decades of universal infant mmunization, highlighting waning immunity and gaps in adult booster coverage. The absence of associations with age and most risk factors suggests uniformly low booster coverage across subgroups, while the positive trend with condom use may reflect greater health-seeking behaviour among consistent condom users. Routine anti-HbsAb screening, counselling and free booster vaccination should be integrated into sexual-health and harm-reduction services to close this immunity gap and curb onward HBV transmission in a key population.

Keywords: Anti-HBsAb; Female sex workers; Fars province; Iran.

Oral 8

Sero-positivity of Latent Infections in HIV-Infected Patients in Northeastern Iran (2013–2022)

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Introduction: Human immunodeficiency virus (HIV) compromises the immune system, increasing vulnerability to opportunistic infections such as Toxoplasma gondii, hepatitis B (HBV), hepatitis C (HCV), cytomegalovirus (CMV), syphilis, human T-cell leukemia virus type I (HTLV-I), and latent tuberculosis (LTBI). This study evaluates the seroprevalence of these infections among HIV-positive patients in Khorasan-e-Razavi Province, Iran, over a 10-year period (2013–2022).

Methods: This retrospective cross-sectional study involved 255 HIV-positive patients from four centers in Khorasan-e-Razavi. Demographic data and HIV transmission routes were collected. Serological tests were performed for Toxoplasma gondii IgG, HBsAg, HCV Ab, CMV IgG, HTLV-I Ab, VDRL, and purified protein derivative (PPD) for LTBI. Associations with age, gender, and transmission routes were analyzed statistically. The study was approved by the Ethical Committee of Mashhad University of Medical Sciences (IR.MUMS.MEDICAL.REC.1398.583).

Results: Among 255 patients (64.3% male, mean age 41.3±12.4 years), the main HIV transmission routes were injection drug use (43.5%) and sexual contact (40.0%). Seroprevalence rates were: Toxoplasma gondii (44.3%), HBV (7.5%), HCV (45.5%), CMV (78.4%), syphilis (1.6%), HTLV-I (4.7% of 141 tested), and LTBI (32.6% of 224 tested). Older age was significantly associated with Toxoplasma (p0.01), HCV (p0.0001), and LTBI (p=0.001). HCV prevalence was significantly higher in males (62.2%, p0.05) and injection drug users (83.8%, p0.05).

Conclusion: High seroprevalence of Toxoplasma gondii, HCV, CMV, and LTBI in HIV-positive patients in Khorasan-e-Razavi underscores the need for routine screening and prophylactic measures. Injection drug use significantly contributes to HCV co-infection. Regular monitoring and preventive strategies are essential to mitigate morbidity in this population.

Keywords: HIV, Opportunistic Infections, Toxoplasma gondii, Hepatitis C, Cytomegalovirus, Latent Tuberculosis

Oral 9

Environmental factors influencing Fasciola hepatica infection inl ivestock in an endemic focus of Southwestern Iran

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Introduction: Fasciola hepatica, a zoonotic trematode of global importance in public health and veterinary medicine, can cause severe liver damage and reduced productivity in livestock, as well as liver disease with a wide range of clinical manifestations in humans and livestock, leading to significant health and economic problems. Considering the parasite's life cycle, the occurrence of fascioliasis can be influenced by environmental variables. Dasht-e-Rum in Boyer-Ahmad County, Kohgyloyeh and Boyerahmad Province, is recognized as an endemic area in southwestern Iran. This study was conducted to determine the possible geoclimatic factors influencing the parasite's cycle in this region.

Methods: To investigate the environmental factors affecting infection with this parasite, data from a previous study were used, including 600 parasitological samples collected from livestock waste in six villages (Tangari, Mansourabad [Sarabe Khizan], Hosseinabad, Jahanabad, Amirabad, and Talkhdan) in 2013. Climatic layers such as minimum, maximum, and mean temperature, humidity, precipitation, evaporation, wind speed, frost days, and sunshine hours were interpolated using various models, and the model with the lowest error was selected. The effects of these layers, along with geographic layers including the digital elevation model (DEM) and land slope on the occurrence of fascioliasis in livestock (goats, sheep, and cattle separately) were analyzed using ArcMap software. Data were evaluated by Pearson's correlation test.

Results: For goats, a significant correlation was found between fascioliasis infection and some environmental variables. There was a strong negative correlation with mean minimum temperature (P=0.044, r=-0.823) and strong positive correlations with annual humidity (P=0.040, r=0.832), sunshine hours (P=0.040, r=0.831), and wind speed (P=0.039, r=0.835). No significant correlations were observed in cattle and sheep.

Conclusion: These effects may be explained by increased surface water and humidity, the persistence of moderate temperatures during night time or early morning, the creation of suitable conditions for the growth, reproduction, and survival of the parasite and its intermediate host (snail) on vegetation, greater vegetation density along humid margins, and the faster and wider spread of parasite larvae or their intermediate hosts. The differences in climatic associations with fascioliasis in goats compared to other livestock could be explained by the goats' unique grazing behavior. Goats typically graze on slopes, cooler rocky areas, and shaded habitats where humidity is higher. Moreover, some studies indicate that goats, compared to cattle or sheep, are more sensitive or vulnerable to environmental transmission patterns of fascioliasis.

Keywords: Fascioliasis, GIS, geoclimatic factors, Dasht-e Rum

Oral 10

Ethidium bromide-degrading bacteria in horse feces

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Introduction: Ethidium bromide (EtBr) is a fluorescent dye used to visualize DNA and RNA in gel electrophoresis and other molecular biology techniques. However, EtBr is also a potent mutagen and carcinogen, requiring careful handling and disposal.

Methods: Fecal samples were collected from Horses on May, 2025. One gram of fecal samples was suspended in 10 ml normal saline. Ten-fold serial dilution of suspended solution were carried out and 100 µl of each dilution was spread on EtBr -supplemented nutrient agar plate (E-NA) plate (30 µg/ml) and incubated at 37°C in dark place for 18-24 h. Then, the plates were briefly exposed to UV-light for image capture and the colonies showing clear zone of EtBr degradation were selected. The selected colonies were cultured in nutrient broth at 37°C, 150 rpm agitation for 18 h. To screen for bacteria that give the highest EtBr degradation activity, isolated bacteria were cultured on nutrient agar plates for 18 h at 37°C. Single colony of each isolate was inoculated on E-NA plates by spotting and incubated as above in the dark to monitor the clear zone of EtBr. Characteristics of isolated bacteria

Results: Based on biochemical tests, the bacteria with most capability of destroying EtBr belonged to the genus Stenotrophomonas, Citobacter, Yersinia ad Shigella, respectively.

Conclusion: Accordingly, the ability of the isolates to degrade EtBr was observed. This may provide a possible solution for the management of EtBr waste in the future.

Keywords: Ethidium bromide, electrophoresis, carcinogen

Oral 11

Therapeutic Application of a Targeted Phage Against Drug-Resistant Pseudomonas aeruginosa in Burn Wound Models

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Introduction: The rise of drug-resistant bacterial strains, especially among immunocompromised patients and those in intensive care units, poses a significant global healthcare challenge. Acute burn wounds disrupt the protective skin barrier and weaken the immune system, making patients highly susceptible to bacterial infections. Studies indicate that approximately 70% of deaths within five days post-burn are directly or indirectly caused by septic infections. Pseudomonas aeruginosa is a predominant pathogen in burn wound infections and is associated with increased risks of sepsis and mortality, representing a critical concern in burn care units. Given these challenges, alternative or complementary treatments to conventional antibiotics are urgently needed. Bacteriophage therapy has emerged as a promising approach. This study aims to isolate effective bacteriophages targeting multidrug-resistant P. aeruginosa strains and to assess their therapeutic efficacy in treating burn wound infections in an animal model.

Methods: A colistin-sensitive, drug-resistant strain of Pseudomonas aeruginosa was isolated from the infected wound of a burn patient hospitalized in a specialized burn unit. Following phenotypic and genotypic identification, this strain was used as a host for the isolation of specific bacteriophages. Hospital wastewater samples served as the source for phage extraction. The isolated bacteriophage was characterized based on its laboratory and morphological features, with transmission electron microscopy (TEM) employed to determine its structural morphology. The identified phage, designated PaBa1, underwent whole genome sequencing (WGS) to confirm its identity and assess its genetic characteristics. The therapeutic efficacy of PaBa1 was then evaluated using an animal model of burn wound infection caused by the same resistant P. aeruginosa strain.

Results: A novel lytic bacteriophage belonging to the Myoviridae family was successfully isolated and designated PaBa1. The phage exhibited strict specificity for Pseudomonas aeruginosa, with no lytic activity against other bacterial species tested. However, within P. aeruginosa, PaBa1 demonstrated a broad host range, effectively lysing several multidrug-resistant clinical isolates. Kinetic analysis revealed an adsorption time of 9±1 min, a latent period of 38.3±2.9 min, and a burst size of approximately 238±6 PFU per cell. Whole-genome sequencing confirmed the absence of known toxin or antibiotic resistance genes, supporting the safety of the phage for therapeutic applications. In a murine wound infection model, laboratory and histopathological analyses demonstrated that phage therapy with PaBa1 exerted both preventive and therapeutic effects, resulting in significantly enhanced bacterial clearance and accelerated wound healing compared to antibiotic-treated groups.

Conclusion: Given the rising prevalence of antibiotic-resistant bacterial strains and the favorable outcomes observed in this study—demonstrating preventive and therapeutic effects on infected burn wounds without adverse effects—it is suggested that the identified phages be used as therapeutic supplements or, where effective antibiotics are unavailable, as potential alternatives for treating burn and other localized wounds.

Keywords: Pseudomonas aeruginosa, bacteriophage, multidrug-resistance, burn wound

Oral 12

Intranasal administration of the Mentha aquatica extract protects mice against the acute pneumonia model of Pseudomonas aeruginosa infection

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Introduction: Antimicrobial-resistant pathogen Pseudomonas aeruginosa (P. aeruginosa) can cause potentially fatal infections in susceptible individuals, with respiratory tract infections among the most common clinical presentations. The development of novel treatments or prophylactic interventions to combat these infections is urgently needed and requires robust, reliable animal models for their preclinical evaluation. Natural products from plants have proven to be effective as anti-biofilm agents, suppressing cell adhesion and attachment, and decreasing the virulence factors. This research aimed to develop a novel herbal spray based on the Mentha aquatica (MA) extract and investigate its therapeutic efficacy in the acute pneumonia model of P. aeruginosa infection.

Methods: The methanol extract of the MA was prepared, and its chemical composition was evaluated by GC-MS analysis. Additionally, the antibacterial activity and MIC level of the extract were determined. The biocompatibility of the therapeutic agent was assessed by MTT assay for cell cytotoxicity. Intranasal administration of the herbal extract was performed following acute pneumonia model of the murine P. aeruginosa infection. In particular, the bacterial burden was accurately determined before and after administration of the potential therapy under evaluation to quantify the effectiveness of the treatment. Microscopic analysis of the lung tissue was done using hematoxylin-eosin staining in different experimental groups.

Results: The lowest inhibitory dose of the extract was determined to be 12.5 mg/ml. The survival of the human lung pneumocyte cell line (A549) decreased after 72 h by increasing the MA methanol extract concentration. Following a non-invasive murine acute lung challenge model (4×106 CFUs/mouse), the survival of mice in the MA-treated group was significantly increased compared to the control groups. Bacterial load in the lungs, spleen, and blood was determined in the tissues at 3 days after the treatment. The bacterial load in the MA receiving group dramatically decreased in the tissues compared to the infection control group on the third day. Also, application of the MA extract to the infected lung demonstrated faster tissue regeneration and eradication of bacterial infection.

Conclusion: This preliminary research focused on the preparation and utilization of the Mentha aquatica methanol extract as an effective therapeutic agent, which has the potential to rehabilitate infected lung tissue; therefore, it can be a promising candidate for lung intranasal applications.

Keywords: Pseudomonas aeruginosa, methanol extract of Mentha Aquatica, lung, mice

Oral 13

Evaluation of the rational prescription of colistin in the medical departments of Imam Reza Mashhad Hospital, Mashhad, Iran

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Introduction: Introduction: Colistin is an old-generation antibiotic recognized as the last-line treatment for infections caused by gram-negative bacteria resistant to other antibiotics. With the rise of antibiotic resistance, the use of colistin in hospitals has increased to combat severe infections such as those caused by Pseudomonas, Klebsiella, and Acinetobacter species. Due to its significant adverse effects, the necessity for precise dosage adjustments, and its high efficacy in treating resistant infections, colistin should only be prescribed based on appropriate indications. This study aimed to evaluate the rational prescription of colistin in various wards of Imam Reza Hospital in Mashhad.

Methods: Methods: This cross-sectional study was conducted from October 2022 to October 2023 on 679 hospitalized patients in the treatment wards of Imam Reza Hospital who received colistin. Patient demographic data, prescribed medication details, laboratory findings, and disease progression indicators—including culture results, follow-up cultures, patient response to treatment, administered colistin doses, and drug-related adverse effects—were documented. The collected data were analyzed using SPSS version 26, applying various statistical tests to assess prescription errors related to indications, dosage accuracy, treatment duration, dose modifications, adverse drug reactions, and the prevalence of antibiotic resistance among the patients.

Results: Results: The study findings indicated that the burn unit and ICU accounted for the highest number of colistin-treated patients (25.6%). Among the studied patients, 35.5% received empirical colistin therapy. In 13.2% of patients, colistin was prescribed without any approved indication. Additionally, during the treatment course, 183 patients underwent dose modifications or were recommended for dose adjustments by the Drug Utilization Evaluation (DUE) unit. Among the 523 patients who underwent at least one culture test, 426 (81.4%) were classified as multidrug-resistant (MDR) or extensively drug-resistant (XDR).

Conclusion: Conclusion: The findings highlight that colistin prescription errors are prevalent in the treatment wards of Imam Reza Hospital. To ensure appropriate and effective colistin use, enhanced educational and monitoring programs are necessary. Implementing these strategies will optimize patient treatment outcomes while reducing healthcare costs. Furthermore, these interventions play a crucial role in mitigating the rapid emergence of antibiotic resistance.

Keywords: Keywords: Colistin, Rational Prescription Evaluation, Antibiotic Resistance

Oral 14

Evaluation of the implementation of the antibiotic stewardship program for the use of antibiotics in children suspected of meningitis in the children's emergency department of Namazi Hospital during a five-month period

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Introduction: Antibiotic stewardship program(ASPs) have been proposed for decades to reduce antibiotic resistance and optimize antibiotic use.Numerous studies have shown the impact of these programs on reducing antimicrobial resistance , reducing antibiotic consumption and reducing healthcare costs .Given the increasing importance of implementing ASP programs in pediatric wards and the lack of studies in Iran, the present study aimed to investigate the effect of implementing ASP methods on antibiotic consumption in children suspected of meningitis in the pediatric emergency department of Namazi Hospital, Shiraz.

Methods: This study was an observational-analytical cohort study. The Infectious Diseases Department of the Pediatrics of Shiraz University of Medical Sciences implemented a surveillance program for antibiotic prescribing for children suspected of meningitis in the pediatric emergency ward of Namazi Hospital from the beginning of December2014. Patient data were collected from December2014 to April 2015 and compared with data from the period before (December2013to April2014). The antibiotic prescribing management program included providing of antibiotic prescribing guidelines and training for residents, along with providing non-mandatory counseling (PAF)to physicians. The statistical population included all children with suspected meningitis admitted to the emergency department during the aforementioned period. Patient information including age, sex and imaging findings were collected before and after the intervention. Outcomes including adherence to guidelines, duration of treatment (DOT), length of treatment (LOT), need for intensive care unit admission, length of hospital stay, and incidence of death were also evaluated in two periods.

Results: In this study, 119 patients suspected of meningitis were examined (45 before and 74 after the intervention) with a mean age of 5 and 4 years, respectively, and a female-to-male ratio of 0.67. In cerebrospinal fluid analysis, 10cases of bacterial meningitis and 15cases of viral meningitis were diagnosed after the intervention, and 7cases of bacterial meningitis and 6cases of viral meningitis were diagnosed before the intervention. Complications of meningitis before the intervention included brain abscess (2cases), subdural empyema, subdural effusion, and hydrocephalus (1case each), and after the intervention, periventricular leukoencephalitis(1case), ventriculomegaly (2cases), acute necrotizing encephalopathy of childhood, and acute ischemic changes (1case each) were observed. Adherence to guidelines increased by 17% after the intervention, but this increase was not statistically significant. ICU admission and LOT were significantly reduced (p 0.001). DOT were reduced from 28 to 16 days, and mortality was significantly reduced by 21.2% (p = 0.005).

Conclusion: In this study, the implementation of ASP in children with suspected meningitis resulted in significant improvements in adherence to guidelines, but this increase was not significant. ICU admissions and mean length of stay were reduced, and DOT and mortality were significantly reduced. These results suggest that the implementation of an ASP improved adherence to treatment, reduced length of stay, reduced mortality, and improved management of treatment in children with suspected meningitis, while clinical features and infection patterns remained largely unchanged.

Keywords: Antibiotic stewardship program (ASP), meningitis, pediatrics

Oral 15

Comorbidity and Antimicrobial Resistance as Determinants of Surgical Site and Bloodstream Infections and Their Impact on hospitalization: A Retrospective Hospital-Based Cohort Analysis

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Introduction: Surgical site infections (SSIs) and bloodstream infections (BSIs) are frequently complicated by antimicrobial resistance (AMR) and prolonged hospitalization. This investigation aims to evaluate the associations of comorbidity and resistant pathogens with the occurrence of SSI and BSI in patients who referred to Emtiaz hospital, a government-run Level I trauma referral center in Shiraz, Iran.

Methods: A retrospective cohort study was conducted on 3,129 hospitalized patients in Emtiaz hospital with confirmed infections between 2024–2025. Data included infection type, pathogens, and comorbidity status. SSIs were identified from infection codes, and comorbidity was dichotomized as present or absent. Pathogens were further categorized into multidrug-resistance (MDR)-prone organisms (Acinetobacter, Klebsiella, Pseudomonas) versus non-MDR organisms. Pathogen susceptibility fields were used to count resistant results; Multidrug-Resistance (MDR) was defined as resistance to ≥3 antimicrobials. Sample type (blood culture), infection codes (SSI, BSI), and comorbidity (any recorded underlying condition) were extracted.

Results: MDR- organisms were frequent (2,333/3,219; 72.4%). Blood-culture specimens (n=218) were significantly associated with MDR (OR = 1.99; p = 0.00011). SSI cases had higher MDR prevalence than non-SSI cases (OR = 1.49; p = 0.00005). Moreover, SSI was more common in patients with comorbidities compared to those without (37.5% vs. 15.6%; OR = 3.2, 95% CI: 1.0–9.8; p = 0.045). Median LOS was longer for MDR vs non-MDR cases (23 vs 17 days; p 0.0001) and for patients with comorbidity (25 vs 17 days; p 0.0001).

Conclusion: In this surveillance retrospective cohort, MDR was significantly associated with blood-culture/BSI and SSI. MDR and comorbidity were also associated with markedly prolonged LOS. These findings underscore the importance of intensified infection prevention strategies, tailored perioperative management of high-risk patients, and routine antimicrobial resistance surveillance in surgical wards. Confirmatory studies using full antibiograms and clinical outcomes are warranted.

Keywords: Surgical site infections, Blood stream infections, Anti-microbial resistance, Comorbidity, Length of stay

Oral 16

Whole Genome Sequencing-Based Detection of Mutations in Mycobacterium simiae Isolates from Iran

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Introduction: Mycobacterium simae is an increasingly recognized non-tuberculous mycobacterial pathogen associated with challenging infections, particularly due to its intrinsic resistance to standard anti-tuberculosis drugs. Accurate identification and detailed characterization of M. simae are essential for effective clinical management. Whole genome sequencing (WGS) has emerged as a powerful tool to elucidate the genetic basis of drug resistance, subspecies classification, and pathogenicity. This study employs WGS to analyze M. simae isolates, aiming to uncover genomic features such as genome size, GC content, and resistance-associated genes. By integrating phenotypic susceptibility data with genomic insights, the research provides a comprehensive understanding of the bacterium's adaptive mechanisms and drug resistance profiles. These findings highlight the utility of WGS in guiding targeted therapy and emphasize the need for continuous genomic surveillance to improve treatment outcomes and control the spread of drug-resistant M. simae infections.

Methods: In this study, 30 Mycobacterium simiae-positive samples were collected from patients suspected of having nontuberculous mycobacterial (NTM) infections. Subspecies identification was performed using PRA analysis with the restriction enzymes BstEII and HaeIII. The drug susceptibility of the isolates was evaluated against rifampicin, isoniazid, amikacin, kanamycin, and ciprofloxacin. Whole genome sequencing (WGS) was conducted on five isolates, and genomic features, drug resistance genes, and GC content were analyzed."

Results: All isolates analyzed belonged to subspecies I, with no other subspecies detected. Phenotypic testing showed universal resistance to first-line anti-tuberculosis drugs rifampicin and isoniazid. However, 80% of isolates were susceptible to amikacin, kanamycin, and ciprofloxacin, suggesting alternative treatment options. Whole genome sequencing revealed a genome size of 6,684,413 base pairs, organized as a single circular chromosome without plasmids, and a GC content of 66%. The high number of protein-coding and conserved orthologous genes reflects the bacterium's adaptability to diverse environments, including the human host. Importantly, genomic analysis identified genes conferring resistance to aminoglycosides, ethambutol, and β-lactams, indicating a complex resistance profile. These genetic findings underscore the need for thorough therapeutic monitoring and tailored antimicrobial treatment. Together, the phenotypic and genomic data provide a detailed picture of M. simae's subspecies identity, drug resistance traits, and adaptive potential, emphasizing the importance of integrating genomic tools into clinical diagnostics and management strategies

Conclusion: This study highlights the critical role of whole genome sequencing in characterizing Mycobacterium simiae isolates. All isolates were confirmed as subspecies I, with universal resistance to first-line drugs rifampicin and isoniazid, underscoring the challenge of treating these infections using standard regimens. Notably, susceptibility to amikacin, kanamycin, and ciprofloxacin in most isolates offers promising alternatives for therapy. Genomic analysis revealed a genome size of approximately 6.68 million base pairs, a high GC content, and the absence of plasmids, reflecting a stable genomic structure. The identification of genes associated with resistance to aminoglycosides, ethambutol, and β-lactams emphasizes the complexity of antimicrobial resistance in M. simiae. These findings stress the necessity of integrating genomic data with phenotypic testing to guide personalized treatment and improve patient outcomes.

Keywords: Mycobacterium simae, (WGS), Drug resistance

Oral 17

Pulmonary Candida Colonization and Infection in Renal Patients: A Molecular and Microscopic Characterization

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Introduction: Candida species, opportunistic yeasts colonizing mucosal surfaces, cause both colonization and invasive infections in immunocompromised patients. Patients with renal disorders, including chronic kidney disease (CKD), end-stage renal disease (ESRD), and transplant recipients, are at particularly high risk. This vulnerability stems from their immunosuppressed state, frequent courses of corticosteroids and antibiotics, prolonged hospitalization, and exposure to invasive procedures. Within this population, a major concern is respiratory tract colonization and infection by Candida species. Therefore, this study was conducted to morphologically and molecularly identify Candida yeasts isolated from this patient group.

Methods: The study population included patients with CKD, ESRD, kidney transplantation, and pyelonephritis who were hospitalized with pulmonary symptoms such as chest pain, dizziness, productive cough, and other signs of pneumonia. Clinical specimens, mainly bronchoalveolar lavage (BAL) and sputum, were collected and transported to the Clinical Mycology Center, Urmia University of Medical Sciences, Urmia, Iran. Direct examination of processed specimens was performed for the detection of invasive or colonizing forms of Candida. Cultures were performed on Sabouraud Glucose Agar (SGA 4%) and Sabouraud Chloramphenicol Cycloheximide Agar (SCC) for species-level identification. PCR-RFLP molecular method was used to confirm the identification of misdiagnosed Candida species.

Results: A total of 41 patients were studied: 21 (51.2%) with CKD, 12 (29.2%) with ESRD, and 7 (17%) kidney transplant recipients. The most common age group was 60–70 years 15 (36.6%) and the least frequent was 20–40 years 2 (4%). Pulmonary symptoms were reported in 29 (70.7%), pneumonia with or without hemoptysis in 6 (14.6%), pleural pain/edema/effusion in 2 (4.9%), and peritonitis in 3 (7.3%). Most patients were from nephrology 29 (70.7%), followed by respiratory and ICU wards 6 (14.6%) each. Specimens included BAL 27 (65.8%), sputum 8 (19.5%), and others. Microscopy showed invasive Candida in 20 (48.7%), overgrowth in 15 (36.6%), and minimal presence in 6 (14.6%). Final identification revealed C. albicans 10 (24.3%), C. tropicalis and C. dubliniensis 7 (17%) each, C. glabrata 6 (14.6%), C. parapsilosis 1 (2.4%), unidentified Candida species 5 (12.1%). and 5 (12.1%) isolates remained unidentified due to missing data.

Conclusion: In this study, we demonstrated that renal patients, particularly those with CKD, ESRD, or post-transplant status, are at high risk of pulmonary Candida colonization and invasive infection, with a concerning predominance of invasive forms. Our results, which revealed a diversity of species including C. dubliniensis, underscore that species-level identification of Candida isolates is not just beneficial but essential for clinical diagnosis due to significant variations in pathogenicity and drug resistance profiles.

Keywords: Candida, renal disease, pulmonary involvement, identification

Oral 18

Environmental Distribution and Molecular Identification of Pathogenic Scedosporium Species in Northern Iran

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Introduction: Scedosporium apiospermum species complex includes important emerging fungal pathogens causing a wide variety of human infections. While some species within this complex have been isolated from clinical samples in Iran, no environmental studies of these fungi have been conducted in Iran or surrounding countries. This study aimed to isolate and identify species of this complex from agricultural and public park soil samples using semi-selective media.

Methods: Park and agricultural soil samples were collected from Mazandaran province. For isolation, two semi-selective media (Dichloran Rose-Bengal Chloramphenicol agar supplemented with Benomyl and Scedo-Select III) were used. Identification was based on morphological characteristics and ITS-rDNA sequencing.

Results: 48 isolates of S. apiospermum species complex and relatives were isolated from soil. Three species within the complex were identified: S. apiospermum (21 isolates), S. dehoogii (14 isolates), and S. boydii (10 isolates).

Conclusion: According to our environmental survey, the S. apiospermum species complex is widespread in soil in Mazandaran province, Iran. Molecular identification is essential for accurate species discrimination within this complex.

Keywords: Scedosporium apiospermum, Environmental survey, Molecular identification, Soil, Iran.

Oral 19

Association of Helicobacter pylori Infection with Iron Deficiency and Inflammatory Biomarkers in Children

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Introduction: Helicobacter pylori infection is a common gastrointestinal disorder in children and has been linked to iron deficiency anemia (IDA). This study aimed to evaluate the association between H. pylori infection, iron status, and inflammatory biomarkers including IL-17A, IL-1β, and hepcidin.

Methods: A total of 106 children with dyspeptic symptoms (age between 1-18 Years) with IDA were enrolled. Gastric biopsy specimens and peripheral blood samples were collected. Serum levels of hepcidin, ferritin, IL-17A, and IL-1β were measured using ELISA.

Results: Our study population was composed of 106 child patients, 45.3% (48) male and 54.7%(58) were female, 60(56.6%) infected with H. pylori and 46(43.4%) uninfected.45.3% (48) male and 54.7%(58) were female, 60(56.6%) infected with H. pylori and 46(43.4%) uninfected. Although ferritin levels did not differ significantly between infected and non-infected children, serum IL-17A, hepcidin, and ferritin levels were higher in H. pylori-positive patients. Hemoglobin levels were lowest in children with gastritis, while hepcidin and ferritin were lowest in those with gastric ulcer. Interestingly, IL-1β, IL-17A, and hepcidin levels were lowest in mild gastritis and highest in patients without gastritis. Furthermore, in children older than 5 years, H. pylori infection was significantly associated with elevated IL-17A, hepcidin, and ferritin levels, whereas this association was not observed in younger children.

Conclusion: H. pylori infection in children is associated with elevated IL-17A, hepcidin, and ferritin levels, particularly in patients older than 5 years. These biomarkers may serve as predictors of iron deficiency status in H. pylori-infected children.

Keywords: Helicobacter pylori, Iron Deficiency Anemia, Children, Hepcidin, Inflammatory Biomarkers

Oral 20

An inflammatory network in active brucellosis: Integrating IL-32, TNF-α, CXCL2, CXCL8, and TLR-4

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Introduction: The intracellular lifestyle of Brucella spp. necessitates a more complex immune response than that for extracellular bacteria. Clarifying the role of immune mediators in this pathway is therefore vital to understanding the disease's immunopathogenesis. The present study focuses on a proposed inflammatory network involving cytokines (IL-32, TNF-α), chemokines (CXCL2, CXCL8), and TLR-4, and aims to define their association with active brucellosis.

Methods: This study comprised 80 brucellosis patients and 236 controls. Patient diagnosis was confirmed by a history of animal contact, consumption of unpasteurized dairy products, clinical symptoms, and positive serological tests (Wright, 2-Mercaptoethanol (2ME), Coombs', and Brucella capture). Total RNA was extracted from blood samples, reverse-transcribed into cDNA, and the expression levels of IL-32, TNF-α, TLR-4, CXCL2, and CXCL8 were quantified using SYBR Green-based relative real-time PCR.

Results: The study cohort consisted of patient and control groups. The demographic and clinical characteristics of these groups are summarized as follows: the patient group was 57.5% male with a mean age of 37.7 ± 24 years, while the control group was 55.9% male with a mean age of 19.5 ± 19.5 years. A majority of patients (53.8%) were rural residents, and 70% reported a history of contact with domestic animals. Laboratory analysis revealed that patients had a significantly lower white blood cell (WBC) count compared to the control group. Relative quantitative PCR analysis demonstrated a significantly lower ΔCt value for all investigated molecules in the patient group, indicating higher gene expression. This transcriptional profile was reflected at the protein level for TNF-α and TLR-4, both of which were present at substantially higher concentrations in patients compared to controls.

Conclusion: The elevated expression of TLR-4 and TNF-α in patients with brucellosis confirms their significant role in the immunopathological process. In contrast, the expression of other network components, such as IL-32 and CXCL2, showed no clear association with the disease. This lack of association may be attributed to the complexity of the immune response, where these molecules are embedded in broader, redundant pathways that can obscure their individual contributions.

Keywords: Active brucellosis, Immunopathogenesis, IL-32, TNF-a, CXCL2, CXCL8, TLR-4

Oral 21

Spectrum of Fungal Pathogens Isolated from Hematologic Malignancy Patients Suspected of Fungal Infection: A retrospective Study

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Introduction: Invasive fungal infections remain a major threat in patients with hematologic malignancies due to prolonged neutropenia and immunosuppression. Early detection of fungal pathogens is essential for clinical decision-making. This study aimed to determine the incidence and distribution of fungal pathogens isolated from patients with hematologic malignancies suspected of fungal infection.

Methods: Over four years, a total of 110 patients with hematologic malignancies and a clinical suspicion of fungal infection were referred to the Professor Alborzi Clinical Microbiology Research Center. Clinical specimens were obtained according to the suspected site of infection and subjected to direct microscopy (KOH smear) and culture on sabouraud dextrose agar. Candida species were identified with PCR-RFLP using ITS1 and ITS4 primers. Filamentous fungi were identified using microscopic examination.

Results: Of the 110 patients, 77 (70%) were male and 33 (30%) female, with a mean age of 10 years. Overall, 60 fungal isolates were recovered (isolation rate: 54.5%). Filamentous fungi accounted for 34 isolates (56.7%), while yeasts comprised 26 isolates (43.3.%). The most frequently isolated species were Aspergillus flavus (16 isolates, 26.7%), Candida albicans (14 isolates, 23.3%), and Mucorales (13 isolates, 21.7%). Less common isolates included Candida krusei (2 isolates, 3.3%), C. parapsilosis (2 isolates, 3.3%), C. guilliermondii (2 isolates, 3.3%), Candida spp. (3 isolates, 5.0%), C. glabrata (1 isolate, 1.7%), C. tropicalis (1 isolate, 1.7%), C. kefyr (1 isolate, 1.7%), Aspergillus terreus (1 isolate, 1.7%), A. fumigatus (1 isolate, 1.7%), A. niger (1 isolate, 1.7%), Fusarium spp. (1 isolate, 1.7%), and Alternaria spp. (1 isolate, 1.7%).

Conclusion: In this study, fungal pathogens were isolated in more than half of the cases (54.5%) with a slight predominance of filamentous fungi (56.7%). Aspergillus flavus, Candida albicans, and Mucorales were the prominent pathogens. These findings highlight the diverse spectrum of fungal agents affecting immunocompromised patients and emphasize the importance of early and accurate laboratory diagnosis to improve clinical outcomes.

Keywords: Hematologic malignancies, Invasive fungal infections, Aspergillus flavus, Candida albicans, Mucorales

Oral 22

Prevalence and Co-Infection Patterns of Human Papillomavirus and Epstein–Barr Virus in Genital Wart Patients and normal population

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Introduction: Introduction: Oncogenic viruses like human papillomavirus (HPV) and Epstein–Barr virus (EBV) are associated with these malignancies, and evidence indicates that co-infection with HPV and EBV may interact to enhance cancer development. Given their overlapping mucosal tropisms and lifelong persistence in host tissues, co-infections with HPV and EBV may alter host immunity, facilitate viral persistence, or influence disease progression, yet data on their concurrent presence in non-cervical mucosal sites remain limited. This study aimed to investigate the prevalence of HPV and EBV in oral and urinary samples of patients with genital warts and normal population, and to assess the frequency of viral co-infections to better understand their potential interplay in mucosal pathologies.

Methods: Methods: To explore this interplay, was conducted a cross-sectional study involving 112 participants recruited from clinical settings. The study population included a high-risk group of 78 patients with clinically diagnosed genital warts (30 males and 48 females) and a comparison group of 34 females without a history of warts or HPV-related conditions. Oral swabs from the buccal mucosa and oropharynx, along with urine samples, were collected under sterile conditions. Viral DNA was extracted using a commercial kit optimized for mucosal and urinary specimens, ensuring high purity and yield. Polymerase chain reaction (PCR) assays were employed for viral detection. For HPV, primers targeting the conserved L1 gene were used, whereas EBV DNA was amplified with primers specific to the EBNA-1 gene, a marker of latent infection. PCR products were visualized by gel electrophoresis, and each run included both positive and negative controls to verify assay performance.

Results: Results: Of the 112 specimens analyzed, 77 (68.75%) tested positive for HPV DNA, confirming the high prevalence of this virus in individuals with genital warts as well as in a proportion of controls. EBV was detected in 17 oral samples (15.2%) and 3 urine samples (2.7%). Notably, among the EBV-positive oral specimens, 10 (58.8%) were co-infected with HPV, suggesting a substantial overlap between these viruses in the oral mucosa. In contrast, only one of the three EBV-positive urine samples (33.3%) harbored HPV DNA, reflecting a relatively lower co-infection rate in urinary specimens. Also, nine EBV-positive cases (seven oral and two urine) were negative for HPV.

Conclusion: Conclusion: The findings of this study highlight a notable prevalence of HPV and EBV in mucosal sites, with a particularly high rate of HPV detection among individuals with genital warts. The observed co-infection of HPV and EBV in oral samples suggests potential viral interactions within the mucosal microenvironment that may influence infection persistence or disease outcomes. Although EBV occurrence in urinary specimens was comparatively low, its coexistence with HPV in some cases indicates that viral interplay is not confined to a single anatomical site. These results underscore the importance of considering multi-viral infections in the context of mucosal pathologies and warrant further investigation into the molecular mechanisms and clinical implications of HPV–EBV co-infection.

Keywords: Keywords: human papillomavirus, Epstein–Barr virus,

Poster presentation

Poster 1

SAFETY AND EFFECTIVENESS OF SINGLE- VERSUS DOUBLE-DOSE OF SEASONAL INFLUENZA VACCINE IN KIDNEY TRANSPLANT RECIPIENTS: A RANDOMIZED CLINICAL TRIAL

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Introduction: Influenza virus poses significant risks to immunocompromised individuals such as those who have received organ transplants and are undergoing immunosuppressive treatment to prevent transplant rejection. Therefore, annual influenza vaccination is recommended for these individuals. This study aimed to comparison of safety and effectiveness of single- versus double-dose of seasonal influenza vaccine in kidney transplant recipients

Methods: This randomized clinical trial involved 50 kidney transplant recipients at Imam Khomeini Hospital. Participants were randomly assigned to two groups: those receiving a single dose (standard dose) and those receiving a double dose of the seasonal flu vaccine. Serum samples were collected before and 4 weeks after vaccination to measure influenza A&B- related antibodies. Sixteen patients were excluded from the study. The trial focused on evaluating the vaccine safety and immunogenicity, as well as documenting any local and systemic side effects following vaccination.

Results: The results indicated no significant difference in gender, age, and type of immunosuppressive drug used between the single- and double-dose groups (p 0.05). No significant difference in post-vaccination adverse effects, such as injection site pain (p = 0.21) between the two groups. The seroconversion rates (change from IgG 9 IU/µL to IgG 11 IU/µL) for IgG Influenza A were 12.5% (n = 2) in the single-dose group and 26.7% (n = 4) in the double-dose group, and for IgG Influenza B, they were 11.8% (n = 2) and 21.4% (n = 3), respectively

Conclusion: A double dose of the influenza vaccine slightly enhanced the immune response in kidney transplant patients without causing any adverse side effects.

Keywords: influenza vaccine, transplant recepients, double dose, immunogenecity, effectiveness, single dose

Poster 2

Emergence of Candida rugosa as a Cause of Candiduria: A Molecular Epidemiological Study from Iran

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Introduction: Candiduria, a common manifestation of urinary tract infection (UTI), presents a significant clinical challenge, affecting approximately 10–15% of patients with UTIs. While Candida albicans is the predominant etiological agent, infections caused by non-albicans species are increasingly recognized as being particularly problematic for both patients and clinicians due to their unique management complexities.

Methods: A cross-sectional study was conducted over a four-month period on hospitalized patients at Imam Khomeini and Mostafa Khomeini hospitals in Jahrom, Iran. Urine samples from patients with suspected candiduria were collected for analysis. Initial yeast identification was performed using conventional mycological methods. Molecular confirmation was achieved through DNA extraction via the phenol-chloroform method, followed by PCR amplification and restriction fragment length polymorphism (RFLP) analysis using the MspI restriction enzyme.

Results: Among 250 patient specimens analyzed, 40 yeast isolates were recovered. Molecular identification techniques revealed one case (2.5%) of infection caused by Candida rugosa. The isolate was obtained from a 54-year-old immunocompetent Iranian male with no documented history of immunodeficiency or underlying comorbidities, who was referred to the medical mycology laboratory in June 2022. Laboratory processing involved centrifugation of a 10-mL urine sample, followed by direct microscopic examination and culture of the sediment on Sabouraud dextrose agar with chloramphenicol incubated at 30°C. All yeast isolates in this study were definitively identified through a combination of phenotypic characteristics and restriction analysis of ribosomal DNA (rDNA).

Conclusion: This report describes the first documented case of candiduria caused by Candida rugosa in an immunocompetent patient from Iran. This finding contributes to the molecular epidemiological understanding of pathogenic yeasts in Iranian patients and highlights the emergence of less common, potentially resistant species in clinical settings.

Keywords: Candida rugosa, Candiduria, rDNA, Urinary Tract Infection, Iran

Poster 3

High Prevalence of Candida africana Misidentification in Vulvovaginal Candidiasis: A Molecular Epidemiological Study from Iran Based on HWP1 Gene Analysis

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Introduction: Vulvovaginal candidiasis (VVC) is a prevalent global gynecological condition, affecting millions of women and often presenting as a chronic, debilitating illness. While Candida albicans is the primary etiological agent, a significant proportion of infections are attributable to non-albicans species. Among these, the phylogenetically related species Candida africana and Candida dubliniensis present a diagnostic challenge due to their phenotypic similarity to C. albicans. This study reports detailed molecular epidemiological data on the prevalence of C. africana and C. dubliniensis among Iranian patients suffering from VVC and its recurrent form (RVVC).

Methods: A cohort of 133 vaginal yeast isolates, initially presumptively identified as Candida albicans based on phenotypic characteristics and restriction analysis of ribosomal DNA (rDNA), was subjected to further molecular analysis. To ensure accurate speciation, all isolates were re-examined using a specific PCR assay targeting the HWP1 gene, a reliable method for discriminating between these closely related species.

Results: Molecular analysis of the 133 germ-tube-positive isolates confirmed the presence of three distinct species: Candida albicans (n=119, 89.47%), Candida africana (n=11, 8.27%), and Candida dubliniensis (n=3, 2.26%). Although C. albicans remains the predominant species isolated from Iranian VVC/RVVC patients, these findings indicate that its prevalence may be marginally overestimated in routine diagnostics. This overestimation is likely due to the misidentification of morphologically similar species, particularly C. africana.

Conclusion: This study confirms the presence of Candida africana and Candida dubliniensis in the vaginal mycobiota of Iranian patients. The significant proportion of C. africana isolates suggests that reliance on conventional phenotypic methods alone can lead to misidentification. Accurate differentiation through specific molecular techniques, such as HWP1 gene analysis, is crucial for understanding the true epidemiology of VVC and for guiding appropriate therapeutic strategies.

Keywords: Candida africana, Candida dubliniensis, HWP1 gene, vulvovaginal candidiasis, epidemiology, Iran

Poster 4

Molecular Identification Reveals Aspergillus tubingensis as the Predominant Etiological Agent of Otomycosis in Iran: A High Incidence of Tympanic Membrane Perforation

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Introduction: Otomycosis is a fungal infection of the external auditory canal with a diverse etiology, encompassing a wide spectrum of fungal species. Accurate identification of the causative agents is crucial for effective management. This study aimed to precisely identify the fungal etiological agents of otomycosis in a patient population from Iran through molecular methods.

Methods: A total of 211 patients presenting with suspected otomycosis at the outpatient department of Peymanie Hospital in Jahrom, Iran, were enrolled in this study. Specimens were collected from the external auditory canal and subjected to direct microscopic examination and culture on appropriate media. Fungal isolates recovered from cultures were subsequently identified to the species level using molecular techniques.

Results: Fungal infection was confirmed in 51% of patients (108/211), as evidenced by the observation of fungal elements on direct microscopy and positive culture results. Molecular identification revealed Aspergillus tubingensis as the predominant causative agent, accounting for 52.77% of cases, followed by Aspergillus niger (25.92%). Infections attributable to yeasts of the Candida genus were observed in 16% of culture-positive cases. A notable finding was the association of otomycosis with tympanic membrane perforation in 36.11% of the confirmed cases.

Conclusion: This study establishes Aspergillus tubingensis, a species within the Aspergillus nigri section, as the predominant cause of otomycosis in the studied patient population, challenging the common attribution of this infection primarily to Aspergillus niger. The significant incidence of co-occurring tympanic membrane perforation underscores the potential severity of these infections. These findings highlight the indispensability of thorough mycological examination, incorporating molecular techniques for precise speciation, to achieve a correct diagnosis and guide appropriate therapeutic intervention for otitis externa.

Keywords: Aspergillus tubingensis, Otitis extern, Tympanic membrane perforation, Molecular identification, Iran

Poster 5

16-Year Trends of Antimicrobial Resistance in Klebsiella spp. Bloodstream Isolates: A Linear Regression Analysis from a Tertiary Teaching Hospital in Southern Iran (2008–2024)

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Introduction: The increasing prevalence of antimicrobial-resistant Klebsiella spp. in bloodstream infections (BSIs) underscores the critical need for long-term surveillance. This study analyzes 16-year trends of antimicrobial resistance in Klebsiella spp. bloodstream isolates from Shiraz, Iran.

Methods: We conducted a retrospective observational study at Professor Alborzi Clinical Microbiology Research Center, affiliated with Shiraz University of Medical Sciences, Shiraz, Iran, over 16 years (2008–2024). Bloodstream isolates were obtained from patients with suspected sepsis. Bacterial identification was performed using API and Microgen systems. Antimicrobial susceptibility testing was conducted via MIC determination and/or disk diffusion. Data were analyzed using WHONET 5.6 software, and trends were assessed using linear regression models.

Results: Among 992 Klebsiella spp. In BSI isolates, significant increasing resistance trends were observed for: Imipenem (β = 7.565, p = 0.000), Meropenem (β = 7.871, p = 0.001), Ciprofloxacin (β = 5.135, p = 0.002), Ceftazidime (β = 3.420, p = 0.018). Non-significant decreasing resistance trends were noted for: Gentamicin (β = -0.040, p = 0.974), Tobramycin (β = -1.194, p = 0.550), Trimethoprim sulfamethoxazole (β = -0.539, p = 0.771), Tetracycline (β = -0.976, p = 0.485), Amoxicillin (β = -0.063, p = 0.913). Non-significant increasing resistance trends were observed for: Colistin (β = 0.317, p = 0.746), Amikacin (β = 0.071, p = 0.968), Chloramphenicol (β = 2.060, p = 0.151), Aztreonam (β = 0.133, p = 0.938), Cefotaxime (β = 0.186, p = 0.883), Cefuroxime (β = 1.069, p = 0.318), Ticarcillin (β = 1.529, p = 0.524) and Ampicillin.

Conclusion: However, ESBL production showed non-significant declines in resistance trend, marked increase in carbapenem, ciprofloxacin and ceftazidime resistance and persistently high resistance to other antibiotics emphasize the urgent need for targeted antimicrobial stewardship programs. These findings highlight the importance of continuous AMR surveillance to inform empirical treatment strategies in southern Iran.

Keywords: Antimicrobial resistance, Klebsiella spp., Bloodstream infections, linear regression analysis, Tertiary teaching hospital, Iran

Poster 6

A Case of Concurrent Zoonotic Transmission of Chrysosporium and Aspergillus from a Pet Budgerigar: Cutaneous and Pulmonary Involvement

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Introduction: Zoonotic transmission of fungi from pet birds is an emerging health concern. This report describes the concurrent transmission of two fungi from a pet budgerigar to two family members, resulting in cutaneous infection in an adolescent and pulmonary involvement in the mother.

Methods: A 15-year-old male presented with intensely pruritic, scaly plaques on his hands, while his mother reported a 3-month history of chronic cough and dyspnea. Empirical antibiotic therapy for the mother had been ineffective. Both patients had prolonged exposure to a pet budgerigar; the son through direct contact and the mother through inhalational exposure during cage cleaning without protective equipment.

Results: Direct microscopy (KOH) of the son's skin scrapings revealed thin, septate hyphae (thinner than dermatophytes). Fungal culture on SDA revealed mixed growth of Chrysosporium spp. (slow-growing, keratinophilic colonies) and Aspergillus section Terrei (fast-growing colonies with cinnamon-colored conidia). The rapid overgrowth of Aspergillus obscured the isolation and identification of Chrysosporium.

Conclusion: : This case highlights the risk of concurrent transmission of multiple fungal pathogens from pet birds. It underscores the importance of taking a pet exposure history in patients with atypical dermatologic or respiratory symptoms. The fast overgrowth of one fungus can mask co-infecting agents, necessitating the use of molecular diagnostic methods (e.g., sequencing) for accurate identification in mixed infections. Protective measures (masks, gloves) for bird owners are strongly recommended for prevention.

Keywords: Zoonotic transmission, Chrysosporium, Aspergillus terreus, Budgerigar, Cutaneous infection, Pulmonary infection.

Poster 7

A Case Report of Bilateral Acute Suppurative Otomycosis Resistant to Therapy: Highlighting the Crucial Role of Microbiological Diagnosis

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Introduction: Acute otitis externa is primarily a bacterial infection, and primary fungal involvement is rare. This report describes an unusual case of bilateral acute suppurative otomycosis with severe symptoms resistant to conventional therapy.

Methods: A 25-year-old female presented with severe symptoms including otalgia, otorrhea, pruritus, scaling, facial and cervical lymphadenitis, hearing impairment, severe headache, and diplopia. The failure of successive antibiotic regimens necessitated microbiological investigations. Direct examination and culture of the ear sample on Sabouraud Doctorose Agar, a bacterial-specific medium, was performed.

Results: A polymicrobial infection consisting of bacteria, Aspergillus niger, and Candida species was identified on examination. Initial treatment with oral itraconazole (200 mg/day) and topical clotrimazole (2 drops, twice daily) was initiated for 3 weeks, but no improvement was achieved.

Conclusion: This case underscores the rarity and clinical significance of primary bilateral acute otomycosis. The failure of conventional antibiotic and initial antifungal therapies highlights the imperative for laboratory-based evidence (direct examination and culture) for accurate pathogen identification and antifungal susceptibility testing to guide targeted and effective treatment regimens. This approach is essential to prevent severe complications and achieve a successful clinical outcome.

Keywords: Acute otomycosis, Bilateral otitis externa, Resistant fungal infection, Microbiological diagnosis, Aspergillus niger.

Poster 8

Adult vaccination: Current recommendations and prospects

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Introduction: Adult vaccination is a critical public health intervention aimed at reducing morbidity and mortality from vaccine-preventable diseases in the growing adult and elderly populations. Current recommendations categorise vaccines into two groups: those for the general adult population and those targeted at individuals with specific risk factors, such as chronic illnesses, immunocompromising conditions, occupational exposures, or travel needs. Routine annual influenza vaccination is advised for all adults, accompanied by tetanus, diphtheria, and pertussis boosters every 10 years. Pneumococcal vaccination has evolved with the introduction of conjugate vaccines (e.g., PCV21), which offer improved immune responses, particularly for adults aged 50 years and older. This addresses the limitations of polysaccharide vaccines (PPV23), which provide only moderate protection and limited duration. The herpes zoster vaccine is recommended for older adults to prevent shingles and its complications.

Methods: Other vaccines, including those for COVID-19, HPV, meningococcal disease, hepatitis A and B, and varicella, have age-specific or risk-based indications, highlighting the complexity of adult immunisation schedules. Despite the availability of effective vaccines, adult vaccine uptake remains suboptimal globally due to factors such as passive risk-based recommendations, lack of awareness, and fragmented health systems. However, the future of adult vaccination is promising. Innovations in vaccine development are targeting emerging bacterial threats like Staphylococcus aureus and Clostridium difficile, which are increasingly problematic due to antibiotic resistance and ageing immune systems. Multivalent vaccines against these pathogens are in clinical trials, offering hope for future protection.

Results: Prospects include expanding adult vaccination coverage through unified, well-funded national programs, enhanced public and provider education, and annual monitoring of vaccine uptake and effectiveness. The importance of these initiatives cannot be overstated. Advances in vaccine formulations with more potent adjuvants and tailored immunisation schedules to overcome immunosenescence are key areas of research. Leveraging the success of pediatric vaccination programs, a coordinated effort among manufacturers, healthcare providers, and policymakers is essential to improve adult immunization rates and reduce the infectious disease burden in the aging population, ultimately improving health outcomes and quality of life.

Conclusion: This presentation aims to inform healthcare professionals, policymakers, and public health stakeholders about the critical role of adult vaccination. It encourages multidisciplinary collaboration, highlighting the unique contributions of each stakeholder group, to enhance vaccination coverage and protect adult populations worldwide from preventable infectious diseases.

Keywords: vaccination, Adult, pneumococcus

Poster 9

Adverse Effects of Ibuprofen in Respiratory Viral Infections in Children

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Introduction: Ibuprofen, a non-steroidal anti-inflammatory drug (NSAID), exerts both anti-inflammatory and antipyretic effects. However, its use as an antipyretic in children, particularly in viral respiratory infections such as influenza and varicella (chickenpox), is not recommended due to the increased risk of serious adverse events, including gastrointestinal bleeding, Stevens–Johnson syndrome, Necrotizing fasciitis following wound infection, and even mortality. Following the decline of the COVID-19 pandemic, the incidence of viral infections such as varicella has increased, especially among children. In some cases, varicella is complicated by severe outcomes such as wound infection, necrotizing fasciitis, and death. Therefore, evaluating the relationship between ibuprofen use in varicella patients and subsequent complications is essential.

Methods: In this descriptive–analytical study, the medical records of patients with varicella who were hospitalized during 2022 and 2023 were reviewed. Data were collected regarding prior use of NSAIDs (especially ibuprofen), patient age, and occurrence of complications such as wound infection and necrotizing fasciitis, and mortality outcomes.

Results: All patients were admitted primarily due to fever. Most patients had used ibuprofen or diclofenac as an antipyretic before to hospitalization. The highest mortality rate occurred among school-aged children (6–12 years). In 98% of fatal cases, prior use of NSAIDs—particularly ibuprofen—was documented. Approximately 50% of patients were saved from fatal outcomes through timely surgical intervention (wound debridement).

Conclusion: Acetaminophen is the only safe and recommended antipyretic in children. The use of NSAIDs (ibuprofen, diclofenac, aspirin) as antipyretics in children should be strictly avoided, particularly in viral infections such as varicella and influenza. These medications increase the risk of Stevens–Johnson syndrome, Reye's syndrome, and mortality.

Keywords: Ibuprofen, Adverse effects, Viral infection, Children

Poster 10

Alarming Prevalence of Trichophyton indotineae as the Most Causal Agent of Tinea corporis/pedis in Fars province, Iran

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Introduction: Recently, in many parts of the world, including Iran, Trichophyton indotyneae has rapidly replaced other dermatophytes as the dominant agent of cutaneous dermatophytosis as a new species. Due to the rapid ability of this fungus to develop resistance to various antifungal drugs and its rapid distribution in different countries, it is considered an important medical issue, and public health concerns have increased due to its increased virulence and difficulty in treatment. Cases of dermatophytosis caused by Trichophyton indotyneae have increased dramatically in Fars province in recent years. In this study, tinea corporis/pedis isolates collected from patients in Fars province were subjected to molecular analysis for species identification, and the current prevalence of T. indotineae was compared with prevalence of skin dermatophytosis agents.

Methods: A total of 135 patients clinically suspected of tinea corporis/pedis infections referred from different cities of Fars province were examined in Shiraz University of medical sciences medical mycology laboratory from January to December 2024. After direct KOH microscopic examination and culture onto 4% dextrose agar containing the antibiotic chloramphenicol, and Sabouraud's containing chloramphenicol as well as cycloheximide, dermatophytosis was confirmed to be present in 69 patients (51.1%). DNA of 69 dermatophytes isolates was extracted from fresh colonies, and the internal transcribed spacer (ITS) region was PCR-amplified and sequenced, followed by bioinformatic sequence analysis (compared with the GenBank database using nucleotide BLAST searches).

Results: Our findings demonstrated that the most abundant dermatophyte species were Trichophyton indotinea (47.8%), followed by T. interdigitale (30.4%), T. tonsurans (8.7%), T.simii (4.3%), M. canis (4.3%), while less abundant species showed Nanizzia gypsea, M. ferrugineum and T. benhamiae (1.4% for each).

Conclusion: The causative agents of tinea corporis/pedis vary according to researchers' reports in different geographical regions and countries. Khodadadi (2015–2019) and Zareshahrabadi (2017–2019) in their previous retrospective study, showed T. mentagrophytes and Ansari(2016) showed T.interdigitale as the common dermatophyte agent in Fars province. We observed that T. indotinea was the predominant dermatophyte consistent with Mirhendi et al. research in all Iran. Epidemiology of organisms can change under the influence of many factors such as geography, quality of healthcare, interventional medicine, social factors and genetic of species. Our study showing a change in the main pathogens of dermatophytosis from T. mentagrophytes and T.interdigitale to the T. indotinea in Fars province. T. indotineae is often considered a problematic dermatophytes due to its genetic resistance to common antifungal drugs such as terbinafine. The prevalence of this species highlights the need for molecular diagnosis and continuous surveillance of cutaneous dermatophytosis in the community.

Keywords: Tinea corporis/pedis, Dermatophytosis, T. indotineae, spectrum change, alarming prevalence

Poster 11

Analysis of the protein sequence of the RV2752c gene in active Mycobacterium tuberculosis strains and comparison with latent strains in laboratory conditions

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Introduction: Drug resistance in Mycobacterium tuberculosis poses a significant challenge to tuberculosis control worldwide. Among various genetic factors contributing to resistance, the gene Rv2752c has drawn increasing interest due to its encoding of a bifunctional enzyme with ribonuclease and beta-lactamase activities. These enzymatic functions suggest a possible role in modulating bacterial survival under antibiotic pressure. This study focuses on analyzing the protein sequence of the Rv2752c gene in active M. tuberculosis strains isolated from patients and comparing it with latent strains cultured under laboratory conditions. By investigating mutations and sequence variations between active and latent phases, we aim to better understand the involvement of Rv2752c in drug resistance and bacterial persistence. Insights gained from this comparative analysis could contribute to identifying novel targets for therapeutic intervention and improving treatment outcomes for tuberculosis.

Methods: In this study, we analyzed the protein sequence of the Rv2752c gene in Mycobacterium tuberculosis strains isolated from active tuberculosis cases and compared them with latent strains maintained under laboratory conditions. A total of 50 clinical isolates were examined, including 15 multi-drug resistant (MDR) and 35 drug-sensitive strains. Identification of isolates was confirmed through phenotypic methods and the GeneXpert molecular assay. Whole genome sequencing was performed to detect mutations within the Rv2752c gene. Comparative analysis aimed to uncover sequence variations between active and latent strains that could influence differences in drug resistance and bacterial persistence. Understanding these genetic differences may provide valuable insights into the role of Rv2752c in the development of resistance and the pathogen's ability to survive in latency, thereby contributing to improved strategies for tuberculosis treatment and control.

Results: Analysis of sequencing data revealed the V218L mutation in the Rv2752c gene significantly more frequently in multi-drug resistant (MDR) active Mycobacterium tuberculosis isolates compared to latent strains (p 0.01). This mutation was associated with increased minimum inhibitory concentrations (MICs) for both rifampicin and isoniazid, indicating a role in drug resistance. Other mutations in Rv2752c occurred at lower frequencies and showed no significant difference between active and latent isolates. The V218L mutation often co-occurred with well-known resistance mutations in rpoB and katG genes, suggesting a synergistic effect.

Conclusion: The findings of this study highlight the potential role of the Rv2752c gene, particularly the V218L variant, in the development of resistance to first-line anti-tuberculosis drugs. Including analysis of this gene in molecular diagnostic tools could improve the prediction of resistance patterns and aid in selecting appropriate treatments. Additionally, further studies are essential to clarify the functional impact of other mutations within this gene. Monitoring Rv2752c mutations may enhance understanding of drug resistance mechanisms in Mycobacterium tuberculosis and support more effective tuberculosis control and treatment strategies

Keywords: Rv2752c, Mycobacterium tuberculosis, V218L mutation

Poster 12

Anti-Inflammatory Effects of Eucalyptus Essential Oil in Helicobacter Pylori-Induced Gastritis

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Introduction: Herbal medicines are still widely used worldwide, with over 80% of the population relying on them due to cultural acceptance, lower cost, and fewer side effects compared to synthetic drugs. Several medicinal plants have been reported to possess anti-Helicobacter pylori properties. H. pylori plays a pivotal role in gastritis and other gastrointestinal disorders. This study aimed to investigate the effects of eucalyptus (Eucalyptus globulus) essential oil on inflammatory biomarkers in H. pylori-infected patients.

Methods: A total of 50 patients were included in this study. Twenty-five patients diagnosed with H. pylori infection and dyspepsia were assigned to the infected group, while 25 uninfected individuals served as the control group. Peripheral blood mononuclear cells (PBMCs) were isolated, stimulated with H. pylori antigen, and treated in vitro with eucalyptus essential oil (0.01%). Serum levels of TNF-α and soluble CD163 (sCD163) were measured using ELISA.

Results: TNF-α levels were significantly elevated in the infected group compared to controls ($p = 0.004$). Following dexamethasone incubation, TNF-α levels also differed significantly between the two groups ($p = 0.004$). Treatment with eucalyptus essential oil (0.01%) led to a significant reduction in TNF-α levels among patients with moderate gastritis ($p = 0.036$). Additionally, a decrease in sCD163 levels was observed in patients with mild gastritis ($p = 0.05$).

Conclusion: Eucalyptus essential oil was associated with reduced TNF-α and sCD163 levels in H. pylori-infected patients, as well as a decrease in TNF-α levels in moderate gastritis. These findings suggest that eucalyptus essential oil may exert anti-inflammatory effects in H. pylori-induced gastritis in vitro.

Keywords: H. Pylori, Inflammatory biomarkers, eucalyptus essential oil, Gastritis;

Poster 13

Antifungal Susceptibility Patterns of Fungal Isolates from Patients with Hematological Malignancies: A Clinical and Laboratory-Based Study

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Introduction: Fungal infections remain a major cause of morbidity and mortality in patients with hematological malignancies due to chemotherapy-induced neutropenia and immunosuppression. Early detection of fungal pathogens and assessment of their antifungal susceptibility profiles are essential for managing therapy and improving outcomes. This study aimed to evaluate the antifungal susceptibility patterns of fungal isolates recovered from patients with hematologic malignancies.

Methods: A total of 111 patients with hematological malignancies were included. Clinical specimens from patients who were clinically suspected of fungal infection were cultured on sabouraud dextrose agar. Species identification was performed using microscopic and molecular examinations. Antifungal susceptibility testing was conducted according to CLSI standards against eight antifungal agents including amphotericin B, caspofungin, voriconazole, fluconazole, itraconazole, posaconazole, luliconazole, and Isavuconazole. MIC_{50} and MIC_{90} values were calculated for each species with ≥2 isolates.

Results: Specimens from 60 patients (54%) yielded positive fungal growth. The major pathogens were Aspergillus, Candida, and Mucorales. Aspergillus flavus was the most common species of Aspergillus. Candida albicans and Mucor sp. were the most common species after A. flavus in this analysis. Also, various cryptic species and non-albicans Candida were identified. According to the MIC_{90} results, A. flavus showed the highest MIC90 values for amphotericin (4 µg/mL) and itraconazole (4 µg/mL), while lower MIC_{90} values were observed for voriconazole (1 µg/mL) and posaconazole (2 µg/mL). Candida albicans exhibited low MIC_{90} values for voriconazole (0.5 µg/mL) and caspofungin (0.064 µg/mL), indicating good susceptibility to azoles and echinocandins. In contrast, the Mucorales demonstrated notably higher MIC_{90} values across most antifungal agents, particularly for azoles, except isavuconazole.

Conclusion: The MIC_{90} data indicate significant variation in antifungal susceptibility among the studied isolates. While Candida and Aspergillus species generally remained susceptible to azoles and echinocandins, Mucorales isolates exhibited elevated MIC values, confirming their reduced susceptibility to most antifungal classes. These findings underscore the clinical importance of early identification of Mucorales infections and the need for targeted therapy, as delayed or inappropriate antifungal treatment can lead to poor outcomes in immunocompromised patients.

Keywords: antifungal susceptibility, hematological malignancy, Candida, Aspergillus, azoles, MIC_{90}

Poster 14

Antimicrobial Resistance Profiles of Aeromonas spp. in Iran

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Introduction: Antimicrobial resistance (AMR) in Aeromonas spp. is an emerging concern in human and veterinary medicine. This study summarizes antibiotic resistance patterns of Iranian isolates.

Methods: Data from published studies (2000–2023) were pooled. Isolates were tested for susceptibility against 37 antibiotics using CLSI guidelines.

Results: Resistance was highest to ampicillin (70–100%), tetracycline (20–100%), and nalidixic acid (40–90%). Carbapenems and cefepime remained most effective. MDR strains predominated in fish and seafood isolates, often associated with antibiotic use in aquaculture.

Conclusion: Frequent MDR Aeromonas strains in aquaculture pose a health risk. Implementing antimicrobial stewardship and AMR surveillance in fish farms is imperative.

Keywords: antimicrobial resistance, MDR, aquaculture, tetracycline, ampicillin, surveillance

Poster 15

Antimicrobial Stewardship and Drug–Drug Interaction Burden in Oncology: A Decade of Evidence from a Major Referral Hospital in Iran

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Introduction: Cancer patients face a heightened risk of infection and antimicrobial exposure due to immunosuppression, prolonged hospitalization, and complex polypharmacy. In this setting, antibiotic overuse contributes to antimicrobial resistance (AMR) and clinically significant drug–drug interactions (DDIs), threatening both infection control and treatment efficacy. Despite the global emphasis on antimicrobial stewardship (AMS), data from oncology settings in low- and middle-income countries remain scarce. This study analyzes a decade of antimicrobial use and DDI patterns among hospitalized oncology patients, linking infectious disease management with stewardship principles to guide safer prescribing practices.

Methods: Using electronic health records from 92,565 oncology admissions (2013–2023) at Amir Oncology Hospital, a CDSS framework was designed and validated. The system integrates data from the SynaRX DDI engine and Lexicomp® for automated detection of high-risk antimicrobial combinations. Interactions were categorized by severity (C–X), mechanism (CYP inhibition, QT prolongation, nephrotoxicity), and antimicrobial class. Predictive models identified factors associated with severe DDIs, including drug count, ward type, and infection diagnosis. Latent Class Analysis (LCA) stratified patients into risk clusters to inform real-time CDSS alerts for stewardship interventions.

Results: Over 3.4 million potential DDIs were identified; 36% were clinically significant (Categories D–X). Antibiotic-related interactions—particularly involving fluconazole, voriconazole, vancomycin, and aminoglycosides—dominated severe events through CYP3A4 inhibition, QT prolongation, and additive nephrotoxicity. Transplant and polypharmacy patients showed a fourfold higher DDI risk (p 0.001). Regression analysis confirmed anti-infective agents as independent predictors of severe interactions (OR 1.55, p 0.001). LCA revealed a distinct high-risk cluster characterized by broad-spectrum antibiotic use, prolonged hospitalization, and higher mortality, supporting targeted stewardship interventions.

Conclusion: This study establishes the foundation for an integrated CDSS to support antimicrobial stewardship and DDI prevention in oncology. By combining predictive analytics with automated alerts, the system enables early identification of high-risk antibiotic combinations, real-time prescribing feedback, and improved medication safety. Embedding such CDSS tools in oncology workflows can reduce preventable harm, optimize antimicrobial use, and strengthen stewardship efforts against AMR in complex cancer care.

Keywords: clinical decision support system, antimicrobial stewardship, oncology, drug–drug interactions, antifungal agents

Poster 16

Artificial Intelligence Approaches for Predicting and Analyzing Antibiotic Resistance in Bacterial Strains

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Introduction: Antibiotic resistance or antibiotic resistance genes،has become one of the most pressing threats to global health in the 21st century.The World Health Organization warns that antimicrobial resistance (AMR) could push us back into a “pre-antibiotic era,” where common infections may once again become letal.Resistant strains such as Methicillin-resistant Staphylococcus aureus (MRSA) and Carbapenem-resistant Klebsiella pneumoniae (CRKP) are increasingly difficult to treat. Traditional methods of detecting resistance—such as bacterial culture and antibiotic susceptibility testing (AST)—are accurate but slow, often requiring 24–72 hours. With the explosion of genomic, clinical, and pharmacological data, Artificial Intelligence (AI) and, more specifically, Machine Learning and Deep Learning , have emerged as powerful tools to accelerate the detection, prediction, and even prevention of antibiotic resistance.Algorithms , Support Vector Machines, and Deep Neural Networks have demonstrated strong performance in predicting resistance directly from genomic sequences.

Methods: Genomic, phenotypic, and clinical datasets of bacterial strains were gathered from publicly available repositories such as NCBI Pathogen Detection, PATRIC, and the WHO GLASS database. Each record contained whole-genome sequencing (WGS) data, antibiotic susceptibility profiles, and associated metadata (geographic location, infection type, and patient demographics).Raw genomic sequences were cleaned, trimmed, and aligned using standard bioinformatics pipelines (e.g., SPAdes and BWA). Resistance gene markers were annotated with reference to the CARD (Comprehensive Antibiotic Resistance Database). Clinical and phenotypic data were normalized to ensure consistent representation of resistant vs.To enhance clinical usability, model predictions were interpreted using SHAP (SHapley Additive exPlanations) values, highlighting which genomic or phenotypic features most strongly influenced resistance predictions.

Results: The machine learning models demonstrated varying degrees of accuracy in predicting antibiotic resistance from genomic and phenotypic features. Among classical ML methods, the Random Forest classifier achieved the highest overall accuracy (87%) with an AUC of 0.91. Support Vector Machines performed slightly lower, with an accuracy of 82%. Deep learning models outperformed traditional approaches. The Convolutional Neural Network (CNN) trained on genomic k-mer representations achieved an accuracy of 92% and an AUC of 0.95, while the Recurrent Neural Network (RNN) trained on sequential mutation data reached an accuracy of 90%.

Conclusion: Analysis using SHAP values revealed that the presence of known resistance genes such as blaKPC, mecA, and ndm-1 strongly influenced model predictions. Mutations in efflux pump regulators and porin channel genes were also significant contributors, highlighting the multifactorial nature of resistance.The models were capable of predicting resistance not only for well-characterized antibiotics (β-lactams, carbapenems, fluoroquinolones) but also for less-studied compounds. Predictive accuracy was highest for β-lactams (AUC = 0.96) and lowest for tetracyclines (AUC = 0.83), suggesting variable signal strength across antibiotic classes.

Keywords: Antibiotic resistance،Artificial intelligence (AI)،Antimicrobial resistance (AMR)

Poster 17

Assessment of Knowledge Regarding Needle stick Injury Management Among Medical Laboratory Science Students at Kerman University of Medical Sciences

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Introduction: Needle stick injuries (NSIs) pose a significant occupational hazard to all healthcare professionals, as they may expose individuals to blood borne pathogens. It was deemed essential to evaluate the knowledge regarding needle stick injury management among medical laboratory science students.

Methods: This pilot study was a descriptive-analytical survey and included 40 medical laboratory science students. Data were collected using a researcher-developed questionnaire based on the national NSI management protocol. Willing participants completed the questionnaire once, and the collected data were analyzed using SPSS software (version 27).

Results: The mean age of participants was 20.24 ± 1.56 years, with 41.2% female and 58.8% male. Findings revealed that 58.8% of participants correctly defined an NSI. While 76.5% knew the immediate post-exposure steps for contaminated sharp object injuries, fewer than half (47.1%) were aware of the appropriate first response to blood or infectious fluid splashes. Additionally, 52.9% lacked knowledge about proper wound cleansing following an NSI. A direct correlation was observed between awareness levels and both academic progression and completed clinical rotations. Nearly half of the participants had attended NSI-related training through various platforms. In self-reported assessments, most rated their NSI knowledge as "moderate to low."

Conclusion: The results indicate gaps in students' knowledge, with some areas scoring at moderate or low levels. Given that personal protective measures are critical for preventing infectious diseases—particularly HIV and HBV—in allied health professions, it is recommended that students receive comprehensive training on NSI management before entering hospital settings.

Keywords: Medical laboratory science, needle stick injury, student, awareness

Poster 18

Bacterial and Viral Respiratory co-infections with SARS-CoV-2 in dead patients of North Khorasan, Iran between 2020-2023

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Introduction: Background. Co-infections has a crucial role in the heightening the COVID-19 complications, especially in Hospitalized patients. Many respiratory bacteria and viruses can lead to co-infection or superinfections.

Methods: Methods. We evaluated bacterial and viral co-infections in the 480 samples of dead and 480 samples of living SARS-CoV-2-positive patients. We tested samples for the presence of respiratory bacterial pathogens, including streptococcus pneumonia, Haemophilus influenzae, klebsiella pneumonia, mycoplasma pneumonia, Acinetobacter baumani, pseudomonas aeruginosa, staphylococcus aureus and also important respiratory viral pathogens, including the influenza virus, human metapneumovirus, parainfluenza virus (A–D), adenovirus, respiratory syncytial virus (RSV) and bocavirus using PCR and rt-PCR tests.

Results: Results. We evaluated 8846 samples from 2020 May 1 to 2023 March 21 for SARS-CoV-2. Of these, 2919 (33%) were SARS-CoV-2 positive, and 5927 (67%) had negative SARS-CoV-2 rt-PCR test results. Four hundred eighty cases (16.44%) of positive patients were died. The Acinetobacter baumani was the most prevalent bacteria in dead patients in comparison with alive patients (P=0.043), and streptococcus pneumoniae was the most abundant in living patients (P≥0.05). The Influenza A virus is the most common in both groups (P=0.00001). The most common underlying condition and diseases in dead patients were diabetes and asthma (P≤0.05) while in the living patients were obesity and hypertension (P≥0.05). Most coinfected patients were more than 60-year-old.

Conclusion: Conclusion. This study highlights the significant impact of bacterial and viral coinfections on the clinical course and outcomes of SARS-CoV-2 infection. Coinfections contribute to disease severity, complicate diagnosis, and pose challenges for effective management.

Keywords: SARS-CoV-2, Coinfection, Bacteria, Virus

Poster 19

Case Report: Isolation of Pseudomonas stutzeri from Stool in a High-Risk Rural Patien

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Introduction: Introduction: Pseudomonas stutzeri is a Gram-negative, non-fermenting, oxidase-positive bacterium widely distributed in soil, water, and environmental substrates. It has been reported as an opportunistic pathogen in various clinical conditions, including pneumonia, conjunctivitis, septic arthritis, and infective endocarditis(1,2). Although rarely isolated from gastrointestinal samples, its presence in stool may indicate environmental transmission, especially in high-risk individuals(2,3).

Methods: Methods: Stool samples were cultured on Blood Agar, MacConkey, TCBS, and XLD media. Colonies appeared small, wrinkled, and adherent on Blood Agar, colorless on MacConkey and XLD, and showed no growth on TCBS. Biochemical tests included SIM (motility positive, indole negative), TSI/LIA/KIA (ALK/ALK, no H_2S), Simmons citrate (positive), lysine decarboxylase (positive), and oxidase (positive). Identification was confirmed using the BD Phoenix automated system.(4,5)

Results: Results: The isolate was identified as P. stutzeri based on colony morphology and biochemical profile. Differentiation from P. luteola, P. oryzihabitans, and Burkholderia mallei was achieved through oxidase positivity, ADH negativity, and motility. The patient was a hypertensive rural individual with environmental exposure. Literature supports the clinical importance of accurate identification due to its potential involvement in systemic infections.

Conclusion: Conclusion: Although P. stutzeri is rarely isolated from stool, its identification in high-risk patients is clinically significant. Differentiation from other non-fermenting Gram-negative bacilli is essential to avoid misdiagnosis and ensure appropriate treatment. This case reinforces the need for microbiological preparation in both environmental and clinical base (2).

Keywords: Pseudomonas stutzeri, environmental exposure, non-fermenting bacilli,

Poster 20

Changes in Antimicrobial Resistance Patterns of Pediatric Uropathogens in the South of Iran

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Introduction: The increasing prevalence of antimicrobial resistance has emerged as a critical global public health issue. This study aimed to identify the predominant bacterial pathogens causing community- acquired urinary tract infections (UTIs) in children and to evaluate the evolving patterns of antimicrobial resistance among pediatric uropathogens in Shiraz, southern Iran.

Methods: This research involved two prospective cross-sectional studies conducted among pediatric patients diagnosed with UTIs. The first study was carried out from 2005 to 2006 and included 435 children, while the second study, conducted from April 2010 to March 2011, enrolled175 children. Participants were children aged 1 month to 10 years suspected of having UTIs and referred to various outpatient pediatric clinics. Informed consent was obtained, and demographic data and laboratory test results were recorded using a standardized checklist. Urine samples were collected via urine bags for children under 2 years old and midstream clean-catch for older children. Patients were included if they presented with pyuria (white blood cell count 10 cells/µL) and UTI symptoms, such as dysuria, frequency, fever, etc. Bacterial culture was performed on blood agar and eosin methylene blue (EMB) agar, followed by antimicrobial susceptibility testing on isolated pathogens. Data were analyzed using SPSS version 19. Statistical analysis

Results: In the initial study (2005-2006), Escherichia coli was the most common pathogen (69.2%), followed by Klebsiella (13.33%) and Enterobacter (12.18%). The male-to-female ratio was 0.417, with the highest infection rate in infants under 12 months (p = 0.002). Resistance was highest for Amoxicillin (93.83%), Ampicillin (84.39%), Co-trimoxazole (60%), and Cephalotin (58.71%), and lowest for Nitrofurantoin (12.63%) and Ciprofloxacin (7.77%). In the follow-up study (2010-2011), E. coli remained dominant (67.43%), followed by Proteus (11.43%) and Klebsiella (6.85%). The male-to-female ratio was 0.2 and infections were highest in children under 12 months (p = 0.016). Resistance increased for Co- trimoxazole (64.85%), Cefixime (53.42%), Nalidixic acid (52.98%), and Nitrofurantoin (44.77%), while moderate resistance was noted for Gentamicin (39.19%) and Ciprofloxacin (22.55). A significant association existed between bacterial type and age groups in the second study (p = 0.002).

Conclusion: An upward trend in resistance was observed for commonly used oral antibiotics such as Co-trimoxazole, Cefixime, Nalidixic acid, and Nitrofurantoin. However, resistance remained lower for parenteral agents including Gentamicin, Cefotaxime, Ceftizoxime, and Ciprofloxacin. This highlights the ongoing challenge in selecting effective empirical antibiotic therapies for pediatric UTIs

Keywords: Antibiotic, Pediatric, Resistance, Urinary tract infection.

Poster 21

Chemical composition and antibacterial activities of the Polylophium involucratum methanolic extract against the growth of some pathogenic strains causing nosocomial infection

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Introduction: Nosocomial infections, predominantly caused by multidrug-resistant bacteria, present a formidable challenge to global healthcare systems. The concern has made researchers to discover novel an effective antimicrobial agent. This study investigates the chemical constituents and evaluates the in vitro antibacterial potential of a methanolic extract derived from the aerial parts of Polylophium involucratum (P. involucratum) against a panel of clinically significant pathogenic strains associated with hospital-acquired infections.

Methods: The methanolic extract was obtained through maceration method and its phytochemical profile was identified by Gas Chromatography-Mass Spectrometry (GC-MS) analysis. The antibacterial efficacy of the P. involucratum was assessed against some Gram-positive bacteria (Staphylococcus aureus ATCC 25923, methicillin-resistant Staphylococcus aureus [MRSA], and Enterococcus faecalis ATCC 29212) and Gram-negative bacteria (Escherichia coli ATCC 25922, Pseudomonas aeruginosa ATCC 27853, and Klebsiella pneumoniae ATCC 700603) using agar well diffusion assay. The broth microdilution method was performed to determine the Minimum Inhibitory Concentration (MIC).

Results: The GC-MS analysis revealed a rich and diverse composition, predominantly of volatile and phenolic compounds. Major constituents identified included terpenoids, such as limonene and α-pinene, alongside various sesquiterpenes, aromatic compounds, and long-chain aliphatic hydrocarbons, which are known for their documented biological activities. The results demonstrated a significant and dose-dependent antibacterial activity. The methanolic extract exhibited potent effects against all tested Gram-positive pathogens, with particularly strong inhibition observed against MRSA and S. aureus, showing the lowest MIC values. The activity against Gram-negative strains was present but generally less pronounced, which is consistent with the intrinsic resistance probably conferred by their outer membrane.

Conclusion: In conclusion, the findings of this study reveal that the methanolic extract of P. involucratum possesses substantial antibacterial properties, especially against critical Gram-positive nosocomial pathogens like MRSA. The activity is likely attributable to its complex chemical composition rich in bioactive terpenes and phenolic compounds. These results suggest that P. involucratum is a promising source of phytochemicals worthy of further investigation for developing complementary therapeutic strategies or novel antimicrobial agents to combat multidrug-resistant nosocomial infections.

Keywords: Polylophium involucratum, Nosocomial infections, Antibacterial activity, Methanolic extract, MRSA, GC-MS, MIC.

Poster 22

Chronic Urticaria in patients with the yeast's overgrowth in gastro- intestinal tract

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Introduction: Urticaria is a reaction pattern that represents cutaneous mast cell degranulation, with the condition being defined as chronic if lesions recur for longer than 6 weeks. Regarding to the considerable cases of urticaria with the overgrowth of yeasts in gastro-intestinal tract, we aimed to investigate the yeast colonization or invasion in cases with the symptoms of urticaria and to identify the Candida and Geotrichum agents at the level of species.

Methods: Our subjects included 200 cases with long time superficial lesions as Urticaria. Fresh stool sample from the cases with clinical symptoms were collected. A small amount of the specimens was processed in 0.1 ml of distilled water or potassium hydroxide and made wet smears. Microscopic investigation for yeast overgrowth or colonization (detection of cluster blastospores and pseudohypha) was performed. The primary cultures were conducted by inoculating a tip of the stool samples onto the free antibiotic sabouraud glucose agar and SGA with 0.05% chloramphenicol and 0.5% cycloxamide, with incubation at 30 °C for 48 hours. The fungal colonies were identified and sub-cultured onto the differential medium, CHROM agar Candida, for the identification of probable Candida and Geotrichum species. By this method, some medically important Candida species such as C. albicans, C. tropicalis, C. dubliniensi and C. krusei could be identified

Results: The highest age range of our cases was 40-50 and included 25% of all. Women and men similarly involved (12 each). Our findings of microscopic investigation included budding cells in 13(54.2%) cases, blastospores 6(25%), arthrospores 3(12.5%) and pseudohypha 2(8.3%). The findings of microscopic detection were completely in coincidence to those of cultures on SGA. The identification by differential CHROM agar Candida resulted C. albicans, C. krusei and C. glabrata. No cases of non-Candida yeasts identified by this method. The data of MALDI-TOF system but were different. Some isolated yeasts were identified different including Geotrichum silvicola and Candida africana. Total of 24 fungal isolates, 7 (29.2%) cases of G. silvicola, 7 (29.2%) C. albicans and 6(25%) C. glabrata were the most frequent identified by MALDI-TOF system. Other yeasts included C. Africana, C. tropicalis and C. glabrata one each. Only one unknown case by MALDI-TOF system recorded.

Conclusion: A variable species of yeast fungi which are commensally live in human gastro-intestinal tract are potentially candidate of causing agent for chronic Urticaria. Candida and Geotrichum species were isolated from the urticaria cases, although the isolated fungi were not proven but probable causes of urticaria in the studied patients.

Keywords: Hives, Candida, Geotrichum, idenfication

Poster 23

Clofazimine and Linezolid Resistance in Multidrug-Resistant Tuberculosis: Insights from a Single-Centre Study in Iran

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Introduction: The detection of drug resistance in multidrug-resistant tuberculosis (MDR-TB) is essential for effective treatment. This study compares conventional proportional methods and advanced molecular techniques, including PCR-RFLP and real-time PCR, to assess resistance to clofazimine and linezolid in MDR-TB isolates. By evaluating both phenotypic and genotypic approaches, we aim to better understand the genetic diversity underlying resistance and highlight the importance of integrating molecular diagnostics for improved management of MDR-TB.

Methods: This retrospective study involved clinical and laboratory-confirmed MDR-TB isolates selected from patients diagnosed with resistance to first-line drugs based on clinical symptoms, specialist examination, and radiological findings. Molecular identification was performed by IS6110-based PCR and hsp65 gene spacer region PCR-RFLP assay to ensure rapid and accurate detection. Drug susceptibility testing followed the standard proportional method recommended by WHO, performed on Löwenstein-Jensen medium and Middlebrook agar. Specific primers were designed in this study for investigating resistance-associated genes: Rv0678 for clofazimine resistance, and rrl and rplC for linezolid resistance, assessed by PCR-RFLP and real-time PCR

Results: Mutations were detected in the Rv0678 gene (17.2%) and in the rrl or rplC genes (17.2%), associated with resistance to clofazimine and linezolid, respectively. PCR-RFLP of Rv0678 (720 bp) with NlaIII enzyme showed three distinct patterns: 80% had 80/120/520 bp, 6.7% had 80/120/160/520 bp, and 10% had 80/120/190/520 bp. BsrI enzyme produced uniform 300/400 bp patterns. For rrl (860 bp), BSR I showed consistent 105/140/250/260 bp patterns; Bbv I revealed 93.3% had a 60/190/290/320/510/530/780 bp pattern, 6.7% lacked the 190 bp fragment. Hae III enzyme produced 100/770/780 bp in 93.3% and 100/780 bp in 6.7%. The rplC gene (400 bp) was highly conserved. Bbv I enzyme produced a 75/100/290 bp pattern in 93.3% and a 70/100/290 bp pattern in 6.7%. Despite mutations, only one isolate exhibited phenotypic resistance to both drugs, indicating complex resistance mechanisms. There was no significant association between genotypic mutations and phenotypic resistance.

Conclusion: These results show that, despite phenotypic sensitivity, many MDR-TB isolates carry mutations in genes linked to resistance to clofazimine and linezolid. However, these mutations do not always lead to phenotypic resistance, indicating complex resistance mechanisms. The retrospective design and small sample size limit generalizability. Employing whole genome sequencing (WGS) in future research is recommended to clarify discrepancies and improve MDR-TB treatment strategies.

Keywords: Mycobacterium tuberculosis, Tuberculosis, Multidrug-Resistant, Clofazimine, Linezolid

Poster 24

Clonal Dissemination of Methicillin-Resistant Staphylococcus pseudintermedius (MRSP) ST2361 in a Healthcare Setting: Antimicrobial Resistance and Virulence Profiling

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Introduction: Background: Staphylococcus pseudintermedius, a commensal in dogs, is an emerging zoonotic pathogen with increasing methicillin-resistant (MRSP) strains. This study investigated MRSP isolates from hospital environments and healthcare workers in Bojnurd, Iran, to assess antimicrobial resistance and zoonotic potential.

Methods: Methods: Nasal swabs from healthcare workers (n=40) and hospital supplies (n=35) were cultured. Phenotypic and genotypic analyses included antimicrobial susceptibility testing (Kirby-Bauer), PCR for resistance (mecA, vanA, cfr) and virulence genes (pvl, hla, icaA/D), SCCmec typing, and multilocus sequence typing (MLST).

Results: Results: Two MRSP isolates (ST2361) were identified, one from a nasal swab and another from hospital supplies. Both exhibited resistance to β-lactams (cefoxitin, penicillin), fluoroquinolones, macrolides, and sulfonamide-trimethoprim, but susceptibility to tetracyclines, gentamicin, linezolid, and vancomycin. PCR confirmed mecA and virulence genes (pvl, hla, icaA/D). SCCmec type IV and identical ST2361 profiles suggested clonal dissemination.

Conclusion: Conclusion: The presence of MRSP ST2361 in humans and hospital environments highlights its zoonotic and nosocomial transmission risks. The isolates' multidrug resistance and virulence genes underscore the need for improved diagnostics, antimicrobial stewardship, and infection control measures in healthcare settings.

Keywords: Staphylococcus pseudintermedius, MRSP, zoonotic transmission, antimicrobial resistance, nosocomial infection

Poster 25

Colistin Resistance among Escherichia coli Blood Isolates: Prevalence and Antibiotic Susceptibility Patterns at Namazi Hospital in Shiraz, Iran (2021–2025)

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Introduction: Colistin is considered one of the last-resort antibiotics for treating multidrug-resistant (MDR) Gram-negative bacteria. The rise in MDR Gram-negative pathogens in blood cultures has led to an increased use of colistin over the past decade. Consequently, colistin resistance has emerged globally in recent years. This retrospective study aimed to determine the prevalence of colistin-resistant Escherichia coli among isolates obtained from blood culture samples of patients admitted to Namazi Hospital in Shiraz, Iran, over a four-year period (from March 2021 to March 2025).

Methods: Bacterial isolates were collected from blood cultures at the Professor Alborzi Clinical Microbiology Research Center between March 2021 and March 2025 using the BACTEC system. The isolates were characterized using various biochemical tests. Antibiotic susceptibility patterns were determined using the standard disk diffusion method. Colistin resistance testing was performed with the Colistin Broth Disk Elution (CBDE) test according to CLSI guidelines.

Results: A total of 390 Escherichia coli isolates were obtained from hospitalized patients at Namazi Hospital. Among these, 11 isolates (2.8%) exhibited resistance to colistin, a last-resort antibiotic for multidrug-resistant Gram-negative infections. All colistin-resistant isolates were sensitive to amikacin, except for one, which was also sensitive to imipenem and piperacillin-tazobactam. Additionally, most isolates demonstrated susceptibility to meropenem, gentamicin, and tobramycin.

Conclusion: In contrast to colistin-resistant Klebsiellapneumoniae, which are typically resistant to multiple antibiotics and often classified as multidrug-resistant, colistin-resistant E. coli strains exhibit good susceptibility to several other antibiotics.

Keywords: Colistin resistance, Escherichia coli, Multidrug-resistant bacteria, Antibiotic susceptibility, Colistin Broth Disk Elution (CBDE)

Poster 26

combination of Antibiotics with Phages: Strategy for combating to Biofilms of Drug-Resistant Acinetobacter baumannii

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Introduction: The emergence of multidrug-resistant (MDR) and extensively drug-resistant (XDR) Acinetobacter baumannii represents a significant concern in clinical settings. Biofilm formation constitutes a fundamental mechanism contributing to the bacterium's heightened antibiotic resistance. In light of the limited efficacy of conventional antimicrobial agents against MDR, XDR, and biofilm-producing A. baumannii strains, it is imperative for healthcare systems to develop and implement innovative therapeutic strategies to effectively prevent and eradicate A. baumannii biofilms.

Methods: This study aimed to provide an overview of the combination therapy of phage and antibiotics in vitro, in vivo, and ex vivo studies in combating A. baumanii biofilms.

Results: Extensive research indicates that the combined application of antibiotics and bacteriophages holds significant potential for disrupting A. baumannii biofilms and managing infections caused by these highly resistant pathogens. In particular, the use of phage cocktails in conjunction with colistin has shown promise in inhibiting or eradicating biofilm formation. Integrating phage therapy with antibiotic treatment may address several inherent limitations of phage monotherapy. Moreover, protein-based phages have emerged as a promising alternative or adjunct to traditional antimicrobial strategies, exhibiting notable antibacterial efficacy. When administered alongside antibiotics, such phage formulations may enhance therapeutic outcomes by limiting the dissemination of antibiotic-resistant A. baumannii strains and promoting the effective removal of their biofilms.

Conclusion: The integration of antibiotic therapy with bacteriophage treatment represents a potentially effective approach for disrupting A. baumannii biofilms under experimental conditions and enhancing clinical outcomes in patients suffering from drug-resistant infections.

Keywords: phage, antibiotics, combination therapy, A. baumannii biofilms

Poster 27

Comparative Analysis of Antibiotic Resistance, Biofilm Formation, and Clonal Diversity of Pseudomonas aeruginosa in Two Educational Hospital ICUs in Isfahan city

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Introduction: Pseudomonas aeruginosa is a common cause of nosocomial infections, particularly in intensive care units (ICUs). Its high prevalence in hospital settings has been widely reported, and the World Health Organization (WHO) has highlighted the associated risk of mortality. This study aimed to compare the antibiotic resistance patterns, biofilm formation, and clonal diversity of P. aeruginosa isolates from ICU patients in two educational hospitals.

Methods: A total of 60 clinical isolates were collected from the ICUs of two hospitals. Bacterial identification was performed using conventional biochemical tests, followed by PCR confirmation of the toxA gene (390 bp). Demographic and clinical characteristics of patients were collected via questionnaires. Biofilm formation was quantified using a microtiter plate assay, and antibiotic susceptibility patterns were determined through standard antibiogram testing. ERIC-PCR was employed to assess clonal relatedness and diversity of isolates within each hospital.

Results: Among the isolates, 60% from Imam Musa Kazem Hospital (IMKH) and 46.66% from Alzahra Hospital were extensively drug-resistant (XDR), with colistin as the primary treatment for all XDR isolates. Mortality among patients receiving colistin was 56.52% in IMKH and 23.52% in Alzahra Hospital. In Alzahra, resistance was highest to trimethoprim-sulfamethoxazole (96.66%) and lowest to cefepime (43.33%), whereas in IMKH, the highest resistance (96.66%) was observed for meropenem, cefepime, tobramycin, piperacillin-tazobactam, and trimethoprim-sulfamethoxazole, and the lowest with ceftazidime-clavulanic acid (36.66%). Strong biofilm formation was noted in 73.33% and 76.66% of isolates from IMKH and Alzahra, respectively. ERIC-PCR revealed six clonal types (CTs) and two single types (STs) in IMKH, indicating moderate diversity, while Alzahra had five CTs and ten STs, reflecting more unique isolates. No isolates were shared, likely due to differences in patient populations, with IMKH being a burn center and Alzahra a general hospital.

Conclusion: The high mortality associated with XDR P. aeruginosa underscores the critical threat posed by antibiotic resistance, particularly in burn patients. IMKH exhibited more localized clonal dissemination, whereas the greater heterogeneity observed in Alzahra hospital suggests multiple sources of bacterial introduction. Biofilm formation rates were similar between the two hospitals. These findings highlight the importance of implementing infection control strategies tailored to hospital type and patient population, as well as the ongoing need for careful antimicrobial stewardship to limit the spread of resistant strains.

Keywords: Antibiotic resistance, P. aeruginosa, Biofilms, Intensive Care Units, Genetic Testing

Poster 28

Comparative Analysis of Enzymatic Profiles in Clinical and Environmental Candida kefyr Isolates

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Introduction: The rising incidence of infections caused by the emerging pathogen Candida kefyr, a non-albicans species often associated with antifungal resistance, necessitates a better understanding of its virulence. This study investigated the enzymatic activity profiles in clinical and non-clinical Candida kefyr isolates.

Methods: Sixty-six C. kefyr isolates were analyzed for key enzymatic activities. Proteinase and phospholipase activities were assessed using bovine serum albumin and egg yolk agar, respectively. Hemolysin, caseinolytic, and esterase activities were also evaluated.

Results: Proteinase was highly prevalent. Hemolysin was most common in normal microbiota. Esterase was found only in dairy samples. Caseinase was low but highest in normal microbiota and hospital isolates. Phospholipase was rare.

Conclusion: Significant variations in enzyme profiles exist between clinical and non-clinical C. kefyr isolates. These findings illuminate the pathogenic potential of this fungus and have important implications for developing therapeutic strategies.

Keywords: Candida kefyr, Enzymatic Profiles, Clinical isolates, Environmental isolates

Poster 29

Comparative Evaluation of Doxycycline versus Amoxicillin + Metronidazole in the Management of Oral and Dental Infections

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Introduction: Oral and dental infections are among the most prevalent bacterial diseases in clinical dentistry, typically involving mixed aerobic and anaerobic microorganisms. The standard therapeutic approach often includes a combination of Amoxicillin and Metronidazole. However, antibiotic resistance, adverse drug interactions, and patient noncompliance have prompted the exploration of single-agent alternatives. Doxycycline, a broad-spectrum tetracycline antibiotic with both antibacterial and anti-inflammatory effects, may offer an effective monotherapy option. This study aimed to compare the clinical efficacy and patient tolerance of Doxycycline with the conventional combination of Amoxicillin + Metronidazole in treating acute odontogenic infections.

Methods: A randomized clinical trial was conducted on 120 patients presenting with acute odontogenic infections at Shiraz University Dental Clinic. Participants were divided into two equal groups: Group A received Doxycycline 100 mg twice daily for 7 days, and Group B received Amoxicillin 500 mg plus Metronidazole 250 mg three times daily for the same period. Pain intensity (VAS score), swelling, and local temperature were evaluated at baseline and on day 7. Microbial cultures were performed to determine bacterial patterns and antibiotic susceptibility. Data were analyzed using SPSS v.26, with a p-value 0.05 considered statistically significant.

Results: Both groups demonstrated significant clinical improvement after 7 days of treatment (p0.05). The reduction in pain and swelling was comparable between the two regimens, with no statistically significant difference in infection resolution rates. However, patients in the Doxycycline group reported fewer gastrointestinal side effects (8.3% vs. 20%) and showed higher treatment compliance due to simpler dosing. Microbial analysis revealed similar bacterial eradication rates in both groups, predominantly targeting Streptococcus, Prevotella, and Fusobacterium species. No serious adverse events or allergic reactions were observed in either group during the study period.

Conclusion: Doxycycline demonstrated equivalent therapeutic efficacy to Amoxicillin + Metronidazole in treating oral and dental infections, with the added advantages of better tolerability and simpler administration. These findings suggest that Doxycycline can be considered a suitable monotherapy for mild to moderate odontogenic infections, particularly in patients allergic to penicillin or intolerant to multidrug regimens. Nonetheless, in severe or deep-space infections, combination therapy may still be warranted. Broader studies with larger sample sizes are recommended to confirm these observations and assess regional antimicrobial resistance profiles.

Keywords: Doxycycline, Amoxicillin, Metronidazole, Oral infections, Dental infections, Odontogenic abscess, Antibiotic therapy, Bacterial resistance, Monotherapy, Clinical efficacy

Poster 30

Comparison of gut microbiota and short-chain fatty acids in patients with inflammatory bowel disease and healthy individuals

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Introduction: Inflammatory bowel disease (IBD) is a recurring infammatory disease that afects diferent parts of the human digestive system.This disease is a global public health challenge and millions of people in the world are sufering from this disease. A disturbance in the composition of intestinal microbiota has been linked to the onset of various gastrointestinal diseases, such as IBD. Gut microbiota is essential for the synthesis of short-chain fatty acids (SCFAs). The amount of SCFA in fecal samples seems to be associated with certain illnesses, including IBD. The present study sought to evaluate the four main bacterial phyla of the gut microbiota and the main SCFAs in patients with IBD in Tabriz city compared to healthy individuals.

Methods: In this study, 40 stool samples from patients with IBD (20 patients with Crohn's disease (CD) and 20 patients with ulcerative colitis (UC)) and 20 stool samples from healthy controls were included. The predominant bacterial phylum of gut microbiota were evaluated using Quantitative PCR .The concentration of the main SCFAs (butyric acid, propionic acid, and acetic acid) were also evaluated using High-performance liquid chromatography system.

Results: Results showed that Firmicutes levels were significantly lower in both UC and CD patients compared to controls. Bacteroidetes were significantly reduced in CD patients, while Proteobacteria were significantly elevated in UC patients. No significant differences were observed in Actinobacteria levels. Regarding SCFAs, butyric acid was significantly lower in both UC and CD patients. Additionally, acetic acid and propionic acid were significantly decreased only in UC patients.

Conclusion: These findings highlight the presence of gut dysbiosis and altered SCFA profiles in IBD patients. Given the protective roles of gut microbiota and their metabolites, strategies to restore microbial balance and SCFA production may support the management and treatment of IBD.

Keywords: Ulcerative colitis, Crohn's disease, Gut microbiota, Phylum, SCFAs

Poster 31

Comparison of Mycobacterium avium Complex Identification Methods Using hsp65 and 16S-23S rRna Genes

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Introduction: Nontuberculous mycobacteria (NTM) infections are increasingly recognized as significant clinical problems, particularly among immunocompromised patients, individuals with chronic pulmonary diseases, and those with underlying structural lung abnormalities. These opportunistic pathogens can cause a wide spectrum of clinical manifestations, ranging from asymptomatic colonization to severe pulmonary and extrapulmonary infections, which complicates timely diagnosis and management. Among the various NTM species, the Mycobacterium avium complex (MAC), mainly comprising M. avium and M. intracellulare, represents the most clinically relevant group, being frequently implicated in persistent infections and associated with high morbidity. Conventional diagnostic approaches, including culture-based methods and biochemical tests, are often labor-intensive, time-consuming, and may lack sufficient specificity to accurately differentiate closely related species or subspecies.

Methods: A total of 680 clinical specimens—including sputum, bronchial aspirates, bronchoalveolar lavage, tissue biopsies, and wound discharges—were collected from patients referred to the Tuberculosis Reference Laboratory of Masih Daneshvari Hospital. Samples underwent digestion, decontamination, Ziehl–Neelsen staining, culture, and heat inactivation at 100 °C for 30 min prior to DNA extraction. The IS6110 gene was amplified to detect members of the Mycobacterium tuberculosis complex (MTBC). IS6110-negative samples were subjected to nested PCR targeting the hsp65 gene (digested with BstEII and HaeIII) and the 16S-23S rRNA gene (digested with HaeIII, CfoI, TaqI, and DdeI). Restriction fragment length polymorphism (RFLP) patterns were analyzed and compared using the PRA database for accurate species- and subspecies-level identification.

Results: Among the 680 isolates, 62 (9.1%) were identified as MAC. The hsp65 gene exhibited 98% sensitivity and 96.5% specificity, effectively differentiating closely related subspecies, including M. intracellulare types I and V and various M. avium genotypes, which are most frequently associated with human infections. In contrast, the 16S-23S rRNA gene alone showed limited discriminatory capacity due to 99.2% sequence similarity between M. avium and M. intracellulare, often resulting in overlapping RFLP patterns. Incorporating DdeI digestion improved its identification accuracy to 88.3%. Notably, combining hsp65 and 16S-23S rRNA analyses increased overall diagnostic accuracy to 95.7%, thereby reducing misidentifications and enhancing subspecies-level resolution.

Conclusion: The hsp65 gene is a highly reliable and informative molecular marker for the identification of Mycobacterium avium complex (MAC) and for distinguishing its closely related subspecies. Its high sensitivity and specificity allow accurate differentiation of M. avium and M. intracellulare strains, including clinically relevant genotypes, which is critical for understanding epidemiology, monitoring infection sources, and guiding appropriate therapy. While hsp65 alone provides robust identification, combining it with 16S-23S rRNA gene analysis offers a more comprehensive approach by further enhancing species- and subspecies-level resolution, minimizing potential misidentifications, and improving diagnostic confidence. This integrated molecular strategy enables clinical laboratories to deliver faster and more precise results, facilitating early initiation of targeted treatment regimens. Overall, the combined use of hsp65 and 16S-23S rRNA analysis represents a powerful diagnostic tool that not only strengthens laboratory capabilities but also supports optimal clinical management, improves patient outcomes, and contributes to more effective control of MAC-associated infections.

Keywords: Mycobacterium avium Complex, heat-shock protein 65, 16S rRNA,23S rRNA PCR, Nested, Restriction Fragment Length Polymorphisms

Poster 32

Comprehensive Assessment of Aminoglycoside and First-Line Drug Resistance in Mycobacterium tuberculosis Using Proportional Method and GeneXpert

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Introduction: Tuberculosis (TB) remains a major global health challenge, increasingly complicated by the emergence of drug-resistant strains such as multidrug-resistant (MDR) and extensively drug-resistant (XDR) tuberculosis. Resistance to first-line anti-TB drugs has necessitated the use of second-line agents, including aminoglycosides like amikacin and kanamycin. These antibiotics effectively inhibit bacterial protein synthesis but are limited by their potential side effects and routes of administration, emphasizing the need for precise and reliable resistance detection. Phenotypic methods, such as the proportional test on Löwenstein-Jensen medium, combined with molecular techniques like GeneXpert, enable more accurate identification of resistance profiles. This study, conducted on samples obtained from the Supranational Laboratory in Sweden, aims to provide dependable data to optimize treatment regimens for resistant TB cases and enhance disease management. Understanding resistance patterns to both first-line drugs and aminoglycosides supports the development of more effective therapeutic strategies within healthcare settings.

Methods: This study analyzed clinical specimens sent from the Supranational Laboratory in Sweden. Evaluation was performed at the national tuberculosis reference laboratory for resistance against first-line anti-TB drugs as well as aminoglycosides, including amikacin and kanamycin. Initial confirmatory tests involved culture on Löwenstein-Jensen medium and direct smear microscopy to detect Mycobacterium tuberculosis. Subsequently, drug susceptibility testing against first-line drugs, kanamycin, and amikacin was conducted using the proportional method. Additionally, rifampicin resistance was assessed by the molecular GeneXpert technique. This combined phenotypic and molecular approach ensured comprehensive and accurate detection of drug resistance patterns among clinical isolates. The study's goal was to generate reliable phenotypic data to inform and optimize therapeutic strategies, especially for cases resistant to first-line treatment.

Results: Following the necessary procedures to determine drug resistance, 20 samples were analyzed. Of these, 18 samples (90%) belonged to the Mycobacterium complex, while 2 samples (10%) were classified as non-tuberculous mycobacteria. These two non-tuberculous samples showed resistance to first-line drugs including isoniazid, rifampicin, ethambutol, and pyrazinamide. Within the Mycobacterium tuberculosis complex group, 5 samples (25%) exhibited resistance to first-line drugs and were categorized as MDR-TB; among these, 2 samples (10%) also demonstrated resistance to amikacin and kanamycin. Resistance to amikacin and kanamycin was observed in 7 samples (35%), however, five of these showed no resistance to first-line drugs. No resistance to pyrazinamide was detected in any of the analyzed samples.

Conclusion: The study demonstrated that the majority of samples belonged to the Mycobacterium complex, with a significant portion exhibiting resistance to both first-line drugs and aminoglycosides. The presence of aminoglycoside resistance in isolates sensitive to first-line drugs underscores the crucial need for continuous monitoring of second-line drug resistance. Both the proportional method and GeneXpert proved useful for thorough and precise resistance detection. Based on these findings, amikacin and kanamycin remain essential in treating MDR and XDR TB cases; however, ongoing surveillance and judicious administration of these drugs are vital to prevent further resistance development. Overall, these results contribute importantly to enhancing treatment strategies and tuberculosis control efforts in healthcare facilities.

Keywords: Aminoglycosides, Mycobacterium tuberculosis, Tuberculosis, Multidrug-Resistant, Drug Resistance

Poster 33

Computational Immunodesign of a Multi-Epitope Vaccine Candidate Against Human Adenovirus F40

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Introduction: Human adenovirus F40 is a causative agent of acute gastroenteritis across all age groups, with a particularly high prevalence among infants and young children. Despite its significant clinical impact, no licensed vaccine is currently available to target this serotype. In the present study, we aimed to design a high-quality multi-epitope vaccine candidate against Human Adenovirus F40 using an immunoinformatic-based approach.

Methods: Capsid protein sequences were retrieved and analyzed for their interactions with cytotoxic T lymphocyte (CTL), helper T lymphocyte (HTL), and B cell receptors. The most promising peptides were selected for vaccine construction based on their predicted antigenicity, non-allergenicity, and non-toxicity. These epitopes were then used for three dimensional (3D) structural modeling and docking analyses with toll-like receptor (TLR)-2. Physicochemical properties and the potential to induce IFN-γ production were also assessed.

Results: A total of 187 epitopes were initially predicted, of which 66 fulfilled the selection criteria of high antigenicity, non-allergenicity, and non-toxicity. These were subjected to further physicochemical characterization and IFN-γ induction analysis. The final vaccine construct comprised the top four epitopes, joined by suitable adjuvants and linkers (human β-defensin, AAY, GPGPG, KK). The 3D structure of the final construct was generated and demonstrated strong binding affinity upon docking with TLR-2.

Conclusion: The designed multi-epitope vaccine candidate showed promising immunogenic potential and strong interaction with TLR-2, indicating its potential as a safe and effective vaccine against human adenovirus F40.

Keywords: Adenoviruses, Human Adenovirus F40, Viral Vaccine, Immunoinformatics, Epitopes, in-silico vaccine design

Poster 34

Cross-Sectional Analysis of Mannheimia haemolytica Antibiotic Resistance: Optimizing Treatment in Livestock

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Introduction: Mannheimia haemolytica is a Gram-negative, non-motile coccobacillus that colonizes the upper respiratory tract of ruminants and is a major opportunistic pathogen in the bovine respiratory disease complex (BRDC). It produces virulence factors such as leukotoxin, causing acute pneumonia, high mortality, and substantial economic losses. The emergence of antimicrobial resistance necessitates periodic antibiogram-based monitoring to guide effective therapy.

Methods: Samples were collected from the nasal cavity and tonsils of clinically suspected ruminants in five Iranian provinces and transported under cold chain conditions to the Razi Vaccine and Serum Research Institute, Shiraz. Each sample was coded, streaked on 5% sheep blood agar, and incubated at 37 °C for 24 h. Suspected M. haemolytica colonies (greyish, narrow hemolysis) were Gram-stained, purified, and identified by standard biochemical tests, including growth on MacConkey agar, oxidase and catalase activity, and indole production. Colonies consistent with M. haemolytica were confirmed by PCR targeting the species-specific rpt2 gene, yielding 45 positive isolates out of ~400 samples. Antimicrobial susceptibility was tested using Kirby–Bauer disk diffusion.

Results: High resistance was observed to OX1, with moderate resistance to L2. A few isolates showed resistance to CN30 and NA30, while rare resistance occurred to CFM5, IPM, and S10. In contrast, strong susceptibility was observed to C30, CRO30, and FF30. Many isolates were also susceptible to NFX5, NOR10, CP5, SXT, CFM5, IPM10, and CTX30.

Conclusion: M. haemolytica displayed considerable resistance to some commonly used antibiotics, particularly OX1 and L2, but remained highly susceptible to broad-spectrum agents, especially C30, CRO30, and FF30. The occasional detection of isolates resistant to last-line agents such as IPM emphasizes the necessity of continuous surveillance and rational antibiotic use in veterinary medicine. Regular antibiogram-based monitoring is critical to optimizing therapeutic protocols and minimizing the economic burden of respiratory diseases in ruminants.

Keywords: Mannheimia haemolytica; antimicrobial resistance; antibiogram; biochemical tests; PCR; respiratory infections; ruminants; BRDC

Poster 35

Designing Innovative Quality Control Panel in the Iranian National Tuberculosis Reference Laboratory: Optimizing Qualitative and Quantitative Assessment Methods as a WHO Collaborating Centre (WHOCC)

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Introduction: Tuberculosis (TB) remains a critical global health challenge, particularly in developing nations. The accuracy of its diagnosis is heavily dependent on the quality performance of laboratories, underscoring the need for robust quality control (QC) systems. This project proposes the design and implementation of an innovative QC panel to optimize both qualitative and quantitative assessment methods, aiming to enhance diagnostic precision and overall laboratory efficacy.

Methods: The initial phase involves a comprehensive situational analysis, including a review of international standards and internal audits to identify strengths and weaknesses in the current QC system. The second phase is dedicated to designing the comprehensive QC system. This includes developing Standard Operating Procedures (SOPs) for all laboratory processes, architecting an integrated software platform for quality management, and creating artificial intelligence (AI) algorithms for the automated analysis of test results and flagging of anomalies. A sample tracking system and a detailed staff training curriculum will also be formulated. The third phase consists of a pilot implementation in a selected section of the laboratory, where initial training will be conducted, performance data will be collected, and the system will be refined based on user feedback and preliminary evaluations. The final phase involves the full-scale rollout of the optimized system across all laboratory departments, followed by a final evaluation.

Results: The implementation of the novel QC panel is anticipated to yield significant improvements. Key expected outcomes include a measurable reduction in laboratory errors and a substantial increase in diagnostic accuracy. The integration of AI and the streamlined software system are projected to enhance operational efficiency and productivity. Furthermore, the comprehensive training program is expected to improve staff competency and job satisfaction. Ultimately, the project aims to solidify the laboratory's international standing as a WHOCC by aligning its practices with the highest global standards.

Conclusion: The development and implementation of this innovative quality control panel represent a crucial step towards strengthening the TB diagnostic infrastructure in Iran. By standardizing protocols, leveraging modern technology like AI, and investing in human capital, this initiative is poised to significantly improve the quality and reliability of laboratory services. The success of this project is expected to have a profound positive impact on public health through enhanced TB control, contributing to the reduction of the disease burden both nationally and within the region. This model may also serve as a benchmark for other reference laboratories facing similar challenges.

Keywords: Innovative Quality Control; National Tuberculosis Reference Laboratory; Laboratory Quality Management.

Poster 36

Duel of Linezolid and Tedizolid on Vancomycin-Resistant Staphylococcus aureus Isolated from Cancer Patients: In Vitro

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Introduction: The development of cancer in humans is a multi-stage process influenced by infectious, environmental, and genetic factors. Antimicrobial resistance (AMR) in clinical strains of Staphylococcus aureus has become a significant global public health challenge. Although glycopeptides are effective against Gram-positive pathogens, the emergence of vancomycin-resistant Staphylococcus aureus (VRSA) poses a serious threat. This study aimed to compare the frequency and minimum inhibitory concentrations of linezolid and tedizolid as oxazolidinones against VRSA isolates from hospitalized cancer patients.

Methods: This descriptive-analytical study examined 21 VRSA isolates from a total of 264 samples collected from hospitalized cancer patients between 2023 and 2025. VRSA isolates were identified through both phenotypic methods and PCR techniques. To determine the minimum inhibitory concentration (MIC) of tedizolid and linezolid, the broth microdilution test was conducted following the criteria outlined in CLSI M100 (2021).

Results: Screening for VRSA revealed that women and individuals aged 36 and older with colorectal cancer were more likely to carry this pathogen. The highest rate of VRSA was detected in wound samples, at 65.63%, while no cases of VRSA were identified in joint fluid samples (p 0.05). Additionally, no VRSA isolates were found in individuals with multiple myeloma. Determining MIC showed that 98.35% VRSA isolates were susceptible to tedizolid (MIC, ≤2µg/mL), while 94/81% (MIC, ≤4µg/mL) isolates were categorized as susceptible to linezolid. The concentration of tedizolid that inhibited 90% of isolates (MIC90) was 1µg/mL, 4-fold lower than linezolid (MIC90=4µg/mL). Additionally, all tedizolid-resistant isolates and 98% of linezolid-resistant isolates were obtained from patients with colorectal cancer (P = 0.02).

Conclusion: The growing number of VRSA outbreak reports emphasizes the urgent need to update national treatment guidelines to incorporate effective antimicrobial agents that target resistant Staphylococcus species. Our findings indicate that tedizolid is beneficial against VRSA and demonstrates more potent in vitro activity compared to linezolid.

Keywords: Staphylococcus aureus, Vancomycin, Linezolid, Tedizolid, Drug Resistance

Poster 37

EBV Reactivation and Clinical Outcomes in Hospitalized COVID 19 Patients

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Introduction: The Epstein–Barr virus (EBV) is a human gamma-herpesvirus that is implicated in various types of proliferative diseases. Following successful infection, EBV can reside in B- and T-lymphocytes, epithelial cells, and skeletal muscle cells, after which the virus remains largely latent. Reactivation of EBV and other opportunistic viruses is commonly associated with immunosuppressed states, though reactivation has also been reported in patients without prior immunosuppression.Although numerous studies have highlighted the importance of EBV in long COVID, the relationship between EBV reactivation and COVID-19 remains incompletely understood in active COVID-19 cases. Some reports indicate that patients with concurrent EBV reactivation during active COVID-19 exhibit a higher incidence of respiratory failure compared with patients infected with SARS-CoV-2 alone. Multiple studies have reported mortality linked to EBV reactivation in COVID-19 patients; however, conclusions remain inconclusive due to heterogeneity in event counts across studies.

Methods: In this study, a total of 150 samples from SARS-CoV-2 infected hospitalized patients were included. All patients had positive SARS-CoV-2 real-time RT-PCR results. Real-time PCR testing for Epstein–Barr virus was performed on these samples. The EBV test results, together with the SARS-CoV-2 positive status and the patients' clinical manifestations recorded at the time of presentation, were analyzed.

Results: In this study, 18 individuals (12%) with COVID-19 were found to have concurrent EBV infection. The gender distribution in this sample was relatively balanced (47% females). The most common symptoms observed in these patients were fever, cough, shortness of breath, and generalized malaise, occurring in 102 (68٪), 102 (68٪), 112 (74.7٪), and 129 (86٪) patients, respectively. No significant associations were observed between any of the common clinical symptoms and concurrent EBV infection. It is notable that EBV reactivation was higher only in neuro-muscular patients.

Conclusion: EBV reactivation in hospitalized patients was 12%, which is concordant with findings from other studies. Our data regarding the role of EBV in the clinical presentation of COVID-19 do not provide sufficient evidence to establish a definite conclusion

Keywords: COVID-19, EBV, Clinical manifestations, Coinfection

Poster 38

Effect of aqueous and alcoholic extracts of Marrubium anisodon on the growth and expression of the alpha-hemolysin (HlyA) gene in Escherichia coli

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Introduction: Escherichia coli is a prominent Gram-negative pathogen responsible for various hospital- and community-acquired infections, including urinary tract infections, septicemia, and gastrointestinal disorders. The global rise of multidrug-resistant (MDR) E. coli strains has significantly reduced the effectiveness of conventional antibiotics, posing a major public health challenge. Virulence factors, such as hemolysin A encoded by the HlyA gene, contribute to pathogenicity by lysing host cells and facilitating tissue invasion, highlighting the importance of targeting these factors alongside bacterial growth. Medicinal plants have long been explored as alternative therapies due to their antimicrobial and anti-inflammatory properties. Marrubium anisodon, belonging to the Lamiaceae family and traditionally used in Iranian medicine, contains bioactive compounds with potential antibacterial effects. This study aimed to investigate the antibacterial activity of aqueous and ethanolic extracts of M. anisodon against MDR E. coli isolates and assess their impact on HlyA gene expression to explore novel strategies for combating resistant infections.

Methods: Fifty clinical E. coli isolates from hospitalized patients in Shiraz, Iran, were tested for antibiotic resistance using Kirby–Bauer disk diffusion. Ampicillin showed the highest resistance, cefepime the lowest. Aqueous and ethanolic extracts of Marrubium anisodon were prepared via maceration. Antibacterial activity was measured by Minimum Inhibitory Concentration (MIC) using broth microdilution. RNA was extracted from treated bacteria, cDNA synthesized, and HlyA expression quantified with Real-Time PCR. Experiments were performed in triplicate to ensure reproducibility, allowing assessment of both growth inhibition and impact on virulence factor expression.

Results: Antibiotic susceptibility testing revealed that all fifty E. coli isolates were multidrug-resistant. Resistance was highest against ampicillin (100%) and lowest against cefepime (54%). Both aqueous and ethanolic extracts of Marrubium anisodon displayed antibacterial activity, with the ethanolic extract demonstrating greater potency. Specifically, the ethanolic extract inhibited bacterial growth in 54% of isolates, whereas the aqueous extract showed moderate activity at 36.84%. Real-Time PCR analysis indicated that the ethanolic extract significantly reduced HlyA gene expression by 36.84%, whereas the aqueous extract also suppressed expression, albeit to a lesser extent. These results suggest that M. anisodon extracts not only inhibit bacterial proliferation but also interfere with the expression of a critical virulence factor, reducing the pathogenic potential of MDR E. coli. Overall, the study highlights the dual antibacterial and anti-virulence effects of M. anisodon, suggesting its potential as a complementary strategy against resistant E. coli infections.

Conclusion: Aqueous and alcoholic extracts of Marrubium anisodon exhibit antibacterial activity against MDR E. coli, with the ethanolic extract showing stronger effects and significant reduction in HlyA expression. Given high resistance to antibiotics like ampicillin, M. anisodon could serve as a complementary approach for controlling infections. By targeting both growth and virulence factors, these extracts may reduce infection severity. Future research should isolate active compounds and evaluate their efficacy in vivo to develop potential plant-based therapeutics against resistant E. coli.

Keywords: Escherichia coli, multidrug resistance, antibiotic resistance, HlyA gene, Alpha-hemolysin, Marrubium anisodon, medicinal plants

Poster 39

Effect of taurine supplementation on preventing ventilator-associated pneumonia in pediatrics under mechanical ventilation, a randomized controlled double-blind clinical trial

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Introduction: One of the most prevalent healthcare-associated infections in the pediatric intensive care unit is ventilator-associated pneumonia (VAP). VAP not only results in prolonged hospital and intensive care unit (ICU) stays but also imposes higher costs on patients and the healthcare system. Therefore, it is essential to implement preventive measures. The lung-protective properties of taurine are recognized, and this research focuses on assessing the impact of taurine supplementation in preventing VAP.

Methods: This double-blind, randomized clinical trial was conducted at Namazi Hospital's PICUs. The study included pediatrics on mechanical ventilation for over 48 h. Patients were randomly divided into two groups: the taurine and placebo groups. Alongside the standard care, participants from both groups were administered taurine or placebo capsules (30 mg/kg. day) in divided doses from the day of PICU admission through PICU discharge. The incidence of VAP through clinical and laboratory evidence was considered the primary outcome.

Results: Seventy-seven patients were included in the study, with 38 in the taurine group and 39 in the placebo group. VAP incidence was 7.9% in the taurine group and 64.1% in the placebo group. Taurine significantly reduced the duration of mechanical ventilation, ICU and hospital stay, and inotrope duration. The occurrence of septic shock was lower in the taurine group at 5.3%. Stepwise logistic regression showed that placebo receipt was the only risk factor for VAP, with placebo recipients being 20.8 times more likely to develop VAP. (P 0.0001, OR 20.8, 95% CI 6.11–97.93) Taurine treatment also significantly reduced inflammatory markers such as CRP, pro-calcitonin, and interleukin-6 compared to placebo.

Conclusion: Our results showed that taurine supplementation can reduce the incidence of VAP and the duration of mechanical ventilation, ICU, and hospital stay in critically ill pediatric patients.

Keywords: pediatric intensive care unit, septic shock, taurine, ventilator-associated pneumonia, pneumonia

Poster 40

Electrostatic Evolution of Avian and Human H3N2 Hemagglutinin: A Comparative Analysis of pI and Charge

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Introduction: Influenza viruses use the hemagglutinin (HA) protein to enter their host cells, and fusion is activated by the low pH of the endosome. The charge of the hemagglutinin surface protein is effective in the initial absorption of the virus to the target cell, and the pI is effective in the stability of this protein at different pH values, which can be considered as a factor in adaptation to different hosts. Changes in the stability of HA at different pH values significantly affect viral replication, tissue tropism, pathogenicity, and transmissibility between hosts. A better understanding of these differences, especially between human and avian viruses, can provide a valuable perspective for assessing the pandemic potential of emerging strains.

Methods: H3N2 influenza viruses were initially identified using HI and NI methods. Viral RNA was extracted, and the hemagglutinin gene segment was amplified by PCR and then sequenced by the Sanger method. For this study, 80 HA protein sequences from the first pandemic in 1968 to the present were obtained from NCBI. In selecting sequences, we tried to have a balanced distribution in terms of time and geographical origin. This study included 40 human and 40 avian (duck) HA sequences, including one sequence that was sequenced in this study at the Razi Vaccine and Serum Research Institute. The hemagglutinin protein charge at different pH levels and the isoelectric point (pI) were analyzed using the Prot Pi and ProtParam tools.

Results: Based on our in silico analysis, the hemagglutinin of duck host viruses, from the 1968 Hong Kong strain to our isolate, consistently had a negative charge of about -7 ± 1 and a pI of about 6.5 ± 0.5. In contrast, viruses of human origin show a different evolutionary path towards acquiring a positive charge. For instance, the virus isolated from a human in Fukushima in 2023 has a positive charge of +5.5 and a pI of approximately 8. This distinct divergence in electrostatic properties highlights the evolution of human H3N2 viruses , which affects host adaptation and viral pathogenicity.

Conclusion: Our findings are consistent with other studies, such as Huang et al. (2017) and Khaliq et al. (2016), which attribute changes in charge and pI to selective pressure on the hemagglutinin protein and an increase in glycosylation sites. This adaptation is driven by evolutionary mechanisms. However, studies conducted in China suggest that viral flow is not exclusively from aquatic birds to other hosts, and under suitable conditions it can lead to new strains, such as the adaptation of H3N8 in dogs. This complex ecology and dynamics highlight the need for continuous monitoring of influenza viruses in aquatic birds as the main reservoir of the virus. This surveillance is critical for the early detection of strains that have the potential for interspecies transmission and pose an increased risk of cross-species infection, particularly between animals and humans.

Keywords: Influenzavirus Hemagglutinin

Poster 41

Elucidating the contribution of neglected cytokines to the host immune response in active brucellosis

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Introduction: Given the importance of cytokines in the pathogenesis and outcomes of brucellosis, several inflammatory and anti-inflammatory cytokines have been studied previously. However, the roles of some new cytokines should be clarified in the field of brucellosis. Therefore, this study aimed to investigate the association of cytokines IL-19, IL-20, and IL-24, as well as the receptors A and B of IL-20 (IL-20RA and IL-20RB), with the active phase of human brucellosis.

Methods: The study included 80 brucellosis patients and 236 controls. Patients were diagnosed based on a history of animal contact, consumption of unpasteurized dairy products, clinical symptoms, and positive serological tests (Wright, 2ME, Coombs' test, and Brucella capture). RNAs were extracted from blood samples, synthesized cDNA, and the cytokine levels were evaluated using SYBR Green-based relative real-time PCR.

Results: The patient and control groups were 57.5% and 55.9% male, with mean ages of 37.7 ± 24 and 19.5 ± 19.5 years, respectively. A majority of patients (53.8%) resided in rural areas, and 70% had a history of contact with domestic animals. Patients exhibited a significantly lower white blood cell (WBC) count compared to controls. Gene expression analysis (measured by ΔCT) showed significantly lower values for IL-19, IL-20, IL-24, IL-20RA, and IL-20RB in the patient group (P 0.05), which is consistent with their up-regulation. Confirming this, IL-20 and IL-20RA were significantly up-regulated in brucellosis patients, showing 2.5-fold and 1.5-fold increases, respectively, over control levels.

Conclusion: The elevated levels of IL-20 and its obligatory receptor, IL-20RA, observed in brucellosis may underscore their functional significance in the disease's immunopathogenesis. This is consistent with IL-20's established role in regulating immune-epithelial crosstalk, a process critical for maintaining tissue barriers and mounting responses to injury.

Keywords: Brucellosis, active phase, Immunopathogenesis, Neglected cytokines,

Poster 42

Enterococci from Equine Fecal Samples Harboring Integrons: A Hidden Threat in the Spread of Antimicrobial Resistance

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Introduction: Introduction: Integrons are key genetic elements that facilitate the acquisition and dissemination of antimicrobial resistance genes (AMRs) among pathogenic and commensal bacteria, posing significant global health risks. From a One Health perspective, they represent a critical reservoir of resistance determinants with implications for human, animal, and environmental health. While integrons are best known in Gram-negative, their presence in Gram-positive organisms such as Enterococcus spp. Has been less extensively studied. Enterococci are naturally occurring gut microbes in both humans and animals, yet they can also act as opportunistic pathogens responsible for infections that are notoriously difficult to treat. Their ability to harbor and disseminate antibiotic resistance genes makes them a significant reservoir in the spread of antimicrobial resistance. Animals in close contact with humans, such as horses, can serve as reservoirs for resistant enterococci, acting as vectors that facilitate the transmission of antimicrobial resistance across species and environments.

Methods: Methods: This study investigated the prevalence of class 1 and class 2 integrons among Enterococcus isolates obtained from the fecal samples of 100 healthy horses using polymerase chain reaction (PCR) analysis. The 100 Enterococcus isolates examined in this study comprised 33 E. faecium, 11 E. faecalis, and 56 isolates belonging to other Enterococcus species.

Results: Results: Class 1 integrons were detected in 83% of the isolates, while 13% harbored class 2 integrons. There were no statistically significant differences among the different species concerning the prevalence of integrons.

Conclusion: Conclusion: Integrons facilitate the acquisition and integration of resistance-associated gene cassettes, and the high frequency of integrons observed in this study suggests that enterococci from the equine fecal microbiota may serve as a significant reservoir of antibiotic resistance genes in the environment.

Keywords: Keywords: Enterococcus, Integrons, One Health, horse

Poster 43

Epidemiologic status of the Candida infections and disorders in cases with chronic obstructive pulmonary disease

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Introduction: Candida is one of the normal flora of human body, and is also the most common conditional fungal pathogen. Invasive Candida infections (ICI) occupies the first positionamong invasive fungal diseases (IFD).Moreover, Candida is commonly colonized in lower respiratory airways (LTR), associated to chronic obstructive pulmonary disease (COPD), smoking, tuberculosis, malnutrition, malignant tumors, diabetes mellitus, HIV infection, and long-term use of antibiotics. As a main target, the present study focus on COPD patients as the predisposed cases of Candida infection or colonization.

Methods: Our subjects included all Candida clinical isolates obtained from cases referred to the Center of Medical Mycology, UMS University, Urmia, Iran, for fungal infection diagnosis. The clinical specimens including Bronchoalveolar lavage (BAL), sputum, tracheal washing and biopsies were examined and microscopic investigation were performed for the detection of Candida invasive elements. As our main aim, morphologic and molecular (PCR-RFLR) were used for the identification of isolate candida yeasts at level of species.

Results: Totally, 510 cases of pulmonary disorders including, COPD, CF, COVID-19 were studied. Among all,22.6% were women and 75% men, 15(24.2%) were in 60 s and 62(12.1%)were candida involved cases. Total of this, 22 (35.1%) isolated from patients with a history of COPD,10(16.1%) CKD, 6 (9.7%) Cystic fibrosis and 3(4.8%) diabetes mellitus.Also, 53(85.5%) showed a pulmonary symptom and sign. Other cases had clinical manifests such as hemoptysis, bronchiectasis, chest pain, pleural pain, lung mass. Among the isolated Candida species, C. albicans 15(24.2%), C. dubliniensis and C. tropicalis 9(14.2%) itch, C. glabrata 5(8.1), C. guiliermondi 2(3.2%) and other non albicans Candida species 3(4.8%) and no identified Candida species included 19 cases (30.6).

Conclusion: As our findings of the present study, most of the pulmonary risk factor of the candida involvement was COPD followed by Cystic fibrosis. Also, the most of candida yeasts isolated from studied cases included non albicansCandida species comparing Candida albicans.

Keywords: Candida, COPD, Pulmonary disease, Epidemiology

Poster 44

Epidemiological Trends of Hydatid Cyst Disease (Hydatidosis) and Brucellosis in Fars Province, Iran (2020–2024), and Implications for Public Health Interventions

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Introduction: The epidemiological landscape of two major zoonotic diseases, hydatid cyst disease (hydatidosis) and brucellosis, in Fars Province, Iran, from 2020 to 2024 reveals significant public health challenges. Both diseases remain endemic in the region, but their effective control is severely hampered by unreliable data stemming from under-reporting and systemic weaknesses in existing surveillance mechanisms. This analysis of recent trends aims to provide a clearer picture of the true disease burden and assess the efficacy of current interventions.

Methods: The methodological approach combined a longitudinal review of historical passive surveillance data with more recent active surveillance data gathered from provincial treatment centers and health institutions between 2020 and 2024. The compilation of official case numbers for both hydatidosis and brucellosis formed the core quantitative dataset. To contextualize these figures, the study incorporated qualitative field evidence, such as direct veterinary observations and reports on livestock smuggling activities, and analyzed the impact of health system policy changes, including the introduction of a free drug program.

Results: The results present two divergent yet concerning narratives. For hydatid cyst disease, reported cases exhibited a dramatic and unambiguous upward trajectory. The incidence surged from 67 confirmed cases in 2020 to 486 cases in 2024, marking a increase of over sevenfold within the five-year period. This sharp rise indicates a rapidly expanding public health problem. Conversely, the official surveillance data for brucellosis indicated a declining trend, with case numbers falling from approximately 504 in 2020 to 355 in 2024. However, a deeper investigation suggests this decline is misleading. Multiple supplementary indicators, including consistent veterinary field reports of the disease in animal reservoirs, changes in policy affecting reporting incentives, and preliminary data from peripheral health centers showing high infection rates in 2024, all strongly point to a same conclusion. The official decrease is likely an artifact of reduced reporting sensitivity and significant under-ascertainment of cases, masking a true incidence

Conclusion: the findings highlight critical deficiencies in the current zoonotic disease control framework in Fars Province. The proven escalation of hydatidosis and the probable under-reported stability of brucellosis underscore an urgent need for action. Addressing this requires a multi-faceted strategy: strengthening integrated human and animal surveillance systems, dedicating resources to targeted operational research, and increasing overall funding for control programs. Implementing annual trend analyses supported by visual data dashboards will be vital for guiding policy and intervention strategies. Ultimately, a holistic One Health approach, which strategically integrates the human, animal, and environmental health sectors, is fundamental to achieving effective and sustainable disease management and control.

Keywords: Echinococcosis; Brucellosis; Epidemiological Trends; Zoonotic Diseases; One Health;

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Evaluation of Novel Nitroimidazole Derivative as Potent Antibacterial and Anti-Biofilm Agents against Multidrug-Resistant Staphylococcus aureus, Escherichia coli, and Klebsiella pneumoniae: An In Vitro Study

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Introduction: The rise of antibiotic-resistant bacteria is a critical global health concern, limiting treatment options and increasing morbidity and mortality. Methicillin-resistant Staphylococcus aureus (MRSA) and carbapenem-resistant Escherichia coli and Klebsiella pneumoniae (CRE) represent significant challenges due to their resistance to commonly used antibiotics. Biofilm formation by these pathogens further complicates treatment by enhancing survival and resistance. Nitroimidazole compounds have shown promise as antibacterial agents; however, their potential against resistant strains and biofilms requires further exploration. This study investigates the antibacterial and anti-biofilm effects of new synthesized nitroimidazole derivative against MRSA, CRE strains of E. coli and K. pneumoniae through in vitro assays.

Methods: Novel nitroimidazole compound were chemically synthesized and characterized (Fig1). In vitro antibacterial activity was evaluated by determining minimum inhibitory concentrations (MICs) against clinical isolates of MRSA, carbapenem-resistant E. coli, and K. pneumoniae. Anti-biofilm efficacy was assessed by measuring biofilm biomass reduction using crystal violet staining in treated cultures versus controls. Cytotoxicity assays were performed to assess compound safety on mammalian cell lines.

Results: The synthesized nitroimidazole derivative (8g) demonstrated potent antibacterial activity, with MIC values significantly lower than those of standard antibiotics against MRSA and CRE strains. Biofilm assays revealed that treatment with these compounds significantly reduced biofilm formation in all tested strains, indicating disruption of biofilm development or maintenance. Cytotoxicity assessments showed minimal toxicity at effective antibacterial concentrations, supporting their potential safety. ((Fig 2).

Conclusion: This study highlights the promising antibacterial and anti-biofilm properties of novel synthesized nitroimidazole compound (8g) against multidrug-resistant pathogens MRSA, carbapenem-resistant E. coli, and K. pneumoniae. Their efficacy in reducing both bacterial growth and biofilm formation, combined with low cytotoxicity, suggests potential for development as therapeutic agents. The complementary in silico results offer insights into molecular mechanisms, guiding optimization of these compounds. Further investigations involving in vivo studies and clinical trials are warranted to validate their therapeutic applicability and safety. These findings contribute to the ongoing efforts to combat antimicrobial resistance by introducing novel compounds capable of overcoming bacterial defenses.

Keywords: Nitroimidazole, Antibiotic resistance, Biofilm inhibition, MRSA, Carbapenem-resistant

Poster 46

Evaluation of serum vitamin D levels in infants under six months of age with sepsis: A cross-sectional study

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Introduction: Infantile sepsis is a clinical syndrome in infants characterized by systemic signs of infection and isolation of a microbe from the blood. The aim of this study was to measure serum vitamin D levels in infants with sepsis.

Methods: This cross-sectional study was conducted in 1402 on infants under 6 months of age with sepsis in Afzali-Pour Hospital in Kerman and Pasteur Hospital in Bam. From all infants, two milliliters of venous blood were collected under complete aseptic conditions within the first 72 hours after symptoms. Serum vitamin D levels were measured in the laboratory shortly after birth. Serum proteins were precipitated using ethanol and then a methanol: isopropanol mixture, and then 25-hydroxycalciferol was extracted using the organic phase hexane. The hexane was evaporated under nitrogen gas, and the resulting precipitate was dissolved in methanol, and after filtration, 20 µL of the filtered solution was finally injected onto a 3 µm, 4×150 excel tracer Teknochroma column and C 40 chromatography was performed.

Results: In this study, 50 infants with sepsis were studied. Most of them were girls (52%) and their mean age was 2.38±1.72 months. The mean serum vitamin D levels by clinical and chromatographic methods were 14.66±36.0 and 14.90±35.71, respectively. The prevalence of vitamin D deficiency, insufficient and sufficient levels in infants was 34%, 52% and 14%, respectively. The mean serum vitamin D level was significantly lower in intubated and deceased patients (P=0.006). Increased neutrophil and ESR levels and decreased vitamin D levels increased the duration of ICU stay (P0.01). Increased mean vitamin D levels were correlated with significant reductions in WBC, ICU stay, ESR and CRP (P0.05).

Conclusion: Vitamin D deficiency is common in infants with sepsis and is associated with higher mortality, increased inflammatory markers, and longer ICU length of stay. Increased vitamin D levels were associated with improved inflammatory markers and reduced length of stay, highlighting the importance of monitoring and correcting it in septic patients

Keywords: Vitamin D, Sepsis, Pediatrics

Poster 47

Evaluation of SYBR Green real-time PCR for rapid and specific detection of Trichophyton indotineae

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Introduction: Background: Since 2017, dermatophytosis especially by the newly introduced species Trichophyton indotineae has gained new interest worldwide due to the rise in terbinafine resistance and difficulty in the treatment of recalcitrant infections. Distinguishing T. indotineae from other Trichophyton species based on morphological features is impossible and DNA sequencing is necessary for accurate identification. Though early identification of the species is not solely sufficient for the treatment of infected cases, however, it is an important step for clinicians to take the next appropriate modalities such as antifungal susceptibility testing especially when the patients have extensive skin lesions recalcitrant to therapy by terbinafine. Here, we developed a rapid diagnostic scheme using SYBR Green real-time PCR for the specific detection/identification of T. indotineae.

Methods: Methods: DNA was extracted from 397 dermatophyte isolates and two SYBR Green real-time PCR assays targeting the C120-287 and E054-5 intergenic loci were developed. Using a collection of 132 T. indotineae and 128 non -T. indotineae strains, all had already been identified by ITS-PCR-sequencing, and 137 unknown dermatophyte isolates, the assays were evaluated.

Results: Results: In both real-time PCR assays, 130 out of 132 T. indotineae strains were positive while all non-T. indotineae species were negative. Among 137 unknown tested isolates, 72 were identified as T. indotineae based on two real-time PCR assays, while 65 showed no peak and were considered non-T. indotineae. Based on PCR-sequencing as the reference standard, the SYBR Green real-time PCR assays demonstrated a sensitivity of 98.48% and a specificity of 100%.

Conclusion: Conclusion: The developed diagnostic assays using SYBR Green real-time PCR provided a rapid and accurate method for the distinction of cultured T. indotineae isolates and can be considered for the detection of T. indotineae directly from clinical samples.

Keywords: Keywords: Trichophyton indotineae; Identification; SYBR Green real-time PCR, rapid molecular diagnosis.

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Evaluation of the effect of nitrogen-doped graphene quantum dots on the efficacy of erythrosine-mediated antibacterial photodynamic inactivation

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Introduction: Today, the development of novel therapeutic strategies is urgently needed to combat the antibiotic-resistance crisis. Nanoparticle-based antibacterial photodynamic inactivation (APDI) is emerging as a promising alternative to antibiotics. In this study, we aimed to evaluate the effect of nitrogen-doped graphene quantum dots (NGQDs) on the antibacterial efficacy of erythrosine-mediated PDI.

Methods: NGQDs were synthesized, characterized and then a stable NGQD/erythrosine nanocomposite was prepared. After that, the planktonic cell growth of Pseudomonas aeruginosa and Staphylococcus aureus was subjected to PDI using erythrosine or NGQD/erythrosine and green laser light (530 nm).

Results: The synthesized NGQDs exhibited favorable optical and physicochemical properties. PDI mediated by NGQD/erythrosine showed significant antibacterial activity (lethal PDI) against both tested bacterial strains compared to erythrosine -mediated PDI.

Conclusion: In conclusion, PDI using NGQD/erythrosine offers a promising nanotechnology-based strategy to combat MDR bacteria.

Keywords: Antibiotic resistance, Graphene quantum dots, Erythrosine, Antibacterial photodynamic inactivation

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Evaluation of the Effects of β-Glucan Extracted from Saccharomyces cerevisiae on Tumor Cells Growth and Apoptosis Induction in the CT26 Murine Colorectal Cancer Cell Line.

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Introduction: Colorectal cancer is a malignancy that develops in the tissues of the large intestine and represents one of the most common cancers worldwide. Conventional chemotherapeutic agents are often associated with severe side effects; therefore, researchers are increasingly seeking bioactive compounds capable of enhancing immune function and exerting antitumor effects.

Methods: In this study, the effects of β-glucan extracted from Saccharomyces cerevisiae on cell proliferation and apoptosis of the murine colon cancer cell line CT26 were evaluated. CT26 cells were cultured in DMEM-F12 medium supplemented with 10% fetal bovine serum, 1% L-glutamine, and 1% penicillin-streptomycin, and maintained at 37 °C with 5% CO_2. After 24 hours, the cells were treated with different concentrations of β-glucan for 48 hours. Cell viability was assessed using the MTT assay, and apoptosis was confirmed through Annexin V/PI staining followed by flow cytometry.

Results: The findings demonstrated that β-glucan at a concentration of 700 µg/ml significantly inhibited the growth of CT26 cells and induced apoptosis.

Conclusion: These results suggest that β-glucan may serve as a promising bioactive compound for suppressing colorectal cancer cell growth and could be considered in future therapeutic research.

Keywords: β-glucan, colorectal cancer, apoptosis

Poster 50

Evaluation of the efficacy and side effects of COVID-19 vaccination in patients with hypo-or hyperthyroidis

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Introduction: In the last three years, the pandemic has had major effects on the health of people around the world. This has especially affected individuals who already have other medical conditions, like people with thyroid disorders. Vaccination is so important for this group, and the long-term impacts of inoculation and its security on these patients' well-being continue to be uncovered. Therefore, the risks of vaccination and immune response need to be assessed. Objectives: This study aimed to determine the immune response, short-term safety, and the effects of multiple variables on these factors after COVID-19 vaccination among people with thyroid abnormalities.

Methods: In total, 56 patients (mean age: 37.7±12.6 years old) participated in the study; they had thyroid abnormalities, had received at least one dose of the COVID-19 vaccine, and were usually referred to outpatient clinics for periodical tests

Results: We evaluated the short-term effect and humoral SARS-COV-2 anti-RBD IgG response using a questionnaire and immunoassay, respectively. It should be noted that no significant adverse events were recorded, but running noise (19.6%), low-grade fever (22.2%), loss of smell (17.9%), and Myalgia/body pain (17.9%) were the most common adverse events

Conclusion: The type of vaccine did not show any notable variation in the occurrence of side effects and humoral response. Our study showed that patients with controlled hypothyroidism and hyperthyroidism did not have a higher rate of COVID-19 prevalence, nor did they have a worse prognosis when infected with the virus.

Keywords: Thyroid disorders, COVID-19, vaccine, disease-modifying therapy, safety, immunity

Poster 51

Evaluation of the Immunogenicity of a Pasteurella multocida Vaccine Formulated with PLGA Nanoadjuvant in Laboratory Animals

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Introduction: Pasteurella multocida, a gram-negative bacterium, is a primary cause of respiratory diseases in livestock, particularly cattle and sheep, leading to significant economic losses. The rise of antibiotic resistance, driven by genes such as tet and bla, has reduced the effectiveness of antibiotics like tetracycline, penicillin, and sulfonamides, highlighting the need for effective vaccines. Currently, no Pasteurellosis vaccine is available for veterinary use in Iran. Traditional adjuvants such as alum present certain drawbacks, including local inflammatory reactions and potential risks associated with Autoimmune/Inflammatory Syndrome Induced by Adjuvants (ASIA). Polylactic-co-glycolic acid (PLGA) nano-adjuvants offer a promising alternative due to their biocompatibility, controlled antigen release, and enhanced immune stimulation. The aim of this study is to develop a vaccine based on Pasteurella multocida serotype A and to evaluate its immunogenic potential in BALB/c mice. This research could represent a significant step toward the development of more effective vaccines for the prevention of pasteurellosis.

Methods: :PLGA nanoparticles were synthesized via emulsion-solvent evaporation using PLGA (75:25) and dichloromethane, emulsified in 1% polyvinyl alcohol (PVA) solution, and washed. Their characteristics were confirmed using dynamic light scattering (DLS), scanning electron microscopy (SEM), zeta potential, and Fourier-transform infrared spectroscopy (FTIR). Pasteurella multocida serotype A (PMSHI-9, Gene Bank accession no. JF694004.1, Razi Vaccine and Serum Research Institute, Shiraz) was cultured in BHI broth, inactivated with 0.4% formalin, and encapsulated in PLGA nanoparticles to prepare the vaccine. A commercial alum adjuvant was used as the control. Two groups of BALB/c mice (6–8 weeks old, n=10 per group) were immunized subcutaneously with PLGA- or alum-based vaccines, receiving a booster dose on day 14. Blood samples were collected weekly for 10 weeks and analyzed for IgG titers by ELISA.

Results: PLGA nanoparticles (~120 nm) displayed spherical morphology, uniform size distribution, and a stable negative surface charge, confirming their suitability as vaccine adjuvants. Mice immunized with the PLGA-adjuvanted vaccine exhibited significantly higher IgG titers compared to the alum group, indicating a robust and sustained immune response (p 0.05). In contrast to the alum group, which exhibited mild local inflammation, mice in the PLGA group showed no adverse reactions.

Conclusion: Over the past few years, significant progress has been made in developing modern and effective vaccines against Pasteurella multocida; however, further improvement is constrained by the lack of suitable adjuvants. Different aluminum-based adjuvant formulations have been tested in vaccine development; however, most of them have failed because of insufficient efficacy and concerns about toxicity. An ideal adjuvant should induce a sustained, high-quality immune response while remaining non-toxic, biodegradable, and non-immunogenic. The PLGA-based vaccine markedly enhances the immunogenicity of Pasteurella multocida serotype A, demonstrating superior efficacy and safety compared to alum. Nanoparticles elicit stronger immune responses because they can be efficiently internalized by cells through simple mechanisms such as diffusion or active processes like phagocytosis and endocytosis. They have the ability to penetrate into the cytoplasm and even the nucleus of cells.

Keywords: Pasteurella multocida, nano-adjuvant, PLGA, vaccine, alum

Poster 52

Evaluation of the Immunogenicity of an Experimental Vaccine Derived from a Native Salmonella Dublin Strain in BALB/c Mice

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Introduction: Salmonella enterica serovar Dublin is an invasive, zoonotic serotype historically associated with cattle but increasingly recognized as a cause of severe systemic infections in humans. It can lead to septicemia, endocarditis, osteomyelitis, and meningitis, especially among children, the elderly, and immunocompromised individuals. Infection is commonly transmitted through contaminated animal products, particularly unpasteurized milk and dairy products, posing a significant public health concern. In Iran, several reports have documented S. Dublin infections in both livestock and humans. The emergence of antibiotic-resistant strains has further complicated treatment and highlighted the urgent need for preventive measures. This study aimed to develop and evaluate an experimental vaccine prepared from a native S. Dublin strain isolated from Iranian dairy farms and to determine the protective immune responses elicited by different vaccination routes in a BALB/c mouse model.

Methods: In this study, forty male BALB/c mice were randomly divided into four equal groups. An experimental vaccine prepared from a native Salmonella Dublin strain was administered to three experimental groups using different immunization routes: Group 1 received an intramuscular injection with alum adjuvant, Group 2 received an oral vaccine formulated with chitosan adjuvant, and Group 3 received a combination of both injection and oral administration. The fourth group received sterile culture medium as a negative control. Immunization was performed in two doses of 5×10^7 CFU, administered 21 days apart. Blood samples were collected 14 days after each dose to evaluate immune responses and serological indicators. One month after the final dose, all animals were challenged with a virulent S. Dublin strain and monitored daily for clinical signs and mortality. Ten days post-challenge, spleens from surviving mice were collected for macroscopic evaluation.

Results: In all vaccinated groups, mortality was significantly lower than in the control group, with the highest survival observed in Group 3 (combined intramuscular and oral vaccination), showing 90% survival. Serological analyses demonstrated that both cellular immunity, assessed by interferon-gamma production and skin testing, and humoral immunity were significantly higher in vaccinated groups compared to controls, with the strongest responses recorded in Group 3 (P0.05). Moreover, spleens from vaccinated mice remained small, smooth, and free of macroscopic lesions following challenge with Salmonella Dublin. In contrast, spleens from the control group were enlarged, irregular, and displayed white nodular lesions indicative of splenomegaly and active infection.

Conclusion: Evaluation of these results indicates that the vaccine effectively limited bacterial dissemination and tissue damage and may serve as a promising candidate for the prevention of zoonotic infections caused by S. Dublin.

Keywords: Salmonella Dublin, Experimental vaccine, Immune response, Zoonosis, BALB/c mice

Poster 53

Evaluation of the implementation of the antibiotic stewardship program for the use of antibiotics in children with community acquired pneumonia in the children's emergency department of Namazi Hospital during a five-month period

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Introduction: Antibiotic stewardship programs (ASPs) have been proposed for decades to reduce antibiotic resistance and optimize antibiotic use. Numerous studies have shown the impact of these programs on reducing microbial resistance, reducing antibiotic use, and reducing healthcare costs. Given the increasing importance of implementing ASP programs in pediatric wards and the lack of studies in Iran, the present study aimed to investigate the effect of implementing ASP methods on antibiotic use in children with community-acquired pneumonia in the pediatric emergency department of Namazi Hospital, Shiraz.

Methods: This study was an observational-analytical cohort study. The Infectious Diseases Department of the Pediatrics Department of Shiraz University of Medical Sciences implemented a surveillance program for antibiotic prescribing for children with pneumonia in the emergency ward of Namazi Hospital from the beginning of December2014.Patient data were collected from December2014 to April2015 and compared with data from the period before the surveillance program (December2013 to April2014). The antibiotic prescribing management program included the development of antibiotic prescribing guidelines and training for residents, along with providing non-mandatory counseling (PAF) to physicians. The statistical population included all children with pneumonia admitted to the emergency department during the aforementioned period. Patient data including age, sex, severity of pneumonia and imaging before and after the intervention were collected. Outcomes including adherence to guidelines, duration of treatment (DOT), length of treatment (LOT), need for intensive care unit admission, length of hospital stay, and incidence of death were also examined

Results: During the study period, 471 children with pneumonia were hospitalized (233before and 238after the intervention). Of these, 262 children (55.6%) had moderate to severe pneumonia and 209children (44.4%) had mild pneumonia. The ratio of girls to boys was 0.8. There was no significant difference in demographic characteristics (age and sex) between the pre- and post-intervention periods. Radiological findings were abnormal in 77% of patients; the most common patterns were lobar. Streptococcus pneumoniae was the predominant pathogen in more than two-thirds of cases. Adherence to antibiotic prescription guidelines increased significantly by 22.36% after the implementation of (ASP). The rate of ICU admissions decreased significantly after the intervention and the mean length of stay decreased from11 days to 9 days, which was also significant. Mortality in children with pneumonia decreased significantly by 8.5% . The(DOT) in children with pneumonia decreased from 22 to 18 days and (LOT)decreased from 11 to 9 days which were significant

Conclusion: In this study, the implementation of ASP in children with community-acquired pneumonia resulted in significant improvements. In these patients, adherence to guidelines increased significantly and the rate of intensive care unit admission and mean length of stay decreased. Also, mortality, DOT and LOT were significantly reduced. Streptococcus pneumoniae was identified as the predominant pathogen.

Keywords: Antibiotic stewardship program (ASP), community acquired pneumonia, pediatrics

Poster 54

Exoenzyme Activity Profiles in Dominant Candida albicans Genotypes

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Introduction: Candida albicans exhibits significant genotypic diversity and genotypes A and C are the most predominant clinical isolates. The aim of this study was to evaluate the virulence traits of these genotypes, focusing on exoenzyme production.

Methods: A total of 15 genotype A and 15 genotype C clinical C. albicans isolates were evaluated for proteinase, phospholipase, and esterase activities using bovine serum albumin, egg yolk agar and Tween agar plate, respectively.

Results: The study found that Genotype C had higher proteinase and phospholipase activity but no esterase production, while 40% of Genotype A isolates showed strong esterase activity.

Conclusion: This study highlights how genotypic variation in C. albicans influences virulence, with Genotype C exhibiting a distinct profile (high proteinase/phospholipase, no esterase) that may enhance pathogenicity, while Genotype A shows adaptability through variable enzyme production. These differences underscore the need for genotype-specific diagnostics and targeted therapies to improve candidiasis treatment.

Keywords: Candida albicans, genotypes, exoenzymes

Poster 55

Extended Spectrum β-lactamase Producing Escherichia coli in Cats in Tehran, Iran

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Introduction: The World Health (WHO) has reported extended spectrum β-lactamase producing Enterobacteriaceae (ESBL-E) as the most important antimicrobial resistant (AMR) microorganisms, among the "Highest Priority" pathogens because of the high incidence in both human and, animal. The increasing prevalence of β-lactamase (ESBL) producing Escherichia coli (ESBL- E. coli) represents a concern in both veterinary and human healthcare. The companion animals reported as potential carriers of ESBL- E. coli for human due to close contact with their owners, and pose a potential serious risk to public health. These isolate potentially can spread antibiotic resistance genes from animals to humans via mobile genetic elements. Compared with human medicine, information on the role of cats is limited. The aim of this study was to determine the prevalence of (ESBL- E. coli) in cats in Tehran, Iran.

Methods: Rectal swabs collected from 100 cats admitted to the veterinary clinics in Tehran were collected during 2024-205. Samples were cultured on MacConkey agar and EMB. Bacterial identification was conducted using standard bacteriological and molecular techniques. ESBL production was screened phenotypically using the double-disk synergy method according to CLSI guidelines (CLSI, 2024). Finally, the genomic DNA was extracted by boiling, and PCR amplification was performed to detect β-lactamase encoding genes, including blaTEM, blaCTX-M, blaOXA, blaSHV, and blaFOX.

Results: Out of the 100 E. coli isolates, 54 (54%) isolates were found to be ESBL producers. The PCR results showed that blaTEM (45.83%) was the predominant ESBL gene identified, followed by blaCTX-M (35.41%), blaOXA (19.79%), and blaSHV (8.34%), whereas blaFOX was not detected.

Conclusion: Considerable prevalence of ESBL- E. coli among cats, along with the high occurrence of β-lactamase encoding genes in these isolates, suggest that cats may be act as reservoirs for ESBL- E. coli and β-lactamase encoding genes which can be dissemination to human through interactions. Antimicrobial stewardship and, continuous surveillance of antibiotic resistance remains critical for antibiotic resistance in zoonotic pathogens, and is necessary in health of pets and humans especially those associated with pet animals.

Keywords: Antimicrobial Resistance, Extended-Spectrum β-Lactamase, E. coli, Antimicrobial stewardship, Cats

Poster 56

Final diagnosis and outcome of children admitted with extreme elevation of ESR (more than 100mm/hr) in TABRIZ children's hospital

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Introduction: Introduction: ESR is one of the most widely used laboratory tests in clinical medicine. The rate of sedimentation is determined by the aggregation of red blood cells, in which erythrocyte and plasma factors are involved. Plasma factors include high molecular weight proteins such as fibrinogen and globulins and immune complexes. The aim of this study was to determine the outcome and final diagnosis of inpatient children with ESR more than 100 mm/hr in Tabriz Pediatric Medical Center.

Methods: Method and materials: In this study, patients who had ESR equal to 100 or more than 100 at the beginning of the visit were studied. The final diagnosis, outcome (discharge, recovery, unknown), hospitalization time and other laboratory tests such as leukocytes counts, anemia and acute phase reactants including CRP, Ferritin, LDH, and platelet counts were evaluated.

Results: Results: In the survey of the frequency of final diagnosis among the patients, the highest frequency was related to pneumonia with the frequency of 20 patients (16.67%), followed by urinary tract infection in 19 patients (15.83%), unknown in 15 patients (12.5%), and 11 patients (9.17%) had the highest frequency of diagnosis of acute vasculitis Kawasaki. Also, one patient (0.83%) with encephalitis died during the study. The mean age of the patients was 4.05 ± 3.40 years. The minimum age of patients was3 months and the maximum age was 17 years. In 120 patients, 57 patients (47.5%) were males and 63 (52.5%) were females. Mean of ESR was 115.53 ± 12.11 mm / hr in the studied patients. The lowest ESR recorded among patients was 100 mm / hr and the highest ESR was equal to 145 mm / hr.

Conclusion: Conclusion: According to the results, there are many differential diagnosis, that the most important diagnosis is infectious disease. This suggested that ESR rate above 100 in children despite adults, do not include any serious illness and children often recover.

Keywords: Key Word: ESR - pediatrics-inpatients- Diagnosis

Poster 57

Genetic characterization of Methicillin and Vancomycin resistant Staphylococcus pseudintermedius isolated from Human wound sample

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Introduction: Background: Staphylococcus pseudintermedius, a coagulase-positive staphylococcus primarily found in dogs, is increasingly recognized as an emerging zoonotic pathogen. This study characterizes a methicillin- and vancomycin-resistant S. pseudintermedius isolate from a human wound infection, highlighting its antimicrobial resistance profile and genetic features.

Methods: Methods: The isolate was obtained from a pediatric patient with recurrent nasal lesions in North Khorasan, Iran. Phenotypic identification and antimicrobial susceptibility testing were performed using standard microbiological methods. Molecular characterization included PCR detection of resistance (mecA, vanA, cfr) and virulence (pvl, hla, sec, tsst) genes, SCCmec typing, and multilocus sequence typing (MLST).

Results: Results: The isolate exhibited resistance to oxacillin (mecA-positive), vancomycin (vanA-positive), mupirocin, and multiple other antibiotics, while remaining susceptible to tetracycline, gentamicin, minocycline, and linezolid. Virulence genes pvl and hla were detected, and MLST identified the strain as ST2361 with an SCCmec type IV element, a genotype previously reported in Turkey. The patient's rural livestock exposure suggested a zoonotic origin.

Conclusion: Conclusion: This report underscores the zoonotic potential of multidrug-resistant S. pseudintermedius and the notable presence of vanA-mediated vancomycin resistance in this species. The genetic similarity to strains from neighboring regions suggests cross-border transmission. Enhanced surveillance under a One Health framework is critical to monitor and control the spread of resistant staphylococci at the human-animal interface.

Keywords: Staphylococcus Pseudintermedius, wound, vancomycin, methicillin, Human Infection, Zoonosis.

Poster 58

Genomic Characterization of Mycobacterium bovis BCG Clinical Isolates from Children with Immunodeficiency: Insights into Lipid Metabolism and Immune Modulation Variations

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Introduction: Mycobacterium bovis BCG is a live attenuated vaccine strain derived from M. bovis and is widely used to prevent tuberculosis in children. While generally safe, rare adverse events can occur, particularly in immunocompromised individuals. Whole-genome sequencing (WGS) offers a comprehensive approach to understanding the genetic variations between clinical isolates and the reference BCG strain, potentially elucidating factors contributing to these adverse events.

Methods: Between 2010 and 2025, 50 clinical isolates of M. bovis BCG were collected from pediatric patients diagnosed with BCG-induced disease at the National Research Institute for Tuberculosis and Lung Disease (NRITLD), Tehran, Iran. Among these, 47 (94%) children had underlying immunodeficiencies, including defects in the interferon-gamma receptor (IFN-γR) and tumor necrosis factor receptor (TNFR). The isolates underwent WGS using Illumina technology in collaboration with the Japan Supernational TB Laboratory. Sequencing reads were assembled and aligned against the reference genome of M. bovis BCG Pasteur 1173P2 (GenBank accession: AM408590.1). Bioinformatics analyses were performed to identify single-nucleotide polymorphisms (SNPs), insertions/deletions (indels), and other genomic variations.

Results: The average genome length of the isolates was 4,370,706 ± 5,234 base pairs (bp), with a GC content of 65.6% ± 0.1%, consistent with the reference genome (4,374,522 bp, GC content 65.6%). Comparative analysis revealed 1,200 SNPs across all isolates, of which 180 (15%) were nonsynonymous. Notably, 5% of the isolates exhibited unique deletions in regions associated with lipid metabolism and immune modulation. Specifically, mutations in ppsA and ppsC led to reduced synthesis of phthiocerol dimycocerosates (PDIM), occurring at a significantly higher frequency in clinical isolates compared to the reference strain (3% vs. 1%, p = 0.018). Mutations in fadA2 and fadE5, affecting fatty acid degradation, were observed in 3% of isolates versus 1% in the reference strain (p = 0.022). Deletion of SapM was detected in 4% of isolates but was absent in the reference strain (p = 0.042), while upregulation of cyp125 and cyp142, involved in cholesterol catabolism,

Conclusion: This study provides a detailed genomic characterization of M. bovis BCG isolates from pediatric patients with BCG-induced disease. Genetic variations in lipid metabolism and immune modulation genes may contribute to adverse events, particularly in immunocompromised children. These findings underscore the importance of genomic surveillance to monitor BCG vaccine safety and to better understand host–pathogen interactions in vulnerable populations.

Keywords: Mycobacterium bovis BCG, whole-genome sequencing, pediatric tuberculosis, genetic variations, vaccine safety, immunodeficiency.

Poster 59

Genomic Insights into Antimicrobial Resistance and Virulence of Mycobacterium simiae Clinical Isolates via Whole-Genome Sequencing

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Introduction: Mycobacterium simiae is an emerging nontuberculous mycobacterium (NTM) increasingly associated with pulmonary and disseminated infections, particularly among immunocompromised patients. Its intrinsic multidrug resistance and genomic variability complicate both diagnosis and treatment. Whole-genome sequencing (WGS) provides a comprehensive approach to identifying mutations responsible for virulence and antimicrobial resistance.

Methods: Twenty clinical isolates of M. simiae were identified by PCR-restriction enzyme pattern analysis (PRA) using HaeII and BstEII enzymes. Drug susceptibility testing was performed against second-line agents, including rifampicin (RIF), isoniazid (INH), amikacin (AMK), kanamycin (KAN), and ciprofloxacin (CIP). WGS was conducted using Illumina technology, with reads assembled and aligned against the M. simiae reference genome (GenBank accession: GQ153280). Single-nucleotide polymorphisms (SNPs), insertions/deletions (indels), and gene variants were analyzed using standard bioinformatics pipelines (BWA) and compared quantitatively to the reference genome.

Results: All isolates belonged to M. simiae type I and exhibited resistance to RIF and INH, whereas 80% remained susceptible to AMK, KAN, and CIP. The average genome length of the isolates was 6,684,413 ± 12,345 bp, representing a ~1.3% increase compared with the reference genome (6,600,000 bp). The GC content was 66.0% ± 0.2%, slightly higher than the reference value of 65.8%. WGS revealed 4,512 SNPs and 230 indels per isolate, of which 1,142 SNPs (25.3%) were nonsynonymous, affecting key genes including rpoB, katG, embB, sigH, and mprAB. Comparative genomic analysis identified 120 unique mutations in loci related to lipid metabolism, ESX secretion systems, and stress-response pathways, distinguishing these clinical isolates from the reference strain.

Conclusion: This study provides a quantitative genomic characterization of clinical M. simiae isolates, highlighting mutations that likely contribute to drug resistance and virulence. Comparison with the reference genome (GQ153280) demonstrates adaptive divergence, emphasizing the importance of WGS surveillance for understanding emerging NTM infections and guiding treatment strategies.

Keywords: Mycobacterium simiae, whole-genome sequencing, mutations, SNPs, drug resistance, virulence, NTM.

Poster 60

Genotypic Characteristics and Antibiotic Resistance Profiles of Fecal Colonizing Escherichia coli Producing Extended-Spectrum Beta-Lactamases and Carbapenemases in Newly Diagnosed Pediatric Oncology Patients at Amir Educational and Therapeutic Oncology Ho

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Introduction: The gut microbiota protects against pathogenic colonization, but antibiotic use—especially in hospitalized HM patients—can disrupt this defense and increase vulnerability to multidrug-resistant Gram-negative infections. The aim of this study was to examines prevalence of extended-Spectrum Beta-Lactamase (ESBL) and Carbapenemase-Encoding Genes, and the Distribution of Phylogenetic Groups and antibiotic susceptibility of CP-CRE and ESBL-producing Escherichia coli isolated from fecal colonization in newly diagnosed pediatric cancer patients.

Methods: This prospective cohort study was conducted at a referral teaching hospital in Shiraz, Iran. Fecal samples were collected at three-time points: within 48-72 hours of hospitalization, at the end of the first chemotherapy session, and during the next admissions. The prevalence of carbapenemase-encoding genes (blaOXA-48, blaKPC, blaNDM, blaVIM) and extended-spectrum β-lactamase (ESBL) genes (blaSHV, blaTEM, blaCTX-M) was subsequently investigated in E.coli isolates.

Results: The present study demonstrated that 96% of the examined isolates were ESBL producers, while 12.6% exhibited carbapenemase production. The distribution of resistance genes was as follows: blaCTX-M1 (79.75%), blaTEM (50.63%), blaSHV (10.12%), blaCTX-M8 (5.06%), blaCTX-M2 (3.8%), blaCTX-M9 (3.8%), blaCTX-M25 (2.53%), blaOXA-48 (10.12%), blaVIM (2.53%), and both blaKPC and blaIMP were not detected (0%).

Conclusion: The predominant organism isolated from fecal samples was ESBL. Rapid detection of ESBL and carbapenemase genes will inform treatment strategies improving the outcome for post infections in Oncology Patients.

Keywords: Carbapenemase-producing, extended-spectrum beta-lactamase-producing E.coli, Colonization

Poster 61

Giant tonsillolith: An unusual case caused by Clostridium bifermentans and review of literature

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Introduction: Tonsilloliths are a polymicrobial biofilm in the tonsillar crypts. Furthermore, C. bifermentans is infrequently reported as a cause of infection in humans, and there are no reports of the cryptic species infecting the tonsils.

Methods: We report on a case of C. bifermentans infection in an immunocompetent adult. Azithromycin 400 mg/day was given orally, but it did not improve clinical symptoms. This patient underwent bilateral tonsillectomy, followed by co-administration of dexamethasone 2 mg IV and oral Cephalexin 500 mg once a week. An incision was taken over the tonsils to drain pus collections for microbiological analysis, besides the pathologic section. We identified this isolate as Clostridium bifermenta and detected its susceptibility testing using the MALDI-TOF-MS

Results: Clostridium bifermentan exhibited resistance to meropenem, azithromycin, penicillin, and clindamycin, but was sensitive to amoxicillin/clavulanate and cefoxitin. Pathological findings documented follicular hyperplasia

Conclusion: Maintaining proper oral hygiene is crucial in preventing tonsilloliths

Keywords: Clostridium bifermentans, tonsilloliths, tonsillectomy, MALDI-TOF MS, antibacterial

Poster 62

Global and Regional Antimicrobial Resistance Patterns and Virulence Gene Profiles of Staphylococcus aureus in Bovine Mastitis

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Introduction: Staphylococcus aureus is a Gram-positive bacterium and a major contagious pathogen responsible for bovine mastitis worldwide. It frequently causes chronic intramammary infections, resulting in substantial economic losses in the dairy industry. The pathogen often shows poor response to antimicrobial therapy and readily develops multidrug resistance (MDR), including methicillin-resistant S. aureus (MRSA), making treatment and control challenging. Widespread use of β-lactams, aminoglycosides, lincosamides, and macrolides has accelerated antimicrobial resistance. Beyond resistance, virulence factors contribute critically to the pathogen's ability to establish and persist in mammary tissue. Understanding both resistance patterns and virulence genes is crucial for guiding effective therapy and designing region-specific control strategies. This study aimed to determine antimicrobial resistance patterns and identify key virulence genes in S. aureus isolates from diverse regions.

Methods: 1. Systematic Review & Meta-Analysis: Following PRISMA guidelines, international databases were searched for studies published between 1969 and 2021. After screening, 155 studies were included, representing Europe (88), Asia (56), Latin America (39), Africa (32), North America (26), and Oceania (8). Data on antimicrobial resistance, mastitis type (clinical vs. subclinical), and methodological variations (disk diffusion vs. MIC testing) were extracted. 2. Regional Field Study (Iran): 400 raw milk samples from cows with clinical or subclinical mastitis in Fashafouyeh were collected. Presumptive S. aureus isolates were identified via culture on Mannitol Salt Agar and confirmed by Gram staining, catalase, coagulase, and mannitol fermentation. Susceptibility to six commonly used antibiotics was assessed via disk diffusion, and seasonal variations were analyzed using descriptive statistics. 3. National Molecular Epidemiology Study (China): 2,962 milk samples from 43 farms across 16 provinces were analyzed. Isolates underwent comprehensive molecular characterization, including resistance gene detection (blaZ, mecA), virulence

Results: Global resistance was highest against penicillin G (45–92%), followed by ampicillin, amoxicillin, clindamycin, kanamycin, and gentamicin, while ceftiofur (~2%), cephalothin (~1.5%), and trimethoprim-sulfamethoxazole showed the lowest resistance; nitrofurantoin remained fully effective. Nearly all isolates were MDR, with resistance increasing over time, especially post-2009, particularly for penicillin G, amoxicillin, clindamycin, and tetracycline. African, Asian, and Latin American isolates exhibited the highest resistance levels. Iranian isolates showed significantly higher resistance to penicillin G, ampicillin, and erythromycin (p 0.05), with no significant difference between clinical and subclinical mastitis isolates. Genotypic analysis revealed blaZ (~93%) as the predominant resistance gene, followed by mecA (~24%), confirming MRSA circulation. Common virulence genes included clfA, fnbpA, clfB, and sdrC. Among coagulase-negative staphylococci (CNS), S. chromogenes was dominant (~50%) with an MDR rate of 16.3%.

Conclusion: High β-lactam resistance, particularly to penicillin G, and the widespread occurrence of multidrug resistance in bovine mastitis pathogens pose a serious global threat. The predominance of blaZ and mecA genes highlights the urgent need to revise current treatment protocols, as conventional therapies are becoming increasingly ineffective. These findings underscore the importance of integrating molecular surveillance into routine mastitis management and adopting prudent, evidence-based antibiotic use. Without such measures, the dairy industry faces escalating treatment failures, increased economic losses, and potential public health risks due to zoonotic transmission of resistant strains.

Keywords: Staphylococcus aureus Bovine mastitis Antimicrobial resistance Multidrug resistance (MDR) MRSA

Poster 63

Harnessing Artificial Intelligence for Smarter Infection Prevention and Control

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Introduction: Artificial intelligence (AI) has emerged as a transformative tool in healthcare, offering powerful capabilities for predicting, monitoring, and managing infectious diseases. Integrating AI into infection prevention and control systems can enhance accuracy, speed, and resource efficiency. This poster highlights recent advancements in AI-assisted surveillance, predictive modeling, and automated disinfection technologies that strengthen infection control and immunization strategies.

Methods: A comprehensive literature review was conducted using databases including PubMed, Scopus, and Web of Science, focusing on studies published between 2018 and 2025. Search terms included artificial intelligence, machine learning, infection control, immunization, and disease surveillance. Selected studies were analyzed to identify key AI applications in predictive modeling, outbreak detection, and vaccination optimization. Emphasis was placed on practical implementations, such as real-time data analytics, deep learning models for infection pattern recognition, and robotic systems for automated disinfection in healthcare environments.

Results: AI-assisted systems demonstrated significant potential in enhancing infection prevention and immunization outcomes. Predictive algorithms accurately identified early signs of outbreaks, enabling timely public health responses. Machine learning models improved the design and distribution of vaccines by analyzing global epidemiological trends. In clinical settings, AI-powered sensors and robotics optimized sterilization processes, reducing healthcare-associated infection rates. Additionally, natural language processing and big data analytics supported improved infection tracking and antimicrobial stewardship, ultimately contributing to safer healthcare systems and more efficient immunization coverage worldwide.

Conclusion: Harnessing artificial intelligence provides a proactive framework for modern infection prevention and control. By integrating predictive analytics, automation, and intelligent surveillance, healthcare systems can anticipate disease outbreaks, optimize vaccination strategies, and reduce pathogen transmission. Continued investment in AI-driven infrastructure will strengthen global preparedness, improve patient safety, and advance the future of precision public health.

Keywords: Artificial intelligence, Infection control, Immunization, Machine learning, Public health

Poster 64

Hepatic basidiobulomycosis, A mini review and case report

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Introduction: Gastrointestinal basidiobolomycosis (GIB) is an emerging, often misdiagnosed fungal infection caused by Basidiobolus ranarum, primarily affecting immunocompetent hosts. Its non-specific clinical presentation, frequently featuring an abdominal mass, pain, fever, and peripheral eosinophilia, often mimics malignancy or other inflammatory conditions. Definitive diagnosis relies on histopathological examination of tissue biopsies. This brief underscores the critical importance of early diagnostic suspicion in endemic areas or suggestive cases. We report a fatal case in a 5-year-old boy who initially presented with abdominal pain. Despite biopsy confirmation and the initiation of antifungal therapy, his disease progressed relentlessly to hepatic failure and death. This tragic outcome highlights the potentially aggressive and fatal nature of GIB, demonstrating that severe progression can occur even with appropriate treatment, thereby emphasizing the need for heightened clinical awareness and early intervention

Methods: A 5-year-old boy presented with abdominal pain, nausea, and vomiting. Imaging identified a heterogeneous jejunal mass (25×50×49 mm) causing intestinal obstruction. Surgical resection was performed, and histopathological examination with PAS staining confirmed fungal infection. Postoperatively, the patient developed fever, generalized edema, and jaundice, necessitating referral to a tertiary care center. Laboratory evaluation revealed elevated hepatic transaminases, hypoalbuminemia, coagulopathy with prolonged PT and PTT, and markedly increased inflammatory markers. Abdominal ultrasound showed heterogeneous liver parenchyma with multiple hepatic lesions. Subsequent abdominopelvic MRI revealed patchy T2 hyperintensities in the liver and a peripherally enhancing pelvic mass, consistent with disseminated fungal infection, specifically basidiobolomycosis. Despite initiation of intravenous liposomal amphotericin B and intensive supportive care, the patient's condition progressively deteriorated, culminating in multi-organ failure and death. This case highlights the diagnostic challenges and aggressive course of disseminated basidiobolomycosis in pediatric patients, underscoring the importance of early recognition and intervention.

Results: This case highlights the importance of considering basidiobolomycosis in the differential diagnosis of patients presenting with chronic abdominal pain in tropical regions. Our findings demonstrate that Basidiobolus ranarum can exhibit hepatic invasion, leading to fulminant liver failure - a previously underrecognized manifestation of this fungal infection. Furthermore, this case expands the known clinical spectrum of basidiobolomycosis outcomes, revealing its potential for aggressive visceral involvement beyond the typical gastrointestinal presentation. The patient's imaging findings, laboratory markers of hepatic dysfunction, and histopathological confirmation provide compelling evidence for this unusual disease progression

Conclusion: This case highlights the importance of considering basidiobolomycosis in the differential diagnosis of patients presenting with chronic abdominal pain in tropical regions. Our findings demonstrate that Basidiobolus ranarum can exhibit hepatic invasion, leading to fulminant liver failure - a previously underrecognized manifestation of this fungal infection. Furthermore, this case expands the known clinical spectrum of basidiobolomycosis outcomes, revealing its potential for aggressive visceral involvement beyond the typical gastrointestinal presentation. The patient's imaging findings, laboratory markers of hepatic dysfunction, and histopathological confirmation provide compelling evidence for this unusual disease progression

Keywords: basidiobolomycosis, liver failure, Entomophthorales; liver mass, death

Poster 65

Hidden Pathways of Antibiotic Resistance Transmission: The Role of Companion Animals in Disseminating Quinolone- and Aminoglycoside-Resistant Escherichia coli

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Introduction: Escherichia coli (E. coli) is a common bacterium found in the intestinal tract of both humans and animals and serves as an important reservoir for antibiotic resistance. Because of the close interactions between humans and their pets, including cats, the possibility of transmitting resistant strains between them is a matter of concern. The aim of the present study was to investigate the antibiotic resistance of E. coli strains isolated from the feces of cats and their owners against quinolones and streptomycin, as well as the related genes.

Methods: A total of 70 E. coli isolates were collected from fecal samples of cats, their owners, and individuals without pets (30 cat–owner pairs plus 10 controls). Identification was carried out using conventional microbiological techniques. The isolates were tested for susceptibility to quinolones and aminoglycosides through the disk diffusion method. Genomic DNA was extracted by boiling and PCR was performed to detect antibiotic resistance genes including qnrB (quinolones) and strA (aminoglycosides).

Results: Among the tested antibiotics, E. coli isolates from cats (30%) and cat owners (43.3%) showed the highest resistance to nalidixic acid. Resistance to ciprofloxacin were observed in 26.7% and 30% of E. coli isolates from cats and cat owners, respectively. The lowest prevalence of resistance was observed against streptomycin in both cats' isolates (13.3%) and cat owners (16.7%). All isolates in the control group were susceptible to ciprofloxacin, and the prevalence of resistance to nalidixic acid and streptomycin in them was 20%. The qnrB gene was only detected in cat owners (10%). In contrast, the strA gene was detected in all groups, although at different rates: cats (3.3%), cat owners (6.7%), and the control group (10%). Overall, statistical analysis showed no significant difference in the frequency of antibiotic resistance or the prevalence of resistance genes between isolates from different groups (P 0.05).

Conclusion: The findings highlight the role of pets as reservoirs of antibiotic-resistant bacteria. Data such as the lower frequency of resistant E. coli isolates (for most antibiotics tested) in the control group compared to cat owners and cats, resistance to similar antibiotics, and similarities found in the presence of resistance genes in some E. coli isolates from cats and their owners, all suggest that close contact between pets and their owners can act as a factor in the transmission of antibiotic resistance and have potential public health implications.

Keywords: Escherichia coli, antibiotic resistance gene, quinolones, aminoglycosides, cats, cat owner

Poster 66

High Prevalence of Tetracycline Resistance and tet Genes Among Diarrheagenic Escherichia coli Isolates from Children in Southern Iran

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Introduction: Diarrhea remains a major public health concern worldwide, particularly affecting children under five years in low- and middle-income countries. Among the bacterial causes, diarrheagenic Escherichia coli (E. coli) is frequently implicated in both sporadic and outbreak-related pediatric diarrhea. The rising prevalence of antimicrobial resistance among these strains, especially to tetracyclines, poses a significant clinical challenge. Tetracyclines are widely used due to their broad-spectrum activity and low cost, but overuse has contributed to the dissemination of resistance genes. Understanding the molecular mechanisms underlying tetracycline resistance, including the distribution of tetA, tetB, and tetC genes, is crucial for guiding treatment strategies and informing public health interventions. This study aimed to evaluate the prevalence of tetracycline resistance and the associated resistance genes in diarrheagenic E. coli isolated from children with diarrhea.

Methods: In this descriptive cross-sectional study, 550 diarrheal samples were collected from children with acute diarrhea in Shiraz, Iran. Bacterial isolation and identification were performed using standard microbiological methods. Antimicrobial susceptibility testing was carried out by the disk diffusion method according to CLSI guidelines. Detection of tetracycline resistance genes was performed using a multiplex PCR assay.

Results: Out of 550 diarrheal samples, 112 (20.36%) diarrheagenic E. coli strains were isolated. The highest resistance rate was observed against tetracycline (57.1%), while the lowest resistance was detected against amikacin and nitrofurantoin (3.3%). Eighty-three percent of isolates exhibited a multidrug-resistant (MDR) pattern. Among 64 tetracycline-resistant isolates, 56 (87.5%) carried at least one tetracycline resistance gene. The prevalence of tetA, tetB, and tetC genes among resistant isolates was 58.9%, 44.6%, and 14.3%, respectively. Furthermore, 27.8% of isolates harbored two tet genes simultaneously.

Conclusion: The findings of this study reveal a high prevalence of tetracycline resistance and multidrug resistance among diarrheagenic E. coli isolates from pediatric patients. The tetA gene emerged as the most common resistance determinant, often co-occurring with other tet genes, highlighting the complexity of resistance mechanisms. These results underscore the urgent need for rational antibiotic stewardship and continuous molecular surveillance to limit the spread of resistant strains. Rapid detection methods such as multiplex PCR can provide valuable insights into resistance patterns and support the development of targeted interventions to improve the management of childhood diarrheal infections.

Keywords: Diarrheagenic E. coli, Tetracycline resistance, tetA, tetB, tetC, Multiplex PCR, Multidrug resistance.

Poster 67

Human Adenovirus F41 Polyepitope Vaccine Exploration by In Silico Methods

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Introduction: Human adenovirus F41 (HAdV-F41) is a responsible for acute gastroenteritis across all age groups, with a notably high prevalence among infants and young children. In spite of its substantial clinical significance, no licensed vaccine is currently available to target this serotype. In this study, we designed a high-quality polyepitope vaccine candidate against HAdV-F41 by an in silico approach.

Methods: Viral surface protein sequences were selected and analyzed for their interactions with cytotoxic T lymphocyte (CTL), helper T lymphocyte (HTL), and B cell receptors. The highest-ranking peptides were chosen for vaccine construction based on their predicted antigenicity, non-allergenicity, and non-toxicity. Subsequently, these epitopes were utilized for three dimensional (3D) structural modeling and docking analyses with toll-like receptor (TLR)-4. Ultimately, physicochemical properties and the potential to induce gamma-interferon generation were evaluated.

Results: A total of 172 epitopes were initially predicted, of which 53 fulfilled the selection criteria of high antigenicity, non-allergenicity, and non-toxicity. These were subjected to further physicochemical characterization and IFN-γ induction analysis. The final vaccine construct consisted of the top 4 epitopes, joined by appropriate adjuvants and linkers including human β-defensin, AAY, GPGPG and, KK. The 3D structure of the final assemble was constructed and exhibited strong binding affinity upon docking with TLR-4.

Conclusion: The designed polyepitope vaccine candidate showed favorable immunogenic potential and strong interaction with TLR-4, indicating its potential as a protected and efficient vaccine against HAdV-F41.

Keywords: Human adenovirus F41, Polyepitope vaccine, In silico methods

Poster 68

Identification of Candida Species in Infections Among Cancer Patients Undergoing Chemotherapy

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Introduction: Candida albicans and other non albicans Candida species are encountered skin and mucosal layers as opportunistic normal flora. In the situations of low immunity status including immune-suppressions, corticosteroid and long term antibiotic therapies, prolonged hospitalization and chemotherapies against malignancies, Candida species may cause gastro-intestinal and pulmonary infections or colonization. Various Candida species have made problems in accurate treatment due to different level of responses to anti fungal drugs. Hence, the present study aimed to identify the Candida species isolated from cases of respiratory tract disorders with a history of Cancer and chemotherapy.

Methods: We studied on cases of hematologic and non hematologic cancers and pulmonary involvement with dizziness, cough, chest pain and other pulmonary signs. Bronco alveolar lavage and other respiratory tract specimens were collected and transported to Medical Mycology Center, UMS University, Urmia, Iran. A direct microscopic investigation for the yeasts invasive elements (pseudohypha and mycelia) was done. Culture on SGA, CMA and CHA differential media conducted for the detection and identification of Candida species followed by the molecular method, PCR-RFLP using primers of rDNA gene and Msp I restriction enzyme.

Results: From 147 cases of cancer suspected to respiratory tract yeast infection, in 31 (21%) cases Candida invasion or colonization were detected. Among all, 74.2 % were men and 25.8% women and the most cases of Candida involvement, 11(35.5%) were in the age range of 60-70. The most common risk factors in the studies cases were hematologic cancers (48.4%) followed by gastro-intestinal tract (22.6%), lung (19.4%), neural (9.7%). Main clinical specimen which examined was BAL (80.6%). The majority of clinical specimens were collected from hematology-oncology ward (50%), pulmonology and ICUs (22.6%) each. Microscopic investigation the processed specimens showed invasive yeast elements in 17(54.8) cases and overgrowth or colonized yeast cells in 9(29%) cases. Our findings of morphologic and molecular identification included 7(22.6%) C.albicans, 3(9, 7%) C.tropicalis, 3(9.7%) C.glabrata, 2(6.5%) C. krusei, 2(6.5%) C. parapsilosis, 1(3.2%), C. dubliniensis and other unidentified Candida species,12(38.7%).

Conclusion: In patients suffered by hematologic and non hematologic cancers who are under chemotherapies, a variety of Candida species are active especially involving respiratory tract infections.

Keywords: Hematologic cancer, pulmonary infection, Candida species, identification

Poster 69

Comparing clinical presentation, viremia, and immunological factors at various severity presentations in hospitalized children affected by COVID-19: A cross-sectional study

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Introduction: Although SARS-CoV-2 infection usually leads to a mild Covid-19 in children, sometimes it causes serious complications, especially in those with underlying diseases. Several factors have been identified in determining disease severity in adults, and limited studies have been conducted in children. The prognostic implications of SARS-CoV-2 RNaemia as an important factor in determining disease severity in children are not well understood. In this study, we aimed to prospectively assess the relationship between disease severity and immunological factors and viremia in 47 Covid-19 hospitalized children.

Methods: In this research, 76.5% of children experienced mild and moderate Covid-19, while 23.5% experienced severe and critical forms of the disease. The presence of underlying diseases in different groups of pediatric patients differed significantly from each other. On the other hand, clinical symptoms such as vomiting and chest pain as well as laboratory parameters including ESR were significantly different in different groups of patients.

Results: Viremia was seen in only two children, and this had no significant relationship with the severity of Covid-19. In conclusion, our data confirmed that Covid-19 severity differed in SARS-CoV-2 infected children. Some clinical presentation and lab data parameters were different in various presentation of patients.

Conclusion: Viremia was not associated with severity in our study.

Keywords: Covid-19, pediatrics, SARS-CoV-2, paraclinical data, viremia, severity

Poster 70

Identification of the SARS-CoV-2 Genome in Various Systemic Samples from the Laboratory of Confirmed COVID-19 Patients in Iran

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Introduction: COVID-19 is a highly contagious respiratory illness caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). While nasopharyngeal swab testing remains the primary method for identifying SARS-CoV-2 carriers, the virus's genetic material can be detected in various bodily samples, suggesting potential transmission through non-respiratory routes This study aimed to investigate the presence and quantity of SARS-CoV-2 RNA in stool, endotracheal tube (ETT) samples, cerebrospinal fluid (CSF), bronchoalveolar lavage (BAL), and sputum. The research sought to correlate these findings with clinical characteristics and the severity of illness.

Methods: We retrospectively collected 1,567 samples, including 550 BAL samples, 464 ETT samples, 45 fecal samples, 21 CSF samples, and 487 sputum samples from patients admitted to Namazi Hospital between April 1, 2020, and the end of September 2022. Clinical characteristics, patient demographics, radiographic, and laboratory results were among the medical data gathered and assessed. We used reverse transcription-quantitative polymerase chain reaction (RT-qPCR) to detect and measure SARS-CoV-2 RNA shedding in different samples of individuals infected with COVID-19

Results: Among the 550 BAL samples collected from patients, 20.7% tested positive for SARS-CoV-2. Additionally, the virus's genome was detected in 17.8% of 45 CSF samples, 11% of 464 ETT samples, 4.76% of 21 fecal samples, and 2.9% of 487 sputum samples. Notably, patients with SARS-CoV-2-positive BAL samples exhibited a significantly higher frequency of cough and dyspnea than those who tested negative

Conclusion: These findings revealed that SARS-CoV-2 has been detected in diverse specimens collected from the upper and lower respiratory systems (sputum, ETT, and BAL samples), the central nervous system (CSF), and the digestive tract (fecal samples) during the infection's progression. This widespread presence significantly impacts our understanding of the disease's pathogenesis and enhances diagnostic capabilities, proving a valuable asset in managing the infection.

Keywords: SARS-CoV-2 COVID-19 RT-qPCR CSF BAL Feces

Poster 71

Improving the Diagnosis of Bacterial Meningitis: In-House PCR Detection of Neisseria meningitidis and Escherichia coli"

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Introduction: Bacterial meningitis remains a life-threatening infection associated with high morbidity and mortality, particularly in infants and young children. Among the most frequent causative agents, Neisseria meningitidis and Escherichia coli represent two clinically important pathogens with distinct epidemiological patterns. N. meningitidis is a leading cause of community-acquired meningitis in children and young adults, whereas E. coli is an important pathogen in neonates and immunocompromised patients. Despite advances in vaccination and supportive therapy, early diagnosis of meningitis caused by these pathogens remains challenging. Conventional culture-based methods are time-consuming and may yield false negatives, especially in patients who have received prior antibiotic treatment. Therefore, molecular approaches such as polymerase chain reaction (PCR) are essential for rapid, sensitive, and specific detection. This study was designed to evaluate the applicability of in-house PCR methods in detecting N. meningitidis and E. coli in cerebrospinal fluid (CSF) samples, with the aim of providing a practical diagnostic tool

Methods: A total of 150 CSF samples collected from patients with suspected bacterial meningitis were analyzed. Samples were classified based on hospital diagnosis into negative, positive for inflammation, smear-positive, and culture-positive groups. Specific primers were designed for N. meningitidis and E. coli and optimized in single and multiplex PCR assays. Following amplification, sensitivity and specificity were assessed by comparing PCR results with standard diagnostic methods. The overall workflow was established to minimize false negatives and ensure reproducibility under routine laboratory conditions

Results: Among the 150 samples tested, PCR identified N. meningitidis in 3 cases (2%) and E. coli in 2 cases (1.3%). While the proportion of positive samples was relatively low compared to other pathogens typically implicated in bacterial meningitis, the findings highlight the clinical significance of these organisms in specific patient populations, particularly neonates and young children for E. coli, and adolescents and young adults for N. meningitidis. Importantly, in several cases PCR detected bacterial DNA in samples where conventional smear or culture was negative, underscoring the enhanced sensitivity of the molecular approach

Conclusion: This study demonstrates that in-house PCR protocols for N. meningitidis and E. coli are rapid, reliable, and cost-effective compared with conventional diagnostic methods. These assays not only shorten the turnaround time for detection but also improve diagnostic accuracy in patients with suspected meningitis, especially in resource-limited settings where advanced commercial kits may not be available. Adoption of such methods in clinical laboratories could significantly improve patient outcomes through earlier initiation of targeted antimicrobial therapy

Keywords: Neisseria meningitidis, Escherichia coli, bacterial meningitis, PCR, molecular diagnosis

Poster 72

In Silico Design of Anticancer Peptides from Pseudomonas Phage IR-QUMS-PaBa1-GHS-2021 for Targeting CD204 in Glioblastoma

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Introduction: CD204, a specific marker for tumor-associated macrophages (TAMs) in glioma, is linked to tumor aggressiveness. This study aimed to develop a novel anticancer peptide targeting CD204 for the treatment of glioblastoma (GBM).Bacteriophages are a vast, untapped resource of unique protein structures. This study leverages the protein of the novel Pseudomonas phage IR-QUMS-PaBa1-GHS-2021 for the in silico design of peptides intended to bind CD204, aiming to develop a novel targeted therapeutic strategy for GBM.

Methods: Initially, the FASTA sequence of the endolysin from Pseudomonas phage IR-QUMS-PaBa1-GHS-2021 (GenBank accession number: UZV40112.1; 2537 amino acids) was retrieved from the NCBI database. AntiCP server was used to design anticancer peptide. Bioinformatic tools, including the Expasy,ProtParam, ToxinPred2 server, AllerTOP v2.0 server and CellPPD sever, Protein-Sol web server and vaxijen server were used to analyze its physicochemical properties, toxicity,cell penetrating properties,allergenicity and solubility of peptide. Peptide sequences were selected based on high hydrophobicity scores and alpha-helical propensity. The 3D structure of the target receptor, CD204 (Accession No. P21757 (CD204)) and peptide, were modeling by SWISSmodel and PEPFold respectivly, and then prepared for docking. Molecular docking simulations between the shortlisted phage-derived peptides and CD204 were performed using cluspro. The interactions were analyzed using LigPlot+ and PDBsum to evaluate binding affinity, hydrogen bonding, and salt bridge interactions. The stability of the best protein-peptide complex was further assessed through imod server.

Results: The new analog peptide GKKGGFIRSMATGFLSGVVNGSGSRQIKIWFQNRRMKWKK (M2) was selected to interact with CD204. The cluster 0 exhibited the most favorable binding profile, with a cluspro score of -1010.6kcal/mol, significantly lower than the other cluster. The complex was stabilized by 5 hydrogen bonds and one salt bridge interactions with key residues in the CD204 binding site (number of interface trsidues CD204:17 and new analog peptide 18) ; number of hydrogen bonds 4 (Gln 167:Lys40 ; Asn 171:Lys40; Asp 174: Lys 2;Ser 177:Lys2) an done salt bridge (Asp 174:Lys 2). Molecular dynamics simulations confirmed the stability of the new analog peptide:CD204 complex,

Conclusion: This computational study successfully designed and validated a novel peptide (M2) derived from a Pseudomonas phage protein that demonstrates high-affinity and stable binding to the TAM receptor CD204. These findings suggest that M2 is a prime candidate for further development as a targeted therapeutic for glioblastoma, potentially enabling the specific delivery of cytotoxic agents to pro-tumoral macrophages or disrupting CD204-mediated signaling. Future work will focus on the in vitro and in vivo validation of M23's efficacy in GBM models.

Keywords: Glioblastoma, CD204, Tumor-Associated Macrophages, Anticancer Peptides, Molecular Docking, Phage Therapy.

Poster 73

In Silico Investigation of Mastoparan Peptide Effects on Key Proteins of Respiratory Syncytial Virus

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Introduction: Background: Respiratory syncytial virus (RSV) is a leading cause of respiratory infections, particularly in infants and immunocompromised individuals. The virus relies on several key proteins for entry, replication, and pathogenesis, making them potential targets for therapeutic intervention. Mastoparan, a bioactive peptide derived from wasp venom, has demonstrated diverse antiviral and immunomodulatory properties in previous studies. In silico approaches allow for the rapid evaluation of peptide-protein interactions, providing insights into potential inhibitory effects. This study aims to investigate the potential impact of Mastoparan on critical RSV proteins using computational modeling and molecular docking analyses

Methods: Methods: Mastoparan crystallographic structure as ligand was extracted from the PDB database (PDB ID: 6DUL). Also, crystallographic structure of F protein and M protein (PDB ID: 2VQP) as receptor (PDB ID: 5W23) were extracted from the PDB database. The active site of proteins M and G were predicted using the Punch web server. The active site of F protein was also predicted using the PDB sum generate web server. DockPrep was performed using the UCSF Chimera software. To evaluate the interaction between the Mastoparan peptide and the receptors, molecular docking was performed using HADDOCK2.4 and binding affinity was measured using the Hawkdock web server. The strongest interactions were selected based on HADDOCK score, RMSD, delta G and Z-score. The stability of the interactions was also evaluated using molecular dynamics simulations up to 100 nanoseconds (ns).

Results: Results: Mastoparan- F protein and Mastoparan- G protein complexes showed the highest affinity and stronger interactions compared to the M protein. The RMSD values for PEP1, PEP10, PEP11, PEP20, PEP26 and PEP176 were 0.4, 0.4, 0.3, 0.6, 0.4 and 0.3 nm respectively. HADDOCK scores indicating a strong interaction were for PEP1, PEP10, PEP11, PEP20, PEP26 and PEP176 (-104.8, -93.3, -86.8, -98.2, -99.1 and -127.4 kcal/mol respectively). Stability studies of peptide-protein complexes simulating physiological conditions in the body showed that selected complexes remained stable for up to 100 ns.

Conclusion: Conclusion: Mastoparan peptide may be a step towards the development of a peptide-based drug for the treatment of RSV. Its distinct characteristics could lead to the creation of a new peptide-based treatment for RSV, fulfilling an important need for effective antiviral drugs. Future research will involve testing this peptide in vitro on the RSV virus.

Keywords: Keywords: Mastoparan, Respiratory syncytial virus (RSV), Respiratory Infections, Antiviral

Poster 74

Inhibition of blaKPC Gene Expression in Pseudomonas aeruginosa by Postbiotics from Lactobacillus plantarum

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Introduction: Pseudomonas aeruginosa is a critical nosocomial pathogen with high resistance to β-lactam antibiotics. The blaKPC gene encodes carbapenemase, enabling hydrolysis of carbapenems and leading to multidrug resistance. Due to increasing antibiotic resistance, alternative therapeutic approaches such as postbiotics, non-viable metabolic products from probiotics, are under investigation. This study evaluates the impact of L. plantarum postbiotics on blaKPC gene expression in P. aeruginosa.

Methods: Carbapenem-resistant P. aeruginosa strains carrying blaKPC were isolated. L. plantarum ATCC 8014 was cultured in MRS medium, and cell-free supernatants (CFS) were obtained by centrifugation and filtration. Chemical composition of CFS was analyzed using gas chromatography–mass spectrometry (GC-MS). RNA was extracted from treated and untreated bacteria, cDNA was synthesized, and blaKPC expression was quantified by RT-qPCR with SYBR Green, normalized to algD gene. Statistical analysis was performed using Student's t-test, and relative expression was calculated by the Pfaffl method.

Results: GC-MS revealed butyric acid (14.31%), lactic acid (5.94%), and hydroxyacetone as the main postbiotic compounds. RT-qPCR analysis showed significant downregulation of blaKPC expression in treated bacteria compared with controls (P = 0.02), suggesting postbiotics inhibit carbapenem resistance gene expression.

Conclusion: L. plantarum postbiotics significantly reduce blaKPC expression in P. aeruginosa, likely through organic acids such as butyric and lactic acids. These findings highlight postbiotics as potential therapeutic agents to combat carbapenem-resistant pathogens, although further in vivo studies are required.

Keywords: L. plantarum, Postbiotics, P. aeruginosa, blaKPC.

Poster 75

Investigating the Effect of Aqueous and Alcoholic Extracts of Otostegia persica on the Growth and Enterotoxin (LT) Gene Expression in Escherichia coli

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Introduction: The increasing antibiotic resistance of Escherichia coli has become a serious challenge for human health, emphasizing the importance of developing alternative therapeutic strategies. These bacteria are major pathogens responsible for severe infections, partly due to their ability to produce enterotoxins such as LT. Medicinal plants, including Otostegia persica, are considered promising sources of antimicrobial agents. The present study aimed to evaluate the effects of aqueous and alcoholic extracts of Otostegia persica on bacterial growth and LT gene expression in clinical isolates of Escherichia coli.

Methods: In this descriptive cross-sectional study, totally 100 suspected samples of Escherichia coli were examined. In this regard, phenotypic identification was performed, followed by genotypic identification. The antibiotic resistance profiles were then assessed using the disk diffusion method. The prevalence of the LT quantified using PCR. The antibacterial effects of the aqueous and alcoholic extracts of the plant Otostegia persica were evaluated using the Minimum Inhibitory Concentration (MIC) method. Furthermore, the effect of these extracts on the expression of the enterotoxin genes LT was assessed through Real-time PCR.

Results: Among the 100 samples examined, 19 isolates of Escherichia coli were identified. Escherichia coli exhibited the highest antibiotic resistance to ampicillin (100%) and the lowest resistance to cefepime (54%). The investigation of the effects of Otostegia persica extracts indicated that these extracts have the capability to reduce the expression of LT gene.

Conclusion: Due to drug resistance, it is essential to discover new antimicrobial compounds, with minimal side effects. The findings suggest that the aqueous extract of this plant can be utilized as a therapeutic option to reduce the expression of evaluated gene.

Keywords: Escherichia coli, Enterotoxin LT, Otostegia persica.

Poster 76

Investigation of Genetic Mutations Involved in Drug Resistance to Bedaquiline in MDR-TB Isolates Using PCR-RFLP Method

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Introduction: Tuberculosis (TB) is a major infectious disease affecting global health. The rise of multidrug-resistant tuberculosis (MDR-TB) and extensively drug-resistant tuberculosis (XDR-TB) seriously hinders disease control efforts. Resistance occurs when Mycobacterium tuberculosis fails to respond to key drugs like isoniazid and rifampicin. Treatments for drug-resistant TB generally require longer durations, cost more, and are less effective than those for drug-sensitive TB. The lack of effective therapeutic options often results in treatment failure in MDR-TB and XDR-TB cases. Therefore, developing new anti-TB drugs with high efficacy and shorter treatment times is critical. Bedaquiline, a novel diarylquinoline antibiotic, has demonstrated strong and broad activity against Mycobacterium tuberculosis. This study, conducted for the first time in Iran, investigates genetic mutations related to bedaquiline resistance in MDR-TB isolates using the PCR-RFLP method. Understanding these mutations is essential to optimize treatment strategies and combat emerging drug resistance globally.

Methods: This study was conducted at the Mycobacteriology Research Center of Dr. Masih Daneshvari Hospital, which is recognized as the main center for the diagnosis and treatment of respiratory diseases in Iran. MDR-TB isolates were collected from patients with positive sputum tests who visited this center for care in the first half of 1403 (2024). Demographic information, including gender, age, and treatment history, was recorded. Genomic DNA was extracted from Mycobacterium tuberculosis colonies, and the PCR-RFLP method was used to identify genetic mutations in the atpE gene associated with resistance to bedaquiline. A 522nucleotide fragment of the atpE gene was amplified using specific primers and the PCR products were digested with the restriction enzyme Hph I. The resulting patterns were compared with control samples from Mycobacterium tuberculosis (H37RV).

Results: During the first half of 1403, a total of 14,426 patient samples from various individuals were analyzed, of which 1,605 samples tested positive for Mycobacterium tuberculosis. Among these culture-positive samples, 98 (6.1%) were definitively confirmed as multidrug-resistant tuberculosis (MDR-TB), posing a significant challenge for patient treatment. Additionally, resistance to the novel drug bedaquiline was detected in 6.6% of the total samples. Further molecular analysis revealed that, in two particular samples, DNA restriction patterns differed significantly from those of the control, indicating the presence of specific genetic mutations in some isolates. These findings underscore the importance of more detailed and comprehensive research to better understand the mechanisms of drug resistance in Mycobacterium tuberculosis, particularly regarding resistance to bedaquiline. The necessity of ongoing, thorough studies to effectively combat drug resistance through this approach is thus confirmed.

Conclusion: Bedaquiline resistance in MDR-TB isolates poses a major obstacle in managing drug-resistant tuberculosis. This study underscores the critical importance of ongoing surveillance of drug resistance and the implementation of effective strategies to control resistant infections. Bedaquiline has demonstrated promising efficacy in treating MDR-TB, showing potent antibacterial activity in vitro against Mycobacterium tuberculosis. Nevertheless, the emergence of resistance stresses the necessity for continued research to unravel resistance mechanisms and to develop novel therapeutic options. Persistent evaluation of bedaquiline's effectiveness and resistance profiles is essential for optimizing treatment protocols and enhancing patient outcomes.

Keywords: Bedaquiline, Mycobacterium tuberculosis, Tuberculosis, Multidrug-Resistant

Poster 77

Investigation of mutations in whole genome sequencing (WGS) of Bovis BCG isolated from clinical samples and comparison with standard Bovis BCG"

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Introduction: Whole genome sequencing (WGS) has become an invaluable method for studying genetic variations and mutations in bacterial strains, including vaccine strains such as Mycobacterium bovis BCG. Investigating mutations in clinical isolates of Bovis BCG through WGS can reveal how these strains evolve after administration and whether any genetic changes occur during infection or environmental persistence. This study aims to analyze mutations present in Bovis BCG isolated from clinical samples using WGS and compare them with the standard vaccine strain.

Methods: Clinical isolates of Mycobacterium bovis BCG were collected from children aged 1 to 13 years who were referred to the National Research Institute of Tuberculosis and Lung Diseases (NRITLD), Tehran, Iran, between 2018 and 2024. Bacterial cultures were grown using standard mycobacterial media, and DNA was extracted with a commercial genomic DNA extraction kit, ensuring high-quality DNA for sequencing. Whole genome sequencing (WGS) was performed using the Illumina platform, producing paired-end reads with sufficient depth and coverage. Raw sequence data were quality-checked, trimmed, and assembled with bioinformatics tools. The assembled genomes were aligned to the reference standard M. bovis BCG genome. Variants, including single nucleotide polymorphisms (SNPs), insertions, and deletions, were identified using variant calling pipelines. Comparative genomic analyses highlighted mutations unique to clinical isolates. Phylogenetic analyses were conducted to evaluate the genetic relationships between clinical strains and the standard vaccine strain, providing insights into genomic evolution and potential impacts

Results: Fifteen Mycobacterium bovis BCG strains were analyzed, comprising 14 Pasteur lineage and one Danish lineage isolate. Whole genome sequencing revealed several notable mutations distinguishing clinical isolates from standard reference strains. Among these, SNPs in the rpoB gene, linked to rifampicin resistance, were found in 20% of the isolates. Mutations in the embB gene, associated with ethambutol resistance, occurred in 30% of the strains. Additionally, a frameshift mutation in the ppe38 gene, which may influence virulence, was identified in 40% of the Pasteur strains. The Danish strain exhibited unique mutations in the ppsA gene, involved in lipid metabolism and potentially affecting bacterial survival. Phylogenetic analysis showed clear separation between the Danish and Pasteur lineages, confirming their distinct genetic backgrounds.

Conclusion: This study demonstrates significant genetic variability among Mycobacterium bovis BCG strains isolated from clinical samples, with 14 strains belonging to the Pasteur lineage and one to the Danish lineage. Whole genome sequencing identified important mutations in genes associated with drug resistance, such as rpoB and embB, as well as mutations potentially affecting virulence, like those in the ppe38 gene. The unique genetic profile of the Danish strain further highlights the diversity within BCG vaccine strains. These findings underscore the dynamic nature of BCG genomes after vaccination and possible environmental exposure, which could influence vaccine efficacy and safety. Continuous genomic surveillance of clinical BCG isolates is essential to monitor emerging mutations that may impact the protective effect of the vaccine and to guide improvements in tuberculosis control strategies.

Keywords: ,M bovis BCG Whole genome sequencing (WGS) Genetic mutations

Poster 78

Isolation and Characterization of a Lytic Phage and Its Efficacy against Multi-Drug Resistant Strains of Pseudomonas aeruginosa

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Introduction: Background: Phages are potent alternatives to antibiotics due to their lytic activity and specificity. We isolated and characterized a specific bacteriophage effective against resistant strains of P. aeruginosa and their biofilms.

Methods: Samples were collected from hospital sewage, morphological, life-cycle characteristics, pH and thermal stability, and host range of the isolated phage. Additionally, the sensitivity of 42 P. aeruginosa strains and their biofilms, were assessed.

Results: Morphological analysis showed that vB-pae-PA01 resembled Podophages. Sensitivity assays revealed that vB-pae-PA01 lysed 57% of the strains. vB-pae-PA01 exhibited strong thermal stability However, extremely acidic and basic conditions reduced its lytic activity. The one-step growth curve revealed a latent period of 10 minutes and a burst size of 105 PFU per cell.

Conclusion: Conclusion: we isolated the lytic bacteriophage vB-pae-PA01, which demonstrated potent lytic activity against P. aeruginosa strains. These properties suggest that vB-pae-PA01 could be a potential candidate to use against antibiotic-resistant P. aeruginosa

Keywords: Bacteriophage, Pseudomonas aeruginosa, Antibiotic-resistance, Biofilm, Phage-therapy

Poster 79

Isolation, Characterization and, Determination of Antibacterial Activity of Two Novel Escherichia Phages Against Avian Pathogenic Escherichia coli

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Introduction: According to the World Health Organization's estimates, five million children death worldwide annually due to acute diarrhea. Escherichia coli, known as an important pathogen and the third causative agent of diarrhea in developing countries. By employing new methods that effectively inhibit the growth of this bacterium, it is possible to combat its increasing prevalence. In addition, increase in antimicrobial resistance (AMR) and, the emergence of multidrug-resistant (MDR) bacterial pathogens, alternative and, innovative approaches such as phage therapy can be employed, which not only possess antibacterial properties but also have no adverse effects on the environment and eukaryotic cells. The main objective of this study was to in vitro determination of antibacterial activity of two novel isolated pages (Escherichia phage AG- MK-2022. Basu) and the Escherichia phage VaT-2019a isolate PE17 (GenBank: MK353636.1) against Avian Pathogenic Escherichia coli (APEC) strains isolated from broiler chickens with clinical signs of colibacillosis in the

Methods: Wastewater samples of poultry slaughterhouses in Hamedan county were collected and, a new phage which named Escherichia phage AG-MK-Basu.2022 was isolated and purified. The phage morphology, and some important characteristics such as phage host range, pH stability, thermal stability, NaCl sensitivity, phage adsorption assay and one-step growth curve were determined. Genome analysis of the two phages was performed, and finally, in vitro antibacterial activity of the newly isolated pages (Escherichia phage AG- MK-2022. Basu) and the previously isolated Escherichia phage (Escherichia phage VaT-2019a isolate PE17: GenBank: MK353636.1) was determined using spot assay test, against Avian Pathogenic Escherichia coli (APEC) strains (n= 100) isolated from broiler chickens with clinical signs of colibacillosis in the poultry farms of Hamedan province, Iran.

Results: In the present study, we isolated and purified a new Escherichia phage (Escherichia phage AG- MK-2022. Basu) from poultry slaughterhouse wastewater. Transmission electron microscopy (TEM) indicated that this phage belongs to the Myoviridae family. This phage showed high stability under different pH and, thermal conditions and also exhibits a broad host range. Genome analysis of the phages showed that no virulence factors genes, and antibiotic resistance genes, were identified, confirming phage safety for therapeutic application. In addition, current study results indicate that 95% of the APEC strains in the spot assay test had formed lytic plaques with both phages, suggesting that the use of these two phages could be considered as an important candidate for the effective control and treatment of avian colibacillosis.

Conclusion: The present study findings indicate that phage therapy could be used as novel and, safe biocontrol method to combat the occurrence of MDR-APEC strains isolated from broilers.

Keywords: Antibiotic Resistance, Multidrug resistant Avian pathogenic Escherichia coli (MDR -APEC), Phage, Broilers chicken, Colibacillosis.

Poster 80

Keratinolytic Potential of Bacillus spp. in the Biodegradation of Chicken Feathers

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Introduction: Chicken feathers are a major by-product of the poultry industry, containing approximately 90% β-keratin, a stable protein with high resistance to degradation. Keratinases are extracellular enzymes that belong to the subgroup of alkaline metalloproteases or serine-like proteases that break disulfide bonds and proteins. Furthermore, Feather-degrading bacteria (FDB) produce keratinases that offer numerous industrial applications, like animal feed production, and have emerged as a commendable and environmentally sustainable method for managing feather waste. In this study, we identify and characterize keratinolytic Bacillus spp. with feather-degrading activity.

Methods: Bacillus spp. were obtained from a laboratory collection at Shiraz University. For primary screening, all isolates were streaked on skim-milk agar to predict the production of proteolytic enzymes. Species of the isolates with proteolytic activity are identified by biochemical tests. Each isolate with a clear zone on skim-milk agar is transferred to minimal salt (MS) media with 0.4%(w/v) feathers as the only source of carbon. As the inoculum, a 2% (v/v) bacterial suspension in the logarithmic phase was transferred to 500 mL of MS media and control MS media, which were incubated for 13 days at 120 rpm and 37°C. Every 48 hours, the soluble protein concentration in both test and control media was measured by using the Bradford assay.

Results: Using biochemical tests, we identified Bacillus cereus and Bacillus subtilis, which produced a clear zone on skim milk agar. B. cereus showed the greatest keratinolytic activity during the 13-day treatment period. The soluble protein concentration produced by B. cereus was 0.243 mg, most of which was observed after day 8. In contrast, B. subtilis produced a steady increase in soluble protein, reaching a concentration of 0.123 mg by day 13.

Conclusion: The findings of this research showed that B. cereus was more capable than B. subtilis in keratinolytic activity. This was due to its higher production of soluble protein. Therefore, it could be considered a suitable candidate for industrial processes related to feather waste management and the production of valuable products such as animal feed. Overall, the utilization of keratinolytic bacteria is a novel, economical, and environmentally friendly approach to reducing feather waste in the poultry industry.

Keywords: Keratin, Bacillus spp., feathers, keratinase

Poster 81

Laeveraging Multi-Task Protein Language Model for Robust Sequence-Only Antibody–Antigen Affinity Prediction

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Introduction: Predicting antibody–antigen (Ab–Ag) binding affinity from sequence alone is vital for accelerating antibody discovery, especially when structural data are unavailable. Existing sequence-based methods suffer from limited labeled data, poor generalization to new antigens, and weak calibration. While foundation models like MAMMAL offer broad protein understanding, they are not optimized for antibody-specific affinity prediction. Structure-based methods achieve higher accuracy but are impractical for early discovery due to 3D data requirements. To address these gaps, we developed a sequence-only, multi-task framework integrating antibody VH/VL and antigen sequences to predict binding at three levels—binary binding detection, affinity class, and continuous strength (–log Kd).

Methods: Antibody VH/VL sequences with cognate antigens (457,889 Ab–Ag records; 309,884 unique antibodies; 170,660 pairs; 4,334 antigens) were input to the MAMMAL foundation protein language model, built for general protein tasks and fine-tuned for antibody affinity prediction. The dataset included heavy and light chains, enriched in short sequences (150 AA), with formats such as nanobodies (70,388 non-patent, 113,380 patent) and scFvs (132,157). Binding annotations spanned quantitative (ΔG, ΔΔG, Kd, –log Kd, IC_{50}, enrichment, ELISA) and qualitative (Boolean, fuzzy) labels. Data were stratified into three confidence levels; only high/very high (80%) supported supervised training, while medium-confidence entries expanded diversity during pretraining. The multi-task model used dual heads: one for classification (binary and categorical) and one for regression (–log Kd). Preprocessing involved outlier removal, assay normalization, and exclusion of clone/antigen variants across splits. Performance was measured with accuracy and AUC (classification), MAE, MSE, and R^2 (regression), plus calibration analysis.

Results: Our model achieved 92% accuracy (AUC = 0.95) for binding classification and an $R^2 \approx 0.41$ (MAE = 0.1) for regression, outperforming prior sequence-only models such as DG-Affinity ($R^2 = 0.35$) and AttABseq ($R^2 = 0.38$). On an independent dataset of unseen antigens, the model maintained 88% accuracy, demonstrating strong generalization. Predictions were well calibrated, with 70% falling within ±0.5 log Kd of experimental values. Together, these results suggest that our framework provides a reliable sequence-only tool that can accelerate antibody discovery and vaccine development when structural data are unavailable.The multi-task design delivers outputs at three levels, reflecting decision pathways of triage, prioritization, and ranking of antibody candidates, thereby fostering early antibody detection and selection.

Conclusion: Our optimized multi-task protein language model demonstrates that accurate antibody–antigen affinity prediction is achievable using sequence data alone, bridging a critical gap in infectious disease research where rapid antibody screening is essential. By integrating classification and regression tasks within a unified architecture, the model generalizes effectively to unseen antigens and delivers robust, calibrated predictions without requiring structural inputs. This approach supports early identification of high-affinity antibodies against emerging pathogens, enabling faster therapeutic and vaccine development during outbreaks. The model's capacity to triage, prioritize, and rank antibody candidates from raw sequence data establishes a scalable foundation for next-generation immunoinformatics tools, facilitating structure-independent discovery pipelines in infectious disease and immunotherapy research.

Keywords: antibody–antigen interaction, protein language model, sequence-based prediction, infectious disease, affinity estimation

Poster 82

Latent Toxocara Infection in Multiple Sclerosis Patients: A Seroepidemiological Study from Northeastern Iran

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Introduction: Toxocariasis, a zoonotic parasitic disease caused by Toxocara species, has been implicated in various health conditions, including autoimmune diseases like multiple sclerosis (MS). This study aimed to assess the seroprevalence of Toxocara antibodies among MS patients in northeastern Iran and explore potential associations with demographic and clinical characteristics.

Methods: A cross-sectional study was conducted on 92 MS patients and 93 healthy controls at the Comprehensive MS Center in Mashhad in 2023. Serum samples were analyzed for Toxocara IgG using enzyme-linked immunosorbent assay (ELISA), with positive results confirmed by Western blot. Demographic data were collected, and statistical analyses were performed to compare seroprevalence and associated risk factors between the two groups.

Results: The overall seroprevalence of Toxocara was 2.2%, with a higher prevalence observed among MS patients (3.3%) compared to controls (1.1%), though the difference was not statistically significant (p=0.368). The seropositive MS patients were generally older and had been diagnosed with MS for an average of 5 years. No significant associations were found between Toxocara seropositivity and other risk factors such as gender, age, or consumption of undercooked meat.

Conclusion: While a slightly higher seroprevalence of Toxocara was observed among MS patients, the findings were not statistically significant, suggesting that latent toxocariasis may not have a robust impact on MS progression. Further research with larger sample sizes is needed to better understand the potential role of Toxocara infection in MS.

Keywords: Toxocariasis, Multiple Sclerosis (MS), Seroprevalence, Zoonotic Infections

Poster 83

Microbial synthesis Ag_Albumin nanoparticles by Bifidobacterium breve

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Introduction: Biological and microbial synthesis processes are a safe and useful option due to their compatibility with the environment and nature and their cost-effectiveness over physical and chemical methods. Advantages of biomass and microbial synthesis methods of silver nanoparticles, compared to other methods (chemical, physical), environmental friendliness, cost-effectiveness, ease of operation and less energy are used. Probiotics are beneficial bacteria for the human gastrointestinal tract, probiotic bacteria prevent bacteria from inflammatory bowel disease. Albumin is a group of water-soluble proteins, one of the most important proteins in the plasma in terms of application in the human body. Albumin can be used in medicine and therapy. Albumin nanoparticles reduce drug side effects and increase drug stability. In this study, protein nanoparticles containing silver were synthesized with the probiotic bacterium Bifidobacterium breve.

Methods: First, the probiotic bacterium Bifidobacterium breve was cultured in MRS Broth culture medium, and after obtaining a single colony, the bacterium was cultured in MRSBroth liquid culture medium, then, centrifuged, the supernatant was filtered and silver nitrate was added. Silver nanoparticles are then synthesized. Albumin protein was used to synthesize protein nanoparticles. A solution of albumin protein and distilled water was prepared and synthesized silver nanoparticles were added, 25% glutaraldehyde was added, acetone and ethanol were added, then albumin protein nanoparticles were synthesized, placed in an oven for XRD and FTIR, TEM, SEM and DLS are prepared.

Results: Albumin and silver protein nanoparticles have spherical, crystalline, semi-crystalline and cubic morphology and structure. Silver albumin protein nanoparticles have O-H, N-H and C-H bonds, C = C bonds in aromatic rings and C-N bonds in amino compounds. Silver nanoparticles have OH bonds, CH bonds in CH2 and CH3 groups, NH bonds, CO bonds in the structure of COc and C-OH functional groups.

Conclusion: The results of this study are the synthesis of albumin protein nanoparticles containing silver nanoparticles with suitable structure and properties. , And this protein nanoparticle can also be used for treatment.

Keywords: Biosynthesis .silver nanoparticles, probiotics.

Poster 84

Modulatory effects of sub-MIC colistin on virulence determinants in Acinetobacter baumannii: implications for antimicrobial stewardship in pediatric infections

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Introduction: The escalating threat of multidrug-resistant Acinetobacter baumannii, a critical-priority ESKAPE pathogen, is particularly acute in pediatric healthcare settings. With colistin serving as a last-resort therapy, understanding its sub-inhibitory effects on bacterial virulence is crucial for optimizing treatment strategies and combating antimicrobial resistance (AMR).

Methods: This study characterized 70 A. baumannii clinical isolates from a tertiary Children's Medical Center. Phenotypic biofilm formation was assessed via microtiter plate assay in the presence and absence of sub-MICs (¼ and ½ MIC) of colistin. The prevalence of biofilm-associated genes (bap, abaI, ompA, csuE, blaPER-1) was determined by PCR. Quantitative real-time PCR (qRT-PCR) evaluated the expression of csuE and ompA under colistin pressure. Furthermore, the adherence and invasion capabilities of selected isolates to human laryngeal epithelial (HEp-2) cells were investigated at sub-MIC levels.

Results: A high prevalence of multidrug resistance (MDR: 84.2%) and extensive drug resistance (XDR: 35.7%) was observed. Notably, 92.9% of isolates were biofilm producers, with a significant inverse correlation observed between strong biofilm formation and MDR/XDR phenotypes. The genes abaI, ompA, and csuE were ubiquitous (100%), while bap and blaPER-1 were present in 22.8% and 24.3% of isolates, respectively. Exposure to sub-MIC colistin resulted in the significant downregulation of csuE and ompA gene expression. Crucially, sub-inhibitory concentrations of colistin significantly reduced bacterial adherence to host epithelial cells, although no invasion was detected.

Conclusion: Our findings reveal that sub-MIC colistin can attenuate key virulence mechanisms in A. baumannii, including biofilm formation and host cell adherence, potentially by modulating the expression of critical biofilm-related genes. This research provides a novel perspective on the pharmacodynamic effects of "last-resort" antibiotics beyond mere bactericidal activity. It underscores the importance of precise dosing regimens within antimicrobial stewardship (AMS) programs to not only treat infections but also potentially suppress virulence, thereby improving clinical outcomes in vulnerable pediatric populations.

Keywords: Antimicrobial Stewardship, ESKAPE Pathogens, Biofilm Regulation, Host-Pathogen Interaction, Pediatric Infectious Diseases, Polymyxins

Poster 85

Molecular Diagnostic Methods for Leishmaniasis

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Introduction: Leishmaniasis, a neglected tropical disease, is widely distributed in different geographical areas and manifests in multiple clinical forms including cutaneous, mucocutaneous and visceral leishmaniasis. Given the existence of approximately 21 species pathogenic to humans, rapid and accurate diagnosis, especially in endemic and resource-limited areas, plays a vital role for effective disease management. This comprehensive review aims to map and summarize molecular diagnostic techniques for leishmaniasis, evaluate their diagnostic performance, sample types, applications and implementation challenges.These techniques have been performed in both laboratory and field settings.

Methods: We followed the PRISMA-ScR guidelines. We assessed the inclusion criteria for review articles published between 2014 and 2025. We reviewed current molecular methods (PCR, qPCR, LAMP, RPA, HRM, sequencing) for the diagnosis of Leishmania in humans, according to the aim of the article. The databases searched included PubMed, Google Scholar and Web of Science and manual screening of reference lists. Next, data from each study including author/year, Leishmania species, sample type, molecular method and main outcomes such as sensitivity and specificity, and advantages and limitations were extracted and analysed.

Results: Twelve articles were included. LAMP and PCR were the most commonly used techniques, with LAMP being known for its speed, sensitivity and field applicability, while PCR stood out due to its large number of articles and its widespread use in the diagnosis of leishmaniasis. HRM showed potential for species differentiation but required specialized equipment, RPA with its rapid detection capability, limited clinical validation and sequencing remained the gold standard for species-level identification despite its high cost and limited field applicability. Overall, the sensitivity and specificity of molecular detection methods were high. This study highlights the main limitations in the application of these methods, including protocol variability, limited clinical validation of some assays and the need for sophisticated laboratory equipment. Consequently, future research should highlight areas such as research gaps, the need for standardized protocols, direct comparisons between techniques and wider integration of point-of-care diagnostics into health systems.

Conclusion: Overall, molecular diagnostic methods significantly improve the diagnosis of leishmaniasis by providing features such as detection of low parasite counts, species differentiation, and rapid application in endemic areas, compared to traditional methods. Among the common methods, PCR and real-time PCR remain very reliable for reference laboratories, while LAMP and NASBA are efficient in endemic areas with limited resources. Multiplex and RFLP also provide additional tools for species-level analysis. Ultimately, to maximize the clinical and epidemiological impact of these methods, standardization and wider availability are needed.

Keywords: Leishmaniasis, Visceral, Molecular Diagnostic Techniques, Polymerase Chain Reaction, LAMP assay, Real-Time Polymerase Chain Reaction, Self-Sustained Sequence Replication

Poster 86

Molecular identification of Burkholderia cepacia from cystic fibrosis patients in northwestern Iran: a research note

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Introduction: The Burkholderia cepacia complex (BCC) is a major cause of secondary infections in patients with cystic fibrosis (CF). Despite advances in global surveillance, reliably detecting of BCC remains challenging in terms of morbidity and mortality worldwide.

Methods: From September 2023 to June 2024, periodic three-month assessments were conducted in northwestern Iran to monitor secondary infections in patients with cystic fibrosis. Sputum samples were collected from each patient and subjected to conventional culture on selective media, followed by biochemical tests for preliminary identification. Concurrently, molecular detection was performed using a polymerase chain reaction (PCR) targeting specific Burkholderia cepacia complex (BCC) genes, enabling precise and rapid identification of B. cepacia. The study also evaluated the potential application of an enzyme-linked immunosorbent assay (ELISA)-based approach using native bacterial strains to develop a rapid and specific diagnostic assay. This study aimed to compare the efficiency, specificity, and reliability of conventional versus molecular diagnostic methods in this patient population by combining culture, biochemical, PCR, and ELISA evaluations.

Results: B. cepacia was not detected in any of the 100 samples using culture and biochemical methods. However, PCR identified five positive samples. These results suggest that conventional culture and commercial biochemical systems may be unreliable for detecting B. cepaciae, whereas molecular methods are highly specific and accurate.

Conclusion: Molecular detection, particularly PCR, is a precise method for identifying B. cepacia. Additionally, developing ELISA assays using native species could improve the speed, specificity, and efficiency of BCC detection in a clinical setting.

Keywords: Burkholderia cepacia complex, Cystic Fibrosis, PCR, ELISA

Poster 87

Molecular typing of Clostridium perfringens strains isolated from clinical and non-clinical cases of livestock in Fars Province

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Introduction: Clostridium perfringens, despite its role as a normal flora of intestine, is the agent of important and dangerous diseases in humans and livestock. Enterotoxaemia is one of these diseases, causing significant mortality in livestock annually. Analysis of genetic diversity or relatedness of isolates with molecular typing methods can be helpful for subtyping pathogenic bacteria and identifying, tracking, and preventing the spread of infectious agents, understanding the epidemiology of these infections, and observing population structures of these bacteria in a region. The present study intended to determine the strain diversity of clinical and non-clinical Clostridium perfringens isolates, based on MLVA (Multiple Locus Variable Tandem Repeat Analysis) typing method.

Methods: C. perfringens isolates from different parts of Fars province of Iran isolated during the years 2009 to 2022 were used in this study. A total of 43 C. perfringens isolates were obtained from intestinal contents of healthy goats, sheep and cattle from slaughterhouses. In contrast, 27 isolates were recovered from confirmed enterotoxemia cases. The isolates were evaluated for the determination of toxin type, and then Genetic typing of isolates was done using specific primers for amplification of eight VNTR loci. PCR was done, and electrophoresis banding patterns of fragments were analyzed by BioNumerics software.

Results: Toxin typing showed most of the isolates belonged to type A, then type D , two type G, and one type C. The results of molecular typing revealed 71 distinct MLVA profiles from 74 strains, Including 70 isolates, three vaccine strains and strain 13 (Gene bank). Clustering of isolates according to the minimum spanning tree showed five different clusters, excluding three orphan isolates. Clinical and non-clinical isolates were scattered in all clusters, and no defined cluster related to health status, date of isolation, kind of host and place of isolation was detected. The discriminatory power of individual VNTR loci D (Nei's diversity index) was 0.09, 0.76, 0.25, 0.82, 0.79, 0.85, 0.8 and 0.84 for loci 7, 24d, 17, O1e, cp42, cp13, cp6 and cp19, respectively. Locus cp13 displayed the highest and locus 7 the lowest allelic diversity. The total diversity index (DI) was calculated to be 0.99 for all loci.

Conclusion: Overall MLVA molecular typing method based on VNTRs used in this study, showed high genetic diversity among C. perfringens isolates. Complementing MLVA with other phylogenetic methods are recommended for a more comprehensive analysis.

Keywords: Clostridium perfringens, MLVA, molecular typing

Poster 88

Monitoring azole resistance in Aspergillus species from clinical and environmental isolates in a hospital setting

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Introduction: Drug resistance in Aspergillus with variable prevalence worldwide is a challenge to the effective management of aspergillosis. Due to the increasing environmental and clinical use of azoles ,acquired resistance to azoles has emerged. In this study, we investigated the frequency of itraconazole- and voriconazole-resistant Aspergillus species (particularly A. fumigatus) in a referral laboratory, defined azole cross-resistance patterns, evaluated detection of the cyp51A gene compared with phenotypic azole resistance, and explored possible epidemiologic links between resistant isolates.

Methods: Over a 24-month period (October 2020–September 2022), we prospectively collected clinical specimens—primarily bronchoalveolar lavage (BAL) and sputum—from 720 patients hospitalized with COVID-19 at a major teaching hospital (UMS University, Iran). Sampling focused on patients in high-risk wards, namely Nephrology, Oncology and Hematology, Pulmonology, and the ICUs. Direct microscopic examination of clinical specimens was performed as an initial diagnostic step for the detection of probable fungi causing HAIs. Morphological identification was performed using Sabouraud glucose agar (SGA 4%), Czapek yeast extract agar (CYA) for filamentous fungi, and cornmeal agar and CHROMagar Candida for pathogenic yeasts. PCR-RFLP was performed to confirm identification and to type Aspergillus isolates, including environmental strains.

Results: A total of 29 Aspergillus isolates were recorded, including 15 clinical cases (51.7%) and 14 environmental samples (48.3%). The most common species were A. flavus (12; 41.4%), A. niger (11; 37.9%), and A. fumigatus (5; 17.2%). Notably, the cyp51A gene was present in the vast majority of isolates (27/29, 80%).Furthermore, a high percentage of these cyp51A-positive isolates harbored mutations—87.5% of A. fumigatus and 83.5% of A. flavus. However, despite this high genetic predisposition for resistance, the MIC ranges for itraconazole were broad (0.031–16 µg/ml) and phenotypic resistance was rare. In fact, only one isolate each of A. flavus and A. fumigatus were resistant to itraconazole, and none showed resistance to voriconazole.

Conclusion: Other studies have reported higher rates of azole resistance under similar conditions. In Iran, amphotericin B remains the preferred treatment for invasive aspergillosis, and thus exposure to azole drugs is relatively limited. Importantly, the presence of the cyp51A mutation did not correlate with acquired resistance to itraconazole or voriconazole in our isolates.

Keywords: Aspergillus, hospital, molecular identification, susceptibility

Poster 89

Mucormycosis in Iranian West Azarbayejan cases of COVID-19, focus on Rhizopus oryzae as the most frequent agent

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Introduction: Mucormycosis, an aggressive infection caused by mucoral fungi was emerged in Iran during the pandemic COVID-19, delta strain. High dose corticosteroid therapy (dexamethasone) in cases with severe COVID predisposed hyperglycaemia and keto-acidosis conditions and the triger of invasive mucormycosis. The increase of invasive mucormycosis in cases of diabetes melitus and COVID-19 as the clusters in Iranian hospitals prompted us to sudy on the identification of isolated mucoral fungi from above patients.

Methods: Our subjects included 70 cases suspected to COVID associated mucormycosis. The clinical specimens, sinus discharge, nasal or facial biopsies and bronco-alveolar lavage were transported from central hospital of COVID patients in Northwest to the Center of Medical Mycology, UMS University, Urmia, Iran. The histopathologic and molecular assays were conducted.

Results: Among studied cases, 53(75.7%) COVID patients and 16(22.8%) were diabetic patients with a history of COVID-19. From all, 63 (90%) mucoral infections were detected. Other fungi including Aspergillus and Candida species were diagnosed. All of the mucoral isolates identified as Rhizpus oryzae with PCR- Sequencing.

Conclusion: Although, the variable mucoral species cause invasive infection in regular diabetic patients, Rhizopus oryzae has been main species in recent studies.

Keywords: Rhizopus arrizus, COVID-19, cortico-steroids

Poster 90

National Burden and Economic Impact of Antimicrobial Resistance in Klebsiella pneumoniae and Acinetobacter baumannii in Iran: A 2000–2021 Analysis

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Introduction: Introduction: Antimicrobial resistance (AMR) represents a major public health challenge globally and in Iran, particularly for pathogens such as Klebsiella pneumoniae and Acinetobacter baumannii. These organisms are leading causes of hospital-acquired infections, with rising resistance to carbapenems and other critical antimicrobials. This study aimed to assess the temporal trends in the burden of AMR for these pathogens in Iran between 2000 and 2021, focusing on mortality, disability-adjusted life years (DALYs), and economic impact.

Methods: Methods: We used data from the Global Burden of Disease (GBD) 2021 AMR project to estimate attributable (resistant infections hypothetically replaced with susceptible infections) and associated (resistant infections replaced with no infection) deaths and DALYs per 100,000 population with 95% uncertainty intervals. Economic burden was estimated using GDP per capita and purchasing power parity (PPP)-adjusted costs. Resistance trends, particularly for carbapenems and cephalosporins, were analyzed. Age-specific trends and infection site contributions (e.g., bloodstream and respiratory infections) were also evaluated.

Results: Results: Between 2000 and 2021, the overall AMR-attributable DALYs for A. baumannii declined from 35,284.5 to 28,085.9, and associated DALYs from 90,391.9 to 69,740.5 per 100,000 population. However, all-age deaths increased, particularly in neonates and adults over 50 years. For K. pneumoniae, deaths rose from 565.9 to 643.5, though age-standardized death rates declined from 1.5 to 0.9 per 100,000. DALYs decreased from 29,523.4 to 18,787.1, with the greatest reductions observed in children under five. Carbapenem resistance in K. pneumoniae increased from 7.5% to 20%, contributing to a rise in attributable deaths from 76.1 to 175.0. Both pathogens showed persistently high resistance to carbapenems and cephalosporins, with bloodstream and lower respiratory tract infections being the primary drivers of DALYs. The combined economic burden of AMR for these pathogens was substantial, with A. baumannii peaking at 584.6 million PPP USD in 2010 and declining to 435.2 million in 2021, while K. pneumoniae

Conclusion: Conclusion: Although the overall DALY burden of K. pneumoniae and A. baumannii AMR in Iran has decreased over two decades, mortality rates, particularly in older adults and neonates, remain concerning. Rising carbapenem resistance underscores the need for strengthened infection prevention and control (IPC) measures, optimized antimicrobial stewardship, and improved water, sanitation, and hygiene (WASH) programs to curb further escalation of AMR and its economic impact.

Keywords: Antimicrobial resistance, Klebsiella pneumoniae, Acinetobacter baumannii, economic burden, DALY, Iran

Poster 91

Network Signatures of Antimicrobial Prescribing in Oncology: Insights from a Decade of Hospital Practice

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Introduction: Antimicrobial prescribing in oncology is a critical challenge for stewardship programs. Immunosuppression, prolonged hospital stays, and invasive procedures expose cancer patients to frequent and often empirical antibiotic use. While essential, such use increases the risk of adverse drug reactions, antimicrobial resistance (AMR), and prolonged hospitalization. In low- and middle-income countries, the burden of medication-related harm is even greater, contributing to significant disability-adjusted life years lost. In oncology, overlapping chemotherapy and antibiotic regimens further amplify these risks. Network-based analysis offers a powerful approach to map antimicrobial prescribing patterns, identify high-risk combinations, and detect influential "hub" drugs driving resistance and toxicity. By shifting focus from individual prescriptions to system-level structures, these insights can inform targeted interventions and enhance antibiotic stewardship in cancer care.

Methods: Electronic health records from 2014–2024 were used to construct a weighted co-prescription network including all inpatient medications. Antimicrobial agents were then isolated within this network to examine their connectivity, frequency, and role in high-risk interaction clusters. Louvain modularity was applied to identify antimicrobial-centered communities, and hub analysis quantified their systemic influence. Time-to-event outcomes, including infection recurrence and mortality, were modeled using Cox regression adjusted for demographics and comorbidities.

Results: 92,565 prescriptions gathered for 18,644 cancer patients. Both networks showed a small-world structure, facilitating the rapid spread of prescribing risks. The co-medication network showed dense interconnectivity (density = 0.26), while the severe DDI network was four times sparser (0.04). DDI-Network centrality shows a modest positive correlation with fatality rate, suggesting hub drugs are not strong standalone predictors of death. Community modularity remained high (0.45), reflecting organ- or disease-specific treatment silos. DDI network robustness simulations suggested that deprescription of the top 5% highest-degree drugs could disrupt 20% of interactions. Centrality analyses reflect cisplatin, dexamethasone, and metronidazole as core DDI hubs. DDI clusters with amphotericin B or fluoroquinolone–chemotherapy pairs, and methotrexate–PPI combinations exhibited elevated mortality. QT-prolonging drug pairs (e.g., ondansetron + SSRIs), corticosteroid + CYP3A4-sensitive agents, and palliative CNS polypharmacy were associated with adverse outcomes. Modularity was 0.95 across tumour types, supporting tailored, community-specific dashboards over hospital-wide alerts. Neuro-oncology, breast, and colorectal

Conclusion: Polypharmacy is highly prevalent in oncology, with antimicrobial use contributing substantially to clinically significant drug–drug interactions. Network modeling captured the real-world complexity of oncology prescribing, revealing small-world and modular structures that facilitate the spread of antimicrobial-related risks across cancer subtypes. High modularity (0.95) highlights disease-specific treatment silos, underscoring the need for tailored antimicrobial stewardship rather than uniform alert systems. A small set of recurrent antimicrobial and adjunct drug pairs—such as fluoroquinolone–chemotherapy, amphotericin B combinations, and methotrexate–PPI—accounted for a large share of severe interactions and adverse outcomes. Targeted deprescription or substitution of high-degree antimicrobial hubs could mitigate more than 20% of interaction burden. These findings support integrating network-informed stewardship dashboards into oncology workflows, enabling precision feedback, rational antibiotic use, and safer, data-driven pharmacotherapy for immunocompromised cancer patients.

Keywords: Antimicrobial stewardship Oncology pharmacotherapy Drug–drug interactions Network analysis Polypharmacy

Poster 92

Novel Recombinant Autolysin-Based Vaccine Elicits Balanced Adaptive Immunity and Dramatically Reduces Systemic S. aureus Load: A Preclinical Study

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Introduction: Staphylococcus aureus is a Gram-positive opportunistic pathogen whose increasing antimicrobial resistance poses a major public-health challenge. Vaccination targeting bacterial adhesins and cell-wall associated factors offers a promising preventive strategy. Autolysin, a multifunctional enzyme implicated in host-cell adherence and cell-division processes, represents a rational antigenic target. This study assessed the immunogenicity and protective efficacy of recombinant autolysin (R-Autolysin) formulated with two adjuvants in a BALB/c mouse model.

Methods: R-Autolysin was expressed recombinantly, purified, and formulated with either aluminum hydroxide (alum) or Montanide ISA-266. BALB/c mice (n=15, per group) received three subcutaneous doses of 20 µg R-Autolysin at two-week intervals; control mice received adjuvant alone or saline. Humoral responses were quantified by indirect ELISA to determine total IgG and IgG1/IgG2a isotypes. Cellular responses were inferred from serum cytokine measurements (IFN-γ and IL-4) by ELISA. Three weeks after the final immunization, mice were challenged intravenously with 5×10^8 CFU of S. aureus. Bacterial burden (CFU/g) in target organs (liver, spleen, kidneys) was enumerated 48–72 hours post-challenge. Survival was monitored for 14 days. Data were analyzed using appropriate parametric or nonparametric tests (ANOVA/Kruskal–Wallis) and survival by Kaplan–Meier with log-rank comparison; significance was set at p0.001.

Results: Vaccination with R-Autolysin induced robust humoral responses: total IgG and both IgG1 and IgG2a isotypes were significantly elevated compared with controls (p0.05), consistent with concurrent Th1/Th2 polarization. Serum IFN-γ and IL-4 concentrations were significantly increased in vaccinated groups (p0.05). Following bacterial challenge, vaccinated mice exhibited a mean reduction in organ bacterial loads of approximately 10^3-fold relative to controls. Vaccinated groups demonstrated significantly improved survival compared with controls (log-rank p0.05).

Conclusion: R-Autolysin, when formulated with clinically relevant adjuvants, elicits balanced humoral and cellular immune responses and confers marked reduction in systemic bacterial burden and increased survival in a murine model of S. aureus infection. These preclinical data support further mechanistic studies and advancement of R-Autolysin toward translational development as a vaccine candidate against S. aureus.

Keywords: Staphylococcus aureus, Autolysin, Vaccine candidate, Recombinant protein, Immunogenicity, Protective efficacy

Poster 93

Oral Candidiasis among Hemodialysis Patients in Iran

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Introduction: Patients undergoing hemodialysis frequently experience immune dysfunction, placing them at high risk for opportunistic infections. Oral candidiasis represents the most frequent fungal infection of the oral cavity, yet its determinants in this population remain underexplored. This study aimed to determine the prevalence of oral candidiasis among hemodialysis patients and to evaluate potential demographic and clinical risk factors.

Methods: A cross-sectional investigation was carried out in Birjand, Iran, including 158 individuals receiving maintenance dialysis. Oral swabs were cultured on CHROMagar Candida medium, and species were confirmed through molecular assays. Logistic regression modeling was applied to identify independent predictors of infection.

Results: Oral candidiasis was detected in 69 patients (43.7%), with 97 Candida isolates obtained. Candida albicans was the predominant species (55.7%), followed by C. glabrata (22.7%). Risk factor analysis revealed that prolonged dialysis duration (OR = 7.48; 95% CI = 1.31–2.05; p 0.001), male sex (OR = 3.07; 95% CI = 1.12–8.39; p = 0.02), and smoking (OR = 7.48; 95% CI = 1.98–28.31; p = 0.003) were significantly associated with increased odds of infection.

Conclusion: Nearly half of the studied dialysis patients were affected by oral candidiasis, with C. albicans as the leading etiologic agent. Male gender, tobacco use, and extended duration of dialysis emerged as major risk factors. Routine oral examination and targeted preventive measures could improve patient outcomes in resource-limited settings.

Keywords: Oral candidiasis, hemodialysis, Candida albicans, opportunistic infection, risk factors

Poster 94

Phylogenetic diversity, biofilm production, and antibiotic resistance profiling of Uropathogenic Escherichia coli isolated from children with vesicoureteral reflux: complicating factors for treatment and recurrent urinary tract infections

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Introduction: Introduction: Uropathogenic Escherichia coli (UPEC) are the most common cause of urinary tract infections (UTI). This study investigated the genetic relatedness, biofilm-forming capacity, and antimicrobial resistance profiles in the extended-spectrum beta-lactamase (ESBL)-producing UPEC collected from children with vesicoureteral reflux (VUR) suffering from UTI.

Methods: Materials and methods: In this cross-sectional investigation, a total of 80 non-duplicated UPEC isolates were collected from children afflicted with VUR. Antimicrobial susceptibility testing and phenotypic production of ESBL were conducted according to the CLSI (2023) recommendations. Furthermore, PCR tests were used to detect the presence of ESBL genes. Biofilm formation in 96-well microtiter plates was assessed. Finally, the clonal diversity of the isolates was examined using the Enterobacterial Repetitive Intergenic Consensus (ERIC)-PCR.

Results: Results: Out of all collected isolates, 71.2% (n= 57/80) were ESBL producers and 31.2% (n=25/80) were multidrug resistant (MDR). The frequency of the blaCTX-M gene was 65.0% and 77.5% of the isolates were biofilm producers. ESBL-producing UPEC isolates were clustered by the ERIC-PCR method into the nine groups labeled A–I.

Conclusion: Conclusion: Our findings indicate a high and rising prevalence of multidrug-resistant and ESBL-producing UPEC among children with VUR. This underscores the urgent need for appropriate empirical antibiotic selection, routine monitoring of resistance patterns, and long-term prophylactic strategies to reduce recurrence and improve clinical management in this vulnerable population.

Keywords: Keywords: Uropathogenic E. coli, Biofilm, Vesicoureteral Reflux, ERIC-PCR

Poster 95

Polyp and tumor microenvironment reprogramming in colorectal cancer: insights from mucosal bacteriome and metabolite crosstalk

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Introduction: Highly frequent colorectal cancer (CRC) is predicted to have 3.2 million novel cases by 2040. Tumor microenvironment (TME) bacteriome and metabolites are proposed to be involved in CRC development. In this regard, we aimed to investigate the bacteriome and metabolites of healthy, adenomatous polyp, and CRC tissues.

Methods: Sixty samples including healthy (H), adenomatous polyps (AP), adenomatous polyps-adjacent (APA), cancer tumor (CT), and cancer tumor-adjacent (CA) tissues were collected and analyzed by 16 S rRNA sequencing and 1H NMR spectroscopy.

Results: Our results revealed that the bacteriome and metabolites of the H, AP, and CT groups were significantly different. We observed that the Lachnospiraceae family depleted concomitant with acetoacetate and betahydroxybutyric acid (BHB) accumulations in the AP tissues. In addition, some bacterial species including Gemella morbillorum, and Morganella morganii were enriched in the AP compared to the H group. Furthermore, fumarate was accumulated concomitant to Aeromonas enteropelogenes, Aeromonas veronii, and Fusobacterium nucleatum subsp. animalis increased abundance in the CT compared to the H group.

Conclusion: These results proposed that beneficial bacteria including the Lachnospiraceae family depletion crosstalk with acetoacetate and BHB accumulations followed by an increased abundance of driver bacteria including G. morbillorum, and M. morganii may reprogram polyp microenvironment leading to tumor initiation. Consequently, passenger bacteria accumulation like A. enteropelogenes, A.veronii, and F. nucleatum subsp. animalis cross-talking fumarate in the TME may aggravate cancer development. So, knowledge of TME bacteriome and metabolites might help in cancer prevention, early diagnosis, and a good prognosis.

Keywords: Colorectal cancer, Gut microbiome, Gut metabolome, Tumor microenvironment, Fusobacterium nucleatum

Poster 96

Prevalence and Antimicrobial Resistance Pattern of Vancomycin-Resistant Enterococci (VRE) Isolated from Blood Cultures of Hospitalized Patients

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Introduction: Vancomycin-resistant Enterococcus (VRE) are critical nosocomial pathogens due to their extensive antibiotic resistance. These organisms can cause severe bloodstream infections, leading to prolonged hospitalizations, increased morbidity, and mortality. Evaluating the prevalence and antimicrobial resistance profiles of VRE is essential for informing infection control measures and optimizing empirical therapy. This study aimed to investigate the prevalence and antimicrobial resistance patterns of VRE isolated from blood cultures of hospitalized patients in a tertiary care center in southern Iran.

Methods: Blood samples submitted to the Professor Alborzi Clinical Microbiology Research Center between March 2023 and March 2025 were analyzed in this cross-sectional study. Enterococcus spp. isolates were identified using standard biochemical methods, including Gram staining, esculin hydrolysis, pyrrolidonyl arylamidase (PYR) activity, catalase reaction, and growth in 6.5% NaCl. Antimicrobial susceptibility was assessed using the Kirby–Bauer disk diffusion method, and vancomycin-resistant isolates were confirmed on Brain Heart Infusion (BHI) agar supplemented with 6 µg/mL vancomycin according to CLSI guidelines. Patient demographic data, including age, sex, and hospital ward, were collected to examine epidemiological patterns.

Results: Out of 96 Enterococcus spp. isolates, 62 (71%) were vancomycin-resistant. Most VRE isolates exhibited high levels of resistance to clinically relevant antibiotics, including ampicillin (61.8%), erythromycin (90.0%), gentamicin (83.3%), high-dose gentamicin (57.3%), tetracycline (66.7%), clindamycin (97.8%), rifampin (87.4%), penicillin G (77.0%), imipenem (62.5%), teicoplanin (62.1%), ciprofloxacin (80.7%), and doxycycline (46.1%), while linezolid remained the most effective agent. Patients ranged from neonates (~5 days) to elderly individuals (up to 93 years), with a mean age of 49 years. Adults (19–65 years, n=37) and elderly patients (65 years, n=33) represented most cases, with pediatric patients (5 years, n=13) less frequent. Gender distribution was nearly balanced (50 males, 46 females). Patients were admitted across multiple hospital wards, including emergency (n=37), medical (n=15), ICU (n=8), NICU (n=5), pediatric wards (n=7), surgical wards (n=2), hematology (n=2), bone marrow transplant (n=2), and special ICU (n=1), demonstrating the widespread presence of multidrug-resistant Enterococcus across clinical settings.

Conclusion: This study confirms a high prevalence of VRE among bloodstream isolates in southern Iran, with extensive multidrug resistance patterns consistent with global reports. The wide age range and distribution across hospital wards indicate that VRE dissemination is not limited to critical care units. These results emphasize the urgent need for hospital-wide infection control programs, continuous antimicrobial resistance monitoring, and judicious antibiotic use. Targeted interventions to prevent transmission and guide empirical therapy are essential to reduce morbidity and mortality associated with VRE bacteremia.

Keywords: Prevalence; Vancomycin-resistant Enterococci (VRE); Blood cultures; Antimicrobial resistance

Poster 97

Prevalence of the CRISPR-Cas System and Its Association with Antibiotic Resistance in Clinical Klebsiella pneumoniae Isolates

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Introduction: CRISPR-Cas is a prokaryotic adaptive immune system that protects bacteria and archaea against mobile genetic elements (MGEs) such as bacteriophages plasmids, and transposons. In this study, we aimed to assess the prevalence of the CRISPR-Cas systems and their association with antibiotic resistance in one of the most challenging bacterial pathogens, Klebsiella pneumoniae.

Methods: A total of 105 K. pneumoniae isolates were collected from various clinical infections. Extended-spectrum β-lactamases (ESBLs) phenotypically were detected and the presence of ESBL, aminoglycoside-modifying enzymes (AME), and CRISPR-Cas system subtype genes were identified using PCR. Moreover, the diversity of the isolates was determined by enterobacterial repetitive intergenic consensus (ERIC)-PCR.

Results: Phenotypically, 41.9% (44/105) of the isolates were found to be ESBL producers. A significant inverse correlation existed between the subtype I-E CRISPR-Cas system's presence and ESBL production in K. pneumoniae isolates. Additionally, the frequency of the ESBL genes blaCTX-M1 (3%), blaCTX-M9 (12.1%), blaSHV (51.5%), and blaTEM (33.3%), as well as some AME genes such as aac(3)-Iva (21.2%) and ant(2'')-Ia (3%) was significantly lower in the isolates with the subtype I-E CRISPR-Cas system in comparison to CRISPR-negative isolates. There was a significant inverse correlation between the presence of ESBL and some AME genes with subtype I-E CRISPR-Cas system.

Conclusion: The presence of the subtype I-E CRISPR-Cas system was correlated with the antibiotic-resistant gene (ARGs). The isolates with subtype I-E CRISPR-Cas system had a lower frequency of ESBL genes and some AME genes than CRISPR-negative isolates.

Keywords: CRISPR-Cas system, Klebsiella pneumoniae, Extended-spectrum β-lactamases

Poster 98

Prophylactic effetcs of Thymol Loaded Chitosan Nanoparticles for Controlling Acute Toxoplasma gondii infection in Mice

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Introduction: Toxoplasma gondii is an intracellular protozoan parasite that can infect all warm-blooded vertebrates, including humans. The conventional pharmacological drugs for toxoplasmosis are linked to considerable adverse side effects, notably the tendency of pyrimethamine to cause bone marrow suppression and hematologic toxicity. Nanoencapsulation represents an innovative and practical field within nanotechnology, especially in relation to the pharmaceutical industry. Given the significant role of chitosan nanoparticles in medicine, the present study aimed to assess the in vivo efficacy of synthesized chitosan nanoparticles coated with thymol (CNCT) in combating toxoplasmosis.

Methods: Mice were administered CNCT orally at dosages ranging from 0.25 to 0.75 mg/kg/day for a duration of 14 days. Following this treatment, they were infected with T. gondii tachyzoites of the Rh strain to induce acute toxoplasmosis. Then, the mortality rate, parasite load, antioxidant activity, and the gene expression level of proinflammatory cytokines were evaluated.

Results: The dimensions of CNTN exhibit variability, with a mean size of 295 nm. The prophylactic administration of CNTN in mice infected with T. gondii resulted in a significant enhancement in survival rates and a considerable decrease in parasite load (P0.001). The CNTN caused a significant decrease in malondialdehyde level, while a notable increase (P 0.001) in the activity of the antioxidant enzymes. The feeding the mice infected with CNTN caused a meaningful elevation in the expression level of TNFα- and IL-1β (P0.001). The biochemical analyses indicated no significant changes in the serum levels of liver and kidney function markers.

Conclusion: The recent study revealed that CNTN demonstrates promising in vivo effects against toxoplasmosis in murine models. These effects are attributed to its antioxidant properties and immunomodulatory capabilities, which increase specific pro-inflammatory cytokines without any noticeable signs of toxicity to liver and kidney function.

Keywords: Toxoplasmosis, pharmacotherapy, nanomedicine, treatment

Poster 99

Rapid Molecular Detection of Fluoroquinolone Resistance in Photochromogenic Mycobacteria Using Real-TimePCR

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Introduction: Photochromogenic non-tuberculous mycobacteria (NTM), particularly Mycobacterium simiae, M. kansasii, and M. marinum, are increasingly recognized as emerging opportunistic pathogens responsible for both pulmonary and extrapulmonary infections, especially in immunocompromised individuals. Accurate identification and early initiation of effective treatment remain major clinical challenges due to the intrinsic resistance of these species to many first-line anti-tubercular drugs. Fluoroquinolones, which target DNA gyrase genes (gyrA and gyrB), are important therapeutic alternatives; however, point mutations within the quinolone resistance-determining region (QRDR) frequently lead to treatment failure. Rapid and precise detection of both species identity and resistance-associated mutations is therefore crucial for optimizing therapy and improving patient outcomes.

Methods: A total of 120 clinical photochromogenic NTM isolates were collected and differentiated from the Mycobacterium tuberculosis complex using IS6110 PCR, hsp65 gene sequencing, and 16S–23S rRNA region analysis. IS6110 PCR allowed accurate differentiation between tuberculous and non-tuberculous species. Species-level identification was further confirmed by hsp65 and 16S–23S rRNA sequencing. Mycobacterial DNA was extracted and analyzed using Real-Time PCR with allele-specific probes targeting QRDR mutations in gyrA and gyrB. A subset of isolates was further evaluated by proportional drug susceptibility testing to confirm fluoroquinolone resistance profiles. Mutation frequencies, codon distribution, and concordance between Real-Time PCR and sequencing were statistically analyzed.

Results: Fluoroquinolone resistance was detected in 18% of the 120 photochromogenic NTM isolates, primarily due to point mutations at codons 90 (A90V) and 94 (D94G/N) in the gyrA gene. Real-Time PCR enabled simultaneous amplification and analysis of gyrA, gyrB, and IS6110, allowing rapid species identification and concurrent detection of resistance-associated mutations in a single assay, substantially reducing diagnostic turnaround time. The subset of isolates tested by drug susceptibility confirmed the fluoroquinolone resistance profiles. Real-Time PCR showed high concordance (98%) with sequencing results, demonstrating excellent sensitivity and specificity. These findings highlight the efficiency of Real-Time PCR in combining rapid species identification with precise resistance detection.

Conclusion: Real-Time PCR represents a highly rapid, sensitive, and cost-effective molecular diagnostic approach for the detection of fluoroquinolone resistance and quinolone resistance-determining region (QRDR) mutations in clinically significant photochromogenic non-tuberculous mycobacteria (NTM). By enabling simultaneous identification of multiple resistance-associated genetic markers, this method allows for precise and timely detection of resistant strains, which is critical in guiding targeted antimicrobial therapy. Its integration into routine clinical workflows not only accelerates the diagnostic process but also reduces the likelihood of inappropriate or empiric antibiotic use, thereby minimizing treatment failures and the development of further resistance. Additionally, Real-Time PCR provides valuable epidemiological data, enhancing our understanding of resistance patterns in NTM populations. Overall, the application of this technique supports personalized patient management, improves clinical outcomes, and offers a practical, reliable, and scalable solution for laboratories dealing with emerging opportunistic mycobacterial infections.

Keywords: Mycobacterium marinum, Mycobacterium kansasii, Real-Time PCR, DNA-Gyrase

Poster 100

Refractory Polymicrobial Ascites and Systemic Dissemination Despite Susceptibility-Concordant Therapy: A Complex Case Amidst COVID-19 and Comorbidities

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Introduction: The management of intractable ascites is particularly challenging in patients with specific comorbidities, including end-stage renal disease (ESRD) and hypothyroidism. We describe a unique case of refractory ascites in a patient with COVID-19, which illustrates the intricate challenges in both diagnosing and managing this condition amidst a polymicrobial infectious milieu.

Methods: : A 27-year-old female with a history of ESRD and hypothyroidism was admitted following a presentation of persistent and progressive epigastric abdominal pain that was refractory to empirical antibiotic treatment. Diagnostic paracentesis was performed, and subsequent analysis of the ascitic fluid revealed a polymicrobial infection. Bacterial culture confirmed bacterial growth, while mycological culture identified multiple fungal isolates, including Fusarium redolens, Candida glabrata, and Candida tropicalis. Despite the initiation of combination antifungal therapy with voriconazole and amphotericin B, in addition to ongoing antibacterial agents, the patient's clinical condition failed to improve, and complete remission was not achieved. Further diagnostic investigation was pursued. A pericardial fluid culture returned with no microbial growth. However, bone marrow aspiration cultures were significant for the presence of C. glabrata and Klebsiella species. Microscopic examination of bronchoalveolar lavage fluid revealed trophozoites morphologically consistent with Lophomonas species. Antifungal susceptibility testing was conducted on the isolated fungi.

Results: The isolates exhibited full in vitro susceptibility to both amphotericin B and voriconazole. Notably, F. redolens demonstrated reduced susceptibility to itraconazole and the echinocandin class, while C. glabrata was found to be resistant to anidulafungin specifically. Concurrently, the isolated Klebsiella species exhibited an extensively drug-resistant profile, demonstrating resistance to a broad range of antimicrobial agents and retaining susceptibility only to tetracycline.

Conclusion: This case highlights the profound diagnostic and therapeutic challenges in managing polymicrobial, refractory ascites in a complex patient with COVID-19, ESRD, and hypothyroidism. Despite appropriate, susceptibility-guided antifungal and antibacterial therapy, the patient failed to achieve remission, underscoring the potential for severe, co-existing occult infections and the critical impact of underlying comorbidities and immunosuppression. It emphasizes the necessity for a comprehensive diagnostic workup beyond the peritoneal cavity in such complex presentations

Keywords: Intractable ascites, end-stage renal disease, COVID-19, Fusarium redolens, Candida glabrata, Mixed infections

Poster 101

Reservoirs and Transmission Pathways of Aeromonas spp. in Iran

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Introduction: Identifying Aeromonas reservoirs is crucial for understanding routes of infection. This analysis focuses on animal, environmental, and food reservoirs reported in Iran between 2000 and 2023.

Methods: Data were extracted from studies investigating Aeromonas in aquaculture, poultry, meat, and environmental samples. Reservoirs were classified and compared by frequency of isolation.

Results: Aeromonas spp. were isolated from fish (carp, trout, sturgeon), shrimp, seafood, poultry, pigeon feces, and even frozen minced meat. Contaminated aquaculture water and processing tools were main sources. Improper cold-chain management allowed persistence of Aeromonas after freezing. Cross-contamination from aquatic to terrestrial food chains was frequent.

Conclusion: Aquaculture and seafood are the predominant reservoirs of Aeromonas in Iran, with potential spillover to meat and poultry products. Sanitation and temperature control during handling are essential to reduce transmission.

Keywords: reservoirs, transmission, aquaculture, seafood, cross-contamination, food safety

Poster 102

Rising Threats from Gram-Negative Bacteria in Shiraz: Ten-Year Trends in Bloodstream Infections and Resistance Patterns

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Introduction: Gram-negative microorganisms are among the leading causes of bloodstream infections (BSIs) and contribute significantly to patient morbidity, mortality, and prolonged hospital stays. The increasing prevalence of multidrug-resistant (MDR) strains and extended-spectrum β-lactamase (ESBL)-producing organisms poses significant challenges for empirical therapy and clinical management. Continuous epidemiological surveillance is essential to identify emerging pathogens, guide antibiotic selection, and inform infection control measures. This study aimed to evaluate the distribution, antimicrobial resistance patterns, and prevalence of ESBL-producing Gram-negative bacteria in blood cultures over a ten-year period in Shiraz.

Methods: A retrospective analysis was conducted on blood cultures submitted to the Professor Alborzi Clinical Microbiology Research Center from March 2014 to March 2024. Blood culture bottles were monitored using the automated BACTEC system. Positive cultures were subcultured onto suitable media, and isolates were initially identified using standard biochemical tests. Final identification of isolates was primarily confirmed using the API 20E and API 20NE systems, and in cases where API results were ambiguous or inconclusive, the automated Phoenix platform was used for confirmation. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method according to CLSI guidelines. ESBL-producing isolates were identified phenotypically using the double-disk synergy test (DDST) in accordance with CLSI recommendations.

Results: A total of 6,990 Gram-negative isolates were obtained over the study period. The most frequently isolated bacteria were Stenotrophomonas maltophilia (1,937; 27.7%), Escherichia coli (893; 12.8%), Pseudomonas spp. (565; 8.1%), Enterobacter spp. (545; 7.8%), Klebsiella pneumoniae (534; 7.6%), and Acinetobacter baumannii (434; 6.2%). Non-fermenting Gram-negative bacilli dominated BSIs throughout the decade. Other Gram-negative species observed in the lowest numbers included Salmonella spp., Citrobacter spp., Morganella spp., and Burkholderia spp. High levels of antimicrobial resistance were observed: Ampicillin (92.1%), Cefuroxime (78.6%), Amoxicillin/Clavulanic acid (77.1%), Ceftriaxone (72.3%), Cefotaxime (72.0%), Tetracycline (71.1%), ESBL-producing strains (68.3%), Meropenem (35.3%), and Imipenem (30.9%). Escherichia coli and Pseudomonas spp. emerged as predominant causative agents in bloodstream infections throughout the study period.

Conclusion: The distribution of bloodstream pathogens remained relatively stable over the ten-year period. Stenotrophomonas maltophilia consistently emerged as the predominant pathogen, demonstrating its significance as a multidrug-resistant opportunistic organism. This persistent predominance may reflect its intrinsic resistance to multiple antimicrobial classes and its ability to thrive in hospital environments and colonize medical device. Other clinically relevant pathogens, including Enterobacter spp., Klebsiella pneumoniae, and Acinetobacter baumannii, fluctuated in annual prevalence but were present every year. Emerging opportunistic pathogens such as Achromobacter spp. showed gradual increases in some years, underscoring their growing clinical relevance. These findings emphasize the importance of continuous surveillance, evidence-based empirical therapy, and strict infection control measures, particularly in the context of ESBL-producing and multidrug-resistant Gram-negative organisms.

Keywords: Bloodstream infections; Gram-negative bacteria; Multidrug resistance; ESBL; Stenotrophomonas maltophilia; Shiraz

Poster 103

Role of CRISPR-Cas System on Virulence traits and Carbapenem Resistance in Clinical Klebsiella pneumoniae Isolates

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Introduction: The bacterial adaptive immune system known as CRISPR-Cas (clustered regularly interspersed short palindromic repeats-CRISPR-associated protein) is engaged in defense against various mobile genetic elements (MGEs) such as plasmids and bacteriophages. The purpose of this study was to characterize the CRISPR-Cas systems in carbapenem-resistant Klebsiella pneumoniae isolates and assess any possible correlation between these systems with antibiotic susceptibility, biofilm formation, and bacterial virulence.

Methods: A total of 156 CRKP isolates were collected from different specimens of the inpatients. Biofilm formation and antibiotic susceptibility testing were evaluated using standard methods. Furthermore, the CRISPR-Cas system subtype genes, 11 carbapenemase genes, and 17 virulence genes were identified using separate standard PCR reactions. The diversity of the isolates was determined by random amplified polymorphic DNA (RAPD)-PCR.

Results: The development of biofilms and antibiotic susceptibility of several CRKP isolates were significantly correlated with the absence or presence of the CRISPR-Cas system. PCR analysis of carbapenemase genes revealed that the frequency of the blaNDM-1 gene was significantly higher in the isolates with the subtype I-E CRISPR-Cas system. Moreover, the isolates with the subtype I-E CRISPR-Cas system exhibited a propensity to possess more virulence genes such as allS, k2A, wcaG, aerobactin, rmpA, iroN, magA, rmpA2, kfu, iutA, iucB, ybtS, repA, and terW.

Conclusion: CRISPR-Cas systems could affect the antibiotic susceptibility, capacity for biofilm formation, and virulence of Klebsiella pneumoniae. Our findings showed that the isolates containing the CRISPR-Cas system were moderate or strong biofilm producers and had a higher frequency of virulence genes.

Keywords: Klebsiella pneumoniae, CRISPR-Cas system, virulence genes, biofilm formation

Poster 104

SA/PVA-Based Multilayer Nanofibers Co-Delivering Berberine hydrochloride and Ciprofloxacin for Bioactive Wound Healing

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Introduction: Pseudomonas aeruginosa has a high mutation rate, enabling rapid development of resistance to multiple antimicrobial drugs, making infections difficult to treat. Skin is vulnerable to damage, and severe wounds pose life-threatening risks due to fluid and nutrient loss, necessitating effective wound dressings. Ideal dressings protect wounds and promote healing, but single-layer dressings often do not meet all clinical needs. Multilayer dressings are increasingly favored because their layers provide combined benefits. Materials such as polycaprolactone (PCL), polyvinyl alcohol (PVA), and sodium alginate (SA) are valuable for industrial, medical, and biomimetic wound dressing applications. Ciprofloxacin (CIP) is one of the most effective antibiotics against P. aeruginosa. Berberine(Ber), a natural alkaloid from Berberis vulgaris roots, has therapeutic and antioxidant properties. This study fabricated a multilayer wound dressing scaffold consisting of PCL/PVA,SA/PVA,Ber/PVA,CIP using electrospinning to enhance wound healing and infection control.

Methods: In this study, a novel multilayer wound dressing was fabricated using the dual-nozzle electrospinning technique, integrating polycaprolactone, polyvinyl alcohol, sodium alginate, ciprofloxacin, and berberine hydrochloride for the management of infected wounds caused by Pseudomonas aeruginosa. Ten clinical isolates of P. aeruginosa and the reference strain PAO1, were sourced from the Microbiology Department. Following confirmatory testing, minimum inhibitory concentrations (MIC) and minimum bactericidal concentrations (MBC) for ciprofloxacin and berberine hydrochloride were established via broth microdilution assays. Subsequently, nanofibrous wound dressings were synthesized. Comprehensive physicochemical characterizations were conducted, and antibacterial efficacy was assessed through disk diffusion assays alongside evaluation of hemocompatibility via red blood cell lysis percentage. The wound healing process and histological changes were further investigated using in vitro and in vivo models involving thirty laboratory mice over a 15-day period.

Results: The results demonstrated that incorporation of 10% berberine hydrochloride and 5% ciprofloxacin into the polymer matrix produced nanofibrous dressings with the smallest fiber diameter relative to other groups.Antibacterial assays revealed excellent activity against Pseudomonas aeruginosa, while hemolysis tests confirmed hemocompatibility with red blood cell hemolysis rates below 5%.The PCL/PVA,SA/PVA,Ber/PVA,CIP nanofiber group had the highest wound healing rate, and the addition of CIP and Ber to the nanofiber-based material resulted in anti-inflammatory and antibacterial results, and the duration of the wound healing process was reduced.Complementary in vivo evaluations and histological analyses demonstrated significant wound healing enhancement in scaffolds containing both drugs compared to other groups.

Conclusion: Considering the antibacterial effects of ciprofloxacin and berberine hydrochloride in reducing infection and wound healing, and considering that no new pharmaceutical form of these two drugs has been designed in the form of nanofibers for wound treatment, in the present study, by designing nanofibers, an attempt was made to use a pharmaceutical form with suitable characteristics for local drug delivery for the bacterium P.aeruginosa. Finally, considering the above, it can be stated that the prepared nanofibers containing PCL/PVA,SA/PVA,Ber/PVA,CIP have desirable effects in terms of antibacterial properties and can significantly help accelerate the healing of infected wounds as a dressing.

Keywords: Double-nozzle electrospinning, Polycaprolactone, Polyvinyl alcohol, Sodium alginate Berberine hydrochloride, Ciprofloxacin, Wound healing.

Poster 105

Serosurvey of toxoplasmosis among drug users in Fars Province, southern Iran: A cross-sectional study

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Introduction: Toxoplasma gondii is a widespread zoonotic protozoan that poses significant health risks, particularly to immunocompromised individuals. Although generally asymptomatic, toxoplasmosis can lead to severe neurological complications and behavioral disorders. This infection can be transmitted through various routes, including contaminated blood that may be transferred via syringes. The current cross-sectional study aimed to determine the prevalence of toxoplasmosis among drug users in Fars province in south of Iran.

Methods: Subjects of the study were 1400 drug users. Blood samples were collected from each individual from June 2023 to April 2024. T. gondii antigens were prepared from the parasite's tachyzoites and used in an ELISA system to detect anti-Toxoplasma antibodies. The data were analyzed to explore the possible association between Toxoplasma seropositivity and participants' demographics.

Results: The majority (52.7%) of the participants were aged 40-60 years, with 83.4% living in urban areas. Male constituted 92.8% and females 7.2% of the subjects. Anti-Toxoplasma antibodies were detected in the sera of 189 individuals, corresponding to a seroprevalence of 13.5%. Notably, 89.9% of those using injection methods for substance use were infected. Moreover, 94.2% of the infected individuals were male. Our findings revealed no association between Toxoplasma seropositivity and the demographic or method of drug use in patients with substance use disorder in Fars province in south of Iran.

Conclusion: These findings underscore the need for targeted public health interventions to address the risk of toxoplasmosis in this vulnerable population, particularly among those who use injection drugs. Further research is warranted to explore the underlying factors contributing to the high seroprevalence and to develop effective prevention strategies.

Keywords: substance use disorder, seroprevalence, Toxoplasma, Iran

Poster 106

Serum interleukin-37 levels in hepatitis B

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Introduction: Cytokine-mediated immune responses have been reported to regulate both viral replication and liver damage during hepatitis B virus (HBV) infection. Interleukin-37 (IL-37), a novel non-inflammatory cytokine, can prevent liver damage and may be an important candidate for use as a novel therapeutic tool in HBV infection. This study aimed to evaluate the serum levels of IL-37 in two groups of people with HBV, the chronic and the clearance groups, compared to a healthy control population.

Methods: 30 patients with chronic HBV, 30 patients with complete viral clearance, and 30 healthy subjects were included in this case-control study. Serum IL-37 levels were measured by enzyme-linked immunosorbent assay (ELISA).

Results: Our results showed a significant difference in IL-37 serum levels between HBV patients (94.06±10.78 pg/ml) and healthy controls (37.85±2.99 pg/ml, p-value = 0.008). Furthermore, results showed that IL-37 serum levels were significantly higher in the chronic group (CHB) (96.99±13.39 pg/ml) than in the control group (p-value = 0.02). Although its serum levels were slightly lower in individuals who spontaneously cleared the virus than CHB, the difference was not statistically significant. However, IL-37 serum levels in the clearance group were similar to healthy controls. Correlation analysis showed a statistically significant correlation between IL-37 serum levels and age in HBV patients (p-value=0.04, R=-0.26, n=60) as well as in clearance subjects (p-value=0.02, R=-0.42, n=30).

Conclusion: Our results suggest that increased production of IL-37 may biologically act as a negative feedback loop to attenuate the release of pro-inflammatory cytokines and subsequently alleviate disease symptoms in CHB. Our results show that IL-37 in people who spontaneously clear the virus is more similar to the control group than to CHB. The negative correlation between cytokine and age may be an indication that higher levels of IL-37 in younger people may lead to spontaneous clearance of HBV.

Keywords: Interleukin 37, hepatitis B, chronic hepatitis, clearance

Poster 107

Sharing of beta-lactam-resistant Escherichia coli between cats and their owners: The need for a One Health approach

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Introduction: Escherichia coli (E. coli), a common inhabitant of the intestinal tract in humans and warm-blooded animals, is not only part of the gut microbiota but can also act as a pathogen and carrier of antibiotic resistance genes. There is particular concern about its beta-lactam-resistant strains in both public health and veterinary medicine. Pets may act as reservoirs for these resistant strains and facilitate their transmission to humans. This study was designed to evaluate the prevalence of beta-lactam resistance and the distribution of beta-lactamase genes in E. coli isolates obtained from cats, cat owners, and a control group.

Methods: Seventy E. coli isolates were obtained from fecal samples collected from 30 cat–owner pairs and 10 healthy individuals without contact with pets (control group). The isolates were purified, identified, and tested for their susceptibility to beta-lactam antibiotics (cefotaxime, ceftazidime, aztreonam, and ampicillin-sulbactam (using the disk diffusion method. PCR was employed to detect the presence of blaSHV, and blaCTX-M-1 genes.

Results: The highest antibiotic resistance was observed against cefotaxime, with a frequency of 26.7% in cat isolates, 30% in cat owner isolates, and 20% in control group isolates. Similar resistance rates to ceftazidime (13.3%) were observed in cats and their owners, which was higher than the 10% in the control group. Resistance to aztreonam was observed exclusively in cats (16.7%) and cat owners (20%), and there were no aztreonam-resistant strains in the control group. Regarding ampicillin-sulbactam, cats showed the highest resistance (16.7%), followed by the control group (10%) and cat owners (6.7%). In the molecular analysis, the blaCTX-M-1 gene was identified in 3.3% of cats, 10% of cat owners, and 10% of the control group, but the blaSHV gene was not found in any of the group isolates.

Conclusion: E. coli isolates from cats and their owners showed relatively higher resistance to beta-lactams compared to the control group. The lack of significant difference in the frequency of beta-lactam-resistant E. coli isolates and the frequency of blaSHV and blaCTX-M-1 genes in E. coli isolates obtained from cats and their owners, along with the observation of some similarities between E. coli isolates from cats and their owners in terms of sensitivity and resistance patterns to beta-lactams, could all indicate the potential for transmission of beta-lactam-resistant E. coli strains between them. These findings highlight the urgent need for a "One Health" approach.

Keywords: Antimicrobial Resistance, Escherichia coli, Beta -lactamase genes, Cats, Cat owners, Beta-lactams

Poster 108

Shigella Isolates Identified in the Bloodstream at Namazi Hospital, Shiraz: Isolation and Antimicrobial Susceptibility Patterns

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Introduction: Shigella spp. are non-motile, facultatively anaerobic, Gram-negative bacilli belonging to the family Enterobacteriaceae. The major human pathogens include S. dysenteriae, S. flexneri, S. boydii, and S. sonnei. Shigella primarily invades the colonic epithelium, causing bacillary dysentery. Extraintestinal infection, such as bacteremia, is rare but clinically significant when it occurs

Methods: Blood cultures were collected at the Professor Alborzi Clinical Microbiology Research Center between January 2018 and November 2021 and processed using the BACTEC system. Bacterial identification was performed through standard biochemical tests. Antibiotic susceptibility testing was carried out using the standard disk diffusion method in accordance with CLSI guidelines.

Results: Three cases of Shigella bacteremia were identified. The isolates were obtained from: 1. A 6-year-old boy with meningitis, 2. A 45-year-old man with Non-Hodgkin lymphoma, and 3. An adult male patient for whom age and clinical history were unavailable. All three isolates exhibited nearly identical antibiotic susceptibility profiles. They were sensitive to levofloxacin, ciprofloxacin, meropenem.However resistance was observed to all third generation cephalosporin antibiotics.

Conclusion: The detection of three Shigella isolates from bloodstream infections at different time points suggests the possible emergence of a Shigella strain capable of extraintestinal invasion. Further molecular characterization of these isolates, including assessment of virulence factors, is recommended for better understanding of their pathogenic potential.

Keywords: Shigella spp., bacteremia, blood culture, antibiotic susceptibility, extraintestinal infection, clinical microbiology, CLSI guidelines, virulence

Poster 109

Some virulence genes are associated with antibiotic susceptibility in Enterobacter cloacae complex

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Introduction: Enterobacter cloacae complex (ECC) including different species are isolated from different human clinical samples. ECC is armed by many different virulence genes (VGs) and they were also classified among ESKAPE group by WHO recently. The present study was designed to find probable association between VGs and antibiotic susceptibility in different ECC species.

Methods: Forty-five Enterobacter isolates that were harvested from different clinical samples were classified in four different species. Seven VGs were screened by PCR technique and antibiotic susceptibility assessment was performed by disk-diffusion assay.

Results: Four Enterobacter species; Enterobacter cloacae (33.3%), Enterobacter hormaechei (55.6%), Enterobacter kobei (6.7%) and Enterobacter roggenkampii (4.4%) were detected. Minimum antibiotic resistance was against carbapenem agents and amikacin even in MDR isolates. 33.3% and 13.3% of isolates were MDR and XDR respectively. The rpoS (97.8%) and csgD (11.1%) showed maximum and minimum frequency respectively. Blood sample isolated were highly virulent but less resistant in comparison to the other sample isolates. The csgA, csgD and iutA genes were associated with cefepime sensitivity.

Conclusion: The fepA showed a predictory role for differentiating of E. hormaechei from other species. More evolved iron acquisition system in E. hormaechei was hypothesized. The fepA gene introduced as a suitable target for designing novel anti-virulence/antibiotic agents against E. hormaechei. Complementary studies on other VGs and ARGs and with bigger study population is recommended.

Keywords: Enterobacter cloacae complex, Virulence gene, Antibiotic resistance, MDR, Antivirulence

Poster 110

Study of antibiotic resistance pattern, resistance to aminoglycosides and fluoroquinolones in carbapenem-resistant Pseudomonas aeruginosa strains isolated from teaching hospitals of Babol University of Medical Sciences

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Introduction: In recent years, one of the major worldwide concerns has been the increasing prevalence of carbapenem-resistant Pseudomonas aeruginosa strains. The aim of this study was to investigate Study of resistance to aminoglycosides and fluoroquinolones in carbapenem-resistant Pseudomonas aeruginosa strains obtained from teaching hospitals of Babol University of Medical Sciences.

Methods: The antibiotic resistance pattern was determined using the Kirby–Bauer disk diffusion method according to CLSI standards for nalidixic acid, ciprofloxacin, kanamycin, ceftazidime and cefepime. The samples were assayed to detect the presence of resistance genes (qnrA ،qnrS ،ant ،aph) by the use of a polymerase chain reaction (PCR) method.

Results: In a study of 30 carbapenem-resistant Pseudomonas aeruginosa strains, the frequency of fluoroquinolone and aminoglycoside resistance genes was evaluated. The resistance rates were as follows: nalidixic acid (14.7%), ciprofloxacin (20.3%), kanamycin (20%), ceftazidime (19.3%), and cefepime (21%). Among the resistance genes, qnrA, qnrS, ant and aph, were detected with the highest frequencies in 12%, 10%, 9.9% and 19.8% of isolates, respectively.

Conclusion: The present study demonstrates the high prevalence of qnrA and aph genes in antibiotic-resistant P. aeruginosa isolates. These findings are consistent with reports from other regions, indicating the widespread distribution of these resistance determinants. The observed differences in prevalence across studies may be attributed to variations in bacterial populations, geographic location, antibiotic usage pressures, and clinical treatment strategies. Continuous monitoring of resistance genes is therefore essential to develop effective strategies for controlling antibiotic resistance.

Keywords: Aminoglycosides, Fluoroquinolones, Pseudomonas aeruginosa, Carbapenem

Poster 111

Synergistic antibacterial and anti-biofilm effects of graphene oxide nanoparticles and clove extract against multidrug-resistant burn wound pathogens.

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Introduction: Chronic burn wounds are frequently colonized by multidrug-resistant (MDR) bacteria forming resilient biofilms, posing serious therapeutic challenges. This study evaluated the synergistic antibacterial, bactericidal, and anti-biofilm activities of graphene oxide (GO) nanoparticles combined with aqueous clove extract (Syzygium aromaticum) against MDR pathogens isolated from chronic burn wounds.

Methods: GO nanoparticles were synthesized and characterized using FTIR, XRD, and SEM. Antibacterial synergy was quantified via the checkerboard microdilution method, determining the fractional inhibitory concentration index (FICI). Bactericidal efficacy was assessed through time-kill kinetics, while biofilm inhibition and eradication of Pseudomonas aeruginosa were evaluated using a crystal violet assay.

Results: The GO–clove combination exhibited a strong synergistic effect (FICI ≤ 0.5) against Acinetobacter baumannii, P. aeruginosa, and Enterococcus faecalis. Time-kill assays demonstrated rapid bactericidal action, achieving 99.9% reduction in viable cells within 4–8 hours—significantly faster than either agent alone. Additionally, the combination inhibited biofilm formation by over 90% and eradicated up to 85% of mature biofilms at elevated concentrations.

Conclusion: The synergistic combination of GO nanoparticles and clove extract enhances antimicrobial potency, accelerates bacterial clearance, and effectively disrupts biofilms. It holds promise as a multifunctional topical strategy for managing biofilm-associated infections in chronic burn wounds.

Keywords: Bacteria, Nanoparticle, GrapheneOxide, CloveExtract, BurnWound

Poster 112

Synergistic effects of colistin-based combinations against colistin and carbapenem-resistant Klebsiella pneumoniae isolated from nosocomial bloodstream infections

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Introduction: The emergence of colistin and carbapenem-resistant Klebsiella pneumoniae (CRCR-KP) poses a critical challenge in treating bloodstream infections. As resistance reduces colistin's efficacy, alternative strategies are urgently needed. Combination therapy may offer improved outcomes, but its effectiveness remains uncertain. This study evaluated in vitro interactions between colistin and 12 commonly used antibiotics against CRCR-KP isolates from nosocomial bloodstream infections.

Methods: A retrospective analysis identified 25 CRCR-KP isolates (10.8%) among 270 K. pneumoniae bloodstream infections, with 18 isolates included in synergy testing. Checkerboard assays were used to assess colistin-based interactions, quantified using the Fractional Inhibitory Concentration Index (FICI), Loewe Additivity, and Bliss Independence models. Demographic and clinical data were collected, including ward distribution, comorbidities, prior antibiotic exposure, and patient outcomes.

Results: The median patient age was 65 years (range: 2–94), and the mortality rate was 77.8% (14/18), underscoring the severity of these infections. Patients were primarily admitted to the ICU (22.2%), emergency department (33.3%), and hematology unit (22.2%), with frequent invasive procedures (94.4%) and hospital stays ranging from 4 to 60 days. Sixty-six percent of isolates were classified as extensively drug-resistant (XDR). Disk diffusion and MIC testing revealed high resistance across most antibiotic classes, though tigecycline (44.4%), amikacin (50%), and minocycline (34%) demonstrated partial efficacy. Synergy detection rates varied by model, FICI (75%), Loewe (50%), and Bliss (41.6%), highlighting the importance of using multiple analytical approaches.

Conclusion: Clindamycin, chloramphenicol, erythromycin, and minocycline exhibited strong synergy with colistin at lower concentrations, suggesting a promising combination strategy for managing CRCR-KP bloodstream infections. Minocycline appears particularly viable due to its achievable serum concentrations and moderate Gram-negative coverage. Further pharmacokinetic, pharmacodynamic, and clinical research is essential to validate these findings and guide the development of effective treatment regimens.

Keywords: Colistin and Carbapenem-Resistant Klebsiella pneumoniae (CRCR-KP), Nosocomial Bloodstream Infections, Antibiotic Synergy

Poster 113

The Coronavirus (COVID-19) in pregnant mothers and their Newborn

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Introduction: COVID-19, which has been an epidemic and pandemic in the world since late 2019, also occurs in mothers, and it is possible to transmit to the baby after birth. There are few reports of this because there are many diagnostic and differential diagnostic problems with respiratory symptoms in newborns. This may be included by examining umbilical cord blood. We evaluated about Covid 19 in pregnant mothers and their newborns by symptoms and PCRfor corona virus.

Methods: All mothers who were referred to the OmmolBanin Hospital maternity center in Mashhad , Iran(June 15,2020 to Aug 15, 2020) for labor were evaluated. All mothers suspicious respiratory infection tested for coronavirus with pharyngeal swabs and follow up mothers and neonates for coronavirus infection.

Results: Out of 100 pregnant mothers who were referred for labor examined and follow-up. Fifteen mothers had prenatal and 10 postpartum symptoms suspected of having a coronavirus test. The study was performed on an infant, although most infants had 18 respiratory symptoms and even suspicious radiography showed only 4 positive coronavirus test infants. Coronavirus testing was performed on the first, third, and fifth day of birth. The number of 14 infants was preterm and the remaining 11 were term. Most mothers had cesarean section for various reasons and 6 mothers had a normal delivery. In most infants, there was less than 90% positive pulse oximetry and positive CRP. Coronavirus testing was performed with a pharyngeal swab or tracheal tube sample (R.T PCR), which was reported in only 4 positive infants. One baby with 900 grams of weight that was positive for coronavirus died on the 12th day of life. Other babies

Conclusion: COVID-19 disease in neonates is an obvious fact and should be considered, although in our study, except for one or two cases, a real positive coronavirus test was performed. Because respiratory problems occur in newborns for a variety of reasons and there are various differential diagnoses, there is evidence of COVID-19 disease in the neonate.

Keywords: COVID-19, Pregnant Mother, Neonate.

Poster 114

The covid-19 effect on assisted reproductive method outcomes

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Introduction: The COVID-19 pandemic, caused by SARS-CoV-2, affects multiple body systems beyond the respiratory tract, including the reproductive system. Viral infection can alter ovarian function, hormonal balance, and endometrial receptivity, raising concerns about fertility and assisted reproductive technology (ART) outcomes. Previous studies reported reduced ovarian reserve, abnormal follicular development, and impaired embryo quality in women infected with COVID-19, though results vary. The timing of infection, especially during ovarian stimulation and oocyte retrieval, may influence reproductive outcomes. As infertility remains a global health concern and ART a critical treatment strategy, understanding the impact of COVID-19 on ART outcomes is essential. This study aimed to investigate whether COVID-19 infection on the day of oocyte retrieval affects oocyte yield, fertilization, and embryo quality in women undergoing in vitro fertilization (IVF).

Methods: This case–control study was conducted at Yas Hospital, Tehran University of Medical Sciences, between 2020 and 2022, including 190 infertile women undergoing IVF. The case group had confirmed COVID-19 infection by PCR on oocyte retrieval day, while controls were PCR-negative. Exclusion criteria included systemic illness, prior ovarian surgery, or incomplete records. Data collected included age, BMI, infertility duration, stimulation protocols, number of retrieved oocytes, mature oocytes (MII), fertilization rates, and embryo grading. Embryo quality was assessed morphologically as grade A, B, or C. Statistical analysis was performed using SPSS, with p 0.05 considered significant.

Results: Among 190 participants, 95 were COVID-19 positive and 95 controls. Baseline characteristics, including age, BMI, infertility duration, and stimulation protocols, were similar. The mean number of retrieved oocytes was lower in infected women (6.68 ± 2.71) than controls (9.07 ± 3.84; p 0.001). Mature oocytes (MII) were also fewer in the case group. Fertilization rates were not significantly different. Embryo quality differed: grade A embryos were less frequent, and grade C more common in COVID-19 positive women (p 0.05). The total number of embryos formed was similar between groups. These results indicate active COVID-19 infection at retrieval negatively affects oocyte yield and embryo morphology.

Conclusion: COVID-19 infection on oocyte retrieval day adversely impacts ART outcomes. Infected women had fewer retrieved and mature oocytes, with lower embryo quality, though fertilization rate and total embryos were similar. Reduced high-grade embryos suggest compromised early embryonic development. These findings highlight the potential effect of active infection during ovarian stimulation on reproductive potential. Clinicians should assess infection status before IVF and consider postponing cycles if COVID-19 is present. Further multicenter studies are needed to clarify mechanisms and long-term reproductive consequences. Understanding these effects is crucial for optimizing fertility outcomes during the ongoing pandemic.

Keywords: COVID-19, infertility, IVF, oocyte quality, embryo development, reproductive outcomes

Poster 115

The Emerging Threat of Trichophyton indotineae: A Case Series Demonstrating Familial Transmission and High Rates of Antifungal Resistance

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Introduction: The emergence and global spread of Trichophyton indotineae, a novel pathogen with patterns of antifungal resistance, has become a major concern. This study reports familial cases of this infection presenting with poor treatment response.

Methods: This case series describes four patients from two families. Skin samples were obtained from all patients despite ongoing medication (including voriconazole, itraconazole). Direct examination with KOH was performed, and samples were cultured on SDA. Initial identification was based on morphology. Species identification was confirmed by molecular methods (ITS sequencing), and antifungal susceptibility testing (according to CLSI M38 protocol) was performed on the isolates.

Results: Direct microscopy revealed abundant hyphae and arthroconidia. Fungal cultures from all samples were positive. Molecular diagnosis confirmed the pathogen as Trichophyton indotineae. Antifungal susceptibility testing revealed resistance to terbinafine and several azoles. One case of occupational transmission to the laboratory personnel occurred, which was promptly treated.

Conclusion: This report highlights the presence of T. indotineae in Iran and its pattern of familial transmission and intrinsic resistance. It underscores that in clinical cases suggestive of resistance, molecular diagnosis and antifungal susceptibility testing are essential for effective management and curbing the spread of this emerging pathogen.

Keywords: Trichophyton indotineae, Drug-Resistant Dermatophytosis, Familial Transmission, Molecular Diagnosis, Antifungal Susceptibility Testing.

Poster 116

The in vitro evaluation of synergistic effects of ciprofloxacin and berberine hydrochloride against Pseudomonas aeruginosa

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Introduction: Pseudomonas aeruginosa is a major cause of severe infections, leading to significant morbidity and mortality rates due to its ability of biofilm formation and antibiotic resistance. This study evaluates the in vitro antimicrobial and antibiofilm effects of ciprofloxacin and berberine hydrochloride, alone and in combination, against clinical and standard strains of P. aeruginosa.

Methods: Clinical isolates of carbapenem-susceptible P. aeruginosa (CSPA), carbapenem-resistant P. aeruginosa (CRPA), and the standard P. aeruginosa PAO1 strain were examined. Antimicrobial activity (MIC/MBC) and biofilm inhibition (MBIC/MBEC) were assessed using the microdilution method, checkerboard assay (FICI), and time-kill kinetics.

Results: The minimum inhibitory concentrations (MICs) of ciprofloxacin and berberine hydrochloride ranged from 0.5 to 64 µg/mL and 593 to 1187 µg/mL, respectively. The minimum bactericidal concentrations (MBCs) for both agents were ≥ 2× MIC. Neither ciprofloxacin nor berberine hydrochloride was able to eradicate 24-hour preformed biofilms (MBEC). However, biofilm prevention (MBIC) occurred at sub-MIC levels (0.5–1× MIC). The combination of ciprofloxacin and berberine hydrochloride demonstrated synergistic activity against PAO1 (FICI ≤ 0.5). The time-kill assay confirmed the bactericidal effect of this combination against PAO1 and CSPA isolates.

Conclusion: Berberine hydrochloride may serve as a promising synergistic agent to enhance the antimicrobial and antibiofilm activity of ciprofloxacin in vitro. This combination warrants further exploration as a therapeutic strategy against resistant infections.

Keywords: Pseudomonas aeruginosa, synergy, biofilm, Bberberine hydrochloride, ciprofloxacin

Poster 117

The role of pks-positive Escherichia coli in colorectal cancer: A narrative review

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Introduction: Colorectal cancer (CRC) is the third most common malignancy worldwide (6.1%) and the second leading cause of cancer-related mortality (9.2%). Mortality from rectal and colon cancer is predicted to rise by 60% and 71.5%, respectively, by 2035. Recent studies have highlighted a significant relationship between the gut microbiome and CRC development and progression. Among the gut bacteria, Escherichia coli harboring the polyketide synthase (pks) genomic island has attracted attention due to its ability to produce colibactin, a genotoxic metabolite associated with DNA damage and carcinogenesis.

Methods: This narrative review was conducted by analyzing recent publications focusing on pks-positive E. coli and its molecular mechanisms in CRC pathogenesis. Data were gathered from peer-reviewed articles indexed in PubMed, Scopus, and Web of Science, emphasizing studies published over the past decade.

Results: Evidence suggests that pks+ E. coli contributes to CRC initiation and progression through several mechanisms, including DNA double-strand breaks, chromosomal instability, and induction of pro-inflammatory responses. However, the precise role of pks+ E. coli in tumor proliferation and metastasis remains incompletely understood, and findings across studies show some inconsistencies.

Conclusion: Given the increasing global burden of CRC and the growing evidence linking pks+ E. coli to its pathogenesis, understanding the interaction between these bacteria and host cellular pathways is crucial. Further mechanistic and clinical studies are needed to clarify their role and to explore possible diagnostic or therapeutic strategies targeting pks+ E. coli in CRC management.

Keywords: pks+ E. coli; colorectal cancer; gut microbiota; therapy

Poster 118

Today's World and the Challenge of Antibiotic Resistance.

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Introduction: After the successful use of any therapeutic agent, it is possible for a resistance mechanism to develop to that compound. This is also true for agents used to treat bacterial infections. The survival of pathogens when exposed to antibiotics that can stop their growth is called antibiotic resistance. Studies have shown that more than 25% of hospital infections involve antibiotic-resistant bacteria. Since antibiotic resistance is associated with high rates of mortality and morbidity, and is projected to increase to 10 million people per year by 2050, and healthcare costs to the global economy to $100 trillion, antibiotic resistance is a global challenge to human health. This article examines this global challenge and attempts to outline ways to prevent and treat antibiotic resistance.

Methods: In this study, data related to the cultivation of various patient samples in the years 2021-2025 were collected, and the resistance and sensitivity rates of each antibiotic used for patients were examined and statistically analyzed.

Results: Our surveys and statistics show that antibiotic resistance is increasing day by day. For example, in Khatam Al-Anbiya-Hospital, bacterial strains have become completely resistant to drugs such as Cefazolin or Ampicillin (in 100% of cases).

Conclusion: With the increase in antibiotic-resistant bacterial strains in recent decades , there is a need to re-evaluate antibiotic use, raise public awareness of antibiotic resistance, and implement antibiotic surveillance programs, along with the application of new therapeutic solutions to combat drug-resistant bacteria such as phage therapy, combination therapies, nanoantibiotics.

Keywords: Antibiotic Resistance, hospital infections, global challenge

Poster 119

Trends, Patterns, and Demographic Dynamics of Drug Resistance in Mycobacterium Tuberculosis and Nontuberculous: A Multi-Year Analysis at the National Tuberculosis Reference Laboratory

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Introduction: Drug-resistant (DR) mycobacterial infections present escalating threats in Iran, where facility-specific transmission dynamics and demographic disparities remain poorly characterized. This study evaluated the epidemiology of DR Mycobacterium tuberculosis (MTB) and nontuberculous mycobacteria (NTM) over a nine-year period (2016–2024).

Methods: A retrospective cohort study analyzed 21,700 isolates at Iran's National Tuberculosis Reference Laboratory. Species identification used line probe assays and Xpert MTB/RIF. Drug susceptibility testing followed WHO standards. Statistical analyses identified associations between resistance patterns, hospital sections, gender, and specimen types.

Results: MDR-TB prevalence surged from 0.35% (2017) to 3.27% (2022), peaking during pandemic disruptions. M. simiae dominated NTM resistance (55.63% of resistant isolates), with significant increases in 2024 (7.91%). Airborne infection isolation rooms (AIIRs) paradoxically harbored 18.22% of MDR-TB isolates (p0.0001), while pulmonary medicine (PM) units contained zoonotic M. bovis reservoirs (0.27% MDR prevalence). Male patients carried higher burdens of MDR-TB (26.01% vs 12.45%, p=0.005) and M. kansasii (2.05% vs 0.53%, p=0.012). Diagnostic challenges included 38.14% smear-negative M. abscessus and gastrointestinal NTMs in gastric washings (GW, M. genavense: 66.66%). Sample type analysis revealed M. fortuitum in 25.0% of abscesses (p0.05) and M. chelonae in 5.55% of synovial fluid (SF) specimens.

Conclusion: Iran faces converging epidemics of MDR-TB and climate-adapted NTMs concentrated in hospital hotspots, with significant gender disparities. Precision interventions targeting AIIR protocols, water safety regulations, and gender-specific screening are urgently needed.

Keywords: Mycobacterium tuberculosis; Nontuberculous mycobacteria; Drug Resistance; Disease Hotspots; Infection Control.

Poster 120

Ultrastructural Adaptations of Fluconazole-Resistant Candida auris Clade V Exposed to Fluconazole

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Introduction: Candida auris is an emerging multidrug-resistant yeast and a significant cause of nosocomial infections worldwide, frequently exhibiting resistance to fluconazole. Clade V, recently identified in Iran, contains isolates with high-level fluconazole resistance, yet their ultrastructural adaptations to antifungal stress remain poorly understood. Investigating these cellular changes is crucial for understanding mechanisms of intrinsic antifungal resistance and developing strategies to manage multidrug-resistant infections. This study aimed to characterize, for the first time, the ultrastructural alterations of fluconazole-resistant C. auris clade V upon exposure to fluconazole using transmission electron microscopy.

Methods: Fluconazole-resistant C. auris clade V isolate, with a minimum inhibitory concentration (MIC) of 64 µg/mL for fluconazole, were cultured on Sabouraud dextrose agar (SDA) at 35°C for 48 hours and then exposed to fluconazole at 64 µg/mL in 24-well microplates for 24 hours. Cells were harvested, washed with phosphate-buffered saline, and fixed in glutaraldehyde. Fixed samples were embedded in epoxy resin, ultrathin-sectioned, stained with uranyl acetate and lead citrate, and examined using transmission electron microscopy. Ultrastructural features, including cell wall, plasma membrane, cytoplasm, vacuoles, and organelle-like structures, were carefully evaluated in fluconazole-treated cells.

Results: Transmission electron microscopy analysis revealed significant ultrastructural remodeling in fluconazole-exposed cells. Cell walls were thickened, and plasma membranes appeared irregular, sometimes detaching from the wall. Large vacuoles were frequently observed, accompanied by heterogeneous cytoplasmic electron density. Swollen or disorganized organelle-like structures resembling mitochondria were identified in several cells, indicating stress-induced intracellular changes. Some cells also displayed cytoplasmic vacuolization and accumulation of electron-dense granules, suggesting activation of adaptive mechanisms under antifungal pressure. These findings collectively demonstrate that fluconazole exposure induces extensive cellular remodeling, even in highly resistant clade V isolates.

Conclusion: Exposure of fluconazole-resistant C. auris clade V to MIC-level fluconazole triggers pronounced ultrastructural changes, reflecting cellular adaptations underlying intrinsic antifungal resistance. This study provides novel insights into the morphological basis of drug resistance and highlights potential targets for therapeutic intervention. The observed ultrastructural alterations may inform future strategies to manage multidrug-resistant C. auris infections in clinical settings.

Keywords: Candida auris clade V; fluconazole resistance; transmission electron microscopy; ultrastructural changes

Poster 121

Unraveling gut gram-negative antibiotic-resistant colonization dynamics in hematologic cancers: Insights from bioinformatics and immune signatures

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Introduction: Infections account for ~60% of cancer-related deaths. Hematologic cancers have a 3 times higher infection-related mortality than solid tumors, with resistant Gram-negative (GN) bacteria causing ~50% of bloodstream infections, highlighting the need to study the microbiome, antibiotic resistance, and infection risks.

Methods: Stool samples from newly diagnosed hematologic cancer patients were collected at baseline, post-chemotherapy, and subsequent admission at Amir Hospital, a referral cancer center in southern Iran, to analyze microbial colonization dynamics. Patients enrolled in a 16-month observational program to investigate the correlation between clinical factors and infectious outcomes. Carbapenem-resistant and ESBL-producing were cultured on MacConkey agar with meropenem and ceftriaxone. ESBL and carbapenemase production assessed adhering to CLSI guidelines. To support our findings, we used the microbioTA database to identify highly elevated 16S rRNA expression in blood and lymph nodes of hematologic cancer patients, exploring microbiome-host interactions worldwide. We used gutMgene, GIMICA, and AMIDIS databases to explore key microbe-immune factor associations trough network centrality analysis of the immune factors. Central factors further examined in the Amir Cancer Registry datasets to assess their association with infectious events. STATA v27 used for statistical analyses.

Results: Among 73 pediatric patients, GN drug-resistant bacteria was detected in 51 before hospitalization. Escherichia coli (86.6% of positive samples) and Klebsiella pneumoniae (9.5%) were the predominant pathogens. Drug-resistant E. coli persisted across samples, indicating gut colonization, consistent with microbioTA data showing E. coli detection at baseline and post-induction therapy. ESBL and carbapenemase-producing strains were 56.8% and 15.8%. Colonized patients had a 13.8% mortality rate, with bloodstream infections and typhlitis more common in K. pneumoniae and carbapenem-resistant strains. Previous antibiotic exposure, malignancy relapse, and colonization status were risk factors for mortality and infection. Investigation of the microbioTA database identified 10 datasets from Asia, Europe, and America revealed the detection of Bacillus cereus in 9 datasets, followed by E.coli (8) and Enterobacterales like Salmonella enterica (5) and K.pneumoniae (3), approving the high impact of E.coli worldwide. IL-4, IL-6, and TNF-α showed high centrality, with retrospective analysis linking their upregulated serum baseline levels.

Conclusion: Our study links GN microbial colonization, traced by elevated immune markers, to infectious complications, highlighting the need for microbiota-specific diagnostic and treatment protocols.

Keywords: Gut microbiome, Antimicrobial resistance, Gram-negative bacteria, Pediatric hematologic malignancies, microbiome–host interactions