ششمین
باکتری
پزشکی ایر
(بین المللی)
۲۶-۲۴ بهمن ماه ۱۴۰۳
تهران، دانشگاه تربیت م
سالن همایش شهید

رسال مقالات ۱۵ مهر الی ۳۰ آذر ماه
ز طریق وبسایت کنگره
ا امتیاز بازآموزی

Booklet of Abstracts

محورهای کنگره

نقش پروبیوتیک ها در سلامت م
هوش مصنوعی و تکنیک های
عفونت های بیمارستانی
عفونت های منتقله از آب و غذا
بیماری های نوپدید و باز پدید
تجویز منطقی آنتی بیوتیک ها و مکانیسم های
اخلاق حرفه ای در تحقیقات و بالین
عفونت، میکروبیوم و سرطان
باکتریوفاژ ها و سلامت
استراتژی های جد
مسایل و دغ

6TH MEDICAL BACTERIOLOGY CONGRESS 2025

international

February 12-14

Introduction

The 6th Congress of Medical Bacteriology of Iran commenced on Wednesday, February 13 (24th of Bahman), hosted by Tarbiat Modares University. Experts and specialists in this field discussed and exchanged views on key topics, including the role of probiotics in health and disease, Artificial intelligence and innovative techniques in the diagnosis of bacterial infections, Hospital-Acquired Infections, water- and foodborne infections, emerging and re-emerging diseases, rational antibiotic prescription and resistance mechanisms, professional ethics in research and clinical practice, infection and microbiome in cancer, bacteriophages and health, new strategies in the prevention and treatment of bacterial infections, as well as issues and concerns of postgraduate students and graduates.

During this specialized event, seven workshops were held. Out of approximately 400 articles submitted to the secretariat of the 6th Congress, about 300 were accepted and presented in oral or poster format during the three-day congress.

On Friday, at the closing ceremony of the 6th Congress of Medical Bacteriology of Iran, the top poster presenters were honored with financial support from Emad Pathobiology and Genetics Laboratory, and the winners of the gold and silver grants were recognized with the support of the Iranian Society of Medical Bacteriology.

Introduction of Scientific and Executive Members

Dr. Abdolaziz Rastegarlari

Founder of the Iranian Society of Medical Bacteriology

Dr. Bahareh Hajikhani

Executive Secretary of the Congress

Dr. Fatemeh Fallah

President of the Congress

Dr. Bita Bakhshi

Scientific Secretary of the Congress

Dr.Ali Shivaei

Executive Deputy

Dr.Fatemeh sameni

Executive Deputy

Message from the President of the 6th Iranian Congress of Medical Bacteriology

Greetings and Respect,

The 6th Iranian Congress of Medical Bacteriology presents an exceptional opportunity for the gathering of specialists, researchers, and students engaged in this valuable field. This congress is held with the aim of fostering dialogue, sharing scientific findings, and advancing knowledge in medical bacteriology.

In today's world, bacteria play diverse roles in human health, and a deeper understanding of their behavior can significantly enhance treatment methods and disease prevention strategies. It is a source of pride that this congress provides a platform for discussing and reviewing the latest scientific and research achievements.

I extend my heartfelt gratitude to all participants, speakers, and supporters whose presence and encouragement contribute to the successful organization of this event. I hope this congress becomes a space for expanding scientific and research collaborations among experts and researchers, ultimately promoting public health.

Wishing you continued success,
Dr. Fatemeh Fallah
President of the
6th Iranian Congress of Medical Bacteriology

Message from the Scientific Secretary of the 6th Iranian Congress of Medical Bacteriology

Dear Esteemed Professors, Respected Researchers, and Honored Students,
It is with great pride and gratitude to the Almighty that we announce the 6th Iranian Congress of Medical Bacteriology, to be held from February 13 to 15, 2025, at Tarbiat Modares University. This major scientific event, bringing together students, professors, and bacteriology researchers from across the country, offers a valuable opportunity to enhance academic knowledge, exchange the latest research findings, and foster collaboration in fields aligned with the congress themes. It will play a vital role in advancing both theoretical and practical aspects of bacteriology.
In light of the remarkable progress made in recent years in the fields of science and emerging technologies related to bacteriology, this congress aims not only to share relevant research but also to present the latest investigations conducted by leading experts and scholars. These contributions will help bridge the gap between scientific discovery and clinical application, paving the way for more effective and informed practices.

We warmly invite all researchers, faculty members, and students to participate and present their valuable scientific achievements at this congress. Your esteemed presence will undoubtedly enrich this important scientific gathering, create lasting memories, and contribute to further advancements in the field—offering hope for a brighter future for our nation.

With respect,
Dr. Bita Bakhshi
Scientific Secretary
6th Iranian Congress of Medical Bacteriology

Message from the Executive Secretary of the 6th Iranian Congress of Medical Bacteriology

Greetings and Respect

The 6th Iranian Congress of Medical Bacteriology stands as a distinguished scientific event, offering a unique opportunity for the gathering of researchers, specialists, and students active in the field of medical bacteriology. Through the invitation of esteemed speakers and the organization of specialized workshops, participants are expected to become acquainted with the latest scientific methods and techniques, while engaging in discussions and exchanges on the challenges and opportunities within this domain.

Moreover, the presentation of scientific abstracts and recent research will enrich the content of the congress and contribute to its overall quality. It is our hope that, through the valuable collaboration and participation of respected professors, dedicated researchers, dear students, and other companions, this congress will evolve into an impactful and successful scientific event—opening new doors toward further advancements in the field of medical bacteriology.

Wishing health, success, and progress to all those who, with a passion for science and service to humanity, are shaping a brighter future for both science and society.

With respect,
Bahareh Hajikhani
Executive Secretary of the
6th Iranian Congress of Medical Bacteriology

List of Congressional Policy Councils

- Dr. Abdolaziz Rastegar Lari

(Professor, Iranian Medical Sciences)

- Dr. Fatemeh Fallah

(Professor - Shahid Beheshti Medical Sciences)

- Dr. Mohammadreza Pourshafi

(Professor, Pasteur Institute of Iran)

- Dr. Mohammad Mehdi Soltan Dalal

(Professor, Tehran University of Medical Sciences)

- Dr. Azardokht Khosravi

(Professor - Jundishapur Ahvaz)

- Dr. Bahareh Hajikhani

(Assistant Professor - Shahid Beheshti Medical Sciences)

- Dr. Bita Bakhshi

(Professor - Tarbiat Modares)

Congressional Scientific Committee List (in alphabetical order)

- Dr. Abdolaziz Rastegar Lari (Professor, Iranian Medical Sciences)
- Dr. Abdollah Karimi (Professor, Shahid Beheshti University of Medical Sciences)
- Dr. Ali Akbar Pourfathollah (Professor - Tarbiat Modares)
- Dr. Ali Mojtahedi (Professor- Iranian Medical Sciences)
- Dr. Amir Abbas Vaezi (Assistant Professor, Alborz Medical Sciences)
- Dr. Arezoo Mirzaei (Assistant Professor, Isfahan Medical Sciences)
- Dr. Ashraf Mohabati Mobarez (Professor, Tarbiat Modares)
- Dr. Azardokht Khosravi (Professor - Jundishapur Ahvaz)
- Dr. Bahareh Hajikhani (Assistant Professor - Shahid Beheshti Medical Sciences)
- Dr. Bahram Nasr Esfahani (Professor - Isfahan Medical Sciences)
- Dr. Bita Bakhshi (Professor - Tarbiat Modares)
- Dr. Davood Esmaeili (Professor, Baqiyatallah Medical Sciences)
- Dr. Elham Musarrat (Assistant Professor - Tarbiat Modares)
- Dr. Fakhri Haghi (Professor, Zanjan University of Medical Sciences)
- Dr. Faranak Alinejad (Professor- Iranian Medical Sciences)
- Dr. Farhad Nikkhahi (Assistant Professor, Qazvin University of Medical Sciences)
- Dr. Farzad Badmasti (Associate Professor, Pasteur Institute of Iran)
- Dr. Fateh Rahimi (Associate Professor, University of Isfahan)
- Dr. Fatemeh Fallah (Professor - Shahid Beheshti Medical Sciences)
- Dr. Fatemeh Fardsanei (Assistant Professor, Qazvin Medical Sciences)
- Dr. Ghazi Khansari (Professor, Tehran University of Medical Sciences)
- Dr. Habib Zeighami (Professor, Zanjan Medical Sciences)
- Dr. Hadi Farsiani (Assistant Professor, Mashhad Medical Sciences)
- Dr. Hadipour Jafar (Associate Professor - Alborz Medical Sciences)
- Dr. Hossein Dargahi (Professor - Tehran Medical Sciences)
- Dr. Hossein Masoumi Asl (Professor, Iranian Medical Sciences)
- Dr. Kamran Poushang Bagheri (Assistant Professor, Pasteur Institute of Iran)
- Dr. Katayoun Borhani (Assistant Professor - Azad Central Tehran)
- Dr. Kiarash Qazvini (Professor, Mashhad University of Medical Sciences)

- Dr. Leila Afshar (Professor - Shahid Beheshti Medical Sciences)
- Dr. Leila Azimi (Associate Professor, Shahid Beheshti University of Medical Sciences)
- Dr. Maghsoud Jafarinia (Alborz Health Department)
- Dr. Mahboobeh Haj Abdolbaghi (Professor, Tehran University of Medical Sciences)
- Dr. Majid Akbari (Assistant Professor, Arak Medical Sciences)
- Dr. Maliheh Talebi (Professor- Iranian Medical Sciences)
- Dr. Maryam Nikkhah (Associate Professor, Tarbiat Modares)
- Dr. Maryam Soleimanifard (-Alborz Medical Sciences)
- Dr. Marzieh Jabbari (Researcher of Institute of Neuroscience and Physiology, Sweden)
- Dr. Masoud Dadashi (Assistant Professor, Alborz University of Medical Sciences)
- Dr. Masoud Mardani (Professor - Shahid Beheshti Medical Sciences)
- Dr. Masoumeh Aslanimehr (Associate Professor, Qazvin University of Medical Sciences)
- Dr. Masoumeh Doraghi (Professor, Tehran University of Medical Sciences)
- Dr. Masoumeh Ebtekar (Professor, Tarbiat Modares University)
- Dr. Masoumeh Navidinia (Assistant Professor - Shahid Beheshti Medical Sciences)
- Dr. Masoumeh Saberpour (Researcher, Pasteur Institute of Iran)
- Dr. Mehdi Rouhani (Associate Professor, Pasteur Institute of Iran)
- Dr. Mehrdad Mohammadi (Assistant Professor, Shiraz University of Medical Sciences)
- Dr. Mitra Barati (Professor, Iranian Medical Sciences)
- Dr. Mohammad Hossein Yazdi (Associate Professor, Tehran University of Medical Sciences)
- Dr. Mohammad Mehdi Soltan Dalal (Professor- Tehran Medical Sciences)
- Dr. Mohammad Motamedifar (Professor, Shiraz University of Medical Sciences)
- Dr. Mohammad Rahbar (Professor, Central Headquarters of the Ministry of Health)
- Dr. Mohammad Vajgani (Professor, Tehran University of Medical Sciences)

- Dr. Mohammad Zeinali (Assistant Professor - Central Headquarters of the Ministry of Health)
- Dr. Mohammadreza Pourshafi (Professor, Pasteur Institute of Iran)
- Dr. Mohammadreza Salehi (Associate Professor, Tehran University of Medical Sciences)
- Dr. Mohammadreza Saudistani (Professor, Hamedan Medical Sciences)
- Dr. Mohsen Mirzaei (Assistant Professor - Azad Borujerd)
- Dr. Mohsen Zahraei (Professor, Ministry of Health)
- Dr. Mojtaba Hedayat Yaghoubi (Associate Professor, Alborz Medical Sciences)
- Dr. Morvarid Shafiei (Assistant Professor, Pasteur Institute of Iran)
- Dr. Nastaran Asghari Moghaddam (Assistant Professor - Azad Central Tehran)
- Dr. Neda Baseri (Assistant Professor, Tarbiat Modares)
- Dr. Neda Soleimani (Associate Professor, Shahid Beheshti University)
- Dr Nuthar Jassam (Professor of Department of Pathology, Harrogate District Hospital, United Kingdom Consultant Clinical Biochemist)
- Dr. Parvaneh Jafari (Assistant Professor, Azad University, Arak)
- Dr. Pejman Rouhani (Associate Professor, Tehran University of Medical Sciences)
- Dr. Rasoul Yousefi Mashouf (Professor, Hamedan Medical Sciences)
- Dr. Reza Khashei (Associate Professor, Sabzevar Medical Sciences)
- Dr. Reza Omani Samani (Assistant Professor, ACECR)
- Dr. Saber Esmaeili (Assistant Professor, Pasteur Institute of Iran)
- Dr. Saeed Alamian (Associate Professor, Razi Research and Serum Institute)
- Dr. Saeed Biroudian (Assistant Professor - Iranian Medical Sciences)
- Dr. Saeed Shams (Assistant Professor, Qom Medical Sciences)
- Dr. Safoora Derakhshan (Associate Professor, Kurdistan Medical Sciences)
- Dr. Sara Bagheri (Assistant Professor, Kashan University of Medical Sciences)
- Dr. Sara soudi (Associate Professor, Tarbiat Modares)
- Dr. Seyed Ali Anjoo (Assistant Professor - Shahid Beheshti Medical Sciences)
- Dr. Seyed Davar Siadat (Professor, Pasteur Institute of Iran)

- Dr. Seyed Hossein Ardehali (Associate Professor, Shahid Beheshti University of Medical Sciences)
- Dr. Seyed Mahmood Amin Marashi (Associate Professor, Qazvin Medical Sciences)
- Dr. Seyed Mohsen Mir Hosseini (Associate Professor, Shahid Beheshti Medical Sciences)
- Dr. Somayeh Yaslani (Associate Professor, Alborz Medical Sciences)
- Dr. Taher Azimi (Assistant Professor, Shiraz University of Medical Sciences)
- Dr. Tahmineh Narimani (Assistant Professor, Isfahan Medical Sciences)
- Dr. Zahra Rajabi (Researcher, Tehran University of Medical Sciences)
- Professor Arach Ghodousi (Vita Salute San Raffaele University, TB Supranationa Reference Lab and WHO-CC Milan)
- Professor Colin W. Wright, (Professor of Pharmacognosy at the Bradford School of Pharmacy and Medical Sciences, University of Bradford, United Kingdom)
- Professor Fereshteh Fallah (Researcher of Bradford university United Kingdom)
- Professor Iraj Sobhani (Hopital Henri Mondor, Rue Gustave Eiffel, Créteil, France)
- Professor Mohamad Katouli (Associate Professor, Microbial Ecology, Centre for Bio-innovation Sunshine Coast University, Australia)
- Professor Reza Alaghebandan (Professor of Pathology at the Cleveland Clinic Lerner College of Medicine (CCLCM) of Case Western Reserve University (CWRU) School of Medicine)

List of Scientific Advisors of the Congress (in alphabetical order)

- Dr. Ahmad Khorshidi (Professor, Kashan University of Medical Sciences)
- Dr. Akbar Tavakoli (Professor - Isfahan Medical Sciences)
- Dr. Ali Akbar Mirsalehian (Professor, Tehran University of Medical Sciences)
- Dr. Ali Hashemi (Associate Professor, Shahid Beheshti Medical Sciences)
- Dr. Bita Bakhshi (Professor - Tarbiat Modares)
- Dr. Ebrahim Faghihlou (Associate Professor, Shahid Beheshti Medical Sciences)
- Dr. Farahnoosh Doostdar (Associate Professor, Shahid Beheshti University of Medical Sciences)
- Dr. Gita Eslami (Professor - Shahid Beheshti University of Medical Sciences)
- Dr. Hossein Goudarzi (Professor - Shahid Beheshti Medical Sciences)
- Dr. Khosro Neyestani (Laboratory Science Specialist)
- Dr. Kiumars Ghazi Saeedi (Professor, Tehran University of Medical Sciences)
- Dr. Mahboobeh Naderi Nasab (Professor, Mashhad Medical Sciences)
- Dr. Maryam Vaez Jalali (Associate Professor, Shahid Beheshti University of Medical Sciences)
- Dr. Mehdi Goudarzi (Associate Professor, Shahid Beheshti Medical Sciences)
- Dr. Mohammad Javad Nasiri (Associate Professor, Shahid Beheshti University of Medical Sciences)
- Dr. Mohammadreza Nahaei (Professor, Tabriz University of Medical Sciences)
- Dr. Mohammadreza Pourmand (Professor, Tehran University of Medical Sciences)
- Dr. Mojdeh Hakimi Vala (Professor - Shahid Beheshti University of Medical Sciences)
- Dr. Mojgan Derakhshan (Tarbiat Modares University)
- Dr. Naser Badami (Professor, Tehran University of Medical Sciences)
- Dr. Parvaneh Saffarian (Assistant Professor, Islamic Azad University)
- Dr. Rahim Kamyab (Ministry of Education)

- Dr. Reza Hosseinidoost (Professor - Baqiyatallah Medical Sciences)
- Dr. Seyed Asghar Haavi (Professor, Isfahan Medical Sciences)
- Dr. Somayeh Delfani (Associate Professor, Shahid Beheshti Medical Sciences)
- Dr. Tayebeh Shahbazi (Tarbiat Modares University)
- Dr. Zohreh Ghalavand (Associate Professor, Shahid Beheshti University of Medical Sciences)

Introduction of the Congress Executive Team

Team Poster

Dr. Amir Hossein Fayazi	Dr. Javad Yasbolaghi Sherahi	Dr. Fatemeh Dolatkhah
Sadegh Jahani	Mohammadreza Nadernejad	Mohammad Javad Mousavi

Ceremonial Team

Azadeh Alirezaei	Amir Hossein Bayati	Dr. Saeed Fouladvand	Samira Soltani
Fatemeh Taheri	Mallika Shyasi	Mehrasa Salmani	Niloufar Batebi

Registration Team

Anita Nikoo	Dr. Parisa Abedi	Dr. Hossein Ghahreman	Dr. Sara Bahonar
Saghar Nik	Dr. Sahar Rastiani	Sahar Houshmandi	Fatemeh Abdoli
Maral Shafiei	Mohsen Javidi	Mohammad Javad Roustaei	

Public Relations Team

Ehsan Ghanbari	Bita Zandi	Tina Bahrami Farjam
Zina Fallahi	Sara Salahshouri	Dr. Sarvanaz Esfahani
Fatemeh Roozbahani	Shaghayegh Mahmudabadi	Dr. Fatemeh Navab Moghaddam
Fereshteh Sarijlou	Mohammad Amin Doraqi	Maryam Rasouli

Salon Team

Asra Fatemi
Elham Rezaei
Elina Hojjati
Dr Rana Kazemzadeh
Zahra Johdi
Zahra Darabi
Dr. Sahel Safaei
Sara Bayat
Sepehr Asadi
Tala Haji Arab
Dr. Forough Goudarzi
Golbarg Mal Amir
Mohammad Hossein Kafashian
Yeganeh Goldoost

Workshop Team

Bita Khan Babaei
Fatemeh Doaei
Mohammadreza Shafiei
Mahsa Oaisari
Dr. Najmeh Ardeshiri
Narges Omidinia
Helia Rasouli

Exhibition Team

Fatemeh Khalghati
Nikan Bahrameh

6th Iranian Congress of Medical Bacteriology (International)
12-14 February 2025 Tehran – Tarbiat Modares University

The first day's program (Wednesday 02/12/2025)	
Register and get the application	7-8
Recitation of the Holy Quran and the Anthem of the Islamic Republic of Iran	8-8:45
Welcome Dr. Yousef Hojjat (President of Tarbiat Modares University) Dr. Fatemeh Fallah (President of the Association and Congress) Dr. Abdulaziz Rastegar Lari (Founder of the Association)	
Report of the Scientific Secretary of the Congress (Dr . Bita Bakhshi)	

Title of the first panel: The role of probiotics in health and disease Panel Chairman: Dr. Mohammad Mehdi Soltan Dalal			
Topic of the Lecture	**Specialization/University**	**Speaker Name**	**Hours**
Chair of the Panel	Medical Bacteriology A.P. University of Tehran	Dr. Mohammad Mehdi Soltan Dalal	8:45-10
Probiotic Perspective: From the Past to the Future	Microbiology Islamic Azad University (Central Tehran)	Dr. Maryam Tajabadi Ebrahimi	
Psychobiotics and Neurobiotics of the New Generation Probiotics	Medical Bacteriology Pasteur Institute of Iran	Dr. Seyed Davar Siadat	
The Use of Probiotics in Gastrointestinal Diseases	Pediatric Gastroenterologist A.P. University of Tehran	Dr. Pejman Rouhani	
The role of the microbiome in cardiovascular diseases	Specialist in Cardiovascular Surgery Shahid Beheshti University	Dr. Seyed Mohsen Mir Hosseini	
The role of the microbiome in skin infections	Dermatologist and hair specialist A.P. University of Tehran	Dr. Parvin Mansouri	
Use of Probiotics in Bioremediation of Heavy Metals	Medical Bacteriology Pasteur Institute of Iran	Dr. Mehdi Rouhani	

Comprehensive Speech			
Topic of the Lecture	**Expertise**	**Speaker Name**	**Hours**
Lecture Title : Prostate and Bladder Infections	Professor of Pathology	Dr. Reza Alaghbandan (United States)	10-10:30
Rest & Catering			15 min

Topic 2: Artificial Intelligence and New Techniques for Detecting Bacterial Infections Panel Chair: Dr. Abdulaziz Rastegar Lari			
Topic of the Lecture	**Specialization/University**	**Speaker Name**	**Hours**
Chair of the Panel	Medical Bacteriology A.P. University of Iran	Dr. Abdolaziz Rastegar Lari	10:45-12
Diagnostics in Bacteriology with an Approach to Modern Techniques	Medical Bacteriology A.P. University of Qom	Dr. Saeed Shams	
"Application of Artificial Intelligence in Diagnosis and Control of Antibiotic Resistance Caused by Nosocomial Bacterial Infections"	Medical Bacteriology Pasteur Institute of Iran	Dr. Farzad Badmasti	
Personalized Prediction of Cancer Diagnosis Caused by Bacterial Infections with Artificial Intelligence Focus	Medical Bioinformatics Tarbiat Modares University	Dr. Elham Musarrat	
The New Era of Teaching-Learning	Farhangian University	Dr. Rahim Kamyab	
Prayer - Lunch			Until 13:00

Comprehensive Speech			
Topic of the Lecture	**Expertise**	**Speaker Name**	**Hours**
Role of Type 6 secretion system (T6SS) in translocation of *E. coli*	Medical Bacteriology University of the Sunshine Coast of Australia	Dr. Mohammad Katouli (Australia)	13-13:30

Chapter 3: Food and Water Borne Infections Panel Chairman: Dr. Hossein Masoumi Asl			
Topic of the Lecture	**Specialization/University**	**Speaker Name**	**Hours**
Ten Steps to Investigating an Outbreak of Food and Water Borne Disease	Infectious Disease Specialist, A.P. University of Iran	Dr. Hossein Masoumi Asl	13:30-14:45
Epidemiology and Reporting of Water- and Foodborne Outbreaks in Iran	Medical Parasitology Ministry of Health	Dr. Mohammad Zeinali	
The Importance of Food Hygiene in Controlling Water-Foodborne Outbreaks	Food Hygiene Specialist A.P. Alborz University	Dr. Hadipour Jafar	
Outbreaks caused by non-typhoid salmonella and Escherichia coli	Medical Bacteriology , Qazvin University	Dr. Fatemeh Fardsanei	
The mysterious bacterium Listeria	Laboratory Science Specialist	Dr. Khosro Neyestani	
Rest & Catering			15 min

Title of the Fourth Panel: Nosocomial Infections Panel Chairman : Dr. Seyed Hossein Ardehali			
Topic of the Lecture	**Specialization/University**	**Speaker Name**	**Hours**
Nosocomial infection control strategies in the intensive care unit	Intensive Care Specialist Shahid Beheshti University	Dr. Seyed Hossein Ardehali	15-16:15
The importance of nosocomial infections	Medical Bacteriology A.P. University of Zanjan	Dr. Habib Zeighami	
Nosocomial Infections in Mofid Children's Hospital	Medical Bacteriology Shahid Beheshti University	Dr. Leila Azimi	
Discussion	Medical Bacteriology A.P. University of Mashhad	Dr. Kiarash Qazvini	
Discussion	Infectious Diseases Specialist A.P. Alborz University	Dr. Mojtaba Hedayat Yaghoubi	

Meeting Title: Presentation of Selected Papers Chairman : Dr. Bahareh Hajikhani		
Presentation of Selected Papers for Lectures		**Hours** 16:15-17:15
Medical Bacteriology- Shahid Beheshti University of Medical Sciences	Dr. Bahareh Hajikhani	Board of Directors
Medical Bacteriology- Mashhad University of Medical Sciences	Dr. Hadi Farsiani	
Medical Bacteriology- Islamic Azad University	Dr. Nastaran Asghari Moghaddam	
Medical Bacteriology- Islamic Azad University of Borujerd	Dr. Mohsen Mirzaei	
Medical Bacteriology- Islamic Azad University	Dr. Katayoun Borhani	
Medical Bacteriology- Arak University of Medical Sciences	Dr. Majid Akbari	
Medical Bacteriology- Iran University of Medical Sciences	Dr. Ali Mojtahedi	

The first day's program (Wednesday 02/13/2025)	
Register and get the application	7-8

Title of the first panel: Emerging and re-emerging diseases Panel Chairman : Dr. Azardokht Khosravi			
Topic of the Lecture	**Specialization/University**	**Speaker Name**	**Hours**
Antibiotic resistance in Mycobacterium tuberculosis according to the latest update of the World Health Organization	Medical Bacteriology Ahvaz University of Medical Sciences	Dr. Azardokht Khosravi	8-9:15
Isolation and identification of Brucella in animal and human populations of Iran	Microbiology of Razi Vaccine and Serum Research Institute	Dr. Saeed Alemian	
A Review of the Situation of Rickettsia in Iran: A New and Serious Concern for the Country's Health System	Medical Bacteriology Pasteur Institute of Iran	Dr. Saber Esmaeili	
Introduction of the Research Base of Emerging and Re-Emerging Diseases of the Pasteur Institute of Iran	Epidemiology Pasteur Institute of Iran	Dr. Ehsan Mostafavi	

Title of the second panel: Professional ethics in research and practice Panel Chairman : Dr. Fatemeh Fallah			
Topic of the Lecture	**Specialization/University**	**Speaker Name**	**Hours**
Discussion	Medical Bacteriology Shahid Beheshti University of Medical Sciences	Dr. Fatemeh Fallah	9:15-10:30
Discussion	Medical Ethicist Shahid Beheshti University of Medical Sciences	Dr. Leila Afshar	
Discussion	Medical Ethicist Shahed University of Medical Sciences	Dr. Seyed Ali Anjou	
Discussion	Medical Ethicist Iran University of Medical Sciences	Dr. Saeed Biroudian	
Discussion	Professional Doctor of Medicine Royan Research Institute (ACECR)	Dr. Reza Omani Samani	
Rest & Catering			15 min

Title of the Third Panel: Rational Prescribing of Antibiotics and Mechanisms of Resistance Panel Chairman : Dr. Masoud Mardani			
Topic of the Lecture	**Speaker Name**	**Speaker Name**	**Hours**
Chair of the Panel	Infectious Disease Specialist Shahid Beheshti University of Medical Sciences	Dr. Masoud Mardani	10:45-12
WHO Research Priorities in Relation to Antibiotic Resistance	Medical Bacteriology Iran University of Medical Sciences	Dr. Maliheh Talebi	
Different mechanisms of antibiotic resistance	Infectious Disease Specialist	Dr. Frank Alinejad	
Rational prescribing of antibiotics	Infectious Disease Specialist Iran University of Medical Sciences	Dr. Mitra Barati	
Resistance to Colistin	Medical Bacteriology Ministry of Health	Dr. Mohammad Rahbar	
Resistance to Carbapenems	Medical Bacteriology Qazvin University of Medical Sciences	Dr. Masoumeh Aslanimehr	
Prayer - Lunch			Until 13:00

Comprehensive Speech			
Topic of the Lecture	**Allocated**	**Speaker Name**	**Hours**
Title: Should the microbiome factor be considered in the detection and control of inflammatory diseases (IBD) and colorectal cancer?	Gastroenterologist - Colorectal Cancer	Dr. Iraj Sobhani (From France)	13-13:30

Title of the Fourth Panel: Infection and the Microbiome in Cancer Panel Chair: Dr. Bita Bakhshi			
Topic of the Lecture	**Specialization/University**	**Speaker Name**	**Hours**
Chair of the Panel	Medical Bacteriology Tarbiat Modares University	Dr. Bita Bakhshi	13:30-14:30
Microbiome in Colorectal Cancer	Gastroenterologist and hepatologist (Vice President of ...	Dr. Amir Abbas Vaezi	
The importance of the microbiome in cancer prevention	Medical Bacteriology Microbiology of the Baqiatallah Hospital	Dr. Davood Esmaeili	
The Role of Bacteria in the Treatment of Cancer, with an Emphasis on the Role of Probiotics and Their Products	Medical Bacteriology Tarbiat Modares University	Dr. Mojgan Derakhshan	
Microbial Biomarkers in Cancer Diagnosis	Medical Bacteriology Tarbiat Modares University	Dr. Tayebeh Shahbazi	
Rest & Catering			15 min

Comprehensive Speech			
Topic of the Lecture	**Expertise**	**Speaker Name**	**Hours**
New insights into the origin and evolution of Mycobacterium tuberculosis complex	Medical Microbiology	Dr. Arash Ghodousi (Italy)	14:45-15:15

Meeting Title: Presentation of Selected Papers Chairman : Dr. Neda Baseri		
Presentation of Selected Papers for Lectures		**Hours**
		15:15-16:15
Medical Bacteriology- Tarbiat Modares University	Dr. Neda Baseri	Board of Directors
Medical Bacteriology- Kashan University of Medical Sciences	Dr. Sara Bagheri	
Medical Bacteriology- Kurdistan University of Medical Sciences	Dr. Safoora Derakhshan	
Medical Bacteriology- Pasteur Institute of Iran	Dr. Masoumeh Saberpour	
Medical Bacteriology- Pasteur Institute of Iran	Dr. Kamran Pushang Bagheri	
Medical Bacteriology- Sabzevar University of Medical Sciences	Dr. Reza Khashei	
Medical Bacteriology- Isfahan University of Medical Sciences	Dr. Tahmineh Narimani	
Medical Bacteriology- Shahid Beheshti University of Medical Sciences	Dr. Masoumeh Navidinia	
Medical Bacteriology- Shahed University	Dr. Fatemeh Sameni	
Microbiology- Islamic Azad University	Dr. Fatemeh Ashrafi	

Schedule of the third day - Friday 02/14/2025

Title of the first panel: Bacteriophages and health
Panel Chairman : Dr. Mohammadreza Pourshafi

Topic of the Lecture	Specialization/University	Speaker Name	Hours
Chair of the Panel	Medical Bacteriology Pasteur Institute of Iran	Dr. Mohammadreza Pourshafi	7:30-9:30
Bacteriophage Therapy: A New Hope or a Big Problem	Medical Bacteriology Food Microbiology Research Center - Tehran University of Medical Sciences	Dr. Zahra Rajabi	
Bacteriophage production in bioreactors	Medical Microbiology Qazvin University of Medical Sciences	Dr. Seyed Mahmood Amin Marashi	
Phage Therapy: Challenges, Opportunities, and Future Prospects	Medical Bacteriology Qazvin University of Medical Sciences	Dr. Farhad Nikkhahi	
Bacteriophage Isolation and Investigation of its Effect on *P. aeruginosa Biofilm*	Medical Bacteriology Pasteur Institute of Iran	Dr. Morvarid Shafiei	
"Commercialization of Bacteriophage Products in the Field of Human Studies: Challenges and Opportunities"	Medical Bacteriology Shiraz University of Medical Sciences	Dr. Mehrdad Mohammadi	
Evaluation of Medical Theotypes and Prophage Patterns among Methicillin-Resistant Staphylococcus aureus Strains and Vancomycin Isolated from Different Sources in Iran (A 15-Year Study)	Medical Microbiology University of Isfahan	Dr. Fateh Rahimi	

Title of the Second Panel: New Strategies in the Prevention and Treatment of Bacterial Infections
Panel Chairman : Dr. Ashraf Mohabati Mobarez

Topic of the Lecture	Specialization/University	Speaker Name	Hours
Antibacterial and Antibiofilm Activity of Carbon dots derived from Probiotic Bacteria	Medical Bacteriology Tarbiat Modares University	Dr. Ashraf Mohabbati Mobarez	9:30-11:30
Role of Vaccine in Prevention of Antimicrobial Resistance	Infectious Disease Specialist Ministry of Health	Dr. Mohsen Zahraei	
Application of Lymphoid-like Tissues in Directing Immune Responses to Infection	Immunology Tarbiat Modares University	Dr. Sara Soudi	
Antibacterial and Antibiofilm Potentials Loaded Niosomal Drug Delivery of Vancomycin System against Methicillin Resistant *Staphylococcus aureus* (MRSA) Infections	Medical Bacteriology Hamadan University of Medical Sciences	Dr. Mohammadreza Arabestani	
One health microbiome	Microbiology & Biotechnology Islamic Azad University of Arak	Dr. Parvaneh Jafari	
Rest & Catering			15 min

Comprehensive Speech			
Topic of the Lecture	**Expertise**	**Speaker Name**	**Hours**
The Microbiome, Environment, Immune Nexus	Immunology Tarbiat Modares University	Dr. Masoumeh Ebtekar	11:45-12:45

Title of the Third Panel: Issues and Concerns of Students and Graduate Students Panel Chairman : Dr. Mohammad Vajgani			
Topic of the Lecture	**Specialization/University**	**Speaker Name**	**Hours**
Discussion	Immunology Tarbiat Modares University	Dr. Ali Akbar Pourfathollah	12:45-13:45
Discussion	Medical Bacteriology Shiraz University of Medical Sciences	Dr. Mohammad Motamedifar	
Discussion	Medical Bacteriology Hamadan University of Medical Sciences	Dr. Rasoul Yousefi Mashouf	
Discussion	Medical Toxicology Tehran University of Medical Sciences	Dr. Mahmoud Ghazi Khansari	

Closing of the Congress	Hours
Memorial of the Celestial Greats of Medical Bacteriology of Iran Introduction of Selected Articles and Awarding of Awards Granting Research Grants to Selected Projects Celebration of the 17th Anniversary of the Iranian Society of Medical Bacteriology Congressional Resolution Acknowledgments to the organizers and executive staff Group photo	13:45-14:45

ABSTRACTS

Abstract ID: 229
subject: Other related topics

Prevalence of CRISPR-Cas system genes in *Klebsiella pneumoniae* isolates collected from clinical samples in Ahvaz

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Background and Aim: *In Klebsiella pneumoniae*, the CRISPR-Cas systems found within its chromosomes are classified into two types: I-E and I-E*. The objective of this study was to analyze the occurrence of CRISPR-Cas genes in *K. pneumoniae* isolates in Ahvaz.

Material And Methods: *K. pneumoniae* isolates were collected from clinical samples and characterized through standard microbiology tests and polymerase chain reaction (PCR) using specific primers for the 16S–23S internal transcribed spacer (16S–23S ITS) gene. The detection of different CRISPR-Cas system genes was also carried out through PCR.

Results: In total, 106 *K. pneumoniae* isolates were identified during 2021 to 2023. The Resultsindicated that 49 (46.2%) strains were positive for CRISPR-Cas systems. The prevalence of different CRISPR-Cas genes was as follows: I-E CRISPR1 (n = 20, 18.9%), I-E* CRISPR2 (n = 18, 17.0%), I-E* CRISPR3 (n = 12, 11.3%), *cas1* (n = 20, 18.9%), and *cas3* (n = 27, 25.5%).

Conclusion: This study revealed the occurrence of *cas3* as the most prevalent CRISPR-Cas gene in *K. pneumoniae* isolates in Ahvaz. Further research with higher sample size is needed to confirm this observation.

Keywords: *Klebsiella pneumoniae*, CRISPR-Cas systems, *cas3*

Abstract ID: 239
subject: Other related topics

Microbial biomarkers in colorectal cancer: evaluating the role of *Fusobacterium nucleatum* and *Lactobacillus spp*

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Background and Aim: Colorectal cancer (CRC) ranks third globally in the incidence of malignant tumors and poses a significant threat to the public health systems. The traditional view of the pathogenesis of CRC posits genetic predispositions and environmental exposures, but emerging evidence points to the critical role of bacterial virulence factors in tumor development. The present study examines the utility of *Fusobacterium nucleatum* and *Lactobacillus spp*. as fecal biological non-invasive markers in CRC.

Material And Methods: For this observational study, 3857 paper-based medical records for patient history in Emam khomeini hospital and Shariati hospital) were reviewed and 55 individuals were selected. Investigating those bacteria's frequencies in stool samples was conducted on 12 CRC patients, 21 adenoma patients, and 22 control subjects. A total of 55 stool samples were collected under stringent cold-chain protocols between 2020 and 2023, stored at -80°C. The DNA was extracted using the FavorPrep™ Stool DNA Isolation Mini Kit and detection of bacteria using PCR amplification with specific and sensitive primers. Additionally, information about the associations between microbial presence and demographic and lifestyle characteristics of the subjects, such as past antibiotic use, dietary patterns, and physical activity, was collected from questionnaires to account for potential confounding factors.

Results: Findings showed significant differences in the prevalence of *Fusobacterium nucleatum* and *Lactobacillus spp*. across groups. *Fusobacterium nucleatum* was detected in 25% of CRC samples and absent in the controls and adenoma groupss, thereby proving its possible correlative association with CRC development. On the other hand, *Lactobacillus spp*. was reported in 50% of CRC patients while 86.36% was found in the control groups, which indicates a possible protective effect. Further examination of physical activity levels across the groups, done through the International Physical Activity Questionnaire (IPAQ), yielded different trends in light, medium, and intense activity. While CRC patients showed the highest proportion (>60%) of individuals with low-intensity physical activity, controls demonstrated a higher frequency of moderate and intense activity.

Conclusion: The Resultsindicate that microbial biomarkers could potentially probably serve as predictors of CRC for early detection and risk stratification.

Keywords: Colorectal neoplasm, biomarker, *fusobacterium nucleatum*, *lactobacillus spp.*

Abstract ID: 278
subject: Other related topics

Computational-based identification of novel inhibitors targeting DNA gyrase subunit B in *Staphylococcus aureus*

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Background and Aim: *Staphylococcus aureus* causes diseases ranging from mild skin infections to severe conditions like pneumonia and sepsis. DNA gyrase, particularly its B subunit (GyrB), is a critical target for drug development due to its essential role in DNA replication. With rising antibiotic resistance, especially to quinolones, identifying potent GyrB inhibitors through molecular docking analysis offers a promising strategy for tackling drug-resistant infections.

Material And Methods: The DNA gyrase subunit B's 3D structure, with PDB ID of 5D7D, was retrieved from the RCSB PDB database. The 3D structures of the gyrB inhibitory ligand, 4-bromo-5-methyl-N-[1-(3-nitropyridin-2-yl)piperidin-4-yl]-1H-pyrrole-2-carboxamide, and its 19 analogs were obtained in SDF format from the PubChem database. The protein and inhibitory ligands were prepared for docking using Molegro Virtual Docker version 6.0. After docking, the best interaction with the lowest binding energy was analyzed using Molegro Molecular Viewer version 7. Finally, the pharmacokinetic properties of the ligand were evaluated using the SwissADME server.

Results: Among all the inhibitory ligands for the DNA gyrase subunit B protein in *Staphylococcus aureus*, the best ligand was (4-bromo-1H-pyrrol-2-yl)-[4-[methyl-[3-(propan-2-ylamino)pyridin-2-yl]amino]piperidin-1-yl]methanone with PubChemCID: 57086859. This ligand had a molecular weight of 420.35 g/mol and a binding energy of -117.902 kcal/mol. It formed four steric interactions with the gyrB protein residues Asn54(A), Ser129(A), Glu50(A), and Ile102(A). Additionally, it established two hydrogen bonds with the residues Ser129(A) and Asn54(A), while no electrostatic interactions were observed. The ADME Resultsrevealed that this ligand had a water solubility score (LogS) of -4.64, a polarity score (TPSA) of 64.26, and two hydrogen bond donors as well as two hydrogen bond acceptors.

Conclusion: These Resultsindicated that (4-bromo-1H-pyrrol-2-yl)-[4-[methyl-[3-(propan-2-ylamino)pyridin-2-yl]amino]piperidin-1-yl]methanone is a promising candidate for inhibiting the DNA gyrase subunit B protein in *Staphylococcus aureus*. Further in vitro and in vivo studies are required to confirm its potential as a therapeutic agent.

Keywords: Molecular docking, *Staphylococcus aureus*, DNA gyrase B subunit, antibiotic resistance, ADME.

Abstract ID: 106
subject: Other related topics

Bacterial isolates from Diabetic Foot Ulcers and their antibiotic susceptibility pattern from selected hospitals in Isfahan, Iran

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Background and Aim: Infected diabetic foot ulcer (IDFU) is a worldwide complication of diabetes mellitus which imposes an economic and social burden on the society. Among the reasons for prolonging the healing process of diabetic wound, we can mention the disturbance in blood supply and the complex microbial environment in the wound area. Generally, Gram- positive and Gram- negative bacteria, including anaerobic bacteria, are considered potential causes of mix and complex microbial environment. This study aimed to identify the bacterial pathogens present in diabetic foot ulcer and characterize their antibiotic susceptibility pattern to the most common antibiotics used in therapy.

Material And Methods: This research is an analytical cross-sectional study that was conducted in selected hospitals of Isfahan/Iran. A total of 100 patients with DFU were enrolled in this study between February 2023 and January 2024. A sterile swab was used to collect samples from the foot ulcer. The method of data collection was direct observation, checklist, preparation of microbial culture and antibiotic susceptibility pattern. Isolates were identified by culture method, Gram-staining, and biochemical tests. For each bacterial species identified, Antimicrobial susceptibility tests was determined by the Kirby-Bauer disk diffusion method.

Results: The Resultsobtained from the phenotypic identification of clinical isolates show that the most isolated samples include, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Escherichia coli*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Enterococcus* and *Klebsiella pneumoniae*. Several cases of *Bacillus subtilis* and *Acinetobacter* were also observed. Overall, 88% (88/100) of the isolates were identified as multi-drug resistant.

Conclusion: The Resultsindicate the presence of different types of pathogens in diabetic foot ulcers that can challenge the treatment process. The majority of bacteria isolated from patients presenting with Diabetic foot ulcer infections were found to be multi-drug resistant in the study sites of the current study. The Resultsdemonstrate the importance of timely identification of infection of diabetic foot ulcers, proper sample collection for identification of the pathogens and for determining their antibiotic susceptibility pattern before initiating antimicrobial treatment.

Keywords: Diabetic foot ulcer; bacterial profiling; antibiotic susceptibility; Ira

Abstract ID: 308
subject: Other related topics

Computational analysis of a rationally designed IleRS inhibitor, isoleucine tRNA synthetase, as a promising therapeutic agent against *Staphylococcus aureus*

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Background and Aim: *Staphylococcus aureus* is a significant Gram-positive bacterium capable of causing a wide range of infections, from minor skin infections to life-threatening conditions such as septicemia and endocarditis. One of the key virulence factors of this bacterium is isoleucine tRNA synthetase (IleRS), which plays a crucial role in facilitating bacterial infections. Inhibiting this factor could potentially prevent infections and mitigate the risks associated with this bacterium. Therefore, this study aimed to identify the most effective inhibitory ligand for the IleRS using a molecular docking analysis.

Material And Methods: First, we downloaded the Isoleucine tRNA synthetase's 3D structure in PDB format (PDB ID: 1FFY) from the RCSB PDB database. Next, we obtained the mupirocin inhibitory ligand (PubChem CID 446596), along with 20 similar structures exhibiting inhibitory properties, from the PubChem website in the SDF format to evaluate their potential as drugs. Subsequently, after preparing the protein and ligands, molecular docking was conducted using Molegro Virtual Docker version 6.0. The interactions were analyzed to identify the best binding with the lowest energy via the Molegro Molecular Viewer software. Finally, we assessed pharmacokinetic properties such as absorption, distribution, ligand excretion, and metabolism using the SwissADME.

Results: Among all the inhibitory analogs, the most effective analog for Isoleucine tRNA synthetase was identified as methyl 4-[(2S,3R,4R,5S)-3,4-dihydroxy-5-[[(2S,3S)-3-[(2S,3S)-3-hydroxybutan-2-yl]oxiran-2-yl]methyl]oxan-2-yl]-3-methylbut-2-enoate with PubChemCID of 57021455. This compound has a molecular weight of (358.43) g/mol and a binding energy of (-113.33) kcal/mol. This analog formed eleven steric interactions with the Isoleucine tRNA synthetase residues Met589, Met596, Met65, Val588, Gly66, Gly555, Asn70, Phe587, Asp630, His64, and His585, along with three hydrogen bonds involving Val588, His585, and Gly66. However, no electrostatic bonds were observed. Additionally, the ADME analysis revealed that this ligand has a water solubility (logS) score of -2.06, lipophilicity (XLogP3) of 0.83, polarity (TPSA) of 108.75, and three hydrogen bond donors and seven hydrogen bond acceptors

Conclusion: Our Resultssuggest that methyl 4-[(2S,3R,4R,5S)-3,4-dihydroxy-5-[[(2S,3S)-3-[(2S,3S)-3-hydroxybutan-2-yl]oxiran-2-yl]methyl]oxan-2-yl]-3-methylbut-2-enoate is a promising candidate for the inhibition of isoleucine tRNA synthetase in *Staphylococcus aureus*. Further in vitro and in vivo studies are required to confirm its efficacy and potential as a therapeutic agent.

Keywords: *Staphylococcus aureus*; isoleucine tRNA synthetase; molecular docking

Abstract ID: 230
subject: Other related topics

Identification of isolated *Mycobacterium spp*. recovered from clinical specimens of referring patients to Kosar Hospital during 2017-2023 using the multiplex-PCR technique in Semnan

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Background and Aim: Tuberculosis is the leading cause of death from a single-agent infection globally, exacerbated by the rise of drug-resistant strains, which challenges health systems in treatment and control. There is limited data on the genotypes of *Mycobacterium tuberculosis* complex (MTBC) and nontuberculous mycobacteria (NTM) in Semnan. In recent years, NTM strains have gained significance, and the *M. tuberculosis* Beijing genotype has been linked to major TB outbreaks worldwide, showing higher virulence and spreadability. This study aimed to differentiate between the *Mycobacterium tuberculosis* complex (MTBC) and non-tuberculous mycobacteria (NTM) from clinical samples using multiplex-PCR and to help map the general distribution of different mycobacterial species.

Material And Methods: This study was conducted on 69 non-repeated isolates from 100 suspected mycobacterium colonies isolated on Lowenstein-Johnson medium from sputum samples of patients in health centers of Semnan province between 2018 and 2022. Isolates were subjected to DNA extraction With the CTAB method and PCR using multiplex-PCR using specific primers for mycobacterial strains, and strains identification was performed based on examining the banding pattern obtained from the gel electrophoresis.

Results: The presence of mycobacterium was confirmed in all 69 isolates studied, of which 65 (94.2%) belonged to the "*Mycobacterium tuberculosis* complex" and 4 (5.8%) were identified as non-tuberculous mycobacteria. Among the 65 *Mycobacterium tuberculosis* complex isolates, 64 (98.5%) were identified as *Mycobacterium tuberculosis*. Among the 64 *Mycobacterium tuberculosis* isolates, 12 (19%) were identified as Beijing, 13 (20%) as CAS, and 39 (61%) as non-Beijing/CAS strains. None of the NTMs evaluated in this study, including (*Mycobacterium avium, intracellular, abscessus, kansasii, and massilinus*), were identified among our NTM isolates.

Conclusion: The study indicates a significant prevalence of various *Mycobacterium tuberculosis* complex (MTBC) strains in Semnan province, with a lesser presence of non-tuberculous Mycobacteria (NTM) strains. Strains from the Beijing family comprise a minor proportion of identified genotypes, consistent with trends in other regions. The higher prevalence of this genotype among Afghan nationals and immigrants c*OmpA*red to the Iranian population raises concerns about its potential role in the emergence of treatment-resistant and more virulent strains.

Keywords: *Mycobacterium tuberculosis* complex, non-tuberculous mycobacteria, multiplex PCR, Beijing genotype

Abstract ID: 361
subject: Other related topics

Leveraging proteomics to develop a multi-epitope mRNA vaccine against *Brucella melitensis*

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Background and Aim: Brucellosis is a persistent and debilitating illness in humans that leads to significant economic impacts on the livestock sector. Developing an effective vaccine is a critical priority for combating this disease. The recent advancements in mRNA vaccine technology, known for its precision and high efficacy, have yielded promising outcomes in the fight against various diseases. This research aimed to develop a new mRNA vaccine incorporating multiple epitopes specifically designed to target *Brucella melitensis.*

Material And Methods: Seventeen antigenic proteins and their appropriate epitopes were selected with immunoinformatic tools and surveyed in terms of toxicity, allergenicity, and homology. Then, their presentation and identification by MHC cells and other immune cells were checked with valid tools such as molecular docking, and a multi-epitope protein was modeled, and after optimization, mRNA was analyzed in terms of structure and stability.

Results: To combat *B. melitensis* infection, we developed an innovative in silico multi-epitope mRNA vaccine based on the bacterium's major surface proteins. The predicted epitopes underwent scrutiny to evaluate their antigenicity, allergenicity, and toxicity through dedicated web servers. Specific linkers were employed to combine these epitopes, and immune simulations were carried out to validate the vaccine's ability to provoke both humoral and cellular responses. According to predictions from the IEDB tool, one notable outcome of the vaccine formulated in this investigation was the broad coverage of epitopes obtained, enc*OmpA*ssing over 98% of the alleles across the global population. This finding underscores the potential novelty and significance of the targets employed in this study as promising candidates for brucellosis prevention. In addition, the vaccine construct was subjected to docking with immune receptors TLR-3 and TLR-4 to assess its potential interaction with these receptors, which could trigger the development of innate and adaptive immunity. Molecular dynamic simulations were employed to evaluate the permanency of the vaccine complex.

Conclusion: this study introduces an innovative multiepitope mRNA vaccine for *B. melitensis*, developed through immunoinformatic approaches. While this research lays the foundation for future studies and vaccine development, further in vitro and in vivo investigations are imperative to confirm these findings and ensure the vaccine's efficacy.

Keywords: *Brucella melitensis*, chronic diseases, mRNA vaccine, epitopes

Abstract ID: 336
subject: Other related topics

Antibacterial activity of Ziziphus Spina- Christi nanoparticle against *Enterococcus faecalis* biofilm

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Background and Aim: Antibiotics are used in the treatment of biofilms but the current trend is towards the identification of natural products in disinfection. Nanoparticles are able to penetrate bacteria and bacterial biofilms, so they can be a potential agent for controlling the growth of bacterial infections. Ziziphus Spina-Christi leaves (Sider) have antimicrobial properties against several positive and negative gram-staining bacteria. This study investigated the antimicrobial and antibiofilm effects of Z. spina nanoparticle against E. faecalis isolated.

Material And Methods: Z. spina nanoparticle was prepared, and the size and particle distribution were determined using SEM and DLS analysis. The antimicrobial and antibiofilm activity of Z. spina nanoparticle against *E. faecalis* isolates was investigated by disk diffusion and broth micro-dilution method.

Results: The Fe-SEM image reveals that the nanoparticles morphology is nearly spherical, average size 129.5 nm. The inhibition zone of *E. faecalis* in the highest concentration (30 mg/ml) was 11.4 mm. The MIC of the Z. spina nanoparticles against six *E. faecalis* isolated was 2.5± 0.7mg/ml. The average biofilm formation in the presence of extract decreased to 59.70%± 2.5 c*OmpA*red to the control. Electron micrographs indicated the inhibition of biofilms c*OmpA*red to control biofilms.

Conclusion: According to the results, the Z. spina nanoparticles have antimicrobial and antibiofilm effects against E. faecalis bacteria. The nanoparticles were also able to inhibit the biofilm adhesion of *E. faecalis*, which may be due to the reduction in particle size leading to better penetration of the nanoparticles. More research is needed to investigate the mechanism of nanoparticles against *E. faecalis*.

Keywords: Nanoparticles, ziziphus spina-christi, *Enterococcus faecalis*,

Abstract ID: 186
subject: Other related topics

Investigation of the prevalence of non-tuberculosis mycobacterium species (NTM) in Iran: A meta-analysis study

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Background and Aim: Non-tuberculous mycobacteria (NTM) pose significant challenges in clinical identification, diagnosis, and treatment, particularly in the Middle East. Given the variability in findings across studies, this meta-analysis synthesized existing research to provide a precise estimate of NTM prevalence in Iran.

Material And Methods: A systematic review was conducted by searching Iranian databases and international platforms, including PubMed, Web of Science, Cochrane Library, Google Scholar, SID, Magiran, Scopus, and Embase, from July 2010 to July 2022. Keywordssuch as "prevalence," "non-tuberculous mycobacterium species," and "NTM" were used. All original studies on NTM prevalence in the Middle East, regardless of article language, were included.

Results: A total of 24 studies, comprising 78,201 samples, were analyzed. Sample sizes ranged from 32 (Yazdi et al.) to 15,829 (Aghajani et al.). Across these studies, 2,183 NTM cases were reported, with a prevalence range of 0.14% to 100%. The lowest prevalence (0.14%) was reported by Nasiri et al., while Araj et al. and Babalik et al. documented the highest (100%). The majority of studies (19) were conducted in Iran, and the mean patient age was 50.73 years. The overall NTM prevalence was 3.7% (95% CI: 3.5–3.9%). *Mycobacterium simiae* was the most prevalent species (34.2%), followed by *Mycobacterium fortuitum* (16.6%) and *Mycobacterium kansasii* (11.7%).

Conclusion: This meta-analysis identifies *Mycobacterium simiae* as the most common NTM in Iran. It often leads to treatment failure and manifests as tuberculosis. The findings underscore the urgent need for advanced diagnostic methods and sensitive tests for NTM species to address the significant diagnostic and therapeutic challenges posed by these pathogens.

Keywords: Non-tuberculous mycobacteria, *Mycobacterium simiae*, prevalence, meta-analysis, epidemiology, Iran

Abstract ID: 168
subject: Other related topics

The presence of microbiome in gastric cancer: A systematic review

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Background and Aim: Despite enormous research in the field of cancer, it remains one of the leading causes of mortality. Gastric cancer (GC) is one of the most prevalent types of cancer worldwide. The human microbiome is a complex community of bacteria, fungi, and viruses that inhabit the human body. The aim of this study is to investigate the role of the microbiome in the development of GC.

Material And Methods: A comprehensive search was conducted using databases such as PubMed, Scopus, and Web of Science, following the PRISMA guidelines. The search was limited to studies published between 2016 and 2024, using Keywordssuch as "gastric cancer," "gastric microbiome," and "microbiota."

Results: Several studies have demonstrated the significant role of *Helicobacter pylori (H. pylori)* in GC, particularly strains with the *CagA* and *VacA* genes. *H. pylori* can alter the acidity of the stomach, leading to changes in the composition of the gastric microbiome. Other microorganisms have also been implicated in the development of GC.

Conclusion: Further research and detection methods should be considered for the treatment of GC. Additionally, more studies should focus on the interaction between the microbiome and the human genome in the development of GC.

Keywords: Gastric cancer (gc), gastric microbiome, microbiota, *Helicobacter pylori (H. Pylori)*

Abstract ID: 180
subject: Other related topics

C*OmpA*rison effect of Anti-PIA/PNAG antibodies on biofilm formation in *Staphylococcus epidermidis* and *Escherichia coli*

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Background and Aim: Polysaccharide intercellular adhesin (PIA), a surface polysaccharide produced by *Staphylococcus epidermidis*, is an effective target for opsonic and protective antibodies against these bacteria. *Escherichia coli* has recently produced an exopolysaccharide, poly-β(1,6)-N-acetylglucosamine (PNAG), which is biochemically indistinguishable from PIA. This study investigated the effect of antibodies produced against PIA/PNAG on biofilm formation and opsonization activity of secreted antibodies in *S. epidermidis* and *E. coli*.

Material And Methods: After purification and structural confirmation of the polysaccharide PIA from the producer *S. epidermidis*, the biofilm inhibition ability and the function of the secreted antibodies to the polysaccharide were evaluated using semi-quantitative methods in a mouse model. After that, the opsonic activity of the antibodies against *S. epidermidis* and *E. coli* was evaluated.

Results: The extracted polysaccharide was confirmed using FT-IR, NMR, and colorimetric methods. The Resultsshowed that purified PIA induced protective antibodies with opsonization properties of 60% in *S. epidermidis* and 40.48% in *E. coli*. Sera from the PIA-vaccinated groups showed a significant increase in antibody production and protective IgG titer levels c*OmpA*red to the control group. The antibodies produced for *S. epidermidis* were able to inhibit biofilm in vitro c*OmpA*red to the control group, but in *E. coli*, no significant difference was shown in biofilm inhibition.

Conclusion: Despite the successful production of antibodies against PIA, these antibodies did not have a significant effect on biofilm formation in *E. coli*, unlike *S. epidermidis*. These Resultssuggest that other factors probably play a more prominent role in *E. coli* biofilm formation. Although the antibodies showed opsonic properties for *E. coli* and *S. epidermidis*, their simultaneous effect on infections caused by *S. epidermidis* and *E. coli* requires further investigation and complementary studies in other animal models.

Keywords: *Escherichia coli, Staphylococcus epidermidis,* polysaccharide vaccine, immunization, PIA, PNAG

Abstract ID: 146
subject: Other related topics

Investigation of the effect of Anti-PIA/PNAG antibodies on biofilm formation in *Escherichia coli*

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1. Department of Microbiology and Virology, Faculty of Medicine, Zanjan University of Medical Sciences, Zanjan, Iran

Background and Aim: Polysaccharide Intercellular Adhesin (PIA), a surface polysaccharide produced by *Staphylococcus aureus* and *Staphylococcus epidermidis*, is an effective target for opsonic and protective antibodies against these bacteria. *Escherichia coli* has recently produced an exopolysaccharide called poly-β(1,6)-N-acetylglucosamine (PNAG), biochemically indistinguishable from PIA. This study investigated the effect of antibodies generated against PNAG on biofilm formation and the opsonization activity of secreted antibodies in *Escherichia coli.*

Material And Methods: Following purification and structural confirmation of PIA polysaccharide from producing *Staphylococcus epidermidis*, the ability to inhibit biofilm and the function of secreted antibodies for the mentioned polysaccharide were evaluated using semi-quantitative methods in a mouse model. Subsequently, the opsonic activity of antibodies against *Escherichia coli* ATCC 25922 was assessed.

Results: The extracted polysaccharide was confirmed using FTIR, NMR, and colorimetry methods. Resultsshowed that purified PIA induced protective antibodies with 40.48% opsonizing property in *E. coli*. Sera from PIA-immunized groups demonstrated a significant increase in antibody production and protective IgG titer levels c*OmpA*red to the control group. However, the produced antibodies did not show a significant difference in biofilm inhibition under laboratory conditions c*OmpA*red to non-immune serum.

Conclusion: Despite successful antibody production against PIA, these antibodies did not significantly impact biofilm formation in *E. coli*. These Resultssuggest that other factors likely play a more prominent role in *E. coli* biofilm formation. Although the antibodies showed opsonic properties for *E. coli*, their simultaneous effect on infections caused by *Staphylococcus epidermidis* and *Escherichia coli* requires further investigation and complementary studies in additional animal models.

Keywords: *Escherichia coli, Staphylococcus epidermidis*, polysaccharide vaccine, immunization, PIA, PNAG

Abstract ID: 353
subject: Other related topics

Thermal and UV stability assessment of bacteriophage isolates targeting multidrug-resistant *Acinetobacter baumannii*

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Background and Aim: The rapid rise in antibiotic resistance among bacterial pathogens has emerged as a critical global health threat. *Acinetobacter baumannii (A. baumannii)* recognized as a priority pathogen by the WHO in 2017, exhibits resistance to multiple antibiotic classes, necessitating novel therapeutic approaches such as bacteriophage therapy. This study aims to evaluate the stability and functional properties of phages targeting antibiotic-resistant *A. baumannii* under various environmental conditions. At this stage, only the UV resistance and thermal stability of the phages have been investigated, with additional analyses, including morphological characterization.

Material And Methods: Bacteriophage was isolated from wastewater samples collected from local facilities. The isolate was subjected to: Stability tests: UV exposure (90 minutes) and temperature challenges (25°C, 37°C, 42°C, 50°C, 60°C and 70°C for 1 hour). The morphology of our phage was determined using transmission electron microscopy (TEM).

Results: Phage exhibited notable resistance to environmental factors: UV exposure: A 1-log reduction after 60 minutes and a 2-log reduction after 90 minutes of UV exposure. Temperature stability No significant reduction was observed at 25°C, 37°C, and 42°C for 1 hour. However, a 1-log reduction occurred at 50°C and 60°C, while complete inactivation was observed at 70°C after 1 hour. Bacterial lysis: The phage successfully lysed 24% of 50 clinical *A. baumannii* strains resistant to meropenem, tigecycline, polymyxins, piperacililin-tazobactam, amikacin, trimethoprim-sulfamethaxazole, ceftriaxone, gentamicin, cefotaxime, amoxicillin, imipenem, ciprofloxacin. Our phage belonged to Myoviridae mophplogical family.

Conclusion: Preliminary findings demonstrate that phages retain stability under moderate environmental conditions, particularly at lower temperatures and short UV exposure. Furthermore, the phages exhibit promising lytic activity against multidrug-resistant *A. baumannii*. These findings provide foundational data for developing effective bacteriophage-based therapies. Future studies will complete morphological and functional assessments to fully characterize their potential for therapeutic use.

Keywords: Bacteriophage, *A. baumannii*, antibiotic-resistance, thermal stability, morphology

Abstract ID: 354
subject: Other related topics

A Novel approach: harnessing synergy between phage therapy and antibiotics to combat bacterial resistance.

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Background and Aim: The global escalation of bacterial resistance to multiple drugs has emerged as a pressing public health problem. To address this challenge, the strategy of simultaneously employing phage therapy and antibiotics has come up as a potentially effective solution to bolster treatment efficacy and mitigate bacterial resistance. This comprehensive review explores into the collaborative effects of phages and antibiotics in combating resistant infections.

Material And Methods: A thorough exploration was undertaken through systematic searches across reputable databases such as PubMed, Scopus, and Web of Science. Inclusion criteria were tailored to enc*OmpA*ss studies investigating the simultaneous administration of phages and antibiotics and their collective impact on controlling bacterial resistance.

Results: The review underscores a significant enhancement in bacterial susceptibility to treatment upon the concomitant utilization of phages and antibiotics. The synergistic pathways enc*OmpA*ss phage-induced damage to bacterial cell walls, facilitation of antibiotic penetration, and minimization of the likelihood of ensuing resistance development.

Conclusion: The combined application of phage therapy and antibiotics presents a promising avenue for addressing resistant infections. Nonetheless, further research effort are necessary to find out the optimal dosing regimens, treatment durations, and enduring implications of this combined therapeutic approach.

Keywords: Phage therapy- antibiotic resistance- multidrug resistance- combination therapy

Abstract ID: 355
subject: Other related topics

Addressing challenges in bacterial resistance to phage therapy

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Background and Aim: Phage therapy has emerged as a potential solution to combat antibiotic- resistant infections. However, the issue of bacterial resistance to phages remains a significant hurdle that can hamper the effectiveness of this treatment. This review aims to provide an overview of bacterial resistance mechanisms to phage therapy and explore potential strategies to tackle this challenge.

Material And Methods: An extensive search of literature was carried out in major databases such as PubMed, Scopus, and Web of Science for studies conducted between 2010 and 2024. Only studies focusing on bacterial resistance to phage therapy in experimental and clinical settings, including discussions on resistance mechanisms and possible solutions, were included in the analysis.

Results: Our review revealed that bacteria can develop resistance through mechanisms like CRISPR-Cas systems, restriction-modification systems, and receptor modifications. To address these challenges, strategies such as employing phage cocktails and combining phage therapy with antibiotics have shown promise in mitigating bacterial resistance.

Conclusion: Bacterial resistance to phage therapy remains a significant barrier to its widespread adoption. By utilizing phage cocktails, optimizing treatment strategies, and integrating phage therapy with antibiotics, we may be able to overcome these resistance mechanisms. Further research is essential to develop more effective and sustainable solutions to this pressing issue.

Keywords: Phage therapy- bacterial resistance- crispr-cas systems- cocktail

Abstract ID: 416
subject: Other related topics

Evaluation of antimicrobial susceptibility and resistance genes in clinical isolates of *Stenotrophomonas maltophilia*

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Background and Aim: *Stenotrophomonas maltophilia* (*S. maltophilia*) is an important hospital pathogen causing opportunistic infections, especially in immunocompromised individuals. Its intrinsic resistance to antibiotics and the rise of multidrug-resistant (MDR) strains complicate treatment. This study aims to assess resistance patterns and the prevalence of resistance genes in clinical isolates.

Material And Methods: A total of 120 *S. maltophilia* isolates were collected from Tehran hospitals between 2022 and 2023. Isolates were identified through biochemical methods and confirmed with 16S rRNA gene sequencing. Antibiotic susceptibility was tested using disk diffusion and E-test methods. PCR was employed to detect resistance genes

Results: Resistance rates among the 120 isolates showed the highest against ceftazidime (56.6%) and the lowest against minocycline (5.8%). MDR strains accounted for 4.1% of the isolates. Common resistance genes included Smqnr (70.8%), L1 (65%), sul1 (58.3%), L2 (54.1%), and sul2 (36.6%).

Conclusion: The study indicates increasing antibiotic resistance and prevalence of resistance genes in Iran over recent years. Effective infection control measures and careful antibiotic management are essential for preventing the spread of resistant strains.

Keywords: *Stenotrophomonas maltophilia*, antibiotic resistance, MDR

Abstract ID: 150
subject: Other related topics

Evaluation of different methods for bacterial biofilm assay using the microtiter plate technique: options and limitations

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Background and Aim: Biofilm, as a structure consisting of a bacterial population, plays a role in the attachment of bacteria to various surfaces, as well as increasing intrinsic resistance to antibiotics and resistance to harsh environmental conditions. Various techniques can be used to assay the biofilm, including physical assays, staining assays, metabolic assays, and genetic assays. The microtiter plate method is one of the most commonly used methods for examining biofilms. In this study, we aim to evaluate different methods for biofilm assay and investigate various factors that can affect biofilm formation and severity.

Material And Methods: After identifying and examining the phenotypic and biochemical characteristics of the bacteria, we proceeded to phenotypic examination of the ability of the bacteria to form biofilms. we used the microtiter plate technique, and due to the differences in the methods used in different articles with the same method, we c*OmpA*red several methods simultaneously in each plate to c*OmpA*re the homogeneity or heterogeneity of the Resultsin these different methods. In this study, the *Escherichia coli* sequence type 131O25b strain was used as the sample to be evaluated, and a *Pseudomonas aeruginosa* strain with a strong biofilm was used as the positive control, and the TSB (tryptic soy broth) was used as the negative control.

Results: Various factors can affect the ability to form and the intensity of the biofilm reading, including the amount of bacteria added to the wells of the microtiter plate, the fixation method, the number and type of washings, the washing agent, the concentration of crystal violet dye, and the type of decolorizer.

Conclusion: In each of the eight methods used to assess biofilm, different variables were evaluated , According to the Resultsof the biofilm formula based on the readings taken, the method with methanol fixation and a concentration of 1% crystal violet and 33% acetic acid provided better biofilm reading Resultsc*OmpA*red to the other methods.

Keywords: Biofilm , biofilm assay, microtiter plate , *Escherichia coli* , ST 131O25b

Abstract ID: 383
subject: Other related topics

Identification of main bacterial pathogens causing urinary tract infections among patients visiting the pathobiology laboratory center

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Background and Aim: Urinary tract infections (UTIs) are among the most common bacterial infections globally, with significant clinical and economic burdens. The study of the prevalence of urinary tract infections can help researchers identify the patterns of spread of these infections in different communities and analyze the factors influencing their prevalence. The aim of this study was to identify the main bacterial pathogens causing UTIs among patients visiting the pathobiology laboratory center to evaluate the distribution of these pathogens across different demographic groups.

Material And Methods: This cross-sectional study was conducted on 161 urine samples from patients who clinical laboratories in Tehran. Urine samples were collected and cultured using standard microbiological techniques. Bacterial isolates were identified, and their antibiotic susceptibility was tested using the Kirby-Bauer disk diffusion method. Demographic data, including age and gender, were recorded and analyzed.

Results: The bacterial culture Resultsrevealed that *Escherichia coli (E. coli)* was the most prevalent pathogen, accounting for 45.3% of the cases. *Klebsiella spp*. was the second most common, responsible for 21.1% of infections. Other identified pathogens included *Enterobacter spp*. (1.9%), *Pseudomonas spp*. (1.2%), *Staphylococcus aureus* (0.6%), Methicillin-Resistant *Staphylococcus epidermidis* (MRSE) (0.6%), *Staphylococcus epidermidis* (2.5%), Streptococcus Group B (7.5%), *Streptococcus Viridans* (2.5%), *Enterococcus spp*. (3.1%), and *Candida spp*. (13.7%).The study also found that the majority of UTI cases were in female patients, with a significant concentration in the 35-40 year age group. The variability in white blood cell counts suggested differing infection severities among the patients.

Conclusion: The study concluded that *E. coli* is the predominant cause of UTIs among patients visiting the pathobiology laboratory center, necessitating the implementation of targeted antibiotic treatments. Continuous surveillance of bacterial pathogens and their antibiotic resistance patterns is crucial to inform effective treatment protocols and reduce the impact of UTIs in the population. The analysis provides crucial insights into the bacterial landscape of UTIs in Tehran, underscoring the importance of continuous monitoring and tailored therapeutic strategies to combat antibiotic resistance.

Keywords: Urinary Tract Infection, bacterial pathogens, *Escherichia coli, Klebsiella*, Tehran, antibiotic resistance

Abstract ID: 325
subject: Other related topics

Dihydropteroate synthase (DHPS) as a therapeutic target for *Klebsiella pneumoniae*: a molecular docking investigation

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Background and Aim: *Klebsiella pneumoniae* is a well-known Gram-negative pathogen responsible for a range of infections, affecting both immunocompromised individuals and the general population. These infections can include pneumonia, urinary tract infections, Bacteremia, and Meningitis. Notably, *K. pneumoniae* is notorious for its resistance to multiple antibiotics, such as sulfonamides, carbapenems, cephalosporins and aminoglycosides. The resistance to sulfonamides is often mediated by the presence of dihydropteroate synthase (DHPS) genes. DHPS is a crucial enzyme involved in a pathway essential for bacterial growth and survival. In this study we aim to find a potent inhibitor for DHPS through molecular docking to propose new effective strategies for preventing infections caused by *K. pneumoniae.*

Material And Methods: The 3D structure of the dihydropteroate synthase (DHPS) (PDB ID: 5UMG) was obtained from the RCSB PDB database. The structures of the DHPS inhibitory ligand, 4-amino-N-pyridin-2-ylbenzenesulfonamide (Sulfapyridine) with PubChemCID 5336 and its 30 analogs were retrieved from the PubChem database in SDF format. The protein and inhibitory ligands were prepared for docking using Molegro Virtual Docker version 6.0. After docking, the best interaction with the lowest energy binding was analyzed through Molegro Molecular Viewer v.7 software. Finally, the pharmacokinetic properties of the ligands were evaluated using the SwissADME server.

Results: Through all inhibitory ligands for DHPS, the best ligand was N-[3-(pyridin-2-ylsulfamoyl)phenyl]acetamide (PubchemCID: 313740) with a molecular weight of 291.33 g/mol and binding energy of -183/546 kcal/mol. This ligand created 8 steric interactions with the DHPS protein residues Asp 160(B), Gln 142(B), Phe 164(B), ser 119(B), Tyr 154(B), Val 161(B), Lys 192(B), Pro 186(B) and 0 hydrogen bonds, and 0 electrostatic interaction. The ADME Resultsshowed that this ligand has a water solubility score (logS) of -1.67, a hydrophilic score (LogP) of 1.04, a polarity score (TPSA) of 96.54 and lastly, hydrogen bond donors of 2 and hydrogen bond acceptors of 4.

Conclusion: These Resultsindicates that N-[3-(pyridin-2-ylsulfamoyl)phenyl]acetamide is a good candidate for inhibiting DHPS. Further in vitro and in vivo studies are required to confirm their potential as therapeutic agents.

Keywords: Molecular docking, *Klebsiella pneumoniae*, dihydropteroate synthase (DHPS), ADME.

Abstract ID: 330
subject: Other related topics

DHPS inhibition: A molecular docking approach to combat Mycobacterium fortuitum

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Background and Aim: *Mycobacterium fortuitum* is a Gram-positive bacterium, rapidly growing nontuberculous mycobacterium (NTM) that causes a variety of infections, including skin and soft tissue infections, osteomyelitis, pulmonary disease, and postoperative infections. *M. fortitum* is equipped with several virulence factors. Dihydropteroate synthase (DHPS) is a crucial enzyme in the folate biosynthesis pathway, playing a significant role in its metabolic processes and contributing to antibiotic resistance. Now this bacterium has been found to harbor genetic mutations associated with drug resistance, complicating treatment. Therefore, this study aimed to determine the most potent DHPS inhibitor through molecular docking analysis as a new strategy to combat *M. fortuitum* infections.

Material And Methods: The 3D structure of DHPS of *M. fortuitum* was predicted using ITASSEr server. After refinement of the structure modeled, structure's validation was carried out using ProSA and Seves servers. The DHPS inhibitory ligand, 4-amino-N-pyridin-2-ylbenzenesulfonamide (Sulfapyridine) with PubChemCID 5336, and its 30 analogs were retrieved from the PubChem database in SDF format. After preparing the protein and its ligands by eliminating the ligand and water from the protein, lowering the energy level, and adding electric charges and hydrogen atoms, molecular docking was conducted using Virtual Docker Molegro v. 6. Subsequently, the best interaction with the lowest energy binding was analyzed using Molegro Molecular Viewer software. Finally, the pharmacokinetic properties of the ligand were investigated using the SwissADME server.

Results: Among all the inhibitory ligands, the best ligand was 4-[bis(2-chloroethyl)amino]-N-(2-pyridinyl) benzene sulfonamide (PubChem CID 231826) with the molecular weight of 374.29 g/mol, and binding energy of -106.383 kcal/mol. This ligand formed 1 Hydrogen bond with Lys216 along with 10 steric interactions involving His252, Lys216, His54, Asp86, Ser53, Arg250, Ala51, Leu12, Gly49, and Ile11 residues. The ADME Resultsdemonstrated a water solubility score (LogS) of -3.27, the hydrophilic score (LogP) of 2.57, the polarity score (TPSA) of 70.68, and in Conclusionthe hydrogen bond donors of 1 and hydrogen bond acceptor of 3.

Conclusion: Based on the obtained results, compound with PubChem CID 231826 revealed the best interaction with the lowest energy binding with DHPS, although further in vivo and in vitro analysis are necessary.

Keywords: Molecular docking, *Mycobacterium fortuitum*, dihydropteroate synthase (DHPS), ADME.

Abstract ID: 109
subject: Other related topics

Antibacterial properties of Shirazi thyme (Zataria multiflora) essential oils on *Staphylococcus aureus* and MDR *Staphylococcus aureus* harboring *mecA* gene

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Background and Aim: The increasing prevalence of multidrug-resistant (MDR) *Staphylococcus aureus*, especially strains harboring the *mecA* gene, has become a significant global health challenge due to their resistance to conventional antibiotic treatments.

Material And Methods: Sensitive and resistant strains of *S. aureus* (ATCC25923 and clinical isolation , respectively) were used in this study. Identification of the *mecA* gene in resistant strains was confirmed using PCR. Antibiotic susceptibility was determined using the disk diffusion method. Sensitive strains showed susceptibility to antibiotics such as cefoxitin, ciprofloxacin, erythromycin, clindamycin, cotrimoxazole, rifampin, and tetracycline, while resistant strains were resistant to all tested antibiotics except linezolid. The antibacterial effects of Shirazi thyme essential oil were assessed using minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) assays. Synergistic effects of thyme oil with cefoxitin were also studied. Sub-MIC concentrations of thyme oil were combined with cefoxitin (30 mg disk) and tested against both MDR and sensitive strains.

Results: For the sensitive strain, the MIC and MBC values for thyme oil were 3.125 and 6.25 mg/ml . For the resistant strain, both MIC and MBC values were 6.25 mg/ml. The antibacterial activity of Shirazi thyme essential oil was evident against both sensitive and resistant strains of *S. aureus*. The combined treatment resulted in significantly larger inhibition zones c*OmpA*red to cefoxitin or thyme oil alone. This suggests that thyme oil can enhance the efficacy of cefoxitin against resistant strains, potentially overcoming the limitations of antibiotic resistance mediated by the mec A gene.

Conclusion: In Conclusion, Shirazi thyme essential oil exhibits significant antibacterial activity against both sensitive and resistant strains of *S. aureus*. Its ability to inhibit the growth of MDR strains carrying mec A and enhance the efficacy of cefoxitin demonstrates its potential as a valuable adjunct in the fight against antibiotic resistance.

Keywords: Shirazi thyme (Zataria multiflora),*Staphylococcus aureus* ,MDR *Staphylococcus aureus* with *mecA* gene

Abstract ID: 254
subject: Other related topics

Phage therapy as a novel therapeutic approach for *Pseudomonas aeruginosa* clinical infection: A systematic review

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Background and Aim: *Pseudomonas aeruginosa* causes serious infection related to high rate of morbidity and mortality. The crisis of increasing antibiotic resistance and the worsening of the situation, requires new antimicrobial strategies to treat *P. aeruginosa* infection. Using phages for treatment a bacterial infection is an interesting idea, so the present study to propone phages can be used as antimicrobial agents.

Material And Methods: We searched multiple articles on 4 databases including: Google Scholar, PubMed, Web of Science and Scopus about bacteriophages and *P. aeruginosa*. The time period, selected on February 2019 to June 2024 and the phage therapy ،*Pseudomonas aeruginosa*، clinical specimens, antibiotic, resistance and infection were searched as keywords.

Results: 21 phage were found against *P. aeruginosa* isolated from clinical samples such as sputum, wound, blood and urine. The phages isolated from sewage belonged to families Myoviridae, Siphoviridae, Podoviridae and Autographiviridae. Studies show that phages affect antibiotic resistance and biofilm formed by *P. aeruginosa*. Antibiotic resistance was investigated, and 100 % resistance of isolated strains to ampicillin, amoxicillin, lincomycin, cotrimoxazole, ceftazidime and penicillin antibiotics was shown that can be treat by phages with Multiplicity of infection (MOI) was 0.01, 0.1 and 1.

Conclusion: Although phage therapy is an excellent alternative for the treatment of bacterial infections, especially *P. aeruginosa* optimisation of formulations and long-term stability data is required before it can be widely used within a clinical setting.

Keywords: Phage therapy ،*Pseudomonas aeruginosa* ،clinical specimens, antibiotic, resistance, infection

Abstract ID: 415
subject: Other related topics

A c*ompa*rative study of miRAN16 expression in *Helicobacter pylori*-infected individuals and gastric cancer patients using real-time PCR

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Background and Aim: *Helicobacter pylori*, a Gram-negative bacterium, is a known cause of gastric cancer. MiRNAs are molecules that can be affected by this bacterium's pathogenicity. MiRNA16 can target the Bcl2 molecule and induce apoptosis. This study aims to evaluate miRNA16 expression in individuals infected with *H. pylori* c*OmpA*red to those with gastric cancer

Material And Methods: This case-control study included 72 individuals: 30 with gastric cancer and *H. pylori* infection (group 1), 12 healthy controls (group 2), and 30 healthy individuals with *H. pylori* infection (group 3). Blood samples were collected, RNA was extracted from white blood cells, and cDNA was synthesized using specific primers. MiRNA16 expression was investigated using Real-Time PCR with specific primers and Syber Green stain. Data were analyzed using SPSS, paired T-tests, and ANOVA.

Results: MiRNA16 expression was higher in group 1 than in groups 2 and 3. ANOVA analysis showed a significant difference among the three groups (p-value = 0.035). Conclusions: Increased miRNA16 expression may increase the risk of gastric cancer due to its ability to target the *Bcl2* gene involved in apoptosis.

Conclusion: Increased miRNA16 expression may increase the risk of gastric cancer due to its ability to target the *Bcl2* gene involved in apoptosis.

Keywords: *Helicobacter pylori*, miRNA16, apoptosis, gastric cancer, increased expression.

Abstract ID: 165
subject: Other related topics

A systematic review of the avian antibody (IgY) therapeutic effects on human bacterial infections over the decade

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Background and Aim: The overuse of antibiotics worldwide, especially during the Coronavirus pandemic, has raised concerns about the rise of antibiotic resistance and its side effects. Immunoglobulin Y, a natural protein that specifically targets foreign antigens, holds promise as a potential therapeutic option, particularly for individuals with sensitive immune systems. Despite numerous studies on IgY, the optimal administration method, effective dose, target antigen, and potential side effects of this antibody remain areas of active research and challenge.

Material And Methods: This review selected and evaluated articles published in the last ten years from databases such as PubMed and Science Direct with appropriate Keywordsdiscussing the therapeutic effects of immunoglobulin Y in human infections in vivo. Out of all the reviewed articles, 35 articles met the inclusion criteria.

Results: The Resultsshowed that the specific antibody against dental, respiratory and skin infections has an acceptable effectiveness. In contrast, some infections, such as neurological infections, including tetanus and botulism, still need further investigation due to the short survival time of mice. On the other hand, reporting side effects such as antibody-dependent enhancement (ADE) in some infections limits its use.

Conclusion: Based on these results, the specific antibody against dental, respiratory, and skin infections has shown acceptable effectiveness. However, further investigation is needed for some infections, such as neurological infections, including tetanus and botulism, due to mice's short survival time.

Keywords: Adverse ieactions, IgY, immunoproteins, infection control, passive immunity, therapeutic effects

Abstract ID: 269
subject: Other related topics

Production of IgY antibodies against *Helicobacter pylori* and determination of its stability in environmental conditions and interaction with Salmonella and *Escherichia coli*

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Background and Aim: *Helicobacter pylori*, a pathogenic bacterium related to gastritis and gastric carcinoma, poses challenges due to decreasing treatment effectiveness caused by antibiotic resistance. Therefore, alternative treatment approaches are being explored. This study aimed to investigate the stability of specific IgY antibodies against *Helicobacter pylori* in different environmental conditions and its interaction with other bacteria such as Salmonella and *E. coli.*

Material And Methods: White Leghorn hens were immunized with inactivated *H. pylori* to produce specific IgY. The IgY was purified using polyethylene glycol precipitation and analyzed using SDS-PAGE and western blotting. The efficacy of the IgY antibody was evaluated using the ELISA method. The present study investigated the inhibitory effect of the specific IgY antibody on the growth of *H. pylori*, *Salmonella enterica* serovar Typhi, and *E. coli.*

Results: The IgY antibody demonstrated specific targeting against *H. pylori* as confirmed by ELISA, resulting in a remarkable growth inhibition rate. According to the findings, this antibody had no inhibitory effect on *E. coli* and *Salmonella enterica* serovar Typhi.

Conclusion: IgY antibodies have the potential to reduce and inhibit the growth of *Helicobacter pylori*, making them a viable alternative therapy.

Keywords: *Helicobacter pylori*, IgY antibodies, gastric cancer, gastritis, treatment

Abstract ID: 266
subject: Other related topics

Investigation of the inhibitory and therapeutic effect of IgY antibody against inactivated *Helicobacter pylori* in AGS cell line and C57BL/6 mice

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Background and Aim: Increasing resistance of *Helicobacter pylori* to antibiotics presents great challenges in the treatment of gastric ulcer. The use of IgY antibodies against *Helicobacter pylori* is an attractive strategy. The present study assessed the prevention and synergistic effect of IgY antibodies and pantoprazole in the treatment of *Helicobacter pylori* infection

Material And Methods: In this study, the specific inhibitory effect of IgY was investigated in the AGS cell line infected with *Helicobacter pylori*. Subsequently, the synergistic activity of IgY with pantoprazole, along with its preventive and therapeutic effects, were examined in male C57BL/6 mice.

Results: The findings revealed that IgY antibodies have a high inhibitory effect on the attachment of *Helicobacter pylori* to AGS cell line. IgY antibodies demonstrated a significant reduction ($P<0.05$) in the count of *Helicobacter pylori* and the severity of gastritis in infected C57/BL6 mice in both the treatment and prevention groups. Notably, the best result was achieved through the simultaneous use of IgY and pantoprazole.

Conclusion: Administration of IgY can not only improve the damaged cells, but also can be used to prevent infection by reducing the binding of bacteria to gastric epithelial cells. Moreover, given its synergistic effect with pantoprazole, it can be recommended as a suitable candidate combined to pantoprazole.

Keywords: IgY antibodies, prophylaxis, therapy, *Helicobacter pylori*, AGS cell line, C57BL/6 mouse model, gastritis

Abstract ID: 349
subject: Other related topics

The effect of tele nursing on the self-efficacy of patients with meningitis

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Background and Aim: With the spread of meningitis and its extensive effects on the healthcare system, the need for new and efficient methods was felt more than ever. One of these methods is telenursing, which was proposed as an effective solution in the management and care of patients with meningitis. telenursing allows nurses to provide services to patients in their homes and monitor their health status using new technologies.

Material And Methods: This research was a semi-experimental study with the participation of 70 patients with meningitis referred to teaching hospitals in Zahedan city in 1402. The samples were divided into intervention and control groups using the random block method. In the intervention group, in addition to routine training, mobile health training was provided by mobile phone software designed and built by the researcher under the Android system. In the control group, only routine training was done. The data collection tool in this research was a questionnaire that was completed in two phases, pre-test and post-test (3 months after the intervention), and at the end of the research, the collected data was analyzed by SPSS version 22 software.

Results: The independent t-test did not show a significant difference between before and after the intervention in the control group, but it showed a significant difference in the test group, and this difference was observed in all dimensions of self-efficacy. (p0.001).

Conclusion: telenursing as a new approach in providing healthcare services can have significant effects on the self-efficacy of meningitis patients. Therefore, investing in the necessary infrastructure for the development and expansion of telenursing services is of great importance and can be considered as an effective solution in improving the health and well-being and, as a result, the self-efficacy of this group of patients.

Keywords: Telenursing, self-efficacy, meningitis

Abstract ID: 296
subject: Other related topics

Investigation of the role of *Escherichia coli* strains in the development and progression of colorectal cancer

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Background and Aim: Colorectal cancer (CRC) accounts for about 9.2% of global cancer deaths, ranking among the most lethal cancers worldwide. Recent cellular and molecular studies reveal that the gut microbiome, despite its protective role in host-pathogen defense, can regulate inflammation and contribute significantly to CRC development and progression. The aim of this study was investigation of the role of *Escherichia coli* (*E. coli*), one of the most abundant gut microbiota, in the development and progression of CRC.

Material And Methods: We assessed the frequency of toxin-producing *E. coli* strains in the tumor tissue vs. adjacent healthy tissue of CRC patients, association of bacterial biofilms with tumor progression, and the potential mechanisms by which *E. coli* strains may promote tumorigenesis and cancer progression within the colorectal tissue.

Results: Increased levels of *E. coli* were found in tumor tissues of patients with CRC c*OmpA*red with normal mucosa tissue. A high prevalence of cycomodulin-producing *E. coli* was detected in biopsies of patients with CRC. In addition, pathogenic cyclomodulin-positive *E. coli* strains were more prevalent on mucosa of patients with stages III/IV than those with stage I colon cancer. Cyclomodulin toxins such as pks-encoded toxin hijack the eukaryotic cell cycle. pks-positive *E. coli*, but not pks-negative *E. coli*, induced DNA double-strand breaks and triggered genomic instability in cells. Transient contact of malignant cells with colibactin-producing *E. coli* (pks+ *E. coli*) increased tumor growth. Furthermore, colibactin has been found to promote colon tumor growth by modifying the tumor microenvironment. On the other hand, it was observed that phylogroups which have the capacity to produce biofilms, have a higher tumorigenicity than other groups. Remarkably, enteropathogenic *E. coli* suppressed the expression of DNA mismatch repair proteins which can be contributed to the development of CRC.

Conclusion: These findings indicate that pathogenic *E. coli* strains can be contributed to CRC tumorigenesis. However, further research is required to further illustrate *E. coli* roles in CRC progression.

Keywords: *Escherichia coli* strains, colorectal cancer, tumorigenesis, cancer progression.

Abstract ID: 414
subject: Other related topics

The effect of *Lactobacillus* and coffee caffeine as acne treatment in a mouse model

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Background and Aim: Acne is a common skin disorder, primarily linked to inflammation and changes in sebaceous gland function. Recent studies have focused on natural treatments, such as probiotics and plant-based compounds. *Lactobacillus*, a probiotic with anti-inflammatory properties, and caffeine found in coffee, known for its antioxidant and anti-inflammatory effects, may help in acne reduction. This study investigates the combined effect of *Lactobacillus* and coffee caffeine in a mouse model of acne.

Material And Methods: In this study, laboratory mice were divided into five groups: Control group (no treatment) Group receiving *Lactobacillus* Group receiving coffee caffeine Group receiving *Lactobacillus* Group receiving a combination of *Lactobacillus* and coffee caffeine The treatments were administered for four weeks. Afterward, parameters such as the number and size of pimples, skin inflammation levels, antioxidant enzyme activity, and sebaceous gland secretion were measured.

Results: The Resultsshowed that the group receiving the combination of *Lactobacillus* and coffee caffeine had a significant reduction in the number and severity of acne lesions. Additionally, this group demonstrated a notable decrease in skin inflammation and sebaceous secretion. Positive changes were observed in antioxidant enzyme activity, with increased antioxidant levels. The combination of the two agents helped reduce oxidative stress and improved sebaceous gland function.

Conclusion: The combination of *Lactobacillus* and coffee caffeine showed positive effects in reducing acne in the mouse model. This combination works by reducing inflammation, regulating sebaceous secretion, and enhancing antioxidant activity, leading to acne reduction. These findings suggest that the use of this combination may serve as an effective natural treatment for acne, particularly in reducing skin inflammation and improving sebaceous gland function in animal models.

Keywords: *Lactobacillus,* coffee caffeine,

Abstract ID: 287
subject: Other related topics

Molecular docking study of equilenin and its analogues as *Pseudomonas aeruginosa* inhibitors: a novel therapeutic strategy

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Background and Aim: *Pseudomonas aeruginosa*, is a well-known opportunistic pathogen that causes chronic lung infections in individuals with weakened immune systems and is a common hospital pathogen. It exhibits high intrinsic resistance to antimicrobial agents due to its robust nature and ability to form biofilms. A crucial protein in the metabolic pathway of Pseudomonas is steroid delta-isomerase, which plays a role in lipid metabolism. Recent studies focus on targeting key genes or proteins in Pseudomonas to overcome infections. Therefore, in this study, we explore the most potent steroid delta-isomerase inhibitor using molecular docking analysis.

Material And Methods: The 3D structure of Steroid Delta-isomerase of *Pseudomonas aeruginosa* (PDB ID: 3MSO) was obtained from the RCSB PDB database in PDB format. The structures of equilenin (DrugBank ID: DB03515) and its 30 analogs were obtained in SDF 3D format from the PubChem database. After preparing protein and ligands by removing water molecules and ligand from the protein structure and energy minimization, molecular docking was performed using the Molegro Virtual Docker v. 6. Only the top 1 pose of each ligand was selected in Molegro Virtual Viewer v. 7, and the best ligand with the lowest energy binding was evaluated. Finally, the pharmacokinetic properties of ligand were estimated using the SwissADME database.

Results: The best ligand for Steroid Delta-isomerase of *Pseudomonas aeruginosa* was 3-Hydroxy-19-nor-1,3,5(10)-cholatrien-24-oic acid (PubChem CID: 130467), with a molecular weight of 356.50 g/mol and the most negative ?Gbind (-116/392 kcal/mol). This ligand formed 4 hydrogen bonds with the Steroid Delta-isomerase residues, Ala 44(A), Ser 41(A), Arg 72(B), Val 82(A), and 11 steric interactions involving Glu 113(A), Val 114(A), Lys 96(B), Ser 41(A), Ala 44(A), Ile 98(B), Glu 85(B), Arg 72(B), Ile 98(A), Ile 101(A), Val 82(A). Moreover, the ADME Resultsindicated that this ligand had a water solubility score of (LogS) -5.72, 3 hydrogen bond acceptors, 2 hydrogen bond donors, a lipophilicity score of (XLOGP3) 5.98, and a polarity score (TPSA) of 57.53.

Conclusion: Based on the obtained results, 3-Hydroxy-19-nor-1,3,5(10)-cholatrien-24-oic acid (PubChem CID: 130467) ligand may serve as an inhibitor candidate drug for Steroid Delta-isomerase of *Pseudomonas aeruginosa*, although further in vivo and in vitro analysis are necessary.

Keywords: *Pseudomonas aeruginosa*, steroid delta-isomerase, molecular docking

Abstract ID: 223
subject: Other related topics

A review of antibacterial effects of thyme essential oil against *Streptococcus mutans* based on Iranian studies

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Background and Aim: *Streptococcus mutans*, a Gram-positive bacterium, is a primary contributor to dental caries, a significant global public health issue. Due to rising antibiotic resistance and the limitations of conventional treatments, natural alternatives like thyme (Thymus spp.) have gained attention. Thyme, from the Lamiaceae family, is rich in bioactive compounds with antimicrobial, antioxidant, and anti-inflammatory properties, making it valuable in healthcare and disease prevention. This study evaluates the antibacterial efficacy of thyme essential oil against *Streptococcus mutans* and explores its potential mechanisms of action, aiming to provide alternatives to conventional antibiotics for oral health applications.

Material And Methods: A systematic review was conducted using Keywordssuch as Thymus vulgaris, *Streptococcus mutans*, and essential oil across PubMed, Scopus, ScienceDirect, SID, and Google Scholar. Articles published between 2020 and 2025 were selected for relevance and recent findings. This rigorous approach ensures a comprehensive analysis grounded in credible scientific data.

Results: The review analyzed 102 studies from Iran, demonstrating a strong correlation between the antimicrobial properties of thyme essential oil and its concentration. Resultsconfirm that thyme essential oil significantly inhibits the growth of *Streptococcus mutans*, supporting its potential as a natural antimicrobial agent for managing oral health issues.

Conclusion: These findings underscore the promise of thyme essential oil as a viable alternative to synthetic antibiotics in combating oral pathogens and addressing antibiotic resistance. Its proven effectiveness in reducing bacterial viability highlights its potential for therapeutic applications in oral healthcare. This study contributes to understanding the role of medicinal plants in preventive healthcare and emphasizes the need for further research into their applications in developing natural antimicrobial agents.

Keywords: Antimicrobial effects, thymus vulgaris, *Streptococcus mutans*, essentioal oil

Abstract ID: 228
subject: Other related topics

Association between colorectal cancer and the abundance of *Fusobacterium nucleatum* and *Bacteroides fragilis*: A systematic review and meta-analysis

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Background and Aim: Colorectal cancer (CRC) is well-documented as the second most prevalent cancer worldwide and is recognized as a multifactorial disease. Recent studies have highlighted the potential role of bacterial colonization, specifically the presence of *Fusobacterium nucleatum* (*F. nucleatum*) and *Bacteroides fragilis* (*B. fragilis*), in the development and progression of CRC.

Material And Methods: A systematic review and meta-analysis were conducted using a comprehensive search strategy. Keywordsincluded "*Fusobacterium nucleatum*," "*Bacteroides fragilis*" and "colorectal cancer," obtained from three major databases: Embase, Web of Science and PubMed. The search was limited to English-language articles published between 2000 and 2024. Statistical analyses were performed using CMA software.

Results: The analysis revealed that among CRC patients, the prevalence of *F. nucleatum* was reported in 19 countries, with a prevalence rate of 38.9% and *B. fragilis* was reported in 10 countries, with a prevalence rate of 42.5%. Notably, the highest prevalence of *F. nucleatum* was observed in Asian countries, while European countries reported the highest prevalence of *B. fragilis* isolates. Furthermore, diabetes was identified as the most common underlying disease among CRC patients.

Conclusion: This systematic review and meta-analysis emphasize the high prevalence of *F. nucleatum* and *B. fragilis* among CRC patient. based on the Resultsof this study, in CRC patients modulation of gut microbiota could be a promising strategy to enhance the efficacy of CRC treatment.

Keywords: Colorectal cancer, *Fusobacterium nucleatum*, *Bacteroides fragilis*, meta-analysis.

Abstract ID: 158
subject: Other related topics

Biosynthesis of silver nanoparticles using oscillatoria extract and evaluation the anticancer and antibacterial activities

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Background and Aim: The emergence of nanotechnology is one of the most promising areas for medical research. Today, biological methods of synthesizing nanoparticles have been considered in the fight against many diseases.

Material And Methods: In the present experimental study, the silver nanoparticles biosynthesis was performed using silver ions regeneration with cyanobacteria acetate extracts. Techniques such as X-ray diffraction, scanning electron microscopy and transient evaluation of silver nanoparticles were evaluated. In order to investigate the antibacterial activity of synthesized nanosilver, serial dilution method was used for broth microdilution test to determine minimum inhibitory concentration (MIC). The effects of silver nanoparticle toxicity on T47D breast cancer cell line were evaluated using MTT colorimetric method. Also, the proximal anxine 0.5 propidoid yodide kit and flow cytometry system were evaluated to evaluate the percentage of apoptosis and necrosis in cancer cells treated with silver nanoparticles.

Results: Characterization of biosynthetic silver nanoparticles indicated that these nanoparticles had a mean size of 30 nm with dominant spherical morphology. The evaluation of the antibacterial properties of biosynthetic nanoparticles showed that the minimum inhibitory concentration for *Escherichia coli*, *Acinetobacter bumanni* and *Staphylococcus aureus* was 25, 50 and 12.5 µg / ml, respectively. The Resultsof cell proliferation of nanoparticles showed that its effect depends on the concentration and time of treatment of silver nanoparticles on cancerous cells. In addition, flow cytometric Resultsshowed an apoptotic cell death rate of 35% in the T47D cell line.

Conclusion: Biosynthesis nanoparticles have anticancer and antibacterial activity and can be studied further in the treatment of breast cancer and infections caused by pathogenic bacteria.Since the genus Osillatoria has more biologically active compounds, it seems that it has the regenerating ability of silver salt. Therefore, the use of their extract for the biosynthesis of metal nanoparticles is of great importance.

Keywords: Osillatoria- nanoparticles- anti bacterial- T47D cell line

Abstract ID: 309
subject: Other related topics

Discovery of effective inhibitors targeting the protein kinase B (*PknB*) from *Mycobacterium tuberculosis* via molecular docking

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Background and Aim: Tuberculosis, caused by *Mycobacterium tuberculosis*, is a potentially fatal contagious disease affecting the lungs. Despite ongoing efforts, the emergence of drug-resistant strains and diagnostic challenges continue to make tuberculosis a major global health issue in 2025. The protein kinase *PknB* plays a vital role in *M. tuberculosis*, facilitating bacterial growth, division, and adaptation to stressful environments, including evasion of the host's immune response. Therefore, targeting *PknB* presents a promising strategy for developing alternative therapies to combat against tuberculosis.

Material And Methods: The crystal structure of *M. tuberculosis PknB* was retrieved from the RCSB Protein Data Bank (PDB ID: 2FUM). Fostamatinib and Mitoxantrone, known *PknB* inhibitors (PubChem CID: 11671467 and 4212, respectively) along with their 20 analogs from the PubChem database, were selected in SDF format. Protein and ligand preparation involved removing the ligand from the protein structure, energy minimization, and adding charges and hydrogen atoms. Molegro Virtual Docker v. 6 was employed for molecular docking, and the best interaction with the lowest binding energy was analyzed using Molegro Molecular Viewer software. The pharmacokinetic properties of the ligand were then evaluated using the SwissADME server.

Results: Among the ligands investigated 2-[[4-[2-(Dimethylamino)ethylamino]-5,8-dihydroxy-9,10-dioxoanthracen-1-yl]amino]ethyl-hydroxy-dimethylazanium (PubChem CID: 1430920980((molecular weight: 429.49g/mol) demonstrated the most energetically favorable binding (?Gbind = -131.31 Kcal/mol) to the target protein *PknB*. This ligand formed 1 hydrogen bonds with *PknB* residues Leu 31 (B), and engaged in 7 steric interactions involving residues His34[B],Asp232[C],Arg239[C], Leu31[B], Arg32[B],Glu231[c],Glu227[c].The ligand exhibited a Log S score of -4.39 and a Log P score of -1.17. It also possessed 5 hydrogen bond donors and 6 acceptors, with a polarity index (TPSA) of 122.13 ?².

Conclusion: In Conclusion, the aforementioned findings highlight the potential of the mentioned ligand (PubChem CID: 143092098) as a promising compound for further optimization. This ligand may serve as a suitable starting point for the development of novel therapeutic agents targeting *Mycobacterium tuberculosis*. Therefore, further in vitro and in vivo analysis are required.

Keywords: *M. tuberculosis*, *PknB*, fostamatinib, mitoxantrone.

Abstract ID: 347
subject: Other related topics

Bioinformatics analysis of *Salmonella*-specific bacteriophage endolysins as antibiotic alternatives

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Background and Aim: Phage endolysins are enzymes that play a crucial role in the lytic cycle of bacteriophages by degrading bacterial cell walls. Their remarkable specificity toward host bacterial species positions them as cutting-edge candidates for the development of innovative antibacterial therapies. This study examines Salmonella-specific bacteriophage endolysins as molecular markers, investigates their evolutionary dynamics, and assesses their potential as alternative therapeutic agents to antibiotics for addressing resistant bacterial infections.

Material And Methods: In this study, 35 endolysin sequences from Salmonella-specific bacteriophages were obtained from Reputable sources, including the NCBI database and peer-reviewed experimental studies on endolysins. These sequences were analyzed separately at the nucleotide and amino acid levels. Repeated sequences, Sequences with lengths significantly deviating from the average, and phages with significant evolutionary divergence were excluded. Analyses included multiple sequence alignment and phylogenetic tree construction using the web-based tool Clustal Omega, identification of conserved motifs using MEME server, functional annotation with InterPro, homology modeling, and structural analysis of conserved motifs with Phyre2. Homology was further assessed at both nucleotide and protein levels using BLASTn and BLASTp tools from the NCBI database.

Results: Based on the phylogenetic tree results, 24 endolysins were grouped, and all previous analyses were c*OmpA*red across nucleotide and protein levels. Among the grouped phages, XF2-1 and LPSE1 exhibited the highest similarity, underscoring potential functional or structural parallels, whereas TYM102 and Meda demonstrated significant evolutionary divergence, indicative of unique adaptations or distinct evolutionary trajectories. The identified motifs were linked to lysozyme activity (GO:0003796), peptidoglycan catabolic processes (GO:0009253), and macromolecule catabolic processes in the cell wall (GO:0016998). The phylogenetic analysis highlighted significant evolutionary diversity among these endolysins. Protein-level homology indicated convergent evolutionary relationships between Salmonella-specific endolysins and the lysozymes of Salmonella bacteria (autolysins), suggesting an example of biological adaptation and horizontal gene transfer that provides survival and functional advantages to both phages and their bacterial hosts.

Conclusion: The nucleotide-level conservation of Salmonella-specific phage endolysins establishes their utility as precise molecular markers, facilitating the accurate identification of Salmonella-targeting phages. This in-depth evolutionary insight into these enzymes paves the way for the development of advanced biotools with transformative applications in medicine, agriculture, and biotechnology.

Keywords: Endolysin, bacteriophage, *Salmonella*, enzybiotics, antibiotic resistance

Abstract ID: 317
subject: Other related topics

CmaA3 as a therapeutic target for *Mycobacterium tuberculosis*: A computational investigation

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Background and Aim: *Mycobacterium tuberculosis*, a gram-positive and acid-fast bacterium, is the primary cause of tuberculosis, leading to chronic infections in many individuals. A significant challenge in managing this disease is the rise of multi-drug resistant (MDR) and extensively drug-resistant (XDR) strains, which complicates treatment. The enzyme CmaA3 in *M. tuberculosis* is crucial for synthesizing cyclopropane mycolic acids, which are essential for maintaining the cell wall and protecting the bacterium from environmental stresses. Inhibiting CmaA3 can disrupt the cell wall structure, making the bacterium more susceptible to antibiotic treatments. This study focuses on identifying potent and efficient inhibitors for CmaA3 using molecular docking analysis.

Material And Methods: The 3D structure of CmaA3 of *M. tuberculosis* was extracted from the RCSB PDB database (PDB ID: 1L1E). The Pretomanid inhibitory ligand of CmaA3 with DrugBank ID (DB05154), and a total of its 30 analogs, was retrieved from the PubChem database in SDF format. After preparing the protein and its ligands by eliminating the ligand and water from the protein, lowering the energy level, and adding electric charges and hydrogen atoms, molecular docking was conducted using Virtual Docker Molegro v. 6. Subsequently, the best interaction with the lowest energy binding was analyzed using Molegro Molecular Viewer software. Finally, the pharmacokinetic properties of the ligand were investigated using the SwissADME server.

Results: Among all the inhibitory ligands, the best ligand was (6S)-2-nitro-6-[[4-(2,2,2-trifluoroethoxy)phenyl]methoxy]-6,7-dihydro-5H-imidazo[2,1-b][1,3]oxazine (PubChem CID:15888325) with the molecular weight of 373.28 g/mol , and binding energy of -149.958 kcal/mol. This ligand formed 5 Hydrogen bonds with Gln226(A), Tyr37(A), Lys163(B), Tyr37(B), and Gln226(B) along with 8 steric interactions involving Tyr 37(A), Gln226(A), Lys163(B), Lys59(B), Lys59(A), Gln226(B), Glu286(A), Tyr37(B) residues. The ADME Resultsdemonstrated a water solubility score (LogS) of -3.69, the hydrophilic score (LogP) of 2.42, the polarity score (TPSA) of 91.33, and in Conclusionthe hydrogen bond donors of 0 and hydrogen bond acceptor of 9.

Conclusion: Based on the obtained results, compound with PubChem CID 15888325 demonstrated the best interaction with the lowest energy binding with CmaA3, although further in vivo and in vitro analysis are necessary.

Keywords: Molecular docking , *Mycobacterium tuberculosis* , CmaA3, MDR

Abstract ID: 16
subject: Other related topics

Biological characteristics and anti-biofilm activity of a lytic phage against vancomycin-resistant *Enterococcus faecium*

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Background and Aim: An important leading cause of the emergence of vancomycin-resistant enterococci, especially *Enterococcus faecium*, is the inefficiency of antibiotics in the elimination of drug-resistant pathogens. Consequently, the need for alternative treatments is more necessary than ever.

Material And Methods: A highly effective bacteriophage against vancomycin-resistant *E. faecium* called vB-EfmS-S2 was isolated from hospital sewage. The biological properties of phage S2 and its effect on biofilm structures were determined.

Results: Phage S2 was specifically capable of lysing a wide range of clinical *E. faecium* isolates. According to Electron microscopy observations, the phage S2 belonged to the Siphoviridea family. Suitable pH spectra for phage survival was 5–11, at which the phage showed 100% activity. The optimal temperature for phage growth was 30–45°C, with the highest growth at 37°C. Based on one-step growth curve results, the latent period of phage S2 was 14 min with a burst size of 200 PFU/ml. The phage S2 was also able to tolerate bile at concentrations of 1 and 2% and required Mg2+ for an effective infection cycle. Biofilms were significantly inhibited and disrupted in the presence of the phage.

Conclusion: According to the results, phage S2 could potentially be an alternative for the elimination and control of vancomycin-resistant *E. faecium* biofilm.

Keywords: *Enterococcus faecium*, vancomycin-resistant *Enterococcus faecium*, phage therapy, antibiotic-resistance, biofilm

Abstract ID: 96
subject: Other related topics

Phage therapy a novel and safe approach to combat drug-resistant infections: A systematic review

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Background and Aim: Bacteriophages, independently isolated by Frederick Twort and Félix d'Hérelle in 1915 and 1917, respectively, showed early promises. The wider availability of antibiotics reduced their use, and now, with increasing resistance, there has been a new interest in phage therapy. Because lytic bacteriophages target bacteria very specifically, this minimizes damage to the healthy flora, thus reducing side effects. Evidence in recent times indicates that their clinical impact should not be underestimated against so many multi-resistant infections. This review revisits a review on the safety and efficiency of phage therapy as well as its growing relevance nowadays in current medical practices - both globally

Material And Methods: For this systematic review, a bibliographic search was conducted across three databases: ScienceDirect, PubMed, and Google Scholar. The Keywordsused were “phage therapy” and “multidrug resistant,” combined using Boolean operators. The inclusion criteria consisted of full-text articles and clinical case reports from the last ten years. Articles involving animal studies and metagenomic research without human application were excluded. Titles and abstracts were initially screened for evaluation, followed by full-text review to exclude irrelevant articles. Data management was performed using software such as EndNote and Excel.

Results: The studies on bacteriophage therapy showed that the clinical improvement, reduction in bacterial load, and eradication of infection were seen in more than 80% of cases, while adverse effects due to phage therapy were absent in over 90% of cases. Routes of administration included intravenous 60%, topical 25%, and oral 15%. Infections that are resistant to antibiotics, where treatment was successful, involved 70% of patients treated, although some particular studies also reported success as high as 100%. These figures all point toward the high potential of the phage therapy method.

Conclusion: Phage therapy is promising and safe for drug-resistant infections. The efficacy of phage therapy depends on the precise selection of specific phages, access to extensive phage libraries, and the synergistic use of antibiotics. Combining this method with other medical treatments enhances efficacy and minimizes the risk of potential treatment failure.

Keywords: Multidrug fesistance, bacteriophages, antibiotic synergy

Abstract ID: 97
subject: Other related topics

Efficacy of phage therapy in treating localized infections (wounds, burns) caused by antibiotic-resistant bacteria: A systematic review

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Background and Aim: Since the discovery of bacteriophages, viruses that infect bacteria exclusively, as a promising tool in combating bacterial infections in humans, the rise of antibiotic-resistant bacteria has revived interest in phage therapy. The current review discusses the treatment of localized infections like wounds, burns, diabetic foot ulcers, and other cases using bacteriophages and their efficacy against resistant bacteria.

Material And Methods: A comprehensive bibliographic search was conducted in three databases: PubMed, Scopus, and Google Scholar. The Keywords"phage therapy" and "local infections" were combined using Boolean operators. Inclusion criteria included clinical human studies with therapeutic outcomes for local infections, use of specific phages with defined dosages and administration methods. Exclusion criteria included studies unrelated to local infections or those lacking sufficient information about the type of phage and treatment methods. Outcomes were evaluated based on wound healing and pathogen elimination.

Results: Phage therapy was evaluated in 470 patients across 11 studies, showing significant outcomes. Infected burns (30 patients) showed *Pseudomonas aeruginosa* elimination in 40% and wound healing in 50%. Diabetic ulcers (6 patients) achieved a 100% healing rate. Among 231 surgical wound cases, healing rates were 68–90% across studies. Phage titers ranged from 10^3 to 10^{10} pfu/ml, with topical, oral, and injection methods applied. Resultshighlight phage therapy's potential against resistant pathogens like *Pseudomonas aeruginosa* and *Staphylococcus aureus*.

Conclusion: Phage therapy demonstrates high efficacy in combating localized infections such as wounds, burns, and diabetic ulcers. This method facilitates the wound healing process and eradicates resistant bacteria like *Pseudomonas aeruginosa* and *Staphylococcus aureus*. The diverse application methods and varying phage dosages offer significant potential for replacing antibiotics and addressing drug resistance. The obtained Resultshighlight the importance of ongoing research and the development of clinical applications for phage therapy.

Keywords: Phage therapy, localized infections ,resistant bacteria

Abstract ID: 312
subject: Other related topics

Investigation of potent inhibitors to control *Acinetobacter baumannii* by targeting its outer membrane protein A (*OmpA*) using molecular docking

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Background and Aim: *Acinetobacter baumannii* is a gram-negative bacterium that acts as an opportunistic pathogen, primarily affecting individual with compromised immune system and causing hospital-acquired infections. Its pathogenicity is significantly enhanced by Outer membrane protein A (*OmpA*), which facilitates biofilm formation, contributes to antibiotic resistance, and influences immune responses. Given the increasing prevalence of multi-drug resistant Acinetobacter strains, targeting *OmpA* presents a promising strategy for developing alternative therapies. This study utilized molecular docking analysis to identify potential *OmpA* inhibitors, aiming to address drug-resistant infections effectively.

Material And Methods: The 3D structure of the *OmpA* protein (PDB ID 6gie) was obtained from the RCSB PDB database. Its potential inhibitory ligands, Isosakurnetin (PubChem CID:160481), FIA (PubChem CID:334207), FII (PubChem CID:79859), FIC (PubChem CID:1714209), Gallic and Cinnamic acids, and five analogs for each ligand were extracted from PubChem database in SDF format. Then, molecular docking was performed using Virtual Docker Molegro v.6. Subsequently, the best interaction with the lowest energy binding was analyzed among these ligands using Molegro Molecular Viewer software. Finally, the pharmacokinetic properties of the best ligand were investigated using the SwissADME server.

Results: The best ligand for *OmpA* was identified 2-(Dodecyloxy) ethanol (PubChem CID: 24750) with a molecular weight of 230.39 g/mol and a binding energy of -93.86 kcal/mol. This ligand formed 2 hydrogen bonds with the *OpmA* residues Ser217 and His235, as well as 4 steric interaction with the residues Ser217, Phe191, Glu189, and His235. Moreover, the ADME Resultsindicated that this ligand had a LogS water solubility score of -3.63, a lipophilicity (XLoGP3) of 5.11, a polarity (TPSA) of 29.46, and hydrogen bond donors and acceptors of 1 and 2, respectively.

Conclusion: Consequently, after conducting further in vitro and in vivo tests, 2-(Dodecyloxy) ethanol can be considered as a potential candidate for the design of inhibitory drugs to inhibit *A. baumannii* pathogenesis.

Keywords: *Acinetobacter baumannii*, molecular docking, isosakurnetin.

Abstract ID: 342
subject: Other related topics

The frequency of Verrucomicrobia in intestinal mucus of patients with cancer clorectal

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Background and Aim: Members of the phylum Verrucomicrobia, especially *Akkermensia muciniphila*, have been identified as beneficial gut bacteria. Changes in the gut microbiota are associated with the occurrence of metabolic diseases, such as diabetes, obesity, and irritable bowel syndrome; however, there is conflicting information about their role and changes in colorectal cancer.In the present study, the prevalence of this bacterial phylum was investigated in the intestines of individuals with colorectal.

Material And Methods: Mucus samples were obtained from the colons of 69 individuals with colorectal lesions (CRC and PCL) and 65 individuals without lesions during colonoscopy. DNA extraction from mucus samples was performed using a specialized kit and the presence of Verrucomicrobia was determined using a specific 16S rRNA primer followed by the application of conventional PCR.

Results: Healthy individuals exhibited a higher prevalence of Verrucomicrobia (75.4%) compared to those with either cancer or precancerous gut lesions (59.7%) (P-value = 0.038)

Conclusion: The significant reduction in Verrucomicrobia in people with cancer and precancerous lesions demonstrates the importance of members of this phylum of the microbiota in maintaining health. Since *Akkermansia Muciniphila* belongs to this phylum, these results could confirm the role *of Akkermansia Muciniphila* in gut health.

Keywords: Verrucomicrobia, colorectal cancer, microbiota ,Akkermansia

Abstract ID: 25
subject: Other related topics

Detection of *Brucella spp*. in aborted small ruminant's fetuses by polymerase chain reaction

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Background and Aim: Brucellae are Gram-negative intracellular pathogens that cause important diseases in humans and various species of animals. In small ruminants, the disease mainly causes late gestation abortion in pregnant females. Humans may get the infection through consumption of raw milk, inhalation of infected aerosols and direct contact with aborted materials of infected animals. The main control way for human brucellosis is reducing the disease in sheep and goats. Brucella excretes from animal's discharges mainly following abortion and close contact with the abortion materials may lead to human infection. The aim of the present study was to detect Brucella in aborted fetuses which are considered as an important source of human brucellosis especially during breeding season.

Material And Methods: A total of 17 aborted fetuses in Fars province were transmitted to the laboratory for the detection of Brucella. DNA was extracted from fetal tissues and abomasal fluid using commercial DNA extraction kit (CinaGen). Then the samples were examined by a conventional polymerase chain reaction using primers recommended by WOAH.

Results: Brucella positive amplified products showed band 223bp which was visible in 12 samples (70.6%) using the molecular method.

Conclusion: Brucella was detected in most of the samples which indicated the risk of human infection who have high interaction with sheep and goats. No vaccine is available for human use so the key of prevention of human brucellosis is controlling the disease in animals. The policy of Iran for control of brucellosis is utilization of Rev.1 vaccine in sheep and goats. The vaccine reduces abortion in small ruminants. However, vaccination alone cannot eliminate brucellosis effectively. The successful implementation of a national brucellosis control program requires enough compensation, improving vaccine coverage, improvement of the vaccine quality, farmers' cooperation, accurate diagnosis of infected animals, controlling the disease among dogs and wild animals.

Keywords: Brucellosis, malta fever, PCR, small ruminant, vaccination

Abstract ID: 44
subject: Other related topics

A report of septicemia caused by *Capnocytophaga spp* in dog

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Background and Aim: *Capnocytophaga* is an anaerobic, gram negative, commensal and slow-growing bacteria belonging to the family Flavobacteriaceae. The genus *Capnocytophaga* has eight known species of which *C. canimorsus* and *C. cynodegmi* are zoonotic pathogens. The bacterium is found in oral microbiota of dogs and cats, which can be transmitted to humans by scratches and bites of the animals. It rarely leads to infection in humans, with the infection rate between 0.5 and 0.67 cases per million. Infection usually affects men over the age of 50, and it is more common and severe in asplenic or immunocompromised patients. Infections caused by *C. canimorsus* start 3-5 days after the exposure and can lead to sepsis, septic shock, gangrene, high grade bacteremia, endocarditis, and meningitisand abscesses in human. Septicemia or sepsis, caused by *Capnocytophaga* is a life-threatening infection that happens when the bacteria enter the bloodstream and infect various parts of the body. There is no report of animal's infection with *Capnocytophaga* except for a rabbit case which was bitten by a dog. The aim of the present study was to report the isolation of *Capnocytophaga* in a dog with sudden death.

Material And Methods: A mature dog with the symptom of sudden death was necropsied. The samples were taken from bone marrow and paranchymal tissues such as kidney, liver and lungs. Cultures were prepared on blood agar and MacConkey agar and were incubated both aerobically and anaerobically for 48 hours in 37 °C.

Results: None of the tissues showed any growth of bacteria but bone marrow. The colonies belonged to bone marrow samples on Blood agar and MacConkey agar were stained by gram staining method and gram negative bacilli were visible. Biochemical tests confirmed the isolation of *Capnocytophaga* .

Conclusion: In the current result *Capnocytophaga* was isolated from bone marrow which shows the role of the bacterium in the septic condition of the dog. To our best knowledge the current study is the first report of the bacterium involvement in dog septicemia which indicates the requirement of more investigations in terms of the importance of *Capnocytophaga* in animals and human.

Keywords: Bone marrow, *Capnocytophaga*, dog, human, septicemia

Abstract ID: 149
subject: Other related topics

Comparative investigation of synergistic effects of thymol/cefotaxime on *Staphylococcus epidermidis* and *Escherichia coli*

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Background and Aim: This study aims to compare the synergistic antimicrobial effects of thymol/cefotaxime on *Staphylococcus epidermidis* and *Escherichia coli*.

Material And Methods: Antimicrobial effects of thymol/cefotaxime were performed first individually and then combined on *S. epidermidis* ATCC 1457 and *E. coli* ATCC 25922 by the MIC-MBC method. Therefore, the antimicrobial effects of the compounds that had a synergistic impact were performed on clinical strains using the MIC-MBC method. The identification of chemical bonds, functional groups, and molecular interactions of the mentioned compound was investigated using an FT-IR device. Checkered method, biofilm inhibition on *S. epidermidis* ATCC 1457 and *E. coli* ATCC 25922, and cytotoxicity investigation on red blood cells (RBCs) by hemolysis and human skin fibroblast cells (Ffk) by MTT method were performed. Finally, the results of the tests were compared between the two bacteria.

Results: The results of this study showed that the antimicrobial effects of the thymol/cefotaxime (16/4 µg/ml) were on *S. epidermidis* better than on *E. coli* (128/16 µg/ml) in both clinical and ATCC strains. In the examination with the FT-IR device, had bonds of OH carbohydrates proteins, polyphenols, C=O Amide I band, C-O-C polysaccharide, and C-N amide III band, but one band named C=C conjugated, C?C in compound showed the connection between thymol with cefotaxime. The biofilm inhibition effects of thymol/cefotaxime on *S. epidermidis* ATCC 1457 (61.81%) were better on *E. coli* ATCC 25922 (39.28%). Cytotoxicity of the synergistic compound on RBCs and human Ffk cells was not different and was lower than that of Triton X-100.

Conclusion: Considering the antibiotic resistance of cefotaxime in the treatment of diseases caused by *S. epidermidis* and *E. coli*, thymol/cefotaxime showed better antimicrobial effects in *S. epidermidis* than in *E. coli* in this study. After further studies, this compound can be used as a new drug in patients.

Keywords: *Staphylococcus epidermidis*, *Escherichia coli*, Thymol, cefotaxime, synergistic

Abstract ID: 366
subject: Other related topics

The relationship between Tuberculosis and breast cancer in a mouse model

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Background and Aim: Tuberculosis (TB), caused by *Mycobacterium tuberculosis*, is a chronic infectious disease with systemic effects on the body. Breast cancer is also one of the most common cancers among women. This study investigates the interplay between TB and breast cancer in mouse models.

Material And Methods: Laboratory mice were divided into the following groups: Healthy control group, TB-infected group, Breast cancer group. Group with both TB and breast cancer Changes in cellular processes, immune responses, and tumor growth were analyzed in each group. Additionally, gene expression related to inflammation and cell growth regulation was examined.

Results: Mice with both diseases exhibited increased tumor growth compared to other groups. TB induced alterations in immune responses and promoted chronic inflammation, facilitating tumor progression. Inflammatory markers such as IL-6 and TNF-α were significantly elevated in TB-infected groups, creating a favorable environment for cancer growth. Immunosuppressive cells, such as regulatory T cells (Tregs), were more abundant in mice with both TB and breast cancer.

Conclusion: The study demonstrated that TB can accelerate breast cancer progression through chronic inflammation and immune system modulation. These findings underscore the importance of considering breast cancer risk in TB patients and developing tailored therapeutic strategies to mitigate the effects of both diseases.

Keywords: Tuberculosis , breast cancer, mouse model of breast cancer

Abstract ID: 200
subject: Other related topics

Comparative assessment of bactericidal and synergistic effects of mentha pulegium (oregano) and cinnamomum verum (cinnamon) essential oils against methicillin-resistant *staphylococcus aureus* (MRSA)

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Background and Aim: Methicillin-resistant *Staphylococcus aureus* (MRSA) poses a significant global health threat due to its resistance to various antibiotics. Essential oils from medicinal plants, such as Mentha pulegium (oregano) and Cinnamomum verum (cinnamon), have demonstrated antimicrobial properties. This study aimed to assess and compare the bactericidal effects and potential synergistic interactions between these essential oils and the antibiotic cefoxitin against MRSA strain.

Material And Methods: We utilized MRSA strains confirmed by the presence of the *mecA* gene. The essential oils of Mentha pulegium and Cinnamomum verum were extracted and tested for minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) against both clinical MRSA isolates and standard *Staphylococcus aureus* (ATCC 25923) strains. Antibiograms were performed using cefoxitin and other antibiotics. Synergy testing involved loading sub-MIC concentrations of the essential oils onto cefoxitin discs and evaluating inhibition zone diameters on agar plates.

Results: The essential oil of Cinnamomum verum showed the most potent antibacterial activity, with lower MIC and MBC values compared to Mentha pulegium. Against the MRSA isolates, the MIC and MBC values for cinnamon were 6.25 mg/mL, while for oregano, they were 50 and 100 mg/mL. In synergy testing, the combination of cinnamon essential oil and cefoxitin produced a larger inhibition zone (12 mm) compared to oregano and cefoxitin, indicating a stronger synergistic effect. The solvent used for essential oil extraction, methanol, showed no inhibitory effect on bacterial growth, confirming the antimicrobial activity was due to the oils.

Conclusion: This study highlights the potential of Cinnamomum verum essential oil as a more effective antibacterial agent against MRSA compared to Mentha pulegium. Furthermore, the synergistic effect of combining cinnamon oil with cefoxitin could be a promising strategy to enhance antibiotic efficacy against resistant strains. Further studies are recommended to explore the mechanisms underlying these interactions and to evaluate their clinical applications in combating antibiotic-resistant infections.

Keywords: MRSA, cinnamon, oregano

Abstract ID: 365
subject: Other related topics

Evaluation of the effect of chitosan-BCG microparticles on the expression of genes involved in colorectal cancer signaling pathways in the caco2 cell line

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Background and Aim: Colorectal cancer (CRC) is one of the most common and serious cancers worldwide. Due to the side effects of existing therapies, innovative approaches, such as bacterial-based methods like the BCG vaccine could be effective for cancer management. This study aimed to investigate the effects of BCG encapsulated in chitosan nanoparticles on the modulation of apoptosis and also expression of genes involved in signaling pathways in Caco2 cancer cells.

Material And Methods: The chitosan-BCG microparticles (Ch-BCG) were synthesized using the ionotropic gelation method. Ch-BCG microparticles were characterized by FTIR, DLS, zeta potential, and SEM tests. MTT assay was carried out to assess cytotoxicity and cells were subsequently treated with a concentration of chitosan nanoparticles, BCG, and Ch-BCG that ensured at least 70% viability, followed by RNA extraction. An uptake assay was conducted to assess the cellular internalization of the microparticles. Furthermore, the expressions of apoptosis-related genes (caspase9 and bcl2) and genes involved in the colorectal cancer signaling pathways such as Wnt/β-catenin, PI3K, hes1, gli2, and TGF-β were detected by Real-time qPCR.

Results: The average size of Ch-BCG particles was estimated at approximately 1.8 µm. SEM images showed a remarkable increase in the size of C-BCG microcapsules. The uptake assay results showed a good facility for Ch-BCG to enter Caco2 cells. The mRNA expression of apoptosis-related genes was upregulated, with a 50-fold increase in caspase9 while the 14.5-fold decrease in bcl2 demonstrated down-regulation. Moreover, the PI3K gene involved in the PI3K/AKT pathway was down-regulated 4-fold by Ch-BCG. In the Ch-BCG group compared to the control group, the mRNA expression of β-catenin, hes1, TGF-β, and gli2 genes which belong to the Wnt/β-catenin, Notch, TGF-β, and Hedgehog signaling pathways was decreased by 14, 14.7, 5 and 13.5-fold, respectively.

Conclusion: C-BCG targets colorectal cancer cells by promoting apoptosis and inhibiting critical pathways. The significant changes in gene expression indicate a potential mechanism of action, though further studies are needed to confirm its potential.

Keywords: Bacillus Calmette Guerin, vaccine, chitosan, colorectal cancer, Caco2

Abstract ID: 279
subject: Other related topics

Identification of a promising ligand for inhibiting carbapenem-hydrolyzing KPC enzyme in carbapenem-resistant *klebsiella pneumoniae*; molecular docking investigation

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Background and Aim: *Klebsiella pneumoniae* is a significant pathogen responsible for severe infections, including pneumonia, bloodstream and urinary tract infections. The bacteria's ability to produce the KPC enzyme, carbapenem-hydrolyzing beta-lactamase, is a key factor in its resistance to carbapenem antibiotics. As carbapenem-resistant *K. pneumoniae* strains countinue to rise alarmingly, targeting the KPC enzyme offers a promising strategy for developing novel therapies to combat drug-resistant infections. Therefore, in this study, we explored the most effective inhibitory ligand for the KPC protein through a molecular docking approach.

Material And Methods: The 3D structure of the carbapenem-hydrolyzing beta-lactamase KPC protein, with PDB ID: 2OV5, was obtained from the RCSB PDB database. The structures of the KPC inhibitory ligand, [(2S,5R)-2-carbamoyl-7-oxo-1,6-diazabicyclo[3.2.1]octan-6-yl] hydrogen sulfate, and its 20 analogs were retrieved in SDF format from the PubChem database. The protein and ligands were prepared using Molegro Virtual Docker 6.0. Docking simulations were conducted to identify the best interaction and the lowest binding energy, which was then analyzed via Molegro Molecular Viewer 7. Furthermore, the pharmacokinetic properties of ligand were evaluated using the SwissADME server to assess its potential for drug developement.

Results: Among the analyzed ligands, [2-[(2-amino-2-oxoethyl)carbamoyl]-7-oxo-1,6-diazabicyclo[3.2.1]octan-6-yl] hydrogen sulfate with PubChemCID: 21942042 emerged as the most effective. This ligand had a molecular weight of 322.30 g/mol and a binding energy of -87.0067 kcal/mol. It formed eight steric interactions with the KPC protein residues, including Tyr60(C), Arg61(C), Glu64(C), Glu188(B), Lys192(B), Gly156(B), Glu63(C), and Ala62(C). Moreover, it established six hydrogen bonds with residues Ala62(C), Glu63(C), Lys192(B), Gly156(B), Glu188(B), and Arg61(C), while no electrostatic interactions were observed. The ADME analysis revealed a water solubility score (LogS) of 0.13, a hydrophilic score (LogP) of 0.25, a polarity score (TPSA) of 167.72, along with three hydrogen bond donors and seven hydrogen bond acceptors.

Conclusion: This study identified a promising ligand, [2-[(2-amino-2-oxoethyl)carbamoyl]-7-oxo-1,6-diazabicyclo[3.2.1]octan-6-yl] hydrogen sulfate, for inhibiting the KPC enzyme. Its strong binding energy, favorable interactions, and pharmacokinetic properties highlight its potential as a therapeutic agent against carbapenem-resistant *Klebsiella pneumoniae*, warranting further in vitro and in vivo validations to combat drug-resistant infections effectively.

Keywords: Carbapenem-hydrolyzing beta-lactamase KPC, *Klebsiella pneumoniae*, molecular docking, carbapenem resistance

Abstract ID: 183
subject: Other related topics

A comparative study on the synergistic effects of thymol/ceftazidime against *Escherichia coli* and *Staphylococcus epidermidis*

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Background and Aim: This study compares the synergistic antimicrobial effects of thymol/ceftazidime on *Escherichia coli* and *Staphylococcus epidermidis*.

Material And Methods: Antimicrobial effects of thymol/ceftazidime were performed first individually and then combined on *E. coli* ATCC 25922 and *S. epidermidis* ATCC 1457 by the MIC-MBC method. Therefore, the antimicrobial effects of the compounds that had a synergistic impact were performed on clinical strains using the MIC-MBC method. The identification of chemical bonds, functional groups, and molecular interactions of the mentioned compound was investigated using an FT-IR device. Checkered method, biofilm inhibition on *E. coli* ATCC 25922 and *S. epidermidis* ATCC 1457, and cytotoxicity investigation on red blood cells (RBCs) by hemolysis and human skin fibroblast cells (Ffk) by MTT method were performed. Finally, the results of the tests were compared between the two bacteria.

Results: The results of this study showed that the antimicrobial effects of the thymol/ceftazidime (16/2 µg/ml) were on *S. epidermidis* better than on *E. coli* (16/4 µg/ml) in both clinical and ATCC strains. In the examination with the FT-IR device, it had bonds of OH carbohydrates proteins, polyphenols, C=O Amide I band, C-O-C polysaccharide, C-N amide III band, but one band named C=C conjugated, C?C in compound showed the connection between thymol with ceftazidime. The biofilm inhibition effects of thymol/ceftazidime on *E. coli* ATCC 25922 (75.51%) were better on *S. epidermidis* ATCC 1457 (49.09%). The cytotoxicity of synergistic compounds on RBCs and human Ffk cells was not different and was lower than that of Triton X-100.

Conclusion: Considering the antibiotic resistance of ceftazidime in the treatment of diseases caused by *E. coli* and *S. epidermidis*, thymol/ceftazidime showed better anti-biofilm effects in *E. coli* than in *S. epidermidis* in this study. After further studies, this compound can be used as a new drug in patients.

Keywords: *Escherichia coli*, *Staphylococcus epidermidis*, thymol, ceftazidime, cynergistic

Abstract ID: 388
subject: Other related topics

Genetic diversity and protein structural variations in *flaA* and *flaB* of *H. Pylori*: insights from Iranian strains

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Background and Aim: The *flaA* and *flaB* genes in *Helicobacter pylori* encode two key proteins that form the bacterium's flagella which is crucial for its motility, ability to traverse gastric mucus, and infection of the stomach lining. Proper coordination of these genes is essential for flagella assembly and function, making them central to *H. pylori*'s pathogenicity. This study investigates the genetic diversity of these genes based on whole-genome sequencing of Iranian strains, to uncover their role in disease development.

Material And Methods: A total of 30 gastric biopsy samples from patients diagnosed with *H. pylori* infection were collected and cultured. The isolated *H. pylori* strains underwent whole genome sequencing to obtain extensive genetic data. For analysis, a customized Python-based alignment tool was developed, incorporating BLAST+ for efficient sequence alignment. Using this tool, novel allelic variants of *flaA* and *flaB* were identified. Additionally, the three-dimensional structures of their proteins were predicted using AlphaFold2, and structural comparisons were performed using PyMOL.

Results: Among the 30 sequenced genomes, 3 lacked the *flaA* gene. A total of 12 novel allelic variants of the *flaA* gene and 12 novel variants of the *flaB* gene were identified, none of which were recorded in reference databases. For *flaA*, two distinct protein structures were observed among the 12 alleles, with one structure differing from the other 11. For *flaB*, four unique protein structures were identified, while the remaining variants shared the same structure. The RMSD values for these structures ranged from 0.206 to 0.618, reflecting a high degree of structural similarity.

Conclusion: This study provides a comprehensive analysis of the genetic diversity in the *flaA* and *flaB* genes of *Helicobacter pylori* isolated from Iranian patients. By identifying novel alleles and examining their potential association with clinical outcomes, we aim to enhance the understanding of *H. pylori* pathogenicity in this region. These findings could inform future therapeutic strategies and improve the management of gastrointestinal diseases caused by *H. pylori*. Future research will focus on the functional implications of the observed structural variations in these proteins to better understand their role in bacterial pathogenesis.

Keywords: *Helicobacter pylori*, whole genome sequencing, *flaA*, *flaB*, pathogenicity

Abstract ID: 410
subject: including the role of probiotics in health and disease

The relationship between oral microbiome and stomach cancer

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Background and Aim: Stomach cancer is a major cause of cancer-related deaths worldwide. While factors like *Helicobacter pylori* infection, diet, and genetics are well-known contributors, recent research suggests the oral microbiome may also influence gastric cancer development. This study explores the role of oral bacterial composition in gastric carcinogenesis, focusing on inflammation and immune responses.

Material And Methods: Saliva and oral swab samples were collected from stomach cancer patients and healthy controls. Using 16S rRNA sequencing, bacterial diversity and species were analyzed. Some groups received probiotics or antibiotics to modify the oral microbiota, and their effects on gastric cancer were assessed. Tumor progression, *H. pylori* levels, and inflammation-related gene markers (e.g., IL-6, TNF-α) were evaluated through histological and molecular methods.

Results: Cancer patients exhibited oral dysbiosis, marked by an increase in pathogenic bacteria like Fusobacterium and Porphyromonas and a decrease in protective species like *Lactobacillus*. Oral dysbiosis correlated with higher *H. pylori* levels in the stomach and increased inflammation, contributing to mucosal damage and tumor development. Modifying the oral microbiome with probiotics or antibiotics reduced gastric inflammation and slowed cancer progression in animal models.

Conclusion: Oral microbiome dysbiosis plays a significant role in stomach cancer by promoting inflammation and immune dysfunction. Restoring oral microbial balance may offer a potential strategy for preventing or managing gastric cancer, though further clinical studies are needed.

Keywords: Oral microbiome , stomach cancer

Abstract ID: 405
subject: including the role of probiotics in health and disease

The effect of cosmeceutical probiotics on treating skin lesions in psoriasis: modulating skin microbiota and reducing inflammation

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Background and Aim: Psoriasis is a chronic autoimmune skin disease characterized by scaly plaques, inflammation, and alterations in skin appearance. Dysbiosis of skin microbiota and increased inflammation are key contributors to disease progression. Cosmeceutical probiotics, by modulating skin microbiota and reducing inflammation, may aid in alleviating psoriasis symptoms. To evaluate the effectiveness of cosmeceutical probiotics in reducing skin lesions, lowering inflammatory markers, and improving skin appearance in patients with psoriasis.

Material And Methods: This study was conducted on 40 patients with plaque psoriasis. The intervention group applied probiotic-enriched creams containing *Lactobacillus plantarum* and *Bifidobacterium* breve for 12 weeks. The severity of plaques was assessed using the Psoriasis Area and Severity Index (PASI). Inflammatory markers (TNF-α and IL-17) and changes in skin microbiota composition were also analyzed.

Results: After 12 weeks of treatment, a significant reduction in PASI scores (40% decrease) was observed. Skin lesions appeared less prominent, and skin inflammation was markedly reduced. Microbial analyses showed an increase in beneficial species such as *Lactobacillus* and a decrease in pro-inflammatory taxa.

Conclusion: Cosmeceutical probiotics, by regulating skin microbiota and reducing inflammation, can serve as an effective adjunctive therapy for improving skin lesions and managing psoriasis symptoms. These findings highlight the potential of probiotic-based products in treating inflammatory skin conditions.

Keywords: Cosmeceutical probiotics, psoriasis treatment, skin microbiota modulation, inflammation reduction

Abstract ID: 290
subject: including the role of probiotics in health and disease

Evaluation of the potential effects of *Lactobacillus crispatus* on antitumor immune responses in breast tumor

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Background and Aim: *Lactobacillus crispatus* is a rod-shaped and lactic acid producing bacterial species located in the genus *Lactobacillus*. *L. crispatus* have previously been identified and isolated from the human gastrointestinal tract. This species is also one of the main *Lactobacillus* species found in the healthy vaginal microbiome and is thought to be beneficial to health. The aim of this study was evaluating the potential effects of *L. crispatus* on antitumor immune responses in breast tumor.

Material And Methods: Breast tumor cells (4T1 mammary carcinoma cells) were inoculated to 20 female Balb/c mice. After two weeks, mice were divided into two groups. Heat-killed *L. crispatus* (1×108 bacteria) was injected intraperitoneally to mice of the first group. The second group was considered as control group in which mice received only phosphate buffered solution. On day 40 after tumor inoculation, RNAs were extracted from tumor tissues and gene expression levels of cyclooxygenase-2, arginase and inducible nitric oxide synthase were assessed using real-time RT-PCR technique.

Results: Real-time RT-PCR data analysis showed that cyclooxygenase-2 gene expression levels decreased in tumor tissues of mice treated with *L. crispatus* in comparison with tumor tissues of control group. The gene expression levels of arginase and inducible nitric oxide synthase increased in the tumor tissues of those treated with *L. crispatus*.

Conclusion: Overexpression of cyclooxygenase-2 augments tumorigenicity and local tumor invasion. Arginase plays a pivotal role in tumorigenesis and metastasis and increased arginase activity is associated with potent suppression of T-cell immune responses. Inducible nitric oxide synthase expression has been correlated with increased tumor grade and aggressiveness of breast cancer cells. Tumor-expressed inducible nitric oxide synthase has a critical role in the recruitment and induction of functional myeloid-derived suppressor cells. Our findings suggest that *L. crispatus* can suppress tumorigenicity and local tumor invasion by decreasing cyclooxygenase-2 expression in the breast tumor tissue but can also dampen antitumor immune responses by suppression of T cells activity and induction of functional myeloid-derived suppressor cells in the tumor microenvironment through induction of increased expression of arginase and inducible nitric oxide synthase, respectively.

Keywords: *Lactobacillus crispatus*, antitumor immune responses, breast tumor.

Abstract ID: 288
subject: including the role of probiotics in health and disease

Lmpact of *Bifidobacterium* populations on human health and fitness parameters

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Background and Aim: The gut microbiota plays a critical role in human health and fitness, with *Bifidobacterium* species recognized as key contributors to a balanced and functional microbiome. Regular consumption of traditional fermented dairy products, which often serve as natural source of *Bifidobacterium*, has been associated with improved gut microbiota composition and various health benefits, including enhanced immune function, reduced intestinal inflammation, and improved gut barrier function. These effects may also influence fitness parameters such as metabolic efficiency and energy balance. This study investigates the relationship between *Bifidobacterium* populations and human health indices, focusing on a cohort monitored for their consumption of traditional dairy products compared to commercially pasteurized alternatives. By quantifying *Bifidobacterium* levels and evaluating key health and fitness parameters, the research highlights the probiotic potential of *Bifidobacterium* and its critical role in functional nutrition and overall well-being.

Material And Methods: DNA was extracted from 50 stool samples using the FavorPrep™ Stool DNA Isolation Kit. Genomic DNA from *Bifidobacterium* bifidum PTCC No. 1644 at different concentrations was also extracted for standardization. Real-time PCR with genus-specific primers was used to quantify bifidobacterial counts per gram of sample. The relationship between bifidobacterial counts and fitness indices, as assessed through a completed questionnaire, was then analyzed.

Results: Real-time PCR analysis showed a significant reduction in *Bifidobacterium* spp. abundance in overweight individuals ($P \leq 0.01$) compared to those with a normal BMI. The average bacterial count in normal-weight samples was approximately 2.5×10^5 CFU/g, while in overweight individuals, it was around 1.7×10^5 CFU/g. Questionnaire analysis indicated that daily dairy consumption was reported by 36% of individuals with a healthy weight, compared to only 20% of those classified as obese.

Conclusion: This study highlights the critical role of *Bifidobacterium* spp. in maintaining gut health and fitness, highlighting a notable reduction in their abundance in overweight individuals. The study emphasizes the importance of dietary interventions, particularly through probiotic-rich dairy products, in improving gut microbiota composition and offer a potential solution for addressing obesity-related metabolic issues.

Keywords: *Bifidobacterium*, gut microbiota, probioti, dairy products, physical fitness

Abstract ID: 39
subject: including the role of probiotics in health and disease

The effects of oral probiotics supplementation on glycemic control and lipid profile in type 2 diabetes mellitus (T2DM): systematic literature review

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Background and Aim: Type 2 diabetes mellitus (T2DM) continues to be a significant global health issue. The gut microbiome, which is a complex community of microorganisms, has been associated with various metabolic disorders, including T2DM. Some research indicates that using probiotics may help foster a healthier gut microbiome in those with T2DM, potentially enhancing disease management. This literature review examines the evidence regarding the effectiveness of probiotics in managing T2DM.

Material And Methods: Following our inclusion and exclusion criteria, we searched for open-access English articles and guidelines up to October 2024 across databases like PubMed, Scopus, Web of Science, and Google Scholar. The records were assessed and categorized based on the types of microbiota and interventions. Then, the full texts of the selected articles were reviewed.

Results: This systematic review summarizes thirty-three clinical trials (CTs) that explored the use of oral probiotics for T2DM management. Out of these, twenty-one studies (64%) reported improvements in at least one glycemic measure, while fifteen studies (45%) noted enhancements in at least one lipid measure.

Conclusion: Probiotic strains may positively influence glycemic control and lipid levels in individuals with T2DM, potentially leading to better overall glycemic profiles. The generally positive results across these studies, along with minimal adverse effects, support the need for further high-quality clinical trials. Certain *Lactobacillus* species, such as *L. acidophilus*, *L. casei*, and *L. plantarum*, as well as *Bifidobacterium* strains like B. longum and *B. bifidum*, have shown promise in managing T2DM. However, many studies in this review lacked consistency regarding biochemical parameters and data collection, highlighting the necessity for more research to fill these gaps, particularly concerning specific probiotic strains, dosages, and intervention strategies. An intriguing observation from this review was the positive trend associated with the co-administration of metformin and probiotics.

Keywords: Probiotic; type 2 diabetes mellitus; T2DM; glucose; gut health

Abstract ID: 392
subject: including the role of probiotics in health and disease

The role of prebiotics and *Bifidobacterium* in multiple sclerosis in a mouse model

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Background and Aim: This study investigates the impact of prebiotics and *Bifidobacterium* on Multiple Sclerosis (MS) in a mouse model. MS is a chronic autoimmune disorder in which the immune system abnormally attacks the central nervous system. Recent research has shown that the gut microbiome may play a crucial role in regulating immune responses and could serve as a novel therapeutic target for autoimmune diseases like MS. This study explores the role of prebiotics and *Bifidobacterium* in modulating immune responses and their potential effects on MS progression.

Material And Methods: In this study, a mouse model of MS was induced using chemicals such as MOG (Myelin Oligodendrocyte Glycoprotein) to provoke the disease. Mice were then treated with prebiotics and various strains of *Bifidobacterium*. The treatments were applied over different periods, and their effects on MS progression and immune responses were assessed. Tissue samples from the brain and spinal cord were collected to evaluate inflammation, neural damage, and changes in gut microbiome composition.

Results: The results of this study demonstrated that prebiotic administration and *Bifidobacterium* treatment positively affected the reduction of inflammation and the enhancement of anti-inflammatory immune responses in the MS mouse model. Mice treated with *Bifidobacterium* exhibited reduced clinical symptoms and less neural damage. Additionally, molecular analysis showed that these treatments modulated immune pathways, reducing levels of inflammatory cytokines such as TNF-α and IL-17, which are involved in inflammatory processes and neural damage in MS.

Conclusion: This study suggests that prebiotics and *Bifidobacterium* can effectively reduce the progression of MS in the mouse model and play a key role in modulating the immune system and reducing inflammation. These treatments could be considered as an adjunctive therapeutic approach for managing MS. Suggestions for Future Research: Further studies are needed to understand the precise molecular mechanisms by which prebiotics and *Bifidobacterium* modulate immune responses and reduce inflammation in MS. Additionally, combining these treatments with standard MS therapies may offer a complementary strategy to improve clinical outcomes in MS patients.

Keywords: Probiotic, *Bifidobacterium*, MS , mouse model of MS,

Abstract ID: 201
subject: including the role of probiotics in health and disease

Study of the effect of *Lactobacillus acidophilus*, *Lacticaseibacillus casei*, and *Lactobacillus* delbrueckii on the expression of the tir gene in intestinal *E.coil* bacteria

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Background and Aim: Recently, there is a lot of evidence supporting the beneficial effects of probiotics. In general, probiotics are defined as live microorganisms that are beneficial for health when administered in sufficient quantities. *Escherichia coli* is one of the common causes of food poisoning. Some species are abundantly found in the intestines of animals and humans. The aim of the present study was to investigate the effects of most probiotics *Lactobacillus Acidophilus*, *Lacticaseibacillus casei*, and *Lactobacillus delbrueckii* on the expression of the tir gene in *Escherichia coli*.

Material And Methods: In this study, the nucleic acid DNA of EPEC was carefully extracted along with three probiotic samples, *Lactobacillus Acidophilus*, *Lacticaseibacillus casei*, and *Lactobacillus delbrueckii* then polymerase chain reaction (PCR) was performed using gene-specific primers.The RNA of the bacterial isolates was extracted and finally, quantitative RT-PCR was performed to investigate the effect of probiotics on the expression of the pathogenic tir gene.

Results: It was shown that probiotics have a significant effect on the expression of the tir gene. This means that it indicates a significant decrease in the expression of the tir gene in the presence of three types of probiotics, *Lactobacillus Acidophilus*, *Lacticaseibacillus casei*, and *Lactobacillus delbrueckii*. Therefore, the research hypothesis that the presence of probiotics leads to a decrease in the expression of the tir gene in EPEC can be confirmed

Conclusion: From the results obtained, it can be concluded that the use of lactic acid bacteria, including *Lactobacillus Acidophilus*, *Lacticaseibacillus casei*, and *Lactobacillus delbrueckii*, which are part of the popular probiotics, has a therapeutic and preventive effect on intestinal infections caused by EPEC.

Keywords*: Lactobacillus Acidophilus*, *Lacticaseibacillus casei*, *Lactobacillus delbrueckii*, EPEC, tir gene, q-RTPCR

Abstract ID: 264
subject: including the role of probiotics in health and disease

In vitro assessment of synergetic activity of engineered *Lactobacillus plantarum* produced nisin with fusaric acid and thymoquinone against *S. aureus*, *C. innocuum* and *R. gnavus*

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Background and Aim: Inflammatory bowel disease (IBD) is a gastrointestinal tract disease that manifests as ulcerative colitis and Crohn's disease. Research has shown the importance of probiotics on intestinal microbiota in IBD. Nisin as a bactericide can improve gut health but the *Lactococcus lactis* that normally produces nisin, cannot thrive in the intestinal environment. Also, some organic compounds such as antioxidants and essential oils, has been shown to improve nisin's activity. In this study we aim to use genetically engineered *Lactobacillus plantarum* to produce nisin and later assess fusaric acid and thymoquinone on its antibacterial activity against *Staphylococcus aureus*, *Clostridium innocuum* and *Ruminococcus gnavus*

Material And Methods: *nisA* gene was cloned in *Lactobacillus plantarum* through pET-21a plasmid. Nisin presence was confirmed in the *Lactobacillus plantarum* culture media. engineered *Lactobacillus plantarum* survival and culture in intestine simulated environment was assessed. In three groups of 1) engineered *Lactobacillus plantarum* (nisin) 2) nisin + fusaric acid 3) nisin + thymoquinone, zone of inhibition was measured.

Results: genetically engineered *Lactobacillus plantarum* produced active nisin. engineered *Lactobacillus plantarum* string was able to make biofilm in intestine simulated environment. Nisin's activity in combination with fusaric acid and thymoquinone was improved.

Conclusion: genetically engineered *Lactobacillus plantarum* as a resistant bacterium to bowel environment is an optimal probiotic to deliver nisin as an antibacterial that modulates intestine's microbiota. Organic compounds can be used to elevate nisin's activity

Keywords: Nisin - probiotic - thymoquinone - fusaric acid

Abstract ID: 74
subject: including the role of probiotics in health and disease

Effects of native *Lactobacillus* probiotic strains on oxidative stress and inflammatory pathways induced by nickel in lung tissue

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Background and Aim: Recent studies indicate that heavy metals, particularly nickel, significantly impact lung cells, contributing to the occurrence and severity of respiratory diseases. Nickel, commonly found in the water, soil, and air of industrial cities, induces oxidative stress in both humans and animals. To mitigate the oxidative stress associated with nickel exposure, the antioxidant and anti-inflammatory properties of probiotics may help open new avenues for addressing nickel's deleterious effects. This research aims to explore the effect of native potential probiotics on inflammatory signaling pathways and oxidative stress in lung tissues, ultimately enhancing lung protection against the toxicity of heavy metals.

Material And Methods: In this study, NMRI male mice were exposed to nickel to determine the oxidative stress and inflammatory effects of this heavy metal agent. Subsequently, the mice received probiotic treatments comprising *Lactobacillus spp*. and *Bifidobacterium* spp. To evaluate the impact of probiotics on the antioxidant system and inflammatory responses, molecular analyses using Real-Time PCR were conducted on lung tissues, facilitating an assessment of gene expression patterns.

Results: The findings indicate that the consumption of native potential probiotic strains, simultaneously with nickel exposure, markedly enhanced the expression of key antioxidant genes, including SOD, CAT, GPX, HO-1, and KEAP. Concurrently, there was a notable reduction in the expression of genes associated with inflammatory signaling pathways, specifically RELA, IKKA, and IKKB. Mice exposed only to nickel demonstrated a decrease in antioxidant gene expression alongside an increase in inflammatory gene expression.

Conclusion: This research's findings underscore the harmful impact of nickel, a heavy metal, on lung tissue health while highlighting the benefits of native potential probiotic strains, particularly their antioxidant and anti-inflammatory properties. In light of the substantial risks associated with heavy metal exposure, the consumption of probiotics presents a viable approach to mitigate oxidative stress and inflammation in mucosal tissues, including the lungs. This strategy offers potential benefits for respiratory health and contributes to the prevention of various respiratory disorders.

Keywords: Probiotics, *Lactobacillus*, *Bifidobacterium*, oxidative stress, inflammation, lung

Abstract ID: 408
subject: The role of probiotics in health and disease

Case report: Synergistic effects of retinol and probiotic creams in transforming acne scars

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Background and Aim: This case report examines the impact of retinol and probiotic creams on improving acne scars in a group of 10 patients with varying degrees of scarring. The treatment outcomes were systematically evaluated over 12 weeks.

Material and Methods: Patient Profile Sample Size: 10 individuals Gender: 7 females, 3 males Age: 22–35 years Skin Condition: Deep acne scars, dark spots, and uneven skin texture Treatment Method Retinol: Nightly application of a cream containing 0.5% retinol to stimulate collagen production and promote cellular renewal. Probiotics: Daily use of a probiotic cream to reduce inflammation and strengthen the skin's barrier. Duration: 12 weeks Monitoring: Skin changes were assessed every 4 weeks.

Results: Week 4: 60% of patients reported reduced inflammation and brighter dark spots. Week 8: 7 patients showed visible improvement in acne scar depth. Week 12: 8 patients experienced smoother skin texture and a significant reduction in scars. 2 patients developed mild skin sensitivity (redness and dryness), requiring a lower retinol dose. All patients reported overall improvement in their skin appearance.

Conclusion: The findings suggest that the combination of retinol and probiotics is effective in improving acne scars and enhancing overall skin health. Retinol promotes cellular renewal and reduces scar depth, while probiotics mitigate inflammation and reinforce the skin barrier. Although mild sensitivity was observed in some cases, adjusting the dosage helped manage side effects.

Keywords: Case report, retinol, probiotics, acne scars, group treatment, skin regeneration

Abstract ID: 324
subject: The role of probiotics in health and disease

Investigating the NMDA neurotransmitter receptor in the hippocampal tissue of Alzheimer's rat model treated with native Iranian probiotics and naringenin

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Background and Aim: Alzheimer's disease is a neurodegenerative disease that usually begins slowly and gradually worsens. Alzheimer's disease is the cause of 60 to 70% of dementia cases. The most common early symptom of the disease is impaired short-term memory and difficulty remembering recent events. The NMDA gene is involved in the transmission of nerve messages and memory. In people with Alzheimer's Changes in genes associated with NMDA receptors can lead to brain damage and decreased cognitive function. The combination of native Iranian probiotics & naringenin may have positive effects on brain health & reduce the risk of Alzheimer's. These compounds can facilitate improved mental function and Memory, reduced inflammation, and improved overall health. Probiotics are live microorganisms that are promoted with claims of providing health benefits when consumed, usually by improving or restoring the microbial flora of the gastrointestinal tract. Main Aim: To investigate changes in the NMDA neurotransmitter receptor in Alzheimer's model rat treated with native Iranian probiotics and naringenin

Material and Methods: thirty- six male laboratory rats were randomly divided into six different groups (control group, Alzheimer's group and three groups of treatment).

Results: Based on the behavioral test (shuttle box), it was show that Alzheimer's rat stayed in the white part of box less than the control group, indicating that the beta-amyloid injection was well done in them.

Conclusion: According to the results and data obtained from our research, we showed that native Iranian probiotics& naringenin and their combination mix (probiotic & naringenin) Were able to have a significant increasing effect on NMDA gene expression due to their antioxidant Properties, and as a result, our work can be used as an adjunct treatment in preventing Alzheimer's.

Keywords: Alzheimer's, native Iranian probiotics, naringenin, hippocampus, NMDA

Abstract ID: 409
subject: The role of probiotics in health and disease

The effects of deproherb and *Lactobacillus plantarum* on MS: A mouse model study

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Background and Aim: Multiple sclerosis (MS) is an autoimmune disease affecting the central nervous system. Natural anti-inflammatory compounds and gut microbiota modulation are promising strategies for managing MS. This study evaluates the effects of Deproherb (herbal anti-inflammatory) and *Lactobacillus plantarum* in an experimental autoimmune encephalomyelitis (EAE) mouse model.

Material and Methods: Animal Groups: Control (healthy, untreated), EAE (untreated), EAE + Deproherb (250 mg/kg/day), and EAE + Deproherb + *Lactobacillus plantarum* (2×10^9 CFU/day). Assessments: Clinical EAE scoring (0–5), histopathology for inflammation and demyelination, inflammatory markers (TNF-α, IL-6, IL-10) via ELISA, and gut microbiota analysis using 16S rRNA sequencing. Disease Induction: MS was induced using MOG35-55 peptide.

Results: Clinical Improvement: Combination therapy reduced EAE scores (1.2 vs. 3.8 in untreated EAE). Reduced Inflammation: Histopathology showed less demyelination in the combination group. Gut Microbiota: Beneficial bacteria (Lactobacillus and Bifidobacterium) increased, while pro-inflammatory species decreased. Inflammatory Markers: TNF-? and IL-6 decreased, while IL-10 increased in the combination group.

Conclusion: Deproherb and *Lactobacillus plantarum* reduced inflammation, improved symptoms, and modulated gut microbiota in an EAE mouse model. This combination shows potential as a complementary MS therapy.

Keywords: MS, EAE, deproherb, *Lactobacillus plantarum*, inflammation

Abstract ID: 398
subject: The role of probiotics in health and disease

The impact of nutrition and skin microbiota on skin cancer: Linking environmental and biological factors in skin immunity regulation

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Background and Aim: Skin cancer is one of the most common types of cancer globally, resulting from a complex interplay of genetic, environmental, and biological factors. The role of skin microbiota and nutrition in modulating immunity and skin health is increasingly being recognized as critical in preventing and managing skin cancer. This study focuses on the relationship between diet, skin microbiota, and skin cancer. To investigate the effects of dietary patterns and skin microbiota composition on immune mechanisms and the progression of skin cancer.

Material and Methods: Patients with skin cancer and healthy control groups were studied. Dietary habits were assessed using nutritional questionnaires. Skin samples were collected for microbiota analysis using next-generation sequencing (NGS). Additionally, skin inflammatory and immune markers were measured using ELISA.

Results: Preliminary findings revealed a significant association between diets rich in antioxidants and omega-3 fatty acids with a reduced risk of skin cancer progression. Moreover, alterations in the diversity and ratio of skin microbiota were observed in skin cancer patients. Beneficial species such as *Staphylococcus epidermidis* were reduced, while pro-inflammatory pathogenic species were increased.

Conclusion: These findings highlight the potential role of healthy nutrition and balanced skin microbiota in regulating skin immunity and reducing the risk of skin cancer. Dietary interventions and probiotics may serve as complementary approaches in the prevention and treatment of this disease.

Keywords: Nutrition, skin microbiota, skin cancer

Abstract ID: 89
subject: The role of probiotics in health and disease

Isolation and identification of *Lactobacillus plantarum* with probiotics properties from Iranian sour fruits

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Background and Aim: According to the definition of the World Health Organization (WHO) and The Joint Food and Agriculture Organization of the United Nations (FAO), the following definition is provided for probiotics: " live microorganisms that, when administered in adequate amounts, confer a health benefit to the host". Probiotics have many benefits, some of which can be mentioned: causing microbial balance in the digestive tract, reducing serum cholesterol, reducing the symptoms of lactose intolerance, reducing the risk of developing colon cancer, preventing or reducing allergies in susceptible people, and improving the response Immunity in people. The purpose of this study was to isolate and identify LAB from sour fruits and investigate their probiotic properties.

Material and Methods: Acidic fruits such as strawberries and barberries were collected from different parts of Iran. Each of the samples was well homogenized and placed in MRS broth for 72 h at 37°C. Then, the above suspension was cultured on MRS agar and colonies whose phenotypic characteristics were similar to those of *Lactobacilli* were selected and maintained. Each of the samples was examined in terms of probiotic tests such as acid resistance, bile resistance, resistance to simulated gastrointestinal conditions, binding to HT29, 2,5-diphenyl-2H-tetrazolium bromide (MTT) assay, hemolysis test, cell surface hydrophobicity, and antibiotic sensitivity. The strains with probiotic properties were sequenced and the Lactobacillus strains with probiotic properties were confirmed.

Results: Forty strains of LAB were isolated based on phenotypic characteristics. Among the strains that had the best probiotic properties, two strains were identified and confirmed based on sequencing, *L. plantarum*. These strains had the highest resistance to acid, bile, and simulated gastrointestinal conditions. In addition, they had high binding ability and no antibiotic resistance was observed in them. In terms of safety, none of the strains were hemolysis positive.

Conclusion: Fruits and vegetable products, like dairy products, can contain probiotic bacteria with functional properties that are beneficial to human health. Although the processes of isolation and identification of probiotics are carried out on various products all over the world, this seems necessary and essential, given the important role that these strains play in the prevention and treatment of various diseases.

Keywords: probiotics, LAB, *L. plantarum*

Abstract ID: 210
subject: The role of probiotics in health and disease

Phenotypical and molecular identification of Lactobacilli from traditional dairy products distributed in the areas covered by Tehran university of medical sciences and determination of their inhibitor

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Background and Aim: Gram-positive, catalase-negative bacilli were extracted from dairy samples and analyzed using biochemical techniques. To assess the probiotic potential of the isolates, their growth rates were evaluated across a range of acidic and alkaline pH levels, as well as varying concentrations of bile salts and sodium chloride. The antimicrobial efficacy of the isolates against pathogenic bacteria was assessed through the well-plate method, and susceptibility to commonly used antibiotics was determined via the disk diffusion technique. Molecular identification of the isolated strains was conducted through 16S rDNA gene sequencing.

Material and Methods: A total of 70 strains were analyzed, with 32 found to be similar to *Lactobacillus*. Thirteen of these strains demonstrated probiotic potential, displaying the ability to thrive in various pH and salt concentrations, as well as exhibiting antimicrobial activity against common pathogens. Molecular evaluation revealed high similarity with several known probiotic *Lactobacillus* species. These findings highlight the presence of lactobacilli with probiotic properties in Tehran's dairy farms, indicating their potential use in dairy food production and improving livestock and poultry feed quality.

Results: Out of the 70 Gram-positive and catalase-negative strains studied, 37 were found to be biochemically comparable to Lactobacilli. Thirteen of these strains were capable of growth at pH levels between 3 and 9, as well as in various concentrations of bile salts and NaCl. These bacteria exhibited antimicrobial activity against common pathogens and demonstrated resistance to clindamycin, vancomycin, and ampicillin. Molecular evaluation indicated that 13 strains had a similarity of 100% and 99.82% with strains of *Lactobacillus plantarum*, *Lactobacillus paracasei*, *Lactobacillus casei*, *Lactobacillus delbrueckii*, *Lactobacillus pentosus*, *Lactobacillus acidophilus*, *Lactobacillus gasseri*, and *Lactobacillus fermentum*, showcasing enhanced probiotic properties.

Conclusion: To conclude, the findings of this study indicated that the bacteria obtained from a range of dairy products were indeed probiotic lactic acid bacteria, possessing beneficial probiotic attributes. These isolates hold potential for future research in the formulation of probiotic dairies. The research establishes a basis for the advancement of functional foods and starter cultures that could contribute positively to human health by integrating probiotic microorganisms.

Keywords: *Lactobacillus*, probiotics, traditional dairy products, biochemical identification, antibiotic resistance

Abstract ID: 208
subject: The role of probiotics in health and disease

Investigating the relationship between gut microbiome, probiotic consumption, and guillain-barré syndrome; An integrative review

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Background and Aim: The Investigation of the relationship between gut microbiome, probiotic consumption, and Guillain-Barré Syndrome (GBS) represents a novel area in medical science, contributing to a deeper understanding of the connections between gut microorganisms and the immune system. GBS is a rare autoimmune disorder that typically occurs following viral or bacterial infections. On the other hand, the consumption of probiotics has gained attention as a potential strategy to modulate these changes. This study Investigates these relationships and clarifies the groundwork for future research.

Material and Methods: The search for relevant studies involved utilizing keywords related to "probiotics", "gut microbiome", "normal flora" and "Guillain-Barré Syndrome" in international databases, including PubMed, ScienceDirect, Medline, ProQuest and Web of Science, and national resources like SID, Magiran, and IranDoc, and also Google Scholar search engine. The initial search yielded 256 studies, including criteria was pertinent to the study's focus, excluding animal studies, reviews, conference presentations, and editor letters. No time limitations were applied. After eliminating duplicates and maintaining ethical standards to avoid biases, the final analysis comprised 12 selected studies.

Results: 50% of the studies (6 articles) reported only a general connection between gut microbiome and GBS, attributing it to the Gut-Brain Axis. 33% (4 articles) indicated that *Helicobacter* is one of the causes of GBS and considered it part of the normal gut flora. However, 16% of the studies (2 articles) noted that probiotic consumption in these patients resulted in protective effects and reduced autoimmune reactions.

Conclusion: The findings of this research indicate that the relationship between gut microbiome and GBS is not yet fully understood and requires further investigation. While some studies have pointed to a general connection and the role of Helicobacter, only a limited number have reported positive effects of probiotics in reducing autoimmune responses. These ambiguities and variability in results highlight the necessity for more precise clinical research in this area. Therefore, future investigations should focus on the biological mechanisms underlying these relationships to achieve a better understanding of this complex disorder.

Keywords: Probiotics, microbiome, guillain-barré syndrome

Abstract ID: 76
subject: The role of probiotics in health and disease

Effects of microbiome-based therapies on the progression and severity of inflammatory bowel disease

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Background and Aim: Inflammatory bowel disease (IBD), which includes Crohn's disease (CD) and ulcerative colitis (UC), is marked by alternating phases of remission and active intestinal inflammation, resulting in symptoms such as stomach discomfort, diarrhea, rectal bleeding, malnutrition, and exhaustion. In response to the rising incidence and prevalence of IBD in recent years, several research have been undertaken to investigate the pathophysiology of the disease and associated therapies. This facilitated the discovery of the significant role of the gut microbiota and the evaluation of microbiome-based therapies' impact on inflammatory bowel disease (IBD). This systematic review seeks to evaluate the effectiveness of microbiome-based therapies on inflammatory bowel disease (IBD).

Material and Methods: PubMed was searched for randomized controlled studies on microbiome treatments in inflammatory bowel disease till December 2024. The risk of bias was evaluated using Cochrane instruments. Outcomes included disease activity, endoscopy, histology, quality of life, and adverse events.

Results: Twenty-five randomized controlled trials fulfilled the inclusion criteria. Results demonstrate the remarkable performance of fecal microbiota transplantation (FMT) and probiotics, with FMT yielding superior outcomes in enhancing clinical response rates and achieving clinical and endoscopic remission. Furthermore, *Bifidobacterium* and *Lactobacillus* species seem to be more effective in enhancing clinical remission and diminishing clinical recurrence. The key mechanisms may include the synthesis of regulatory compounds by advantageous bacteria, alteration of the pro- to anti-inflammatory cytokine ratio in colonic tissue and plasma, control of oxidative stress in the colon, and enhancement of intestinal barrier integrity.

Conclusion: Microbiome-targeted therapies suggest a viable strategy for enhancing IBD results.

Keywords: Crohn's disease, fecal microbiota transplantation, prebiotics, probiotics, synbiotics, ulcerative colitis.

Abstract ID: 391
subject: The role of probiotics in health and disease

The impact of *Lactobacillus rhamnosus* on parkinson's disease: Investigating the role of gut microbiota in neurological disorders

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Background and Aim: Parkinson's disease (PD) is a progressive neurodegenerative disorder caused by the loss of dopaminergic neurons in the brain. Recent evidence suggests that the gut microbiota plays a pivotal role in the gut-brain axis and may influence the progression or modulation of neurological disorders. This study examines the effects of the probiotic *Lactobacillus rhamnosus* on Parkinson's disease-related symptoms. The aim of this research is to investigate the impact of *Lactobacillus rhamnosus* consumption on improving motor functions, reducing inflammation, and regulating the gut-brain axis in Parkinson's patients or animal models.

Material and Methods: In this study, a Parkinson's disease model was induced in animals using 6-hydroxydopamine (6-OHDA). Experimental groups received *Lactobacillus rhamnosus* orally for 4 weeks. Motor functions were evaluated using rotational and open-field tests. Additionally, inflammatory markers (IL-6 and TNF-α) were measured, and gut microbiota composition was analyzed using metagenomics.

Results: The consumption of *Lactobacillus rhamnosus* led to significant improvements in motor function and a reduction in anxiety-related behaviors. Microbiota analysis indicated an increase in beneficial species and a decrease in inflammatory species. Additionally, inflammatory marker levels were significantly reduced in the treated groups.

Conclusion: The findings of this study suggest that *Lactobacillus rhamnosus* can have positive effects on Parkinson's symptoms by improving the gut-brain axis, regulating gut microbiota, and reducing inflammation. These results support the potential use of probiotics as a complementary approach in managing neurological disorders.

Keywords: *Lactobacillus rhamnosus*, parkinson's disease, gut microbiota, neurological disorders

Abstract ID: 72
subject: The role of probiotics in health and disease

Comparison of the binding rates of probiotics *Lactobacillus plantarum* and *Lactobacillus reuteri* and the standard strain *Salmonella typhimurium* using a competitive assay in the HT-29 cell line

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Background and Aim: *Salmonella typhimurium* is a primary enteric pathogen infecting both humans and animals. Infection begins with the ingestion of contaminated food or water so that salmonellae reach the intestinal epithelium and trigger gastrointestinal disease. Various antibiotics are used to treat this disease. It is important to reduce the use of antibiotics and discover new therapeutic agents. One solution is the use of probiotics.

Material and Methods: First, HT-29 monolayer cells were prepared in 6-well plates. Overnight culture (16 hours) of *Lactobacillus plantarum*, *Lactobacillus reuteri*, and *S. typhimurium* (107 CFU/ml) was prepared. Then, each strain was cultured of HT-29 cells for 1 hour at 37°C. After 1 hour of incubation, the cells are washed to remove unattached bacteria. The attached bacteria were removed by adding 1 ml of 0.04% Tween 80 and PBS, and the appropriate dilution was plated on MRS agar plates. CFUs were counted after overnight growth at 37°C to determine the number of bacteria attached to the HT-29 cell monolayer.

Results: The results of counting each of the strains using the Pour Plate method, which had an OD = 1 at a wavelength of 600 nm, were calculated to be 7×108 CFU/ml for *L. plantarum* and 2×108 CFU/ml for *L. reuteri*. The results of measuring the adhesion of probiotic strains *L. plantarum* and *L. reuteri* to the HT-29 cell line showed that the studied strains have potential adhesion properties to HT-29 cells, and the number of adhered and attached bacterial cells for both probiotic strains was calculated to be 2×107 CFU/ml, which was only 1 log lower than the control. CFU calculation showed that the number of free-form *S. typhimurium* cells was 2×109 CFU/ml, and the results from the adhesion assay were calculated to be 4×107 CFU/ml.

Conclusion: Compared to *S. typhimurium*, *L. plantarum* and *L.reuteri* have a stronger ability to adhere to HT-29 cells; These probiotics can be used in foods. If food is contaminated with pathogenic bacteria, it is possible to prevent the pathogen from attaching to intestinal cells without the use of antibiotics. The use of probiotics can prevent the development of gastrointestinal diseases caused by *S. typhimurium*.

Keywords: Probiotics, disease, *Salmonella typhimurium*, *Lactobacillus plantarum*, *Lactobacillus reuteri*

Abstract ID: 95
subject: The role of probiotics in health and disease

Comparison of novel native probiotics and paraprobiotics in modulating oxidative stress and inflammation in DSS-induced colitis: implications for enhanced therapeutic strategies in high fat diet

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Background and Aim: Aim IBD is a condition that may result from the presence of oxidative stress. The objective of this research is to evaluate and compare the potency of probiotics and paraprobiotics to modulate oxidative stress and inflammation

Material and Methods: Methods and results in the initial phase, the antioxidant capabilities of 88 strains from *Lactobacillus* and *Bifidobacterium* were evaluated. In the subsequent phase, during the in-vivo stage, four experimental groups were established, consisting of a high-fat diet (HFD)+PBS, HFD+DSS, HFD+DSS+10^9 cfu/ml of 6 selected native probiotic, and HFD+DSS+10^9 cfu/ml of paraprobiotic (from 6 selected strains), with male wild-type C57BL/6 mice being assigned to these groups. The phenotypical indices and pathological scores along with the evaluation of the expression of genes associated with the NF-kB and Nrf2 signaling pathways, as well as enzymes linked to oxidant/ anti-oxidant activities, and proinflammatory/inflammatory cytokines were performed

Results: A significant difference was noted among the groups exposed to DSS and groups that given our native agents. The mice receiving a blend of probiotics and paraprobiotics alongside DSS demonstrated a mitigation of the harmful impacts caused by DSS, both regarding phenotypic traits, including pathological scores and also the level of cytokines and antioxidant markers and also molecular indicators like the Nrf2 and NF-kB associated genes. Also, there was no notable difference between our native probiotic and paraprobiotic.

Conclusion: The study's findings provide evidence that the expression of inflammation can be successfully alleviated by utilizing our native probiotics and paraprobiotics, with a greater emphasis on the latter due to its inherent safety.

Keywords: Probiotic, paraprobiotic, inflammation, oxidative stress, IBD

Abstract ID: 255
subject: The role of probiotics in health and disease

The gut microbiome as a key modulator of immunotherapy and chemotherapy response in colorectal cancer: A systematic review

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Background and Aim: The gut microbiome plays a critical role in regulating immune responses and metabolism, influencing the efficacy of cancer therapies. Recent studies highlight the impact of specific gut bacteria on the response to immunotherapy and chemotherapy in colorectal cancer (CRC). This systematic review explores the molecular mechanisms by which beneficial and pathogenic bacteria modulate treatment outcomes.

Material and Methods: A comprehensive literature search was conducted across PubMed, Scopus, and Web of Science (2010–2024) using keywords ("gut microbiome," "colorectal cancer," "immunotherapy," "chemotherapy," "PD-1 inhibitors," "*Fusobacterium nucleatum*") and MeSH terms ("Gastrointestinal Microbiome," "Colorectal Neoplasms," "Immunotherapy," "Drug Resistance, Neoplasm," "Molecular Mechanisms"). Inclusion criteria focused on studies investigating microbiome-mediated molecular mechanisms in CRC treatment, including human or preclinical models with mechanistic insights. Articles not related to CRC, reviews, editorials, or studies lacking molecular data were excluded. After screening 1,235 articles, 45 studies were included. Data extraction emphasized study design, microbiome composition, molecular pathways, and treatment outcomes.

Results: Beneficial bacteria like *Bifidobacterium* and *Lactobacillus* enhance immunotherapy response by stimulating cytotoxic T-cell activity via short-chain fatty acids (SCFAs), downregulating PD-L1 expression, and promoting T-cell infiltration through IFN-γ production. In contrast, *Fusobacterium nucleatum* promotes chemotherapy resistance by activating NF-κB, altering drug metabolism via β-glucuronidase, and inhibiting apoptosis through the Wnt/β-catenin pathway. Microbiome modulation strategies, including probiotics, prebiotics, and fecal microbiota transplantation (FMT), show promise in improving treatment outcomes by reducing inflammation and restoring microbial balance.

Conclusion: The gut microbiome significantly influences CRC treatment outcomes through complex molecular mechanisms. Beneficial bacteria enhance immunotherapy efficacy, while pathogenic bacteria like *Fusobacterium nucleatum* promote treatment resistance. Modulating the gut microbiome represents a promising strategy to personalize cancer therapy and improve patient outcomes. Future research should focus on developing microbiome-based interventions to optimize CRC treatment.

Keywords: Gut microbiome, colorectal cancer, immunotherapy, chemotherapy, PD-1 inhibitors, *Fusobacterium nucleatum*, molecular mechanisms

Abstract ID: 178
subject: The role of probiotics in health and disease

Evaluation of the frequency of *Lactobacillus* and *Bifidobacterium* in obese and normal weight elderly

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Background and Aim: Probiotics are now recognized for several health benefits and they have been recommended as a complementary therapeutic agent for metabolic disorders. Obesity is an altered health condition, which is a resultant of irregular energy intake and energy balance, changes in gut microbiota, and improper diet with the influence of genetic makeup and environmental factors. In this study, we investigated the abundance of *Lactobacillus* and *Bifidobacterium* in the oral microbiota, which is the most important microbiota after the gut, in the elderly individuals

Material and Methods: This study includes 27 elderly people over 65 years old whose body mass index (BMI) is above 30 kg/m2 and 25 elderly people with BMI between 18.5 and 25 kg/m2. Their saliva (fasting) samples were collected and stored at - 80 degrees. Exclusion criteria were periodontitis, smoking, antibiotics and immunosuppressive drugs, mental disorders and having artificial teeth. DNA was extracted from saliva and quantitative real time PCR was utilized to measure bacterial abundance. Statistical analysis was performed using spss.

Results: In this study, the average age of the obese group is 70.32 years and the average age of the normal weight group is 72.64 years old. The abundance of *Lactobacillus* and *Bifidobacterium* was measured. The frequency of *Lactobacillus* was almost the same in both groups, but *Bifidobacterium* was more in obese people, although it was not statistically significant.

Conclusion: There are differences of opinion regarding the oral microbiota and probiotics in obese and normal weight individuals. In our study, no significant difference was seen, but in some studies, they showed that probiotics are related to reducing obesity, since in this field There is little information, more studies are needed to investigate this issue

Keywords: Microbiota, elderly, obesity, probiotics

Abstract ID: 384
subject: The role of probiotics in health and disease

Dietary *Lactobacillus farciminis* and *Bacillus pumilus* ameliorated the growth performance, immune system and resistance against *Candida albicans* in zebrafish (*danio rerio*)

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Background and Aim: This trial investigated the efficacy of *Lactobacillus farciminis* and *Bacillus pumilus* on the growth performance, immunity, biochemical parameters, and resistance against *Candida albicans* of zebrafish (*Danio rerio*).

Material and Methods: A total of 240 zebrafish were randomly allocated to 12 tanks with 20 fish per tank (4 treatments with 3 replications) and fed with diets containing1×108 CFU/g *Lactobacillus farciminis* (T1), 15 g/kg *Bacillus pumilus* (T2), and 1×108 CFU/g *Lactobacillus farciminis* + 15 g/kg *Bacillus pumilus* (T3) for 45 days; a basal diet with no probiotics was used as control (T0). Then, serum non-specific immune factors (lysozyme, total protein, immunoglobulin and protease enzyme), Serum antioxidant factors (catalase, SOD, GPx), and expression of genes involved in immunity (lyz, TNF-α, IL1β, IL8, and IL10) were measured.

Results: Based on the result, the final body weight, weight gain, and specific growth rate were significantly higher in T3 treatment compared to the control group ($P<0.05$). Immune factors including ACH50, lysozyme in T2 and T3 showed the highest values ($P<0.05$) but no significant difference was observed in total immunoglobulin among the treatments ($P>0.05$). Combination dietary of probiotics (T3) increased activities of serum glutathione peroxidase (GPX), superoxide dismutase (SOD), and catalase ($P<0.05$). The expression of lyz, TNF-α, IL-8, and IL-1β genes in T3 was higher than the control ($P<0.05$) but had no effect on IL-10 gene expression ($p>0.05$).

Conclusion: Fish fed both probiotics supplemented diet had highest survival rate after experimental challenge with pathogenic *Candida albicans*. The present study demonstrated that the administration of *L. farciminis* and *B. pumilus* could improve the growth, immunity, and antioxidant parameters, as well as enhance disease resistance against *Candida albicans* in zebrafish.

Keywords: Probiotics, immune system, growth performance, antioxidant enzyme activity

Abstract ID: 188
subject: The role of probiotics in health and disease

Impact of native iranian probiotic mixture on the expression of tau protein, memory impairment and antioxidant markers in a beta-amyloid-induced Alzheimer's rat model

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Background and Aim: Alzheimer's disease, a prevalent neurodegenerative disorder affecting the elderly, is characterized by the accumulation of amyloid-beta and tau proteins. Recent research suggests that a well-balanced microbiome, modulated by probiotics, may alleviate AD symptoms by enhancing antioxidant production and neutralizing reactive oxygen species in the gastrointestinal tract. This study examined the effects of a probiotic mixture containing *Lactobacillus acidophilus*, *L. paracasei*, *L. rhamnosus*, *L. reuteri*, *L. coagulans*, and *Bifidobacterium longum* on memory impairment and antioxidant levels in a rat model of Alzheimer's induced by beta-amyloid injection.

Material and Methods: Twenty-one rats were divided into three groups: control group, and two experimental groups in which Alzheimer's disease was induced by beta-amyloid injection into the CA1 region. One experimental group received probiotics for three weeks, while the other was given distilled water. The study involved conducting behavioral assessments such as the shuttle box and elevated plus maze tests. Additionally, ELISA analyses levels of antioxidant markers, and western blot was used to assess the Tau protein expression.

Results: The results showed that beta-amyloid injection significantly decreased cognitive function, increased tau protein expression and MDA serum level, and decreased SOD activity. However, probiotic treatment significantly improved learning, reduced oxidative stress, and enhanced neuronal regeneration.

Conclusion: These findings suggest that indigenous Iranian probiotics can enhance cognitive function and mitigate AD symptoms through their antioxidant effects.

Keywords: AD, iranian probiotics mixture, tau protein, antioxidant

Abstract ID: 367
subject: The role of probiotics in health and disease

The effects of gold nanoparticles and *Lactobacillus acidophilus* on esophageal cancer cells

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Background and Aim: Esophageal cancer is one of the most aggressive gastrointestinal cancers with a high mortality rate. Due to the limitations of conventional treatments such as chemotherapy and radiotherapy, innovative therapeutic approaches are gaining importance. Gold nanoparticles (AuNPs) have garnered attention due to their unique properties, including biocompatibility and the ability to target cancer cells. Additionally, *Lactobacillus acidophilus*, as a beneficial probiotic, has shown potential anti-cancer effects by inhibiting tumor growth and enhancing immune responses. This study investigates the combined effects of AuNPs and *L. acidophilus* on the growth of esophageal cancer cells.

Material and Methods: Gold nanoparticles were synthesized and prepared using standard methods. Esophageal squamous cell carcinoma (ESCC) cells were cultured in vitro and treated with AuNPs, *L. acidophilus*, and their combination. Cell viability and apoptosis were evaluated using the MTT assay and flow cytometry.

Results: The results demonstrated that AuNPs alone significantly reduced the growth of esophageal cancer cells. *L. acidophilus* also exhibited inhibitory effects on cell proliferation. The combination of AuNPs and *L. acidophilus* showed synergistic effects, inducing higher rates of apoptosis and inhibiting cancer cell growth more effectively. Additionally, the production of reactive oxygen species (ROS) increased significantly, indicating that ROS generation was the primary mechanism of cell death.

Conclusion: This study suggests that the combination of gold nanoparticles and *Lactobacillus acidophilus* could serve as a novel and effective approach to inhibiting the growth of esophageal cancer cells. Further research is recommended to explore the clinical applications of this combination therapy.

Keywords: Esophageal cancer, gold nanoparticles, *Lactobacillus acidophilus*, apoptosis, cancer therapy

Abstract ID: 32
subject: The role of probiotics in health and disease

Isolation and identification of the anti-diabetic effects of probiotic bacteria effective in reducing blood sugar from the stomach of worker bees

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Background and Aim: In recent years, Diabetes disease has increased rapidly worldwide and its frequency has been equaled in the last two decades. This research aim was studied to the isolation and identification of probiotic anti diabetic in reducing blood sugar from the stomach of worker bees on diabetic patients

Material and Methods: Isolation of probiotic bacteria from the stomach of bees by using biochemical tests such as catalase, oxidase, gram staining, examination of different temperatures, carbohydrate fermentation, antibiotic resistance and resistance in acidic conditions and resistance to bile salts. Then facility to tolerate Glucose by using dextrose medium for ability of bacteria to reduce blood sugar in diabetic patients was investigated. For identification of the isolated strains, DNA extraction from them and molecular studies were performed based on 16SrRNA.

Results: Results shown among 30 isolates were sequestered, 9 probiotic isolates had the ability to reduce blood sugar in diabetic patients. These isolates included *Lactobacillus*, *Leuconostoc* and *Bacillus subtilis*, which showed a significant decrease in glucose tolerance by using dextrose medium, as well as in the reduction of blood sugar in diabetic patients at different times.

Conclusion: The strains of *Lactobacillus acidophilus*, *Lactobacillus plantarum*, *Bacillus subtilis*, and *Leuconostoc* had a significant reduction in blood sugar of diabetic patients in a period of 6 hours. Therefore, could be use these probiotic strains as effective therapeutic agents for reducing blood sugar in diabetic patients.

Keywords: Probiotic bacteria, diabetes, blood sugar, *Lactobacillus*

Abstract ID: 31
subject: The role of probiotics in health and disease

Effect of cytotoxicity of probiotic bacteria isolated from bee honey stomach on HT29 clone cancer cell line and analyzing the expression of apoptotic genes Bcl2, BAX and P53

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Background and Aim: Cancer is a global health burden that requires the discovery of new treatment approaches. Probiotic bacteria, especially those isolated from honey bee stomachs, have attracted attention for their potential anticancer properties. This study aim was investigation the cytotoxic effect of probiotic bacteria isolated from the stomach of bee honey on the cancer cell line clone HT-29 and analyzing the expression of apoptosis genes Bcl2, BAX and P53.

Material and Methods: Probiotic bacteria were isolated from bees and identified using molecular and chemical techniques. The cytotoxic effect of these bacteria on HT-29 cells was evaluated using MTT assay. Real-time PCR was used to analyze the expression of Bcl2, BAX and P53 genes.

Results: Among the 30 isolated colonies, 6 probiotic isolates, among which *Lactobacillus plantarum* and *Lactobacillus acidophilus* significantly decreased the viability of HT-29 compared to the control. *Lactobacillus plantarum*, there was a significant decrease in the expression of the anti-apoptotic Bcl-2 gene and an increase in the expression of the pro-apoptotic BAX and P53 genes in the treated cells.

Conclusion: *Lactobacillus plantarum* strains isolated from honey bee stomachs showed strong anti-proliferative effects on colorectal cancer cells through changing the expression of apoptotic genes. These probiotic strains have potential as accessory therapeutic agents against colon cancer.

Keywords: Probiotic bacteria, cancer cell line HT-29, Bcl2, BAX, P53

Abstract ID: 246
subject: The role of probiotics in health and disease

Investigating the relationship between gut microbiome, probiotic consumption, and sexual health: An integrative review

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Background and Aim: Sexual health is a key aspect of human life that significantly affects the quality of interpersonal and social relationships, as well as mental and physical well-being. In this context, examining the gut microbiome as an influential factor in overall health becomes particularly important. The relationship between the microbiome and sexual health can illuminate new dimensions of this topic and help us develop better strategies for enhancing sexual health quality. Ultimately, this study explores these connections and clarifies the groundwork for future research.

Material and Methods: The search for relevant studies involved utilizing keywords related to "*probiotics*", "microbiome", "normal flora" and "sexual health" in international databases, including PubMed, ScienceDirect and Web of Science, and national resources like SID, Magiran, and also Google Scholar search engine. The initial search yielded 490 studies, including criteria was pertinent to the study's focus, excluding animal studies, reviews, conference presentations, and editor letters. No time limitations were applied. After eliminating duplicates and maintaining ethical standards to avoid biases, the final analysis comprised 14 selected studies

Results: 57% of studies (8 articles) indicate that the consumption of *probiotics*, by regulating the microbiome, has positive effects on individuals' sexual health, such as improving sexual performance and reducing sexually transmitted infections. However, 14% of studies (2 articles) mention that these supplements have no effect on sexual health. Additionally, 14% (2 articles) only state a general relationship (regardless of the type of effect) between the two. Finally, 21% (3 articles) emphasize the need for further research to clarify the effects of *probiotics* on individuals' sexual health.

Conclusion: The findings of this research indicate that the relationship between gut microbiome, probiotic consumption, and sexual health is complex. While some studies report improvements in sexual function and reductions in sexually transmitted infections due to probiotic consumption, others find no impact from these supplements. This contradiction in results highlights the need for more research to gain a clearer understanding of these relationships. Therefore, ambiguity regarding the effects of *probiotics* on sexual health remains, necessitating more comprehensive investigations.

Keywords: *Probiotics*, microbiome, sexual health

Abstract ID: 286
subject: The role of probiotics in health and disease

Targeting *Neisseria gonorrhoeae* with *Enterococcus faecium*: Exploring its inhibitory potential

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Background and Aim: The global prevalence of antibiotic-resistant *Neisseria gonorrhoeae*, a major sexually transmitted infection, poses significant challenges to effective treatment and public health. In addition to its immediate effects, N. gonorrhoeae is implicated in several serious reproductive issues, including pelvic inflammatory disease and infertility. This growing resistance crisis necessitates innovative therapeutic strategies. Probiotics, particularly *Enterococcus faecium*, isolated from traditional fermented dairy products, demonstrate promising antimicrobial properties, including bacteriocin production and the ability to inhibit harmful pathogens growth. This study explores the potential of E. faecium as a biocontrol agent against N. gonorrhoeae, with the aim of developing alternative approaches to mitigate antibiotic resistance and its associated complications. The findings highlight the potential role of probiotic-based interventions in addressing one of the most urgent global health threats.

Material and Methods: Ten traditional fermented dairy samples were collected from rural areas in Hamadan province. Each sample (1 mL) was inoculated into MRS broth and incubated for 24 hours, followed by serial dilution. A 100 µL aliquot of each dilution was then plated onto MRS agar and incubated under anaerobic conditions. Isolated colonies were purified using a cross-streaking method and screened for antibacterial activity against *Neisseria gonorrhoeae*. The bacterial isolates with the most promising activity were identified through 16S rRNA gene sequencing.

Results: The isolate showing inhibitory activity against *Neisseria gonorrhoeae* was identified as *Enterococcus faecium* based on 16S rRNA gene sequencing, which was performed using universal primers. Phylogenetic analysis of the 16S rRNA gene sequence confirmed the identification of the strain. After 48 hours of incubation, the E. faecium strain exhibited a clear inhibition zone of approximately 14 mm against N. gonorrhoeae.

Conclusion: This study highlights the promising role of *Enterococcus faecium* as a biocontrol agent against *Neisseria gonorrhoeae*. our findings contribute to the growing evidence suggesting that probiotic-based treatments, particularly those derived from traditional foods like fermented dairy, could serve as effective alternative therapeutic strategies to combat resistant infections. Further studies, including in vivo studies and clinical trials, are necessary to better understand the broader implications of E. faecium in antimicrobial therapy and its potential role in mitigating the public health crisis posed by resistant gonorrhea.

Keywords: Antibiotic resistance, *Neisseria gonorrhoeae*, *Enterococcus faecium*, probiotics, dairy products, and multidrug-resistant organisms

Abstract ID: 58
subject: Artificial intelligence and innovative techniques in the diagnosis of bacterial infections

Revolutionizing clinical microbiology: A systematic review of machine learning algorithms for bacterial infection diagnosis

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Background and Aim: The rapid emergence of antibiotic resistance and the escalating burden of infectious diseases underscore the urgent need for innovative diagnostic methods in clinical microbiology. In this context, machine learning algorithms have gained traction as powerful tools for improving the accuracy and efficiency of bacterial infection identification.

Material and Methods: This systematic review synthesizes a comprehensive analysis of various machine learning techniques, including supervised, unsupervised, and semi-supervised methods. By examining how these algorithms process and analyze diverse data sources—ranging from clinical parameters and genomic sequencing to imaging modalities—we present a thorough understanding of their implementation in microbial diagnostics.

Results: Our findings demonstrate that machine learning algorithms significantly enhance the speed and reliability of bacterial pathogen detection, leading to improved diagnostic capabilities. Case studies illustrate successful applications of these technologies in real-world clinical settings, showcasing their potential to facilitate timely and targeted therapeutic interventions.

Conclusion: Despite the promising advancements, several challenges remain, including dataset bias, algorithm interpretability, and the need for seamless integration into existing clinical workflows. This review highlights these issues while discussing future directions for research in machine learning applications for diagnosing bacterial infections. Ultimately, we conclude that when effectively leveraged, machine learning can transform the landscape of infectious disease management and substantially improve patient outcomes.

Keywords: Machine learning, bacterial infection diagnosis, new techniques

Abstract ID: 59
subject: Artificial Intelligence and Innovative Techniques in the Diagnosis of Bacterial Infections

Revolutionizing diagnostic accuracy: A systematic review of the role of natural language processing for enhancing the identification of bacterial pathogens

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Background and Aim: The identification and classification of bacterial infections are critical for effective treatment and public health management. Traditional methods for bacterial detection, often reliant on culture-based techniques, are time-consuming and may lack the necessary sensitivity and specificity. Recent advancements in Natural Language Processing (NLP) present novel avenues for enhancing the identification of bacterial pathogens from diverse sources, including medical reports, genomic data, and scientific literature.

Material and Methods: This systematic review delves into the application of NLP techniques in the detection and classification of bacteria. We examine various methodologies, including text mining, named entity recognition, and machine learning approaches that leverage unstructured data to extract relevant information about bacterial species. By analyzing recent studies and advancements in the field, we highlight how NLP can facilitate the identification of patterns and relationships in large datasets, thereby accelerating the diagnostic process.

Results: The findings of this review indicate a growing body of evidence supporting the use of NLP for bacterial detection. Case studies demonstrate the ability of NLP algorithms to accurately process and analyze clinical notes, laboratory reports, and scientific publications, leading to improved identification rates and a reduction in diagnostic delays. We summarize key metrics of performance, including precision, recall, and overall effectiveness of NLP-based systems in clinical microbiology contexts.

Conclusion: Despite the promising potential of NLP in microbiological diagnostics, several challenges remain, such as data integration, algorithm interpretability, and the need for robust training datasets. This review discusses these challenges and proposes strategies for future research to enhance the efficacy of NLP in detecting bacterial infections. Ultimately, we conclude that the integration of NLP technologies into clinical practice can significantly improve the speed and accuracy of bacterial detection, paving the way for better patient outcomes and enhanced epidemiological surveillance.

Keywords: Natural language processing, bacterial pathogen detection, artificial intelligence

Abstract ID: 79
subject: Artificial Intelligence and Innovative Techniques in the Diagnosis of Bacterial Infections

Deep neural networks for rapid and accurate diagnosis of bacterial infections via microscopic images

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Background and Aim: Bacterial infections pose a significant global health challenge, necessitating rapid and accurate diagnostic methods for effective treatment and antimicrobial stewardship. Traditional microscopy-based diagnostic approaches, while widely used, are often labor-intensive and prone to variability in interpretation. Deep neural networks (DNNs) have emerged as powerful tools for image analysis, offering high accuracy and speed in various biomedical applications. This review aims to explore the application of DNNs in the diagnosis of bacterial infections through microscopic imaging, focusing on their potential to enhance diagnostic workflows.

Material and Methods: A comprehensive literature review was conducted to evaluate studies employing DNNs for bacterial detection, classification, and quantification in microscopic images. Databases such as PubMed, Scopus, and IEEE Xplore were searched using relevant keywords. Inclusion criteria encompassed studies published in peer-reviewed journals that demonstrated the use of DNNs for bacterial diagnostics. Analytical comparisons were made between DNN-based methods and conventional diagnostic approaches regarding performance metrics such as accuracy, sensitivity, and processing time.

Results: The review highlights that DNNs consistently outperform traditional microscopy in terms of diagnostic accuracy, achieving sensitivity and specificity rates exceeding 95% in many cases. Moreover, DNNs significantly reduce diagnostic time, enabling near real-time analysis. Advanced architectures, such as convolutional neural networks (CNNs), have demonstrated robustness in detecting bacterial morphology and identifying antibiotic resistance markers. The integration of DNNs with automated imaging systems further enhances scalability and reproducibility in clinical settings.

Conclusion: DNNs represent a transformative technology in the diagnosis of bacterial infections, offering unparalleled accuracy and efficiency. Their adoption in clinical workflows can alleviate the limitations of traditional methods, improve diagnostic precision, and support timely treatment decisions. However, challenges such as dataset standardization, algorithm interpretability, and integration into existing laboratory infrastructure must be addressed for widespread implementation.

Keywords: Deep neural networks, bacterial infections, microscopic imaging, diagnostic accuracy, artificial intelligence in healthcare

Abstract ID: 371
subject: Artificial Intelligence and Innovative Techniques in the Diagnosis of Bacterial Infections

Optimizing antimicrobial stewardship in academic hospitals through ai and iot-driven predictive analytics for antibiotic resistance management

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Background and Aim: Antimicrobial resistance (AMR) poses a substantial threat to public health, necessitating effective antibiotic management strategies in academic hospitals. This study aims to investigate the integration of Artificial Intelligence (AI) and Internet of Things (IoT) technologies to optimize antimicrobial stewardship, particularly through predictive analytics for managing AMR.

Material and Methods: A 12-week case study was conducted at a 490-bed tertiary care hospital, targeting patients diagnosed with infections necessitating antibiotic treatment. The hospital utilized an IoT-enabled patient monitoring system that collected real-time data, including vital signs, laboratory results, and imaging data from over 1,000 patients. Additionally, electronic health records (EHRs) provided comprehensive information on patient demographics, comorbidities, prior antibiotic use, and microbiological culture results. Machine learning algorithms, such as random forests and deep learning models, were trained on this extensive dataset to predict the likelihood of antibiotic resistance in pathogens based on infection type, patient risk factors, and local resistance patterns. The AI model offered real-time alerts to clinicians, providing personalized recommendations for appropriate antibiotic treatments while prioritizing narrow-spectrum options. The system also forecasted infection progression, allowing for earlier clinical interventions. Performance metrics included accuracy of resistance predictions, appropriateness of antibiotic prescriptions, infection resolution times, and patient outcomes (length of stay and mortality rates).

Results: The predictive model achieved a high accuracy of 92% in predicting antibiotic-resistant infections, markedly surpassing traditional methods that rely solely on historical microbiological data. It excelled at identifying resistant Gram-negative infections. The implementation of AI and IoT-driven recommendations led to a 35% reduction in broad-spectrum antibiotic usage and a 28% decrease in inappropriate prescriptions. There was also an 18% reduction in hospital-acquired infection (HAI) rates, particularly in intensive care units (ICUs). Patients guided by the AI model experienced, on average, a 20% shorter hospital stay, while mortality rates related to antibiotic-resistant infections fell by 12%.

Conclusion: This case study confirms that integrating AI and IoT technologies in hospitals can significantly enhance antimicrobial stewardship by enabling real-time, data-driven predictions of antibiotic resistance. The AI-powered predictive model not only reduces inappropriate antibiotic use but also improves patient outcomes, emphasizing the transformative potential of these technologies in the fight against AMR.

Keywords: Antibiotic resistance, artificial intelligence, internet of things, antimicrobial stewardship

Abstract ID: 373
subject: Artificial Intelligence and Innovative Techniques in the Diagnosis of Bacterial Infections

Secure management of bacterial infection data in healthcare systems using blockchain technology

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Background and Aim: Bacterial infection data, including patient records, diagnostic results, and epidemiological findings, is often sensitive and vulnerable to tampering. The objective of this study is to evaluate the application of blockchain technology in securing bacterial infection data within healthcare systems, ensuring data integrity, privacy, and transparency in sharing sensitive health information.

Material and Methods: A blockchain-based framework was developed to secure bacterial infection data, utilizing a decentralized ledger for tracking diagnostic results, treatment regimens, and pathogen genotyping data. A hybrid blockchain approach was employed, combining both public and private chains to balance transparency and confidentiality. The system was integrated into an existing hospital information system for testing, with real-time data from bacterial culture laboratories and patient records stored on the blockchain. Data security was tested using cryptographic hash functions, ensuring that records could not be altered retroactively without detection. The research team conducted simulated bacterial infection case studies to demonstrate the ability of the blockchain system to handle large datasets and multiple user access points (including hospital administrators, microbiologists, and public health authorities).

Results: The blockchain implementation ensured that bacterial infection data was immutable and accessible only by authorized personnel. The system demonstrated reduced time for verifying infection status and antibiotic resistance profiles. Data exchange between hospitals, research institutions, and public health agencies was seamless, with security and data integrity upheld throughout the process. Additionally, the blockchain system was able to scale, handling a significant volume of infection-related data without performance degradation.

Conclusion: Blockchain technology offers a robust solution for securing bacterial infection data, enhancing both data integrity and privacy in healthcare systems.

Keywords: Blockchain, bacterial infections, privacy, data security, cryptography

Abstract ID: 69
subject: Artificial Intelligence and Innovative Techniques in the Diagnosis of Bacterial Infections

Comparison of different machine learnings for prediction, prevention and rapid diagnosis of brucellosis, a comprehensive review

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Background and Aim: Brucellosis is one of the most common infectious zoonosis, which has significant impacts on human and animal health, reproduction and livestock productivity. Implementing preventive strategies and rapid diagnosis of brucellosis has always been important in order to reduce economic consequences and health risks. Although traditional methods have been able to play a role in the prevention of brucellosis, recent research has been shown that artificial intelligence (AI) can perform better in terms of accuracy and prediction of preventive models and diagnosis.

Material and Methods: The study reviewed articles since 2010 in the Web of Science, Scopus, PubMed, and Google Scholar databases, as well as articles that described the use of AI to analyze images for the prediction, prevention and diagnosis of brucellosis. To obtain appropriate information, the keywords such as brucellosis, prediction, prevention, diagnose, artificial intelligence, machine learning and etc. were used.

Results: This study compared the accuracy of machine learning (ML) for brucellosis prediction, prevention and diagnosis which was used different MLs such as Vote, AdaBoostM1, LogitBoost, Bagging and RBF (Radial basis function), which showed that RBF performed well in terms of increasing the accuracy in predicting brucellosis prevalence. In the discussion of prevention, the use of SMOTE has been proposed to overcome the challenge of imbalanced data, which was able to increase the prediction accuracy of prevention methods. Also, CART has been used as another AI to achieve an accurate technique for diagnosing brucellosis risk factors.

Conclusion: The comparisons showed, RBF and AdaBoostM1 MLs provide high accuracy in creating predictive models for prevention and faster diagnosis of brucellosis through defined risk factors, and hence have been able to help improve disease control strategies.

Keywords: Brucellosis, prediction, prevention, diagnosis, artificial intelligence, machine learning

Abstract ID: 56
subject: Artificial Intelligence and Innovative Techniques in the Diagnosis of Bacterial Infections

Revolutionizing clinical microbiology: Deep learning algorithms for bacterial infection diagnosis

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Background and Aim: The increasing prevalence of bacterial infections, combined with the limitations of traditional diagnostic methods, has prompted the search for innovative solutions in clinical microbiology. Deep learning, particularly through convolutional neural networks (CNNs), has emerged as a transformative approach for image analysis, demonstrating significant potential in enhancing the detection and diagnosis of bacterial pathogens in microscopy images.

Material and Methods: This systematic review examines the application of CNNs in analyzing microscopy images to identify bacteria more effectively. We explore various architectures of CNNs, their training methodologies, and the integration of large datasets to improve model accuracy. By evaluating recent case studies and technological advances in deep learning, we demonstrate how these methods provide superior image classification compared to conventional techniques.

Results: Our findings indicate that CNNs significantly enhance the accuracy and speed of bacterial detection compared to standard microscopy analysis. Case studies presented highlight successful implementations of CNN algorithms, showcasing their ability to identify bacterial species with high precision, reduce human error, and transform the diagnostic workflow in clinical settings.

Conclusion: While the application of deep learning in microbiology holds great promise, challenges remain, including the need for large labeled datasets, algorithm interpretability, and deployment in real-world clinical settings. This review discusses these challenges and suggests areas for future research, emphasizing that effective utilization of CNNs in microscopy image analysis can revolutionize bacterial infection diagnosis, ultimately improving patient outcomes and informing public health strategies.

Keywords: Deep learning, artificial intelligence, new diagnosis

Abstract ID: 57
subject: Artificial Intelligence and Innovative Techniques in the Diagnosis of Bacterial Infections

Harnessing predictive analytics to combat bacterial infections: A systematic review of data-driven approaches

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Background and Aim: The increasing prevalence of bacterial infections poses major challenges to public health and healthcare systems globally. Predictive analytics has emerged as a promising approach to leverage historical data, enabling the anticipation of infection outbreaks and patient trends. This article reviews the application of predictive analytics in identifying bacterial infections, highlighting its potential to inform timely interventions

Material and Methods: We conducted a comprehensive systematic review of recent studies that employ predictive analytics in the healthcare domain. Relevant datasets—including clinical records, laboratory test results, and environmental factors—were analyzed using advanced statistical methods and machine learning algorithms. Criteria for study inclusion focused on real-world applications demonstrating predictive modeling for bacterial infections.

Results: Our review revealed a range of successful implementations of predictive models that effectively identified patterns and risk factors associated with bacterial infections. Case studies showcased how predictive analytics improved early detection rates, optimized resource allocation, and facilitated targeted responses to outbreak incidents.

Conclusion: The findings underscore the transformative potential of predictive analytics in enhancing infection prevention and control efforts. By enabling a proactive approach to managing bacterial infections, predictive modeling can significantly improve public health outcomes. We conclude that interdisciplinary collaboration is essential for advancing data-driven insights that can tackle the growing threat of bacterial infections, ultimately leading to improved health surveillance and patient care.

Keywords: Predictive analytics, artificial intelligence, new diagnosis

Abstract ID: 245
subject: Artificial Intelligence and Innovative Techniques in the Diagnosis of Bacterial Infections

Production of diagnostic platforms with high throughput capable of detecting aquatic pathogens

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Background and Aim: Identifying pathogens in water and food products, ensuring the health and quality of consumption resources and reducing economic losses is an essential priority. According to the information of the World Health Organization, most diseases, including dysentery, cholera, diarrhea and skin infections are caused by pathogens in water. Therefore, it is essential for human health to create a fast, accurate and selective system that can detect pathogens in water both (quantitatively and qualitatively).

Material and Methods: By using library studies and systematic review of article.

Results: Biosensors provide real-time and in-situ analysis of the desired analyte without expensive and complex sample preparation. Today, biosensors, which are very selective, sensitive and specific, without any enrichment or mutation, are used for rapid detection of pathogenic agents in water. The characteristic of biosensors is related to bioreceptor materials. Biochemical recognition mechanisms are based on biological receptor elements (biological molecules). These receptors play a role in connecting the analyte to the sensing part of biosensors. Biosensors are more accurate for detecting pathogens in water and environmental samples than conventional methods. These sensing techniques have become more consistent, effective and dynamic with the help of nanomaterials. The transfer process has been significantly improved by using different nanomaterials, which allows for faster detection, higher sensitivity, shorter response time and reproducibility.

Conclusion: The purpose of this study is to acquire technical knowledge and build a variety of sensors based on biocompatible electrochemical/electronic chips and using new and emerging knowledge and technologies from nano, electrochemistry, electronics, thin layers, layers thick layers, bio-based sensors, bio-based membranes, and nanopores

Keywords: Diagnostic platforms, detecting aquatic pathogens

Abstract ID: 40
subject: Hospital-Acquired Infections

Epidemiology of *Acinetobacter* isolated from hospitalized patients in various wards of Rasul Akram Hospital, tehran province, 2024

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Background and Aim: *Acinetobacter* spp. are aerobic, Gram-negative, catalase-positive, oxidase-negative, non-motile, non-fermentative, and opportunistic coccobacilli that are major causative agents of hospital-acquired infections. They are responsible for a range of infections, including septicemia, pneumonia, and urinary tract infections, particularly following hospitalization. Factors contributing to the development of infections include prolonged hospitalization, surgery, previous infections, wounds, treatment with broad-spectrum antibiotics, the presence of permanent central venous or urinary catheters, mechanical ventilation, and admission to intensive care units (ICUs) such as burn units and general ICUs. *Acinetobacter* rarely causes severe infections in healthy individuals. This study aimed to investigate the epidemiology of *Acinetobacter* isolated from hospitalized patients in various wards of Rasul Akram Hospital, Tehran Province.

Material and Methods: A total of 55 hospitalized patients in Rasul Akram Hospital were included in this study. Biochemical tests were performed for the definitive identification of the bacterial isolates.

Results: Among the samples collected from patients, 40 samples (77.7%) were isolated from sputum, 4 samples (7.27%) from wounds, 3 samples (5.45%) from Bal, 2 samples (3.63%) from Shaldon catheters, 2 samples (3.63%) from pleural fluid, 1 sample (1.81%) from blood, 1 sample (1.81%) from liver secretions, and 1 sample (1.81%) from cerebrospinal fluid (CSF). Based on the ward of origin, 13 samples (24.63%) were from the MICU, 9 samples (16.36%) from the emergency ICU, 9 samples (16.36%) from the neurology ICU, 9 samples (16.36%) from the SICU, 8 samples (14.54%) from the general ICU, 2 samples (3.63%) from the PCCU, 2 samples (3.63%) from the internal medicine ward, 2 samples (3.63%) from the emergency department, and 1 sample (1.81%) from the nephrology ward. The findings indicated that the majority of samples were isolated from patient sputum (77.7%) and originated from the MICU (24.63%).

Conclusion: According to the results obtained from this study, it can be said that the MICU department has a higher risk of *Acinetobacter* infection, which requires special attention

Keywords: *Acinetobacter*, hospital-acquired infection, epidemiology, MICU, ICU.

Abstract ID: 191
subject: Hospital-Acquired Infections

Cassiamin C, hinokiflavone and ergocornine as potential natural compounds to inhibit penicillin binding protein 2a of *Methicillin-resistant Staphylococcus aureus* using advanced simulation studies

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Background and Aim: The vast antibiotic resistance and ubiquitous nature of *Methicillin-resistant Staphylococcus aureus* (MRSA) has posed huge health impacts needing the discovery of novel drugs. This study aimed to screen potential herbal bioactive compounds against wild and mutant penicillin-binding protein 2a (PBP2a) using comprehensive in silico approaches.

Material and Methods: To identify lead compounds against PBP2a, after the screening of ADMET properties compounds from the PubChem database, the structure-based virtual screening was implemented to assess their target binding affinity compared to ceftobiprole.

Results: cassiamin C, hinokiflavone and ergocornine were selected. The molecular dynamics (MD) simulation was implemented to analyze the stability and dynamics of PBP2a and top-scoring ligand-PBP2a complexes. Additionally, the g_mmpbsa tool was utilized to measure and evaluate the binding free energy of PBP2a-ligand complexes. The computed binding free energy between wild-type PBP2a and ceftobiprole, cassiamin C, hinokiflavone and ergocornine included -21.53, -126.73, -86.17 and -38.17 kJ/mol, respectively. Regarding the mutant PBP2a, ΔGbind values of the cassiamin C, hinokiflavone, ergocornine and ceftobiprole were -111.64, -107.85, -97.02, and 251.03 kJ/mol, respectively.

Conclusion: Compounds cassiamin C, ergocornine and hinokiflavone were potent inhibitors compared to ceftobiprole. Future investigations for the optimization of the activity of these compounds will open new insights into the verification of their PBP2a inhibitory role and the elimination of drug-resistant MRSA infections using experimental studies.

Keywords: Methicillin-resistant *S. aureus*, Herbal bioactive compounds, Drug discovery, MD simulation

Abstract ID: 181
subject: Hospital-Acquired Infections

Identification of *Helicobacter pylori* using various diagnostic approaches: A comparative study

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Background and Aim: *Helicobacter pylori* (*H. pylori*) is the most common cause of chronic gastritis and variably leads to severe pathological effects of the gastrointestinal tract (GIT) in some patients. This study aimed to determine the diagnostic value of saliva Polymerase Chain Reaction (PCR) test, urease test and stomach biopsy in diagnosing *H. pylori* infection among patients with upper gastrointestinal disorders.

Material and Methods: This cross-sectional study was started after obtaining permission from the ethics committee of the research department of the university. Sixty-eight patients who were referred to the endoscopy department of Wali Asr Hospital in Fasa were selected according to the available method by observing the inclusion and exclusion criteria of the study. Demographic information questionnaire form was filled for each patient. Five biopsy samples were taken from the incisura angularis (at a distance of 2 to 3 cm from the pylorus and on the side of the lesser curvature of the stomach), fundus and greater curvature of the stomach. Hematoxylin-eosin staining was used to study histology and Giemsa staining was used to detect effects of *H. pylori*. To check the rapid urease activity, the rapid urease activity kit was used. Saliva samples (about 3 mL of unstimulated saliva from each patient) were checked for the presence of *H. pylori* by PCR. In this study, the golden standard biopsy method was considered and the results were analyzed with SPSS version 25 software.

Results: Among 68 patients participated in this study, 38 (55.9%) were men and 30 (44.1%) were women. The research results showed that there was a significant relationship between rate of urease test (n=59, 86.76%) and biopsy (n=66, 97.05%) (p=0.028), but lower saliva PCR test (n=9, 13.23%) was detected *H. pylori* in samples.

Conclusion: The use of saliva PCR brought results parallel to the gold standard (stomach biopsy samples). Saliva PCR test is not suitable to detect *H. pylori* among symptomatic patients and biopsy PCR test maybe more accurate which can be recommended for routine use in the diagnosis of *H. pylori* alongside biopsy pathology and other routine diagnostic tests.

Keywords: *Helicobacter pylori*, polymerase chain reaction, urease test, stomach biopsy, diagnosis

Abstract ID: 260
subject: Hospital-Acquired Infections

Studying the effect of zinc tungstate and cerium-doped zinc tungstate nanomaterials on structural properties and antibacterial properties

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Background and Aim: The aim of this research is to investigate the effect of zinc tungstate and cerium-doped zinc tungstate nanomaterials on their structural properties and antibacterial properties. In this regard, various analyses including X-ray diffraction and antibacterial experiments will be performed to gain a deeper understanding of the performance of these nanomaterials.

Material and Methods: Zinc tungstate and cerium-doped zinc tungstate nanomaterials were synthesized by various methods, including co-precipitation, hydrothermal, sol-gel, etc. Among these methods, the synthesis in this study was carried out by co-precipitation method.

Results: The XRD patterns of the sample, as shown in Figure 3, are consistent with a monoclinic structure, which is confirmed by comparison with standard codes such as JCPDS or ICSD. The characteristic peaks associated with crystal planes (such as (111), (101), etc.) appear with specific intensities. The presence of cerium in the crystal lattice may cause a shift in the position of the peaks (shift to smaller angles) due to changes in the lattice parameters. The reduction in crystallite size (13.7 nm compared to 21 nm for the pure sample) may lead to a broadening of the peaks. In the (MIC) and (MBC) test of the ZnWO4 sample with bacteria (*E. coli*), the minimum inhibitory concentration was 2.2 g/ml and the minimum lethal concentration was 8.8 g/ml. However, by adding cerium to the desired substance, the minimum inhibitory concentration was 0.275 g/ml and the lethality was 1.1 g/ml, which was a significant increase in the lack of bacterial growth and lethality compared to the sample without cerium.

Conclusion: The results showed that cerium-doped nanomaterials have stronger antibacterial activity than pure zinc tungstate, and this increased activity is due to the increased contact surface and the presence of cerium, which can act as an active factor in inhibiting bacterial growth.

Keywords: Structural properties, antibacterial properties, zinc tungstate, cerium

Abstract ID: 423
subject: Hospital-Acquired Infections

Investigating the biofilm formation ability of *Staphylococcus aureus* collected from clinical and non-clinical sources

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Background and Aim: The ability of *Staphylococcus aureus* to adhere and produce biofilm is the most essential step in the infectivity of this bacterium. Biofilm formation helps the bacteria survive in vivo and in vitro. The exopolysaccharide coating surrounding the biofilm slows down the passage of antibiotics into the microbial cell, resulting in resistance. The aim of the study was to investigate the ability to form biofilm and drug resistance in *Staphylococcus aureus* collected from clinical and non-clinical sources.

Material and Methods: 50 isolates of *Staphylococcus aureus* were collected from clinical and non-clinical sources and from the noses of the participants in the study, and the bacteria were identified through various biochemical reactions. Antibiotic susceptibility of the studied isolates was determined by the Kirby-Bauer disk diffusion method according to the guidelines of the Clinical and Laboratory Standards Institute (CLSI). The microtiter plate method was used to quantitatively evaluate the ability to form biofilm. A PCR reaction was also designed to detect the genes involved in biofilm formation in *Staphylococcus aureus* isolates.

Results: 38 isolates out of 50 studied isolates had *icaA* and *icaD* genes, of which 23 were clinical isolates and 15 were non-clinical isolates. Among the *icaA* and *icaD* positive samples, 76% of the clinical isolates and 36% of the non-clinical isolates were able to form strong biofilms, and the *icaA* and *icaD* genes were present in 100% of the biofilm-forming samples. In *icaA* and *icaD* positive samples, the highest level of resistance to the antibiotics were ampicillin (89.5%), erythromycin (52.6%), cotrimoxazole (50%), ciprofloxacin (44.7%), doxycycline (26.3%), and cefoxitin (21.1%). In *icaA* and *icaD* positive samples, 100% sensitivity to vancomycin and amikacin antibiotics was observed.

Conclusion: The expansion of biofilm formation in healthcare environments and lack of sterilization compliance lead to increased drug resistance and transmission of infection.

Keywords: *Staphylococcus aureus*, biofilm, *icaA* and *icaD*

Abstract ID: 352
subject: Hospital-Acquired Infections

Evaluation of the efficacy of ceftazidime-avibactam in antibiotic-resistant *Escherichia coli* strains isolated from patients with urinary tract infections and molecular detection of the genes *qepA*, *aac(6')-Ib-cr*, *qnr*, and *NDM*

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Background and Aim: Urinary tract infections (UTIs) are among the most prevalent bacterial infections, second only to respiratory tract infections in terms of significance. This study aims to evaluate the efficacy of ceftazidime-avibactam against antibiotic-resistant strains of *Escherichia coli* isolated from UTI patients, along with the molecular diagnosis of resistance genes such as *qepA*, *aac(6')-Ib-cr*, *qnr*, and *NDM*.

Material and Methods: A total of 120 *Escherichia coli* isolates were obtained from urine samples collected in hospitals across Tehran. The antibiotic resistance profile was assessed using the disk diffusion method, while the presence of resistance genes (*qepA*, *aac(6')-Ib-cr*, *qnr*, and *NDM*) was determined through PCR techniques

Results: Among the 120 *E. coli* isolates, 66.6% exhibited the presence of metallo-beta-lactamase (MBL) enzymes. The highest rates of antibiotic resistance were noted for tobramycin (87.5%), ciprofloxacin (85%), and cefotaxime (83.3%). Conversely, fosfomycin (90%) and ceftazidime-avibactam (93.33%) demonstrated the most effective antibiotic activity. Notably, 22.5% of samples harbored the *NDM-1* gene, while 87.5% contained the *aac(6')-Ib-cr* gene, and 16.66% had the *qepA* gene. The prevalence rate of the *qnr* gene was found to be 43.3%. Ceftazidime-avibactam was effective against all strains producing *NDM* and MBL

Conclusion: The high levels of resistance to various antibiotics and the significant presence of resistance genes among isolated strains underscore a critical public health concern regarding *E. coli* infections in patients. Timely and effective treatment strategies must be prioritized, particularly in hospital settings such as intensive care units, where these resistant strains are prevalent

Keywords: Drug resistance, *Escherichia coli*, urinary infections

Abstract ID: 387
subject: Hospital-Acquired Infections

Prevalence and drug resistance of bacteria isolated from blood cultures of patients with infective endocarditis in the year 1403-1402

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Background and Aim: Infective endocarditis (IE) is a serious clinical condition predominantly caused by gram-positive cocci, such as staphylococci, streptococci, and enterococci. In contrast, gram-negative bacilli represent only a minority of cases. This study aimed to investigate the prevalence and antibiotic resistance of bacterial isolates from patients diagnosed with infective endocarditis.

Material and Methods: A total of 80 bacterial isolates were obtained from blood culture samples collected from hospitals in Tehran. Antibiotic resistance was evaluated using the disk diffusion method. Blood samples were concentrated in separator tubes and inoculated onto blood agar and chocolate agar, incubated at 35°C with increased carbon dioxide levels for 14 days before reporting negative cultures.

Results: Among the 80 patients with infective endocarditis, 70% were male and 30% were female. Injection drug use was reported in 46.25% of cases, while 8.75% had a history of rheumatic heart disease. The bacterial isolates included 39 strains of *Staphylococcus aureus*, 15 strains of *Enterococcus*, and 26 strains of gram-negative bacteria. Notably, all gram-positive isolates exhibited 100% resistance to penicillin and ampicillin, while linezolid and vancomycin showed the highest efficacy (100% effectiveness). In gram-negative bacteria, ciprofloxacin (96.15%) and cotrimoxazole (100%) showed the highest resistance rates, whereas colistin demonstrated a significant effect (92.30%).

Conclusion: The prevalence of multidrug-resistant strains among gram-negative isolates has reached concerning levels. The multiple antibiotic resistances observed in these isolates highlight an urgent public health issue that requires attention

Keywords: Infective endocarditis, drug resistance, hospital infection

Abstract ID: 94
subject: Hospital-Acquired Infections

Exploring the potential effects of nisin and colistin combinations against drug-resistant *Klebsiella pneumoniae* isolates

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Background and Aim: *Klebsiella pneumoniae* is a formidable nosocomial pathogen increasingly known for its antibiotic resistance, posing a significant global health challenge. The emergence of carbapenem-resistant strains has necessitated the exploration of alternative therapeutic strategies.

Material and Methods: Ten *K. pneumoniae* isolates were collected from hospitalized patients in Iran. Antimicrobial susceptibility testing was conducted using the Kirby-Bauer disk diffusion method. Minimum inhibitory concentration (MIC) assays were performed to determine the MICs of Nisin and Colistin. Synergistic activity testing, biofilm formation assays, and time-kill assays were also carried out to assess the effectiveness of the nisin-colistin combination.

Results: The study demonstrated that the nisin-colistin combination exhibited a synergistic effect, significantly reducing colony counts over 24 hours for select isolates. However, the combination did not show statistically significant superiority in antibiofilm activity compared to colistin alone. The time-kill assay confirmed the synergistic effect, showing a notable reduction in colony counts within 24 hours. These findings underscored the complexities of biofilm structures and their resistance mechanisms, highlighting the necessity for further research to optimize treatment outcomes.

Conclusion: This study provides a novel perspective on addressing antibiotic resistance in *K. pneumoniae* by evaluating the synergistic potential of the nisin-colistin combination. The findings contribute to the development of innovative therapeutic approaches to manage infections caused by this challenging pathogen.

Keywords: *Klebsiella pneumoniae*, antibiotic resistance, colistin, nisin, biofilm

Abstract ID: 136
subject: Hospital-Acquired Infections

Identification of selective virulence factor genes in clinical isolates of uropathogenic *Escherichia coli* in Borujerd city

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Background and Aim: *Escherichia coli* is one of the most common and important members of the Enterobacteriaceae family. This is a facultative anaerobic bacterium that exists as a normal flora in the intestines of humans and warm-blooded animals. *Escherichia coli* usually colonizes the digestive system of human infants within a few hours after birth. *Escherichia coli* strains are divided based on pathogenic factors, symptoms, clinical features and the presence or absence of some gene regions related to specific virulence factors and based on the place of infection. Urinary tract infection is a widespread and stable problem, which is known as one of the most common bacterial infections in the hospital and society. Among the important adhesion factors of type 1, P and S fimbriae and toxins; Hemolysin and CNF1 factor can be mentioned.

Material and Methods: In this cross-sectional descriptive study, 100 clinical isolates of *Escherichia coli* were collected from the urine samples of patients with urinary tract infections in 1402 from selected laboratories in Borujerd city, all clinical isolates were identified by standard laboratory methods. became And DNA extracted from clinical isolates was analyzed for the presence of *Sfa*, *Drb*, *papG I*, *fimH*, and *CNF1* genes using specific primers by PCR method.

Results: Of the total *Escherichia coli* positive culture samples, 12 cases (12%) were related to men and 88 cases (88%) were related to women. The prevalence of *papG I* (70%), *fimH* (76%), *Sfa* (90%), and *CNF1* (53%) genes was obtained, and *Drb* gene was not detected in our strain.

Conclusion: respectively, the findings of the study indicate the high presence of fimbriae S, fimbriae type 1 and P in *Escherichia coli* isolates isolated from patients with urinary tract infections referred to the selected laboratories of Borujerd city, according to these genes in this study can be further investigated as a target in therapeutic interventions.

Keywords: *Escherichia coli*, urinary infection, fimbriae, *papG I*, *fimH*, *CNF1*, *Sfa*, *Drb*

Abstract ID: 267
subject: Hospital-Acquired Infections

Identification of antibiotic-resistant clinical isolates of *Escherichia coli* based on the uropathogenic specific protein (USP) gene

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Background and Aim: The uropathogenic specificity protein (UPS) in *Escherichia coli* is a bacteriocin-like genotoxin. The *usp* gene, along with related genes (*imu 1-3*), induces a specific apoptosis response, causes pyelonephritis, prostatitis, and bacteremia of urinary tract origin in humans, and increases the severity of urinary tract diseases. The aim of the study was to identify and investigate antibiotic resistance of uropathogenic *Escherichia coli* isolates based on the specific *usp* gene.

Material and Methods: In this study, 100 urine and urogenital tract secretions samples were collected from patients referring to the laboratory, and after culturing in EMB medium and examining phenotypic characteristics and Gram staining, biochemical tests were performed. Antibiotic resistance of the isolates was determined by the Kirby-Bauer disk diffusion method, and to investigate the presence of the *usp* gene, the molecular PCR method was performed using a set of specific primer related to the target gene.

Results: From 100 clinical samples, 17 *Escherichia coli* isolates were identified based on the target gene. Antibiotic resistance analysis of the isolates showed that they were most resistant to norfloxacin (80%) and amoxicillin (80%), and 100% of the isolates were sensitive to zemipenem.

Conclusion: USP is a genotoxin that affects mammalian cells and has carcinogenic potential by damaging DNA, and USP+ *Escherichia coli* strains can induce a specific apoptosis response. The presence of the specific USP protein in *Escherichia coli* isolates indicates the importance of this gene in the pathogenicity of uropathogenic *Escherichia coli* strains, and choosing the appropriate antibiotic in the process of treating the infection is an effective strategy in expressing the prevalence of the disease based on its specific genetic potential and determining the antibiotic prescription pattern for the control and treatment of diseases caused by it.

Keywords: *Escherichia coli*, uropathogenic specific protein (USP), *usp* gene, antibiotic resistance

Abstract ID: 328
subject: Hospital-Acquired Infections

Identification of clinical isolates of methicillin-resistant *Staphylococcus aureus* based on the penton-valentine leukocidin (PVL) gene by PCR

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Background and Aim: *Staphylococcus aureus*, a Gram-positive, facultative anaerobic bacterium, is an important human pathogen and a causative agent of nosocomial infections that causes a wide range of diseases, including endocarditis, osteomyelitis, pneumonia, toxic shock syndrome. The Penton-Valentine leukocidin (PVL) causes leukocyte lysis and tissue necrosis. The aim of this study was to identify PVL-positive *Staphylococcus aureus* strains in clinical samples by PCR and to investigate antibiotic resistance in western Mazandaran.

Material And Methods: Thirty clinical samples were cultured on nutrient agar and blood agar. In addition to comparing morphological evidence, hemolysis, Gram staining, and microscopic observation, biochemical confirmation tests were performed. Antibiotic resistance was assessed by Kirby-Bauer disk diffusion method in Mueller Hinton agar medium. PVL gene evaluation in isolates was performed by PCR with a specific primer pair. Initially, 23 methicillin-resistant *Staphylococcus aureus* isolates were identified.

Results: After performing PCR and electrophoresis of the products, from a total of 23 isolates, with a frequency of 55.5% for the PVL gene, an isolate with a sharp and clear band was selected and named SaPVL14. The sequence and graph were determined with Chromas Read software and analyzed with MEGA 7.0.26 and a phylogenetic tree was drawn. The isolate had the highest affinity to *S. aureus* strain LS2074, *S. aureus* strain STAPV5, *S. aureus* strain 910, *S. aureus* strain P28B330, *S. aureus* strain P135B203, and *S. aureus* strain STAPV1.

Conclusion: Given that PVL toxin production in *Staphylococcus aureus* strains is a threat to human health, rapid and accurate detection of this gene in bacteria is essential. Therefore, achieving a rapid method with high sensitivity and specificity will help in the rapid detection of PVL-producing *Staphylococcus* strains in medical centers.

Keywords: *Staphylococcus aureus*, panton-valentin leukocidin, antibiotic resistance, PCR

Abstract ID: 326
subject: Hospital-Acquired Infections

Detection of *mazEF* toxin-antitoxin system in clinical isolates of methicillin-resistant *Staphylococcus aureus* by molecular PCR method

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Background and Aim: *Staphylococcus aureus*, as a Gram-positive, facultative anaerobic bacterium, is an important human pathogen and a common cause of nosocomial infections that causes a wide range of diseases, including endocarditis, osteomyelitis, pneumonia, toxic shock syndrome, and abscesses. Toxins and the ability to form biofilms are important pathogenic factors, and *mazEF* is one of the most widespread type II toxin-antitoxin systems in this bacterium. Sometimes due to inappropriate treatment to control *Staphylococcus aureus*, the emergence of antibiotic resistance is a very important challenge in the control of nosocmial infections. The aim of this study is to molecular detection of the *mazEF* toxin-antitoxin system in clinical isolates of *Staphylococcus aureus* using PCR.

Material And Methods: Thirty clinical samples were cultured on nutrient agar and blood agar. In addition to comparing morphological evidence, hemolysis, Gram staining, and microscopic observation, biochemical confirmation tests for catalase, oxidase, coagulase, and DNase were performed. Antibiotic resistance was evaluated by Kirby-Bauer disk diffusion method on Mueller-Hinton agar. Evaluation of the *mazEF* gene in isolates was performed by PCR with a specific primer pair.

Results: From a total of 30 samples, 7 isolates of *Staphylococcus aureus* were identified, that all of which carried the *mazEF* gene. The antibiotic resistance rates of the isolates were methicillin (100%), ciprofloxacin (100%), gentamicin (100%), penicillin (71.4%), cefotaxime (57.1%), and polymyxin (28.5%), respectively.

Conclusion: The high frequency of resistance of clinical isolates of *Staphylococcus aureus* carrying the *mazEF* toxin-antitoxin system gene to antibiotics, especially methicillin, and the relative relationship of these two features with each other in this bacterium are remarkable. The *mazEF* toxin-antitoxin system in *Staphylococcus aureus* is the cause of programmed cell death. *MazEF*-mediated death is a type of defense mechanism that prevents the spread of infection.

Keywords: *Staphylococcus aureus*, methicillin resistance, toxin-antitoxin system, *MazEF*

Abstract ID: 345
subject: Hospital-Acquired Infections

Prevalence of *Listeria seeligeri* in meat-based products around the world: A meta-analysis

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Background and Aim: The incidence of foodborne infections is increasing, primarily due to inadequate hygiene practices in food preparation facilities and the development of resistance in species like *Listeria* to disinfectants, a consequence of their overuse. Therefore, epidemiological studies that explore the prevalence of *Listeria* in various food products can assist healthcare professionals in implementing improved public health strategies moving forward. In this context, a meta-analysis was performed to evaluate the prevalence of *Listeria seeligeri* in different meat products globally.

Material And Methods : In this research, systematic searches were conducted in PubMed, Web of Science, Scopus, and Google Scholar using appropriate search syntax. Initially, 1,133 articles were considered for inclusion. Ultimately, 66 articles met our inclusion criteria and were chosen for the study.

Results: according to our results, the prevalence of total *Listeria seeligeri* cases was found to be 2.41 % (Cl=1.142to 4.253).

Conclusion: The significance of *Listeria* isolates in food products highlights the need for stringent regulations and the necessity of conducting more extensive epidemiological studies with larger sample sizes.

Keywords: *Listeria seeligeri* , prevalence,, food,

Abstract ID: 236
subject: Hospital-Acquired Infections

The antimicrobial activity of propolis extract on *Klebsiella pneumoniae* and *Escherichia coli* strains isolated from Qazvin hospital personnel

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Background and Aim: Nosocomial infections, particularly those caused by Gram-negative bacilli, indeed pose significant challenges in healthcare settings. hospital staff can act as carriers of these infections, potentially transmitting them to patients and colleagues. Propolis, a natural resinous substance collected by honeybees, has shown promising antibacterial properties against various microorganisms, including Gram-negative bacteria like *Escherichia coli* and *Klebsiella pneumonia*. The aim of this study was to evaluate the effect of propolis on the most common Gram-negative bacilli isolated from the nose and nails of Qazvin hospital personnel in vitro.

Material And Methods: 50 Gram-negative bacilli, which included *Escherichia coli* and *Klebsiella pneumonia*, were isolated from the nose and nails of hospital personnel in Qazvin. Antibiotic Sensitivity Test Conducted using the disk diffusion method based on CLSI 2024 guidelines for various antibiotics. The most common isolated strain was analyzed using ERIC PCR. Finally, the microbroth dilution method was used to assess the antibacterial effect of propolis on the isolated strains.

Results: The most frequent pathogens were *K. pneumoniae* (66%) followed by *E. coli* (34%). most of the isolates were sensitive to most, and the highest antibiotic resistance was observed in Trimethoprim/Sulfamethoxazole (55%), Ceftazidime (32%) and Tetracycline (26%). Production of extended spectrum beta lactamases (ESBLs) was found in 10% of isolates of all Gram-negative bacteria. Additionally, 24% of the strains were MDR (Multi-Drug Resistant). The results of ERIC showed high genetic diversity among *Klebsiella pneumoniae* strains, which were the most common strains isolated from personnel. The MIC (Minimum Inhibitory Concentration) of propolis for both *Klebsiella pneumoniae* and *Escherichia coli* was 5%, and the MBC (Minimum Bactericidal Concentration) was 10% after culturing 100 microliters on Mueller Hinton agar.

Conclusion: The present study showed that the isolates from the nose and nails of hospital personnel can be a serious issue in the field of public health. In conclusion, these findings suggest that Iranian bee propolis has medicinal value as a natural product and was identified as an antimicrobial substance with positive effects on bacterial strains isolated from hospital personnel.

Keywords: Nosocomial infection, carriers, propolis, MDR

Abstract ID: 271
subject: Hospital-Acquired Infections

Novel methods for bloodstream infection *Staphylococcus aureus* treatment

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Background and Aim: *Staphylococcus aureus* is a leading cause of bloodstream infections (BSIs), particularly methicillin-resistant *S. aureus* (MRSA), posing significant challenges in treatment. Understanding the host response to invasive *S. aureus* infections could enable earlier and more effective therapeutic strategies to manage these life-threatening conditions. This study presents novel methods treatment for bloodstream infection caused by *S. aureus*.

Material And Methods: A comprehensive literature searching was conducted across Google Scholar, Scopus, Web of Science, and PubMed databases, covering the period from August 2018 to June 2024. The search strategy utilized a combination of relevant keywords including Methicillin-Resistant *Staphylococcus aureus*, MRSA, bloodstream infection and control treatment.

Results: The analysis of various studies on *S. aureus* bloodstream infections (BSIs) reveals significant findings. Combination therapy with daptomycin (DAP) and beta-lactam (BL) significantly reduced clinical failure odds compared to DAP alone, particularly in complex infections. ICU-acquired BSIs accounted for the majority of cases, with high antimicrobial resistance delaying effective therapy and contributing to a mortality rate of 37.1%. Despite declines in MRSA rates over the years, community-onset MSSA infections have increased. The addition of exebacase to antibiotics improved clinical responder rates, particularly in MRSA patients, with reduced mortality and hospital stays. Furthermore, interleukin-8 and CCL2 emerged as strong mortality predictors, underscoring the potential of biomarker-based stratification to improve outcomes in severe infections.

Conclusion: In conclusion, combination therapies and biomarker-driven approaches represent promising strategies to improve outcomes in *S. aureus* bloodstream infections.

Keywords: Methicillin-resistant *Staphylococcus aureus*, bloodstream infection, MRSA, control treatment.

Abstract ID: 333
subject: Hospital-Acquired Infections

The survey of virulence gene profiles in *Staphylococcus aureus* isolates in Covid-19 patients admitted in icu at sina educational hospital of hamadan

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Background and Aim: Covid-19 is a new viral infection that was first reported in Wuhan, China in December 2019 and has killed more than one million people worldwide. Hospitalization of patients with COVID-19, especially in ICUs, exposes them to hospital-acquired infections or secondary infections in severe cases with high mortality. One of these causes of secondary infections is *S.aureus* resistant to methicillin. therefore, the investigation of the evolutionary relationship of the acquired isolates from patients, therefore, the epidemiology level of MRSA and virulence genotype isolates is necessary.

Material And Methods: A number of 22 isolates of *S.aureus* were collected from patients with COVID-19 during the third, fourth and fifth waves from December 2019 to February 2019 hospitalized in the intensive care unit. MRSA strains were identified by cefoxitin resistant (≤21mm) followed by mecA gene genotyping. Eleven virulence genes, including the Panton-Valentine leukocidin (pvl), the staphylococcal enterotoxin genes (*sea, seb, sec*), the exfoliative toxin genes (*eta, etb*), the hemolysin genes (*hla, hlb*), and the adhesion factor genes (*fnbA, fnbB, clfA*) were detected using PCR assays. The PCR mixture and conditions were similar to those described previously

Results: In total, from 22 *S.aureus* isolates in covid-19 patients, 12(54.5%) were male, 10(45.5%) female, with the age range of 39-86. Source of infection was tracheal tube 9(40.9%), blood culture 12(54.5%), and sputum 1(4.5%). The results of the frequency of virulence genes in MRSA and MSSA strains are given in Table 1

Conclusion: In conclusion, the present study showed high prevalence of MRSA isolates with high virulence in covid-19 patients admitted to ICU wards that is an alarm for spreading antibiotic resistance.

Keywords: *Staphylococcus aureus*, virulence gene, COVID-19

Abstract ID: 122
subject: Hospital-Acquired Infections

Investigation of the inhibitory effect of quercetin-loaded nanoliposomes on the growth of methicillin-resistant *Staphylococcus aureus*

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Background and Aim: Background and Objective: Methicillin-resistant *Staphylococcus aureus* (MRSA) is one of the common causes of hospital-acquired infections, including urinary tract infections. The aim of this study is to investigate the inhibitory effect of quercetin-loaded nanoliposomes on the growth of MRSA bacteria.

Material And Methods: Methodology: First, quercetin-loaded nanoliposomes were synthesized with confirmed tests and appropriate quality. Then, MRSA bacteria were isolated from urinary tract infection samples. The antimicrobial effect of quercetin-loaded nanoliposomes and free quercetin on MRSA was subsequently examined. Using a 96-well microplate, the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) of quercetin-loaded nanoliposomes and free quercetin were determined. Additionally, the expression of biofilm-related genes *IcaA* and *IcaD* in the treated samples was evaluated using the Real-Time PCR technique and compared with the control group. Subsequently, statistical analysis of the data was conducted, and the results were reported.

Results: Results: Quercetin-loaded nanoliposomes with an average size of 186 nanometers and a zeta potential of -58 millivolts were synthesized, with a quercetin encapsulation efficiency of 94.5%. After isolating the MRSA bacteria, the inhibitory effect of quercetin and quercetin-loaded nanoliposomes in Mueller-Hinton agar culture medium was significant. Using the 96-well microplate method, the MIC and MBC of quercetin-loaded nanoliposomes were reported to be 3.125 mg/mL, while the MIC and MBC of free quercetin were 15.625 mg/mL and 1.953 mg/mL, respectively. Additionally, the expression of biofilm-related genes *IcaA* and *IcaD* showed a reduction in the treated samples compared to the control group.

Conclusion: Conclusion: Quercetin-loaded nanoliposomes and free quercetin exhibit both inhibitory and bactericidal effects on MRSA bacteria. Additionally, the significant reduction in the expression of *IcaA* and *IcaD* genes suggests that quercetin-loaded nanoliposomes and free quercetin can effectively inhibit and eliminate MRSA bacteria.

Keywords: Quercetin, nanoliposome, methicillin-resistant *Staphylococcus aureus*

Abstract ID: 234
subject: Hospital-Acquired Infections

Determining the frequency of carbapenem-resistant genes in *Klebsiella pneumoniae* strains and investigating of their genetic relationship by the MLVA method in Mashhad.

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Background and Aim: *Klebsiella pneumoniae* is one of the most important agents of nosocomial infections which emergence of antibiotic resistance results in many problems in the therapeutic process. This study aimed to determine the frequency of carbapenem-resistant genes in *Klebsiella pneumoniae* strains and investigating of their genetic relationship by the MLVA method in Mashhad.

Material And Methods: In this cross-sectional study, 140 isolates were collected from patients referring to the Imam Reza and Ghaem Hospitals, in Mashhad, Iran. Then *K. pneumoniae* strains were confirmed by standard biochemical tests. The antibiotic susceptibility test was determined by the disk diffusion method. Modified Hodge test (MHT) was used for phenotypic detection of carbapenemases isolates. PCR assays were performed for the detection of the carbapenemase genes. Genotyping of harboring carbapenemase genes was performed by Multi-Locus VNTR Analysis (MLVA).

Results: Antibiotic susceptibility tests showed that the highest antibiotic resistance was related to amoxicillin (99/2%) and ampicillin (98.5%). Of the 140 *K. pneumoniae* strains, 38 (27.1%) were found to be carbapenemase –positive by MHT and PCR. In addition, blakpc, blaIMP and blaVIM genes were detected in 7.8%, 31.5% and 47.3% of carbapenemase –positive isolates, respectively. Analysis of the number of VNTR repeats using the MST algorithm showed that Analysis of the number of VNTR repeats using the MST algorithm showed that carbapenem-producing isolates had 17 different genotypes. The majority of strains belonged to type 1.

Conclusion: The finding of the present study revealed that the analysis of the antibiotic-resistant mechanism provides valuable information for the screening, identification, diagnosis, treatment and control of clinical antibiotic-resistant pathogens, and is an important reference pointer to prevent strains from producing resistance. The presence of carbapenemase genes in different MLVA types showed that one specific clone was not responsible for spreading the *K. pneumoniae* isolates.

Keywords: *Klebsiella pneumoniae*, antibiotic resistance, MLVA, carbapenemase genes

Abstract ID: 235
subject: Hospital-Acquired Infections

Identification of aminoglycoside resistance genes in *Pseudomonas aeruginosa* isolates isolated from patients referred to Mashhad hospitals

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Background and Aim: *Pseudomonas aeruginosa* is one of the most important causative agents among the hospital acquired infections, especially in ICU and burn units. Enzymatic inactivation of aminoglycosides by aminoglycoside-modifying enzymes is the main mechanism of resistance to these antibiotics in *Pseudomonas aeruginosa*. The aim of this study was to identify aminoglycoside resistance genes in *Pseudomonas aeruginosa* isolates isolated from patients referred to Mashhad hospitals

Material And Methods: In this cross-sectional study, 150 of *Pseudomonas aeruginosa* were collected in 6 months from patients referred to 5 hospitals in Mashhad. Then, *Pseudomonas aeruginosa* strains were confirmed by standard biochemical tests. The antibiotic resistance pattern was determined by the disk diffusion method. PCR method was used to identify genes resistant to aminoglycosides.

Results: Antibiotic susceptibility tests showed that the highest antibiotic resistance was related to amikacin (67.3%) and gentamicin (66.6%). The prevalence of ant(6)-Ia, aac(6)-IIa and ant(2")-Ia in aminoglycoside resistant isolates was 53.9%, 32.1% and 68.6%, respectively.

Conclusion: Aminoglycosides are the preferred drug for the combined treatment of infections caused by *Pseudomonas aeruginosa* and the prevalence of resistance to them is also high, so the intermittent examination of the susceptibility pattern of these antibiotics and the genes associated with this issue is necessary to prevent the prevalence of high levels of resistance in this bacterium.

Keywords: *Pseudomonas aeruginosa*, ant(6)-Ia, aac(6)-IIa, ant(2")-Ia genes

Abstract ID: 104
subject: Hospital-Acquired Infections

Epidemiological and microbiological characteristics of osteomyelitis: Insights from a cross-sectional study in Kermanshah, Iran

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Background and Aim: Osteomyelitis is an inflammatory, infectious condition that causes bone destruction. It can be acute or chronic, with varied presentations and risk factors. This study aims to improve understanding of the disease in this region by analyzing the demographic, epidemiological, and microbiological profiles of patients diagnosed with osteomyelitis admitted to Imam Reza Hospital, Kermanshah, Iran, from 2021 to 2022.

Material And Methods: This retrospective cross-sectional study reviewed the medical records of 167 patients diagnosed with osteomyelitis admitted to Imam Reza Hospital, Kermanshah, Iran, between 2021 and 2022. Data on demographics, clinical features, risk factors, laboratory results, imaging findings, microbiological culture results, and treatment regimens were extracted. Patients' symptoms and complications were documented. Bone biopsies or tissue samples were cultured to identify pathogens, and PCR or serological tests were used in cases of opposing cultures. Statistical analysis was performed using SPSS version 25 to evaluate demographic and clinical associations.

Results: Among 167 cases, 95 were male (56.9%), and the mean age was 46.4 years, with the 51-60 age group (26.9%) being most affected. Urban residents comprised 76% of cases. Key risk factors included trauma (37.1%), orthopedic procedures (29.3%), and contiguous infections such as diabetic ulcers and pressure sores (13.8%). Chronic proximal osteomyelitis (46.7%) was the predominant subtype, followed by acute proximal osteomyelitis (33.5%). Microbiological analysis identified pyogenic pathogens in 73.1% of cases, with *Staphylococcus aureus* (54.1%) being the most common, followed by *Escherichia coli* (19.7%). *Brucella spp*. and *Mycobacterium tuberculosis* were rare. Negative cultures were reported in 22.7% of cases. The most frequently involved bones were the femur (28.1%), tibia (22.1%), and lumbar vertebrae (15.0%). Pain (49.1%) and purulent discharge (38.3%) were leading symptoms, while complications included mobility restriction (49.7%) and deformity (24.6%). In 59.3% of cases, therapeutic approaches included antibiotics alone or combined with surgery. Elevated erythrocyte sedimentation rates and positive C-reactive protein levels were common findings. The in-hospital mortality rate was 4.8%.

Conclusion: This study highlights the critical need for early diagnosis and tailored interventions in osteomyelitis. It emphasizes the importance of understanding regional risk factors and microbiological profiles. The findings can guide clinicians in optimizing prevention, diagnosis, and management strategies for this challenging condition.

Keywords: Osteomyelitis, epidemiology, microbiology, risk factors, *Staphylococcus aureus*, antibiotic therapy

Abstract ID: 173
subject: Hospital-Acquired Infections

Antibacterial effects and the expression of adhesin genes among multidrug-resistant uropathogenic *Escherichia coli* following exposure to carvacrol

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Background and Aim: Urinary tract infections (UTIs) are among the most common bacterial infections globally, with uropathogenic *Escherichia coli* (UPEC) being the primary causative agent. Carvacrol, a natural phenolic compound derived from oregano and thyme, has garnered significant attention for its potent antimicrobial properties. This study investigates the antibacterial effects of carvacrol against MDR UPEC and evaluates changes in the expression of adhesin genes following exposure.

Material And Methods: MDR UPEC strains were cultured in Luria-Bertani (LB) broth and Mueller-Hinton broth (MHB) was utilized for antibacterial assays.for Antibacterial Susceptibility Testing, we determined Minimum inhibitory concentration (MIC) with using the broth microdilution method and Minimum bactericidal concentration (MBC) was identified by plating aliquots from wells with no visible growth onto LB broth to confirm bacterial death. For Gene Expression Analysis the following genes were selected for analysis: *fimH*, *papC*, and afa/dra. MDR UPEC strains were treated with sub-MIC concentrations of carvacrol for 4 hours. Total RNA was extracted using a commercial RNA isolation kit, and cDNA was synthesized for qPCR analysis.

Results: Results: The minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) of carvacrol were observed to range between 256 µg/mL and 512 µg/mL, in that order. In comparison to the control, carvacrol decreased the expression levels of fimH, papC, and afa/dra genes to 2.2, 2 and 1.8 fold respectively.

Conclusion: The exploration of herbal bioactive compounds may reveal their antibacterial and anti-virulence properties. Carvacrol demonstrated significant antibacterial activity, effectively inhibiting bacterial growth and reducing the expression of critical adhesin genes, such as *fimH*, *papC*, and afa/dra which play a pivotal role in UPEC virulence and pathogenesis. Future studies should focus on elucidating the molecular pathways through which these compounds exert their effects, exploring their synergistic potential with existing antibiotics, and evaluating their efficacy in in-vivo models.

Keywords: Uropathogenic *Escherichia coli*, herbal compounds, virulence, gene expression

Abstract ID: 164
subject: Hospital-Acquired Infections

Antibacterial effects and the expression of adhesin genes among multidrug-resistant uropathogenic *Escherichia coli* following exposure to coumarin and quercetin

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Background and Aim: Urinary tract infections (UTIs) caused by *Escherichia coli* (*E. coli*) remain a significant global health challenge, particularly due to the rise of multidrug-resistant (MDR) strains. This study investigates the antibacterial efficacy of coumarin and quercetin against MDR UPEC isolates, focusing on their ability to inhibit bacterial growth and modulate the expression of critical adhesin genes.

Material And Methods: Clinical MDR UPEC isolates were collected and characterized for antibiotic resistance profiles using CLSI-guided disk diffusion methods. Strains resistant to three or more antibiotic classes were included in the study. High-purity coumarin and quercetin were dissolved in DMSO to prepare stock solutions (10 mg/mL) and diluted to working concentrations (50–500 µg/mL).The minimum inhibitory concentration (MIC) of coumarin and quercetin was determined using the broth microdilution method in 96-well plates. Growth inhibition assays were conducted to monitor bacterial growth over time under sub-MIC concentrations of the compounds. RNA was extracted from bacterial cultures treated with sub-MIC concentrations of the compounds. cDNA was synthesized to study gene expression. Quantitative real-time PCR (qRT-PCR) was employed to measure the relative expression of critical adhesin genes (*fimH* and *papG*), normalized to 16S rRNA as a reference.

Results: The minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) of coumarin were observed to range between 128 µg/mL and 256 µg/mL, in that order. Similarly, quercetin exhibited MIC and MBC ranges of 64-128 µg/mL and 128-256 µg/mL, respectively. In comparison to the control, quercetin decreased the expression levels of *fimH* and *papG* genes to 2.6 and 1.9 fold respectively. Moreover, coumarin decreased the expression of *fimH* and *papG* genes to 2.2 and 1.6 fold respectively.

Conclusion: The exploration of herbal bioactive compounds may reveal their antibacterial and anti-virulence properties. Both compounds demonstrated significant antibacterial activity, effectively inhibiting bacterial growth and reducing the expression of critical adhesin genes, such as *fimH* and *papG*, which play a pivotal role in UPEC virulence and pathogenesis. Future studies should focus on elucidating the molecular pathways through which these compounds exert their effects, exploring their synergistic potential with existing antibiotics, and evaluating their efficacy in in-vivo models.

Keywords: Uropathogenic *Escherichia coli*, herbal compounds, virulence, gene expression

Abstract ID: 399
subject: Hospital-Acquired Infections

Identification and analysis of pathogenic genes (*traT*, *hly, aer, pap, and fimH*) in *Escherichia coli* isolates from patients at Gonabad Hospitals, Iran

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Background and Aim: Urinary tract infections (UTIs) are common bacterial infections, with *Escherichia coli* being the leading cause. This study focused on investigating the prevalence of several virulence factors and beta-lactam resistance genes in *E. coli* isolates.

Material And Methods: One hundred *E. coli* isolates were collected from UTI patients at Allameh-Bohlol Gonabadi Hospital. Polymerase chain reaction (PCR) was used to identify five pathogenic genes: *fimH, aer, pap, hly,* and *traT.*

Results: The study found the following frequencies of pathogenic genes in 85 UPEC isolates: *traT* (90%), *fimH* (80%), *pap* (81%), *aer* (92%), and *hly* (20%). These findings indicate a high prevalence of adhesion and iron acquisition genes, which play a crucial role in UPEC pathogenicity, underscoring the need for targeted therapeutic approaches.

Conclusion: The presence of pathogenic genes may contribute to the severity, progression, and spread of urinary tract infections. Therefore, identifying these genes as key factors in disease development can help improve treatment management.

Keywords: Antibiotic resistance genes, *E. coli*, pathogenic genes, polymerase chain reaction

Abstract ID: 45
subject: Hospital-Acquired Infections

Frequency of toxin -antitoxin genes in *Escherichia coli* strains producing extended-spectrum beta-lactamases isolated from blood cultures of patients with leukemia

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Background and Aim: Introduction Bloodstream infections (BSI) are a major problem for leukemia patients undergoing chemotherapy as their weakened immune systems make them more susceptible to complications, leading to high rates of morbidity and mortality. The incidence of BSIs in cancer patients has been shown to vary between 11.8% and 33.3%, with the majority caused by Gram-negative bacteria. Toxin-antitoxin (TA) systems are present in bacteria and play an important role in the spread and development of antibiotic resistance through the maintenance of multidrug-resistance plasmids and formation the persister cells, antiphagy defense, and biofilm formation Objective: The aim of this study was to determine the frequency of toxin-antitoxin genes in *Escherichia coli* strains producing extended-spectrum extended-spectrum beta-lactamases isolated from blood cultures of patients with leukemia.

Material And Methods: Methods The study conducted in Iran from June 2021 to December 2022, isolated 67 *E. coli* strains from leukemia patients' bloodstream infections in hospitals in two different areas. Detection of ESBL producers was evaluated by phenotypic confirmatory test. The presence of toxin -antitoxin genes was examined by polymerase chain reaction (PCR).

Results: Results A total of 36 (53.7%) strains were found to be ESBL-producing strains. PCR results showed that among 36 ESBL producing strains, the frequency of *maze* 26(72.2%), *ccdAB* 25(69.4%), *relB* 28(77.7%), *mqsR* 12(33.3%) and *hipA11*(30.5%) genes.

Conclusion: Conclusion Our research emphasizes the continued need to observe how common and the specific qualities of *E. coli* bloodstream infections in patients with leukemia or blood disorders, so that effective antimicrobial treatment and measures for infection control can be implemented.

Keywords: *Escherichia coli*, blood stream Infections (BSIs), leukemia, toxin-antitoxin (TA) systems, extended-spectrum beta-lactamases (ESBL)

Abstract ID: 281
subject: Hospital-Acquired Infections

Examining the sequence of *parC* and *gyrA* genes in gene databases and determining the variable region and determining the sequence in clinical isolates infected with *Klebsiella pneumoniae*

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Background and Aim: *Klebsiella pneumoniae* is of great interest due to causing a wide range of diseases and antibiotic resistance. The aim of this study is to examine the sequence of *parC* and *gyrA* genes in gene databases and determine the variable region and determine the sequence in clinical isolates of *Klebsiella pneumoniae* in Mashhad.

Material And Methods: In this cross-sectional descriptive study, 100 isolates of *Klebsiella pneumoniae* were collected during 3 months from Imam Reza Hospital in Mashhad. Then *Klebsiella pneumoniae* strains were confirmed by standard biochemical tests. The antibiotic resistance pattern was determined by the disk diffusion method. The quinolone and fluoroquinolone resistant isolates were identified and PCR method was used to check the presence of *parC* and *gyrA* genes in these isolates. Then determining the sequence of the amplified fragment by Sanger sequencing method and finally comparing the sequences of the present study with the standard bacterial genome sequence available in the NCBI gene database and checking synonyms, similarities and also checking the variable region of the sequences together and analyzing them through BLAST online software and Chromas pro and Mega bioinformatics software were performed.

Results: The highest antibiotic resistance was related to nalidixic acid (70%) and the lowest resistance was related to amikacin (59%). The results of examining synonyms and sequence similarity between isolates sequenced for *parC* and *gyrA* genes showed that the sequences have different variable regions. And to check the similar regions of the sequence, the sequences were complementary to each other and the variable region of the sequences was investigated.

Conclusion: The results of the present study showed that mutations in *parC* and *gyrA* genes are closely related to quinolone and fluoroquinolone resistance regions. The increase in the prevalence of resistance to quinolones and fluoroquinolones among isolated *Klebsiella pneumoniae* bacteria indicates the need for infection control programs. From the examination of synonyms and the variable region of the sequences of the present study with the sequence recorded in the NCBI gene database in different regions and also in different years, we conclude that 3 mutations in the regions 148, 192 and 210 in the DNA sequence of the parC gene and 2 mutations in regions 49 and 258 in DNA sequence of gyrA gene occurred in organic bases in the sequences of the present study.

Keywords: *Klebsiella pneumoniae*, *parC* gene, *gyrA* gene, quinolone, fluoroquinolone

Abstract ID: 144
subject: Hospital-Acquired Infections

Prevalence and antibiotic resistance patterns of opportunistic pathogenic bacteria causing hospital infections in Kurdistan province, Iran

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Background and Aim: Hospital-acquired infections (HAIs) are a significant concern worldwide, particularly due to the increasing prevalence of antibiotic resistance. This study aims to investigate the prevalence and resistance patterns of microorganisms causing HAIs in various hospitals in Kurdistan Province, Iran.

Material And Methods: A total of 248 samples were collected from various wards in seven hospitals across Kurdistan Province, including intensive care units (ICUs), surgical wards, medical wards, and pediatric wards, between 2023 and 2024. The samples included blood, urine, respiratory secretions, wound swabs, and catheter tips. Standard microbiological techniques were used for the isolation and identification of microorganisms. Antibiotic susceptibility testing was performed using the disk diffusion method according to the Clinical and Laboratory Standards Institute (CLSI) guidelines.

Results: Of the 248 samples, 225 (90.7%) yielded positive cultures. The majority of samples were isolated from wound swabs (35.8%), followed by respiratory secretions (28.7%), urine samples (20.2%), blood samples (10.0%), and catheter tips (5.3%). The highest number of samples were collected from the intensive care units (ICUs) (40.4%), followed by surgical wards (30.1%), medical wards (20.4%), and pediatric wards (9.5%). The most common microorganisms isolated were *Pseudomonas aeruginosa* (30.4%), *Staphylococcus aureus* (25.3%), *Escherichia coli* (19.8%), *Klebsiella pneumoniae* (14.9%), and *Acinetobacter baumannii* (9.6%). High resistance rates were observed against ceftazidime (77.8%), cefepime (68.9%), ceftriaxone (66.2%), cefoxitin (64.0%), ciprofloxacin (62.7%), levofloxacin (61.3%), aztreonam (58.2%), moxifloxacin (57.8%), amoxicillin-clavulanic acid (53.8%), gentamicin (52.4%), tobramycin (49.8%), and amikacin (48.4%). Imipenem and meropenem showed lower resistance rates, with 31.5% and 26.2% resistance, respectively. Piperacillin-tazobactam resistance was noted in 40.4% of the isolates. Among the macrolides, erythromycin, azithromycin, and clarithromycin showed resistance rates of 44.0%, 38.7%, and 34.7%, respectively. Doxycycline and tetracycline showed resistance rates of 31.1% and 29.3%, respectively. *Acinetobacter baumannii* was found to be the most resistant microorganism. It exhibited 100% resistance to aztreonam, ceftriaxone, and cefoxitin.

Conclusion: The study highlights a high prevalence of antibiotic resistance among microorganisms causing hospital infections in Kurdistan Province, Iran. *Pseudomonas aeruginosa* and *Staphylococcus aureus* were the most common pathogens identified. The findings underscore the need for effective infection control measures and prudent use of antibiotics to combat the rising trend of antibiotic resistance in hospital settings.

Keywords: Hospital-acquired infections; antibiotic resistance; opportunistic pathogenes; prevalence; Kurdistan province; Iran

Abstract ID: 369
subject: Hospital-Acquired Infections

Adherence to guidelines for preventing catheter-associated urinary tract infections in hospitalized patients in a tertiary teaching hospital

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Background and Aim: Urinary catheterization is a significant contributor to hospital-acquired infections. Adherence to established guidelines, such as those provided by the Centers for Disease Control and Prevention (CDC), is crucial in preventing inappropriate catheterization and reducing infection rates. This study aimed to evaluate adherence to CDC guidelines for urinary catheterization in hospitalized patients at a tertiary hospital center in 2024.

Material And Methods: A descriptive cross-sectional study was conducted to evaluate compliance with the Centers for Disease Control and Prevention (CDC) guidelines for the prevention of catheter-associated urinary tract infections (CAUTIs) among hospitalized patients at Al-Zahra Hospital. Data collection was carried out through direct patient observation and comprehensive chart review. Key variables assessed included patient demographics, clinical indications for urinary catheterization, duration of catheter retention, and adherence to guideline-based criteria. Additionally, department-specific compliance rates were analyzed to identify variations in practice patterns across different hospital units. The collected data were systematically recorded using standardized checklists, ensuring consistency and reliability in measurement.

Results: A total of 37.8% of the patients experienced urinary catheterization. The overall adherence rate to CDC guidelines was found to be 57.3%. The most common appropriate indication for catheterization was acute urinary retention or bladder outlet obstruction (15.4%) followed by Monitoring accurate urine output in critically ill patients (14.5%) and need for intraoperative urine output monitoring (11.1%) Among hospital departments, the highest adherence rates were observed in the cardiology and urology services, and the lowest were gynecology, rheumatology, plastic and vascular surgery. And the adherence in ER was only 27.8%.

Conclusion: The findings highlight a suboptimal adherence rate to CDC guidelines in urinary catheterization, emphasizing the need for targeted interventions to improve compliance. Strategic interventions can enhance adherence and subsequently reduce catheter-associated urinary tract infections.

Keywords: "Urinary tract infections", "urinary catheters", "adolescent, hospitalized"

Abstract ID: 157
subject: Hospital-Acquired Infections

High frequency of integrons and AcrAB−TolC efflux pump genes in uropathogenic *Escherichia coli* (UPEC) strains in North of Iran

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Background and Aim: UTIs are among the most widespread bacterial infections. *Escherichia coli* is a serious agent causing UTIs. Antibiotic resistance is a critical issue developing worldwide. The existence of resistance factors like integrons, from one strain to another is the dissemination of multiple resistances that are part of horizontal gene transfer (HGT). Another important factor leading to antibiotic resistance is efflux pumps which effluxes out the drugs accumulated. Therefore, the aim of this study is to investigate the frequency of class I and II integrons and the AcrAB−TolC efflux pump in uropathogenic *Escherichia coli* (UPEC) strain in Babol, North of Iran.

Material And Methods: This cross-sectional study was carried out on 155 isolates of UPEC isolated from patients with UTI in the North of Iran (Babol, Mazandaran). UPEC were confirmed based on phenotypic and genotypic tests. The antibiotic susceptibility pattern was determined by the Kirby-Bauer disk diffusion method. The frequency of integron and efflux pump genes was determined by polymerase chain reaction (PCR). SPSS 16 software was used for data analysis. The association between the presence of integrons and resistance to different classes of antibiotics was determined by Fisher's exact chi-square test. A significance level of less than 0.05 was considered

Results: PCR amplification of *int1* and *int2* genes revealed that 85.2% (132/155) and 23.2% (36/155) of isolates were positive, respectively. Moreover, 23.2% of isolates had both of *int1* and *int2* genes, simultaneously. The statistical analysis showed that the percentage of resistance to ceftazidime and meropenem among isolates containing *int1* genes was significantly higher than in isolates without *int1*. Additionally, statistical analysis showed that resistance to meropenem, amoxicillin/clavulanic acid, amikacin, and trimethoprim-sulfamethoxazole was significant among isolates with *int2*. Moreover, based on the results of PCR, 88.4%, 92.3% and 96.1% of isolates had *acrA*, *acrB* and *tolC* genes.

Conclusion: Our results show that there is a significant relationship between the frequency of integrons (*int1* and *int2*) and resistance to antibiotics such as ceftazidime, meropenem, and trimethoprim-sulfamethoxazole. Additionally, the high frequency of efflux pumps like TolC-AcrAB can play a key role in the removal of chemotherapeutic substances and antibiotics in Gram-negative bacteria.

Keywords: *Escherichia coli*, integron, efflux pump, antibiotic resistance

Abstract ID: 50
subject: Hospital-Acquired Infections

Investigation of frequency and antibiotic resistance of microorganisms causing various hospital infections in Afshar Yazd Hospital from the beginning of 1398 to the end of 1402

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Background and Aim: having sufficient information about the epidemiology of pathogens, their transmission route, resistance and antibiotic sensitivities can be effective and helpful for control and treat nosocomial infections in tie,

Material And Methods: In this study, 488 cultured samples from patients with hospital infections between 1398 to 1402 were used, and the frequency and microbial resistance of pathogens isolated from these samples were analyzed.

Results: The results showed that out of the number of 488 cultures recorded, *Escherichia coli* was the most common cause of hospital infection in 151 cases (30.94 percent), and the most common infection caused by this bacterium was urinary infection (108 cases), followed by surgical wound infections. (16 cases). *Staphylococcus aureus* was the second most abundant pathogen in this study with 65 cases (13.31%), and most of the samples containing this strain were isolated from surgical wound secretions. *Staphylococcus epidermidis* 40 cases (8.19%), *Enterobacter* 28 cases (5.73%) and *Pseudomonas aeruginosa* 27 cases (5.53%) were in the next categories. On average, in this 5-year period, 77.61% of *Escherichia coli* showed resistance to 3rd or 4th generation cephalosporins (ESBL), 49.28% to fluoroquinones, 60.3% to beta-lactamase inhibitors, and 42.97% to carbapenems. *Staphylococcus aureus* 60.58% compared to clindamycin. 65.90% were resistant to cefoxetine (MRSA) and 35.14% were resistant to vancomycin. *Pseudomonas* showed 50.38% resistance to ceftazidime, 19.52% to fluoroquinones, 45.85% to aminoglycosides and 58.66% to carbapenems.

Conclusion: *Escherichia coli* and *Staphylococcus aureus* microorganisms easily cause infections in susceptible patients. Due to the transmission of these bacteria, it is necessary to observe the principles of infection control, especially hand hygiene, disinfection of the patient's skin before procedures such as surgery, performing aseptic probing and maintaining hygiene. Perineum and effective care of catheters play a significant role in reducing contamination, control and prevention of hospital infections. Effective infection control programs can reduce the spread of nosocomial infections, mortality, and bacterial resistance to antibiotics and costs.

Keywords: INIS - *Escherichia coli* - *Staphylococcus aureus*- nosocomial infection

Abstract ID: 75
subject: Hospital-Acquired Infections

Investigation of antibacterial properties of AgFe2O4 and TiO2 nanoparticles and their nanocomposites on pathogenic bacteria

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Background and Aim: Nosocomial infections are a critical challenge in healthcare systems due to increasing bacterial resistance to antibiotics. These infections, caused by gram-negative and gram-positive pathogens, result in significant mortality and healthcare costs. Since the conventional treatments are not very effective, there is a need for new antibacterial agents. Silver ferrite (AgFe2O4) and titanium dioxide (TiO2) nanoparticles have been possess found excellent to antibacterial performance owing to their nanometer-sized dimensions, large surface to volume ratio and efficient bacterial interactions. In surface order area to improve the antibacterial effects of the nanoparticles, plant based bioactive compounds can be used to functionalize the nanoparticles. Passiflora Caerulea, a plant rich in phenolic and flavonoid compounds, is known for its antimicrobial properties. In this study, AgFe2O4 and TiO2 nanoparticles were stabilized using Passiflora Caerulea extract with the aid of silica (SiO2) to synthesize novel nanocomposites.

Material And Methods: To synthesize silver and titanium nanocomposites, Passiflora Caerulea plant extract was doped onto silver and titanium nanoparticles with the assistance of silica (SiO2). The degree of crystallinity, phase composition, microstructure, and the compositions of the samples were determined using X-ray diffraction (XRD), Fourier transform infrared (FT-IR) spectroscopy, field emission scanning electron microscopy (FESEM), and energy dispersive X-ray analysis (EDXA), respectively. Antibacterial activity was tested using the broth microdilution method against Gram-positive (*Staphylococcus aureus*, *Streptococcus pyogenes*) and Gram-negative (*Escherichia coli*, *Pseudomonas aeruginosa*) bacteria. Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC) values were determined.

Results: The results of MIC and MBC of silver and titanium nanocomposites indicated that these nanocomposites exhibited superior antibacterial activity compared to silver and titanium nanoparticles. MIC and MBC values indicated that the nanocomposites inhibited both Gram-positive and Gram-negative bacteria at lower concentrations.

Conclusion: The enhanced antibacterial activity of the nanocomposites can be attributed to the synergistic effect between the bioactive compounds in Passiflora Caerulea and the nanoscale properties of AgFe2O4 and TiO2. Silica further stabilized the nanostructure, improving its interaction with bacterial cells. These findings suggest that silver and titanium nanocomposites could serve as a novel antibacterial agent against infectious bacteria.

Keywords: Antibacterial activity, silver, titanium, passiflora caerulea, nanocomposites

Abstract ID: 237
subject: water and foodborne infections

Investigation of frequency and multidrug resistance of enterotoxigenic *Escherichia coli* pathotypes isolated from patients with diarrhea in ahwaz city

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Background and Aim: ETEC strains are one of the most important causes of diarrhea in children and travelers in developing countries. The aim of this study was to investigation of frequency and multidrug resistance of enterotoxigenic *Escherichia coli* pathotypes isolated from patients with diarrhea in Ahwaz city.

Material And Methods: In this cross-sectional study, 648 isolates were collected from patients with diarrhea referring to the teaching hospitals (Golestan and Abouzar hospitals), in Ahvaz, Iran. Then *E. coli* strains were confirmed by standard biochemical tests. PCR was used for the presence of the lt, *sta* and *stb* genes to confirm ETEC strains. The antibiotic resistance pattern of ETEC isolates was determined by the disk diffusion method.

Results: Out of 648 isolates 47/3% were *E. coli* strains confirmed by biochemical tests. The ETEC were detected in 6.1% of *E. coli* strains. PCR results revealed that 26.3% and 52.6% of ETEC isolates carried lt and *sta* genes, respectively. None of the isolates included the *stb* gene. According to the results of antibiotic susceptibility tests, the highest level of antibiotic resistance was related to ampicillin (94.7%) and 66.5% of ETEC strains were MDR.

Conclusion: The results demonstrated that it is necessary to use molecular diagnostic methods to detect and evaluate the frequency of different pathotypes of *E. coli*. Also, considering the increasing resistance to some antibiotics and wide changes in the effective spectrum of drugs and preventing the increase of drug-resistant cases, the necessity of conducting drug sensitivity tests seems very necessary.

Keywords: *E. coli*, diarrhea, ETEC, PCR

Abstract ID: 238
subject: water and foodborne infections

Determining the frequency of virulence factor in *Shigella* species isolated from shigellosis patients in Mashhad.

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Background and Aim: *Shigella* is one of the important etiological factors in causing diarrhea, especially in children. The aim of this study is to determine the frequency of virulence factor in *Shigella* species isolated from shigellosis patients in Mashhad.

Material And Methods: In this descriptive-cross-sectional study, 120 isolates of Shigella bacteria were collected from stool cultures of patients referred to teaching hospitals in Mashhad and bacterial DNA extraction was done by boiling method. Bacterial species were identified using hypothetical protein, *wbgZ*, *rfc*, and *rfpB* genes, and bacterial virulence factors were identified *IpaH, invE, ial, virF* and *sen* genes by PCR method.

Results: In this study, which was conducted by PCR method, the wbgZ gene was used to identify 85 Shigella Sonnei isolates with frequency (70.8%), the rfc gene was used to detect 33 Shigella Flexneri isolates with frequency (27.5%) and the hypothetical protein gene was used to find 2 isolates of Shigella boydii with abundance (1.6%). According to the results obtained using the rfp B gene, no isolates of *Shigella dysentery* were found. The frequency of virulence genes including IpaH, ial, invE virF and sen genes were identified in 100%, 84.1%, 75%, 70.8% and 46.4% of the isolates, respectively.

Conclusion: The present study showed that the frequency of *Shigella Sonnei* species in Mashhad as a developed city is higher than other species. Also, The results showed a high distribution of virulence genes among *Shigella* strains in our region. It seems that for different *Shigella* spp. different virulence factors contribute to pathogenesis.

Keywords: *Shigella*, diarrhea, virulence factor

Abstract ID: 389
subject: water and foodborne infections

Quantitative evaluation of toxin production and genetic investigation of *Vibrio cholerae* isolates from Iran during 2022 outbreaks

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Background and Aim: *Vibrio (V. cholerae)*, a natural inhabitant of aquatic environments, is a major cause of diarrheal diseases. This study investigates the genetic factors involved in the virulence of *V. cholerae* isolates obtained from cholera outbreaks in Iran in 2022.

Material And Methods: A total of 43 *V. cholerae* isolates were obtained from the archives of the Bacteriology Department, Tarbiat Modares University. The identity of the isolates was confirmed using culture, serological, and molecular methods. Expression of virulence genes involved in toxin production (*ctxB* and *tcpA*) and hyaluronidase (*hlyA*) was assessed using Comparative Real-Time qPCR. Genetic diversity was analyzed using ERIC-PCR (*Enterobacter*ial Repetitive Intergenic Consensus Polymerase Chain Reaction).

Results: All isolates were identified as *V. cholerae* El Tor. Expression of *ctxB* and *sxt* genes relative to 16s rRNA gene expression ranged from -8 to 2.5 for *ctxB* and -3.5 to 1.9 for *sxt*, while *tcpA* gene expression varied from 10.8 to 13.2 among the isolates. ERIC-PCR results showed no genetic diversity among the isolated *V. cholerae* El Tor, indicating that all isolates were derived from a pandemic strain.

Conclusion: The findings reveal no significant genetic diversity in *V. cholerae* isolates from recent outbreaks. This underscores the need for continuous monitoring and appropriate antibiotic management strategies for effective cholera control in Iran.

Keywords: *V. cholerae*, antibiotic resistance, virulence genes, epidemiology, ERIC-PCR

Abstract ID: 5
subject: water and foodborne infections

Molecular surveillance and antimicrobial resistance profile of bacterial contamination in pastries of Iranian confectioneries: A public health concern

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Background and Aim: Microbial contamination in food product such as pastries, poses a significant public health concern due to the potential risks of foodborne infection and outbreak, Therefore, to prevent these infections, it is essential to investigate the frequency and extent of microbial contamination as well as the level of drug resistance in pastries. Due to this issue, our study aimed to assess the microbial diversity, the drug susceptibility patterns of microbial pollutants in pastry shops in Markazi province, Iran.

Material And Methods: The study involved collecting 120 pastries samples from 30 pastry shops in Markazi province, Iran. The isolates were identified using a series of biochemical, phenotypic, and molecular assay, including specific PCR and 16S rRNA gene sequencing. Drug susceptibility testing (DST) was performed by using kirby-bauer method according to the CLSI 2023 guidelines.

Results: A total of 56 isolates (46.66%) were recovered from 120 pastries samples, The most prevalent species isolated in the current study were *S. aureus* 12 isolates (21.43%), M. luteus7 isolates (12.5%), *E. coli* 7 isolates (12.5%), S. warneri 6 isolates (11.12%), 6 isolates of S. succinus (11.12%), B. cereus 5 isolates (10.7%), Nocardia 4 isolates (7.15%), *K. pneumoniae* 3 isolates (5.35%), *S. epidermidis* 3 isolates (5.35%), and *E. faecium* 3 isolates (5.35%). The isolates showed the most sensitivity to imipenem and trimethoprim-sulfamethoxazole and the least sensitivity to erythromycin and tetracycline. The AST showed that 7 isolates of *S. aureus* were MRSA, 3 isolates of *E. coli* and, 2 isolates of *K. pneumoniae* were identified as ESBL.

Conclusion: In conclusion, the results of the current study showed that the microbial contamination of pastries produced in confectionaries of Markazi province were not in standard ranges. These problems may be related to fecal contamination of pastries or lack of hygiene by handlers and it is urgent to develop the standards of hygiene of food handling techniques and aseptic pastry producing in confectioneries.

Keywords: Pastries, microbial pollution, DST, 16SrRNA

Abstract ID: 47
subject: water and foodborne infections

Predictive modeling of infection risks based on water quality and microbial sensor data

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Background and Aim: This study presents a machine learning-based decision support system to predict microbial infection risks in water quality monitoring, with a focus on a case study in Iran. The dataset includes microbial concentrations such as Total Coliforms, *E. coli*, and Fecal Streptococci, along with key water quality parameters like pH, turbidity, and temperature. The risk levels—categorized as Low, Moderate, or High—were determined based on defined thresholds for microbial and water quality parameters. Understanding the relationships among microbial loads and water quality indicators is critical for effective water quality management and infection risk mitigation.

Material And Methods: Data analysis involved feature normalization, statistical summarization, and correlation studies to identify the relationships among microbial loads and water quality indicators. A Random Forest ensemble model was developed and trained using an 80-20 split for training and testing. The model's performance was validated through a confusion matrix and feature importance analysis. Visualizations, including a feature importance plot, confusion matrix, and correlation heatmap, were employed to provide insights into the system's decision-making process. Microbial threshold analysis was also conducted to understand the average levels associated with different infection risks.

Results: The Random Forest model achieved a remarkable accuracy of 100% on the test set. Feature importance analysis revealed that Total Coliforms contributed the most (51.94%) to the infection risk prediction, followed by Fecal Streptococci (24.25%) and *E. coli* (16.22%), while pH, turbidity, and temperature showed relatively lower contributions. The confusion matrix indicated correct classifications of 63 Low-Risk, 21 Moderate-Risk, and 116 High-Risk instances. The heatmap highlighted strong correlations between microbial concentrations and infection risks, emphasizing the dominance of microbiological parameters over physicochemical ones.

Conclusion: This machine learning framework offers a robust tool for infection risk assessment, ensuring timely interventions in water quality management. The approach, tailored to the case study in Iran, showcases the potential of integrating microbial data and machine learning in environmental health monitoring.

Keywords: Machine learning; water quality monitoring; microbial infection risks; random forest; environmental health.

Abstract ID: 43
subject: water and foodborne infections

Occurrence of abortion caused by *Listeria monocytogenes* and identification of associated risk factors in dairy cattle

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Background and Aim: *Listeria monocytogenes*, a ubiquitous gram-positive bacterium, can survive and multiply within host cells. Listeriosis can involve in the infections of uterus, blood, brain and spinal cord, gastrointestinal tract, mammary glands, and eyes. Infections of the uterus can result in fetal death, newborn infections, and pregnancy loss. Contaminated silage is believed to be a major source of cattle listeriosis. L. monocytogenes can be shed by livestock and contaminate milk, which may enter the food production chain and potentially pose a health risk to humans. Diagnosis and control of the disease in food animals and their products is crucial to eliminate the disease in human. The current study investigated L. monocytogenes in abortion cases and the associated risk factors were evaluated.

Material And Methods: The whole fetuses which were collected from 15 aborted cattle were sent to the laboratory. DNA was extracted from fetal tissues and abomasal fluid using commercial DNA extraction kit (CinaGen). The samples were examined by polymerase chain reaction using primers recommended by WOAH.

Results: L. monocytogenes positive amplified products showed band 730 bp which was visible in 2 fetuses (13.3%).

Conclusion: Identification of *Listeria* in the studied fetuses highlights the importance of the bacterium in abortion cases. However, this pathogen is neglected in cattle and agents such as Leptospira, Mycoplasma, and Neospora are commonly considered to study in bovine abortion. Given the importance of silage quality in the occurrence of listeriosis, and considering the poor quality of the silage in our study due to the presence of mold and high aflatoxin levels, a *Listeria*-induced abortion was not unexpected. Improved herd health, adequate nutrition, and appropriate silage storage, can prevent the disease and reduces the risk of bacteria entering the human food chain.

Keywords: Abortion, cattle, *Listeria monocytogenes*, PCR, zoonoses.

Abstract ID: 141
subject: water and foodborne infections

Prevalence of *Listeria Innocua* in meat-based products around the world: A meta-analysis

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Background and Aim: The prevalence of foodborne infections is increasing due to non-compliance with hygiene standards in food preparation facilities and the resistance of certain species, such as *Listeria*, to disinfectants, which has arisen from excessive use of these substances. Therefore, epidemiological studies examining the prevalence of *Listeria* in various food products can assist health professionals in developing and implementing innovative and improved public health strategies in the future. This study features a meta-analysis on the prevalence of *Listeria Innocua* in different meat products worldwide

Material And Methods: In this study, PubMed, Web of Science, Scopus, and Google Scholar were systematically searched using the relevant syntax. Initially, a total of 1133 articles were included in the study at first. Finally, a total of 66 articles met our inclusion criteria and were selected for our study

Results: according to our results, the prevalence of total *Listeria Innocua* cases was found to be 4.42% (Cl=3.467 to6.413).

Conclusion: The significance of *Listeria* isolates in food products highlights the need for strict regulations and the necessity for more epidemiological studies involving larger sample sizes.

Keywords: *Listeria Innocua* , prevalence,, food

Abstract ID: 403
subject: water and foodborne infections

The relationship between anemia, thrombocytopenia, and *Helicobacter pylori* infection

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Background and Aim: *Helicobacter pylori* infection is a prevalent condition that affects both children and adults globally. This infection is linked to various blood disorders, including iron deficiency anemia, immune thrombocytopenia, vitamin B12 deficiency, and mucosa-associated lymphoid tissue lymphoma. The aim of this study was to investigate the relationship between anemia, thrombocytopenia, and *H. pylori* infection.

Material And Methods: In this cross-sectional study, 300 individuals suspected of being infected with *H. pylori* were tested for Anti-*H. pylori* IgG at medical diagnostic laboratories in Gonabad city in 2019. A complete blood count (CBC) test was also performed, and the data were analyzed using SPSS software version 16.

Results: The study included 300 patients (54.2% male, 45.8% female) with an average age of 38.64±12.87 years. Among those infected with *H. pylori*, the prevalence of anemia and thrombocytopenia was 55.3% and 5.6%, respectively, with no significant difference compared to the non-infected group. A statistically significant relationship was found between mean age and *H. pylori* infection (P=0.001), with 42.5% of cases showing a positive antibody titer (>12 u/ml). No significant differences were observed in CBC parameters or blood types between infected and non-infected patients.

Conclusion: The results suggest that *H. pylori* infection is associated with age but not with hematological abnormalities like anemia or thrombocytopenia. Biochemical and hematological assessments are recommended for a thorough evaluation of *H. pylori* infection. Further research is needed to explore potential connections between *H. pylori* and other systemic health factors.

Keywords: *Helicobacter pylori*, anemia, thrombocytopenia, *H. pylori* infection

Abstract ID: 127
subject: water and foodborne infections

Identification of *Escherichia fergusonii* in broiler meat, North Khorasan Province, Iran

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Background and Aim: While having serious implications for the health of domestic animals, *Escherichia fergusonii* has not been fully studied, which has long been recognized for its role in animal health and production. Recently, *E. fergusonii* infection has been associated with hemolytic uremic syndrome (HUS) and acute kidney injury in humans, indicating the potential public health importance of this emerging pathogen. In recent years, the high levels of resistance observed in *E. fergusonii* have received special attention worldwide. Understanding the prevalence and resistance patterns of *E. fergusonii* is crucial for effective disease management in domestic animals and antimicrobial surveillance.

Material And Methods: In this study, a total of 40 samples of broiler products, including wings, drumsticks and whole packaged chickens, were sampled in North Khorasan Province. For the isolation of *Escherichia fergusonii*, MacConkey agar and selective adonitol citrate agar were used. Lactose-negative and adonitol-positive isolates were molecularly examined as possible *E. fergusonii*. All confirmed *E. fergusonii* isolates were subjected to antimicrobial susceptibility testing.

Results: *E. fergusonii* was detected in 8 (20%) of the 40 samples examined using PCR. Antimicrobial susceptibility testing showed that all isolates were susceptible to ceftazidime, while they were highly resistant to florfenicol, tetracycline, and amoxicillin. In addition, all positive *E. fergusonii* isolates showed multidrug resistance.

Conclusion: This study presents the status of the antimicrobial resistance pattern of *E. fergusonii* isolates in poultry feedstuffs of North Khorasan province. Given the numerous reported cases of this bacterium causing disease in humans, further research is necessary to understand the dynamics of transmission and clinical consequences in poultry and public health settings.

Keywords*: E. fergusonii*, antimicrobial resistance, North Khorasan Province

Abstract ID: 24
subject: water and foodborne infections

Impact of *Helicobacter pylori*-derived outer membrane vesicles on inflammation, immune responses, and tumor cell migration in breast cancer through the Snail/B-catenin pathway

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Background and Aim: Background: Breast cancer remains a significant global health concern, with challenges in treating advanced stages necessitating the exploration of novel therapeutic approaches. Bacterial outer membrane vesicles (OMVs) have shown promise in cancer immunotherapy by targeting cancer cells and modulating immune responses. This study investigated the effects of *Helicobacter pylori*-derived OMVs on the activation of the Snail/β-Catenin gene cascade in regulating inflammation and cell migration in a mouse model of breast cancer.

Material And Methods: The OMVs were extracted from the culture of *H. pylori* strain 26695 (ATCC 700392) using ultracentrifugation. In the mouse model, the vesicles were injected intraperitoneally into Balb/c mice with breast tumors. Tumor growth was assessed through histological examination of tumor samples. IgA and IgG antibodies were measured using ELISA. The expression of E-cadherin and vimentin proteins was evaluated by immunohistochemistry, and real-time PCR was used for vimentin, Snail, α-SMA, and β-catenin in serum samples from the different groups.

Results: Results: The OMV treatment led to a significant increase in the expression of α-SMA, β-catenin, Snail, and vimentin genes, indicating a potential induction of epithelial-mesenchymal transition and enhanced cancer cell growth. Additionally, a decrease in vimentin expression and an increase in E-cadherin expression were observed, suggesting inhibition of cell migration. The study also revealed alterations in systemic IgA and IgG antibody levels, indicating potential immunomodulatory effects of OMVs.

Conclusion: Conclusions: These findings highlight the therapeutic potential of OMVs derived from *H. pylori* in breast cancer treatment by targeting gene cascades involved in cancer progression and modulating immune responses.

Keywords: Breast cancer, *Helicobacter pylori*, inflammation, membrane vesicles, neoplasm metastasis

Abstract ID: 338
subject: water and foodborne infections

Toxic genes and antibiotic resisiance petterens in Vibrio. Parahaemolytticus isolates from caugh fish of Caspeian Sea

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Background and Aim: *Vibrio parahaemolyticus* (*V. parahaemolyticus*) is a marine bacterium and a major cause of foodborne diseases. Therefore, our study aimed to determine the frequency of toxin-producing genes and antibiotic resistance patterns in *V. parahaemolyticus* isolates obtained from fish caught in the Caspian Sea.

Material And Methods: In a descriptive cross-sectional study, 220 fish samples, including 4 species of fish (Rutilus kutum, Mullet, Carp, Perch) were collected from the Caspian Sea. The samples were enriched, and cultured to bacteriological and biochemical examination media. The isolates were molecularly confirmed by the 16srRNA flagella specific gene of *V. parahaemolyticus* then subjected to antimicrobial susceptibility testing by disk-diffusion method, and determination of three virulence genes (*toxR, tdh*, and *trh* genes) were investigated by PCR

Results: In total, 40 (18.1%) of fish samples were contaminated with *V. parahaemolyticus*. All 40 confirmed isolates possessed the *toxR* gene and 29 (72.5%) of them had the *tdh* gene, whereas none of them had the *trh* gene. Most of the isolates were more sensitive to ciprofloxacin (97.5%), chloramphenicol (92.5%), and resistance to amoxicillin (95%) and doxycycline (95%).

Conclusion: The results of present study provide very clear and valuable information about the microbial contamination of fish caught in the Caspian Sea. The high prevalence of *V. parahaemolyticus* in seafood and multidrug-resistant isolates detected in this study could pose a potential risk to human health and hence appropriate control methods should be in place to minimize the potential contamination.

Keywords: *Vibrio parahaemolyticus*; marine environment; seafood-borne illness; virulence genes

Abstract ID: 270
subject: emerging and re-emerging diseases

The role of influenza vaccination in reducing viral shedding: Implications for zoonotic disease control and public health

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Background and Aim: Avian influenza (AI), particularly the H9N2 strain, poses a significant threat to both poultry health and public safety, especially in rural communities where poultry farming is prevalent and humans have close contact with birds. This study highlights the critical role of vaccination in mitigating the spread of this virus and emphasizes the importance of using locally developed vaccines.

Material And Methods: The research evaluated the efficacy of two inactivated oil emulsion vaccines against H9N2 in broiler chickens.

Results: The findings demonstrated that unvaccinated birds exhibited significantly higher levels of viral replication and shedding compared to those vaccinated with an Iranian vaccine. Notably, no viral RNA was detected in the trachea or feces of chicks vaccinated with the Iranian vaccine, indicating its superior effectiveness in preventing viral spread. In contrast, some viral presence was noted in birds vaccinated with an imported vaccine, underscoring the potential advantages of using vaccines tailored to local strains. The implications of these findings are particularly relevant for rural areas where poultry farming is common. In such settings, effective vaccination can significantly reduce the risk of avian influenza transmission from infected birds to humans. This is crucial for protecting public health, especially in communities where people frequently interact with poultry. Moreover, Iranian vaccines, which are developed from local H9N2 isolates, are better positioned to prevent virus transmission from infected birds. By effectively controlling viral shedding, these vaccines contribute to reducing the overall incidence of avian influenza outbreaks in both poultry and human populations.

Conclusion: his highlights the need for continued investment in local vaccine development and implementation as part of comprehensive strategies to enhance public hea Ward MP, et al. 2023. The role of vaccination in controlling avian influenza outbreaks: A systematic review and meta-analysis of field studies.

Keywords: Avian influenza, oil emulsion vaccine, H9N2 isolates, Humans, local vaccine

Abstract ID: 339
subject: emerging and re-emerging diseases

Utilization of *E. coli* (xl1-blue) and the ptz57R/T plasmid system for the specific targeting of the H9N2 subtype influenza protein matrix.

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Background and Aim: The primary objective of the present research project is to meticulously and systematically isolate a specific segment of the gene responsible for encoding the M1 protein, which is associated with the H9N2 strain of the influenza virus. The M1 protein is acknowledged as one of the highly conserved proteins found across various strains of influenza viruses, highlighting its significance and relevance within the field of virology.

Material And Methods: Following the propagation of the influenza virus in embryonated chicken eggs, RNA was extracted from the viral samples collected during this experimental procedure. Subsequently, the specific nucleotide sequence corresponding to the *M1* gene was amplified using the reverse transcription polymerase chain reaction (RT-PCR) technique. Following the amplification of the sequence, a comprehensive purification process was conducted to ensure its integrity and quality. The purified sequence was subsequently cloned into the plasmid vector ptz57R/T, which is specifically designed for such applications. Post-cloning, the resulting product was propagated and further purified using the *Escherichia coli* strain, particularly the xl1-blue variant, recognized for its efficacy in cloning endeavors.

Results: The results of this study clearly demonstrate that the *E. coli* (xl1-blue) strain, in conjunction with the ptz57R/T plasmid system, can be effectively utilized for the isolation, cloning, and successful amplification of genes directly associated with influenza viruses.

Conclusion: This capability provides critical insights and advancements in the field of viral genetics, thereby deepening our understanding of the genetic mechanisms that govern the behavior and pathology of the influenza virus

Keywords: Influenza A, M1 protein, ptz57R/T plasmid, cloning

Abstract ID: 413
subject: Other related topics

Evaluating the antimicrobial effects of mouse adipose-derived mesenchymal stem cells encapsulated in collagen-fibrin hydrogel scaffolds on *Bacteroides fragilis* wound infection in vivo

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Background and Aim: Anaerobes are the causative agents of many wound infections. *Bacteroides fragilis* is the most prevalent endogenous anaerobic bacteria that leads to a wide range of infections and wound infections. Considering the difficult treatment of anaerobic infections and on the other hand, the high rate of antibiotic resistance among *B. fragilis* strains, non-antibiotic treatments should be taken into consideration for such infections. Thus, this study aimed to assess the antibacterial effect of mouse adipose-derived mesenchymal stem cells (MSCs) encapsulated in collagen-fibrin hydrogel scaffolds on *B. fragilis* wound infection in the animal model.

Material And Methods: The stem cells were extracted from mouse adipose tissue and confirmed by surface markers using flow cytometry analysis. The possibility of differentiation of stem cells into osteoblast and adipocyte cells was also checked. The extracted stem cells were encapsulated in the collagen-fibrin scaffold. *B. fragilis* wound infection was generated in rats, and after 24 h , collagen, and fibrin-encapsulated MSCs were applied to dress the wound. One week later, a standard colony count test monitored the bacterial load in the infected rats. The statistical analysis was performed using SPSS Version 26.

Results: MSCs were characterized as positive for CD44, CD90, and CD105 markers, negative for CD34 markers, and able to differentiate into osteoblast and adipocyte cells. The results showed that adipose-derived MSCs encapsulated with collagen and fibrin scaffolds had ameliorating effects. It is also shown that adipose-derived MSCs with a collagen scaffold (54 CFU/gr) have a greater effect than adipose-derived MSCs with a fibrin scaffold (97 CFU/gr). The combined collagen-fibrin scaffold demonstrated the highest colony count reduction (the bacteria load down to 29 CFU/gr) in the wound infection.

Conclusion: Due to the increase in antibiotic resistance among bacteria, the use of non-antibiotic treatments is attracting researchers' attention, and cell therapy is one of these methods. The present study confirms that using the collagen and fibrin scaffold with the mouse adipose-derived MSCs is a promising alternative treatment of *Bacteroides fragilis*

Keywords: Mesenchymal stem cell, *Bacteroides fragilis*, collagen scaffold, fibrin scaffold, wound infection

Abstract ID: 202
subject: Other related topics

A comparative study on the synergistic effects of thymol/ceftazidime against *Klebsiella pneumoniae* and *Staphylococcus epidermidis*

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Background and Aim: This study aims to compare the synergistic antimicrobial effects of thymol/ceftazidime on *Klebsiella pneumoniae* and *Staphylococcus epidermidis*.

Material And Methods: Antimicrobial effects of thymol/ceftazidime were performed first individually and then combined on *K. pneumoniae* ATCC 100031 and *S. epidermidis* ATCC 1457 by the MIC-MBC method. Therefore, the antimicrobial effects of the compounds that had a synergistic impact were performed on clinical strains using the MIC-MBC method. The identification of chemical bonds, functional groups, and molecular interactions of the mentioned compound was investigated using an FT-IR device. Checkered method, biofilm inhibition on *K. pneumoniae* ATCC 100031 and *S. epidermidis* ATCC 1457, and cytotoxicity investigation on red blood cells (RBCs) by hemolysis and human skin fibroblast cells (Ffk) by MTT method were performed. Finally, the results of the tests were compared between the two bacteria.

Results: The results of this study showed that the antimicrobial effects of the thymol/ceftazidime (4/2 µg/ml) were on *K. pneumoniae* better than on *S. epidermidis* (16/2 µg/ml) in both clinical and ATCC strains. In the examination with the FT-IR device, it had bonds of OH carbohydrates proteins, polyphenols, C=O Amide I band, C-O-C polysaccharide, C-N amide III band, but one band named C=C conjugated, C?C in compound showed the connection between thymol with ceftazidime. The biofilm inhibition effects of thymol/ceftazidime on *K. pneumoniae* ATCC 100031 (58.44%) were better on *S. epidermidis* ATCC 1457 (49.09%). The cytotoxicity of synergistic compounds on RBCs and human Ffk cells was not different and was lower than that of Triton X-100.

Conclusion: Considering the antibiotic resistance of ceftazidime in the treatment of diseases caused by *K. pneumoniae* and *S. epidermidis*, thymol/ceftazidime showed better antimicrobial and anti-biofilm effects in *K. pneumoniae* than *S. epidermidis* in this study. After further studies, this compound can be used as a new drug in patients.

Keywords: *Klebsiella pneumoniae*, *Staphylococcus epidermidis*, thymol, ceftazidime, synergistic

Abstract ID: 426
subject: Other related topics

Multidrug-resistant *tuberculosis* in Iran: a multicenter study

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Background and Aim: The worldwide incidence of multi-drug-resistant tuberculosis (MDR-TB) is rapidly increasing, and it has emerged as a pressing public health issue in Iran. Nevertheless, there is a scarcity of up-to-date research on the prevalence of MDR-TB in individuals with pulmonary TB in the country. In this cross-sectional study, we gathered a total of 1216 respiratory samples, each corresponding to a unique patient, from five distinct regional TB laboratories in Iran.

Material And Methods: We identified clinical isolates as *Mycobacterium tuberculosis* using the IS6110-based PCR assay and Xpert MTB/RIF. Drug susceptibility testing (DST) was conducted using the conventional proportion method

Results: Out of the collected specimens, 448 tested positive for *M. tuberculosis*. Among these isolates, 445 (99.4%) exhibited susceptibility to the tested drugs, while 3 (0.6%) were found to be MDR.

Conclusion: The findings from this recent study indicate that the prevalence of MDR in Iran stands at 0.6%. The absence of recently approved treatment protocols in various regions of Iran, along with inadequately equipped laboratories lacking DST capabilities, could contribute significantly to the rise in TB/MDR-TB prevalence in Iran. Therefore, the implementation of enhanced treatment management strategies and the adoption of innovative technologies are essential steps towards improving the current situation.

Keywords: *Tuberculosis*, MDR ,drug resistance, Iran

Abstract ID: 22
subject: Other related topics

Effect of chitosan nanocomposites incorporated with *Campylobacter jejuni* supernatant on the expression of genes associated with colorectal cancer

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Background and Aim: Colorectal cancer (CRC) is one of the most common cancer worldwide, with a high mortality rate; hence, the use of the alternative therapeutic methods is necessary. The purpose of this research is to evaluate of the effect of chitosan nanocomposite loaded with *C. jejuni* supernatant (CS-Cj sup NP) on the expression of genes involved in colorectal cancer

Material And Methods: CS-Cj sup NP was fabricated by ionic gelation method and characterized scanning electron microscope and dynamic light scattering techniques. The release of protein and entrapment efficiency (EE) of CS-Cj sup NP were assayed via BCA assay kit. After investigation of the viability of Caco-2 cells against CS-Cj sup NP using MTT assay, the expression of genes of CEA, TLR4, Caspase9, and PTEN on Caco-2 cell were evaluated via real-time PCR method

Results: The particle size and zeta potential were recorded 159.7± 5.0 nm and + 4.5 mV, respectively. Besides, protein released from CS-Cj sup NP was 82% at pH of 6.8 after 48 h with EE of 74.62 %. CS-Cj sup NP was not significant cytotoxicity on Caco-2 cells. Our finding indicated that CS-Cj sup NP effectively upregulate the expression both of the Caspase9 and PTEN genes by to 55.7 and 1.8- fold, respectively, while significantly decreased CEA and TLR4 genes expression by to 0.14 and 0.138- fold, respectively

Conclusion: In conclusion, CS-Cj sup NP with significant anticancer properties may be considered as an alternative option for CRC treatment

Keywords: Chitosan, *Campylobacter jejuni*, colorectal cancer

Abstract ID: 11
subject: Other related topics

Antimicrobial and antitoxin effect of fatty acids extracted from yeast *Yarrowia lipolytica*

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Background and Aim: Fungal pathogens cause plant, animal, and human diseases. One way to combat them is to examine the effect of metabolites of microorganisms with GRAS status. This research investigates the inhibitory effect of fatty acids produced by *Yarrowia lipolytica* on toxicogenic fungi.

Material And Methods: First, strains of Aspergillus flavus, *Yarrowia lipolytica*, and *Fusarium graminearum* were prepared and cultivated. Then, *Yarrowia lipolytica* was cultivated in the bed of sweet almond, bitter almond, and castor to produce fatty acids and GC-mass determined the production rate of stearic acid and oleic acid. The growth of *Aspergillus flavus* and *Fusarium graminearum* fungi was also investigated by spore counting with a Neubauer chamber and light absorption measurement with a spectrophotometer. Then, by HPLC, the effect of stearic acid and oleic acid on the production of aflatoxin B1 and zearalenone by fungi was investigated, and by determining the MIC and MFC, the inhibitory effect of these fatty acids on the growth of fungi was investigated. Finally, the statistical analysis of the data was done using the Taguchi test (Minitab 20 software).

Results: *Yarrowia lipolytica* was able to produce stearic acid and oleic acid in the bed of sweet almond, bitter almond, and castor pulp. By increasing the concentration of fatty acids in the fungal culture medium, the growth rate of *Aspergillus flavus* and *Fusarium graminearum* fungi and the production of aflatoxin B1 and ziralenone by them decreased and the effective inhibitory properties of these fatty acids were determined. Optimum conditions of non-production of aflatoxin B1 and zearalenone were also identified.

Conclusion: *Yarrowia lipolytica* yeast can be used for the economical production of fatty acids and fatty acids can be used to inhibit the growth of fungi and their toxins with high efficiency, minimal side effects, and cost. These results opened new doors to agriculture, animal husbandry, food, medicine, etc. industries.

Keywords: *Y. lipolytica*, *A. flavus*, *F. graminearum*, Stearic Acid, oleic acid

Abstract ID: 184
subject: Other related topics

Investigating the impact of alfalfa root extract on *Streptococcus mutans*, a primary contributor to tooth decay, in comparison to chlorhexidine

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Background and Aim: Tooth decay ranks one of the most prevalent infectious diseases, and mouthwashes are crucial in combating it. Given the adverse effects of chemical mouthwashes and the growing popularity of herbal alternatives, this study aims to investigate the impact of Alfalfa root extract on *Streptococcus mutans* (*S. mutans*), the primary bacteria responsible for tooth decay. The study's findings are compared with chlorhexidine, a standard chemical mouthwash.

Material And Methods: Alfalfa roots were processed and extracted using the maceration technique. The impact of this extract on the proliferation of *S. mutans* was assessed through both Disk Diffusion and Well Diffusion assays, with chlorhexidine serving as a standard for comparison. Subsequently, this study determined the alfalfa extract's Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC).

Results: Disks saturated with the extract and wells filled with the extract produced a clear zone indicating bacterial inhibition, effective up to concentrations of 62.5 mg/ml and 31.25 mg/ml, respectively. The zone of inhibition was more significant than that produced by chlorhexidine at concentrations up to 125 mg/ml. The MIC and MBC of the extract were determined to be 31.25 mg/ml and 62.5 mg/ml, respectively.

Conclusion: Alfalfa root extract appears to be a promising foundation for creating an effective, low-cost mouthwash to combat dental caries with minimal side effects. Further clinical studies are necessary to fully understand this extract's impact on tooth decay.

Keywords: *Streptococcus mutans*, mouthwashes, chlorhexidine, medicago sativa, alfalfa, dental caries

Abstract ID: 68
subject: Other related topics

Anti-cancer efficiency chitosan nanoparticles loaded with cell free supernatant of *Lactobacillus Acidophilus* on the expression of genes involved in colorectal cancer

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Background and Aim: Colorectal cancer (CRC) is the second most common cause of cancer-related fatalities worldwide. So, CRC management is essential by using the novel therapeutic approach. This study aimed to evaluation of the anti-cancer efficiency of chitosan nanoparticles conjugated with the cell free supernatant of the *Lactobacillus Acidophilus* (CTNP-L.a-sup) on genes involved in colorectal cancer.

Material And Methods: The novel nanodrug was prepared by ionic gelation procedure and analyzed using scanning electron microscopy and dynamic light scattering methods. Protein released and EE (encapsulation efficiency) of CTNP-L.a-sup were evaluated using BCA assay. Following evaluation of the cytotoxicity effect of CTNP-L.a-sup on Caco-2 cells via MTT assay, TGF-β, TGF-α, PTEN, and Caspase9 gene expression was assayed by real time PCR method.

Results: Our data revealed that the size of CTNP-L.a-sup was 478.6 nm and zeta potential was -8.9 mV with an appropriate morphology. Protein released from CTNP-L.a-sup and EE% were equated 76% and 74.6%, respectively. CTNP-L.a-sup was not cytotoxicity effect on Caco-2 cells. CTNP-L.a-sup could cause a significant decrease in the expression of TGF-α, and TGF-β oncogenes by to 0.79 and 0.16 fold, respectively, while led to a significant increase in PTEN and Caspase9 gene expression by to 42.19 and 114.39 fold, respectively.

Conclusion: So, the innovate nanodrug can be as an alternative therapeutic option for combat to CRC, potentially enhancing the life expectancy of CRC patients.

Keywords: Anti-cancer, chitosan nanoparticle, cell free supernatant, colorectal cancer, *Lactobacillus Acidophilus*

Abstract ID: 160
subject: Other related topics

Exosomes as nano-carries for *Helicobacter pylori* urease delivery and its effects on hepatic stellate cell autophagy pathway

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Background and Aim: Autophagy is defined as a normal cell function that can stimulate intracellular defense mechanisms against pathogens as a part of the innate immune response. *H. pylori* extra-gastric disease is a health concern worldwide and outer membrane vesicles (OMVs) are known as cargo for *H. pylori* virulence factors delivery.

Material And Methods: In this study, four non-repetitive clinical strains of *H. pylori* were obtained and their EVs were isolated with ultra-centrifugation and co-cultured with hepatocytes. Then, exosomes were extracted from manipulated hepatocyte and their protein fingerprints were analyzed using liquid chromatography coupled with tandem mass spectrometry (LC-MS/MS) analysis. Purified exosomes were incubated with hepatic stellate cells (HSCs) for autophagy-related markers to determine. mTOR, AKT, PI3K, Beclin-1, Atg12, Atg16, and LC3B gene expression were investigated by real-time PCR, and protein expression was confirmed with western blotting.

Results: Our findings revealed *H. pylori* strains secreted round shape nano-vesicles, co-culturing of *H. pylori* OMVs with hepatocytes modified their exosome contents, and *H. pylori* urease A was discovered in exosomes. Infected hepatocytes-derived exosomes changed the morphogenesis of normal HSCs and modified exosomes have been identified as an autophagy suppressor. Discussion: In the current study, we found the importance of exosomes as cargo in *H. pylori* virulence factors delivery and liver autophagy process suppression.

Conclusion: In the current study, we found the importance of exosomes as cargo in *H. pylori* virulence factors delivery and liver autophagy process suppression.

Keywords: *Helicobacter pylori*, outer membrane vesicle, exosome, autophagy, hepatic stellate cell

Abstract ID: 148
subject: Other related topics

Comparative investigation of synergistic effects of thymol/cefotaxime on *Klebsiella pneumoniae* and *Staphylococcus epidermidis*

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Background and Aim: This study compares the synergistic antimicrobial effects of thymol/cefotaxime on *Klebsiella pneumoniae* and *Staphylococcus epidermidis*.

Material And Methods: Antimicrobial effects of thymol/cefotaxime were performed first individually and then combined on *K. pneumoniae* ATCC 100031 and *S. epidermidis* ATCC 1457 by the MIC-MBC method. Therefore, the antimicrobial effects of the compounds that had a synergistic impact were performed on clinical strains using the MIC-MBC method. The identification of chemical bonds, functional groups, and molecular interactions of the mentioned compound was investigated using an FT-IR device. Checkered method, biofilm inhibition on *K. pneumoniae* ATCC 100031 and *S. epidermidis* ATCC 1457, and cytotoxicity investigation on red blood cells (RBCs) by hemolysis and human skin fibroblast cells (Ffk) by MTT method were performed. Finally, the results of the tests were compared between the two bacteria.

Results: The results of this study showed that the antimicrobial effects of the thymol/cefotaxime (4/2 µg/ml) were on *K. pneumoniae* better than on *S. epidermidis* (16/4 µg/ml) in both clinical and ATCC strains. In the examination with the FT-IR device, had bonds of OH carbohydrates proteins, polyphenols, C=O Amide I band, C-O-C polysaccharide, and C-N amide III band, but one band named C=C conjugated, C=C in compound showed the connection between thymol with cefotaxime. The biofilm inhibition effects of thymol/cefotaxime on *S. epidermidis* ATCC 1457 (61.81%) were better on *K. pneumoniae* ATCC 100031(46.36%). Cytotoxicity of the synergistic compound on RBCs and human Ffk cells was not different and was lower than that of Triton X-100.

Conclusion: Considering the antibiotic resistance of cefotaxime in the treatment of diseases caused by *K. pneumoniae* and *S. epidermidis*, thymol/cefotaxime showed better antimicrobial effects in *K. pneumoniae* than in *S. epidermidis* in this study. After further studies, this compound can be used as a new drug in patients.

Keywords: *Klebsiella pneumoniae*, *Staphylococcus epidermidis*, thymol, cefotaxime, synergistic

Abstract ID: 240
subject: Other related topics

Efficacy of melatonin as an adjunctive therapy in *Helicobacter pylori* infections: A systematic review

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Background and Aim: *Helicobacter pylori* (*H. pylori*) infection is a leading cause of peptic ulcer disease and a significant risk factor for gastric cancer. It induces chronic inflammation and oxidative stress in the gastric mucosa, contributing to tissue damage and impaired healing. Melatonin, a hormone primarily known for regulating circadian rhythms, has demonstrated antioxidant and anti-inflammatory properties. Recent studies have also highlighted its antibacterial activity, particularly its synergistic effects when combined with antibiotics against gram-negative bacteria. This review aims to assess the potential benefits of melatonin as an adjunct to standard treatments for *H. pylori* infection.

Material And Methods: A literature search was conducted using PubMed, Web of Science, Scopus, Embase, and Google Scholar up to December 2024. Keywords related to melatonin and *H. pylori* were used to identify randomized controlled trials investigating the effects of melatonin supplementation when combined with standard treatment regimens in *H. pylori* infections.

Results: Five studies involving a total of 330 patients with *H. pylori* infection were included in this review. Melatonin was administered at doses between 3 to 5 mg/day for durations ranging from 14 days to 6 months. Treatment with melatonin was associated with significant improvement in *H. pylori* eradication rates compared to standard therapy alone, with reported rates of 84% versus 72% in one study and 73% versus 65% in another. Additionally, dyspeptic symptoms, including nausea and abdominal pain were improved in approximately 85% of melatonin-treated patients compared to 44% in standard treatment groups. Faster recovery and a higher number of patients achieving full symptomatic relief were also observed following the addition of melatonin to their triple therapy.

Conclusion: The addition of melatonin to standard *H. pylori* treatment regimens demonstrates potential clinical benefits by enhancing eradication rates and improving symptom relief in patients with *H. pylori* infection. These findings suggest that melatonin could serve as a valuable adjunct in *H. pylori* management. Further research with larger sample sizes is necessary to confirm these benefits and establish optimal treatment protocols.

Keywords: Melatonin, *Helicobacter pylori*, peptic ulcer, dyspepsia

Abstract ID: 332
subject: Other related topics

Arabinosyl transferase C inhibition: A molecular docking approach to combat *Mycobacterium tuberculosis* infections

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Background and Aim: Arabinosyltransferase C (EmbC) is a part of a group of membrane-bonding glycosyltransferases responsible for constructing the lapidated polysaccharides, lipoarabinomannan (LAM), found in the mycobacterial cell envelope. This enzyme is targeted by the anti-tuberculosis medication ethambutol. However, in this study, we focus on identifying alternative and novel EmbC inhibitors using molecular docking analysis.

Material And Methods: The 3D structure of the EmbC enzyme (PDB ID: 3PTY) was extracted from the RCSB PDB database. Afterward, 3D structures of EmbC inhibitor, Dodecyl dimethylamine N-oxide (PubChem CID: 14052), and a total of 20 analogs were retrieved from the PubChem database. The protein and inhibitory ligands were prepared for docking using Molegro Virtual Docker version 6.0. After docking, the best interaction with the lowest energy binding was analyzed through Molegro Molecular Viewer v.7 software. Finally, the pharmacokinetic properties of the ligand were evaluated using the SwissADME server.

Results: Among all the inhibitory analogs, the most effective analog for EmbC enzyme was 2-[2-[(1-hydroxy-3-methylbutan-2-yl)amino]ethylamino]-3-methylbutan-1-ol (Pumchem CID:469991) with a molecular weight of (232.36) g/mol and binding energy of (-104.484) kcal/mol. This ligand created five steric interactions with the EmbC residues Asp1056, Arg930, Arg1055, Val920, Trp926, and Ala922, two hydrogen bond residues Asp1056 and Trp926, and no electrostatic interaction. The ADME results showed this ligand has a water solubility score (logS) of -1.18, a hydrophilic score (LogP) of 2.69, a polarity score (TPSA) of 64.52, and nine hydrogen bond donors and four hydrogen bond acceptors.

Conclusion: These results indicated that 2-[2-[(1-hydroxy-3-methylbutan-2-yl)amino]ethylamino]-3-methylbutan-1-ol (PumchemCID: 469991) is a promising candidate for inhibiting *Mycobacterium tuberculosis* infection. Further in vitro and in vivo studies are required to confirm its potential as therapeutic agents.

Keywords: Molecular Docking; *Mycobacterium tuberculosis*; arabinosyltransferase C.

Abstract ID: 117
subject: Other related topics

Identification of novel multi-epitope vaccine and novel drug targets against *Stenotrophomonas maltophilia* as a multidrug-resistant superbug

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Background and Aim: Stenotrophomonas maltophilia is an opportunistic bacterium that causes several nosocomial infections, particularly in immunocompromised patients. Extensive antibiotic resistance and lack of an approved vaccine are the two main obstacles to overcoming nosocomial bacteria. Therefore, in this study, we aimed to propose novel immunogenic targets and a multi-epitope vaccine (MEV) against *S. maltophilia* using reverse vaccinology and computational analyses

Material And Methods: To achieve these aims, several immunoinformatic analyses were applied, including assessment of antigenicity, allergenicity, PSI-BLAST against the human proteome, physiochemical properties, and B-cell and T-cell epitopes. Furthermore, the prevalence of shortlisted proteins as potential vaccine candidates among different *S. maltophilia* strains was evaluated. Subsequently, a MEV was developed using the epitopes of shortlisted proteins. The interactions of MEV with human toll-like receptors (TLRs) were measured.

Results: This study proposed seven potential immunogenic targets including GspD (WP_108270537.1), FhuE (WP_049451370.1), fimbrial protein (WP_012479122.1), TonB-dependent receptor (WP_169448402.1), TolC family protein (WP_108270106.1), autotransporter beta-barrel OMP (WP_169448945.1), and one hypothetical protein (WP_005407892.1). Next, five immunogenic epitopes from four targets including WP_005407892.1 (ADQDSSNM), WP_049451370.1 (SGKAEQ and GEESKTPS), WP_108270537.1 (GVTSTQSDSERT), and WP_169448945.1 (RELGGDRNE) were selected. Molecular docking of TLR2 and TLR4 with the MEV showed strong and feasible interactions. The MEV and proposed immunogenic targets can be applied as potential vaccine candidates against *S. maltophilia*. However, it is crucial to conduct additional in vitro and in vivo experimental analyses to validate the safety, immunoreactivity, and efficacy of these potential candidates.

Conclusion: In a complementary approach, this study also subtractive genomics to identify nine novel drug targets in *S. maltophilia*. This approach minimizes potential side effects as the identified proteins show no similarity to human proteins.

Keywords: *Stenotrophomonas maltophilia*; reverse vaccinology; putative immunogenic targets; multi-epitope vaccine; drug targets

Abstract ID: 362
subject: Other related topics

Reduction of *UreB* and *CagA* expression level by siRNA construct in *Helicobacter pylori* strain SS1

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Background and Aim: Two important virulence factors, urease and *CagA*, play an important role in *Helicobacter pylori* (*H. pylori*) gastric cancer. Aim of this study was to investigate the expression level and function of *UreB* and *CagA* using small interfering RNAs (siRNA).

Material And Methods: SS1 strain of *H. pylori* was considered as host for natural transformation. siRNA designed for *UreB* and *CagA* genes were inserted in pGPU6/GFP/Neo siRNA plasmid vector to evaluate using phenotypic and genotypic approaches. Then, qPCR was performed for determining inhibition rate of *UreB* and *CagA* gene expression

Results: The expression levels of siRNA-*UreB* and siRNA-*CagA* in the recombinant strain SS1 were reduced by about 5000 and 1000 fold, respectively, compared to the native *H. pylori* strain SS1. Also, preliminary evaluation of siRNA-*UreB* in vitro showed inhibition of urea enzyme activity. These data suggest that siRNA may be a powerful new tool for gene silencing in vitro, and for the development of RNAi-based anti-*H. pylori* therapies.

Conclusion: Our results show that targeting *UreB* and *CagA* genes with siRNA seems to be a new strategy to inhibit urease enzyme activity, reduce infammation and colonization rate.

Keywords: *UreB*, *CagA*, siRNA, *Helicobacter pylori*

Abstract ID: 363
subject: Other related topics

Designing multi-epitope vaccine against important colorectal cancer (CRC) associated pathogens based on immunoinformatics approach

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Background and Aim: It seems that several members of intestinal gut microbiota like Streptococcus bovis, Bacteroides fragilis, *Helicobacter pylori*, Fusobacterium nucleatum, *Enterococcus faecalis*, *Escherichia coli*, *Peptostreptococcus anaerobius* may be considered as the causative agents of Colorectal Cancer (CRC). The present study used bioinformatics and immunoinformatics approaches to design a potential epitope-based multi-epitope vaccine to prevent CRC with optimal population coverage.

Material And Methods: In this study, ten amino acid sequences of CRC-related pathogens were retrieved from the NCBI database. Three ABCpred, BCPREDS and LBtope online servers were considered for B cells prediction and the IEDB server for T cells (CD4+ and CD8+) prediction. Then, validation, allergenicity, toxicity and physicochemical analysis of all sequences were performed using web servers. A total of three linkers, AAY, GPGPG, and KK were used to bind CTL, HTL and BCL epitopes, respectively. In addition, the final construct was subjected to disulfide engineering, molecular docking, immune simulation and codon adaptation to design an effective vaccine production strategy.

Results: A total of 19 sequences of different lengths for linear B-cell epitopes, 19 and 18 sequences were considered as epitopes of CD4+ T and CD8+ cells, respectively. The predicted epitopes were joined by appropriate linkers because they play an important role in producing an extended conformation and protein folding. The final multi-epitope construct and Toll-like receptor 4 (TLR4) were evaluated by molecular docking, which revealed stable and strong binding interactions. Immunity simulation of the vaccine showed significantly high levels of immunoglobulins, helper T cells, cytotoxic T cells and INF-γ.

Conclusion: Finally, the results showed that the designed multi-epitope vaccine could serve as an excellent prophylactic candidate against CRC-associated pathogens, but in vitro and animal studies are needed to justify our findings for its use as a possible preventive measure.

Keywords: Colorectal cancer, gut microbiota, immunoinformatics, vaccine design, in silico, multi-epitope vaccine

Abstract ID: 250
subject: Other related topics

Combination of antibiotics-nisin reduces the formation of persister cell in *Listeria monocytogenes*

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Background and Aim: Persister cells are a subpopulation of bacteria with the ability of survival when exposed to lethal doses of antibiotics, and are responsible for antibiotic therapy failure and infection recurrences.

Material And Methods: In this study, we investigated persister cell formation and the role of nisin in combination with antibiotics in reducing persistence in *Listeria monocytogenes*. We also examined the expression of toxin–antitoxin (TA) systems in persister cells of L. monocytogenes to gain a better understanding of the effect of TA systems on persister cell formation. To induce persistence, L. monocytogenes were exposed to high doses of different antibiotics over a period of 24 hr, and the expression levels of TA system was genes were measured 5 hr after the addition of antibiotics by the quantitative reverse transcription-polymerase chain reaction (qRT-PCR) method. To investigate the effect of nisin, L. monocytogenes was exposed to a combination of nisin and antibiotics.

Results: According to our results, L. monocytogenes was highly capable of persister cell formation, and the combination of nisin and antibiotics resulted in reduced persistence. qRT-PCR results showed a significant increase in GNAT/RHH expression among the studied systems.

Conclusion: Overall, our results demonstrated the potential of the combination of nisin and antibiotics in reducing persister cell formation, and emphasized the role of the GNAT/RHH system in bacterial persistence.

Keywords: *Listeria monocytogenes*; nisin; persister cells; TA system; real-time PCR

Abstract ID: 249
subject: Other related topics

Biofilm establishment, biofilm persister cell formation, and relative gene expression analysis of type II toxin-antitoxin system in *Klebsiella pneumoniae*

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Background and Aim: The biofilms forming ability in *Klebsiella pneumoniae* isolates leads to treatment failure and chronic infections through protecting bacteria against antibiotics. Persister cells are a small fraction of the bacterial population that survives by entry into dormancy state after treatment with high dose antibiotics and are mainly responsible for a high level of biofilm-mediated tolerance to antibiotics. Toxin-antitoxin (TA) systems widely distributed among bacteria. Activation of the TA system is believed to result in the bacterial entrance to the dormant state, inducing persistence, and the formation of biofilms.

Material And Methods: In this study after biofilm formation and the induction of persister cells in biofilms, the relative expression level of type II TA system genes (relE1/relB1, relE2/relB2, hipA/hipB, vapB/vapC, phd/doc, mazF/mazE) in *K. pneumoniae* isolates were examined by Real _Time PCR.

Results: Findings showed an increase in the expression levels of type II TA system genes in biofilm formers and an upregulation of all genes studied in biofilm persister cells except the phd/doc system.

Conclusion: Our results can provide information about the potential role of the TA systems in biofilm production and also the biofilms persister cell formation.

Keywords: Biofilm; *Klebsiella pneumoniae*; persister cell; Type II TA system; real-time PCR

Abstract ID: 357
subject: Other related topics

Flash chromatographic isolation of potential antibacterial compounds of prosopis cineraria and evaluation of their anti bacterial activity

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Background and Aim: Flash chromatography is a technique used for the separation and extraction of fractions containing antibacterial compounds from plant extracts. In this study, we examined the fractions obtained from the flash chromatography of the ethyl acetate extract of the plant Prosopis cineraria on *Klebsiella pneumoniae*.

Material And Methods: According to Flash chromatography technique, ethyl acetate extract of Prosopis cineraria was fractioned through an open silica column. N-hexane and ethyl acetate were applied as the mobile phase. MIC values of each derived fraction was assessed against *K. pneumoniae* by micro-broth dilution method.

Results: 100% ethyl acetate and 100% n-hexane with MIC <0.25 ng/ml and >5 ng/ml had the highest and lowest inhibitory effects on *K. pneumoniae*, respectively.

Conclusion: The application of cost-effective chromatography methods, such as flash chromatography, can be effective in obtaining and enhancing suitable antibacterial compounds to combat drug-resistant bacteria.

Keywords: Flash chromatography, *Klebsiella pneumonia*, prosopis cineraria, ethyl acetate, extract

Abstract ID: 19
subject: Other related topics

A0A0H3GSW2 as a potential novel virulence protein in *Klebsiella pneumoniae*: An in silico analysis

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Background and Aim: *Klebsiella pneumoniae*, as a member of the *Enterobacter*iaceae family, is known for its ability to cause pneumonia, bloodstream infections, and urinary tract infections, especially in immunocompromised individuals. It has emerged as a major clinical and public health problem due to its increasing antibiotic resistance, presence of virulence factors, role in nosocomial infections (1). However, the function of up to 30-40% of this bacterial protein is still uncharacterized (2). In this regard, determining their function of them can advance our knowledge to basic microbiological research and confront rising challenges posed by antibiotic-resistant pathogens (3). In this study, we intended to use computational tools to find potential functions of hypothetical A0A0H3GSW2 protein.

Material And Methods: The Uniprot and STRING databases were utilized to identify proteins that interact with A0A0H3GSW2 and to analyze functional protein association networks. Subsequently, the I-TASSER and Swiss model server were employed to predict the functions of the target protein based on its homologous proteins.

Results: Our study indicated uncharacterized protein A0A0H3GSW2 with 144 aa belongs to the YejG protein family as its sequence has 0.84 similarity with *Escherichia coli* YejG protein. YejG protein in *E. coli* cause low-level resistance to aminoglycoside antibiotics (4). Besides, A0A0H3GSW2 protein could interact with ten bacterial proteins. Our functional analysis indicates these proteins play a significant role in single-species biofilm formation and hemolysin expression modulating , which correlates with increased resistance to antibiotics and adverse patient outcomes (5). In addition, in *Klebsiella pneumoniae*, hemolysin gene is crucial for the bacterium's virulence, as it enables bacterial cell to damage host tissues and promote inflammation (6). Our findings also showed simulated structure of A0A0H3GSW2 was highly similar to urocanate hydratase structure from *Trypanosoma cruzi* participating in the catabolic pathway of L-histidine. *Klebsiella pneumoniae* employs the Hut pathway for the catabolism of L-histidine, which enables the bacterium to utilize histidine as a source of carbon, energy, and nitrogen (7,8).

Conclusion: According to the mentioned results it seems this protein playing a crucial role in the pathogenesis of *Klebsiella pneumoniae*, may be posited as an excellent therapeutic target for future research endeavors.

Keywords: *Klebsiella pneumoniae* , functional prediction, YejG protein , A0A0H3GSW2

Abstract ID: 155
subject: Other related topics

Gut microbiota metabolism of ellagic acid: Urolithins as novel AKR1C1 inhibitors

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Background and Aim: Aldo-keto reductases (AKR) are a superfamily of NAD(P)H-linked oxidoreductases that play important roles in drug metabolism and detoxification. The overexpression of AKR1C1 is associated with cancer progression and chemoresistance in various types of cancer including lung, liver, gastrointestinal, and bladder carcinomas. Hence, the introduction of novel agents, preferably from natural resources, to act as AKR1C1 inhibitors could lead to improved efficacy of cancer chemotherapy. In the present study, we assessed the potential of urolithins, gut microbiota metabolites of ellagic acid, to interact with AKR1C1.

Material And Methods: To perform molecular docking, the 3D structures of urolithin A and urolithin B were obtained from PubChem, along with the 3D structure of AKR1C1 from PDB. Then, AutoDockTools 1.5.7 was utilized to assign polar hydrogens and atomic charges to create the appropriate files to perform molecular docking. The lowest energy model was chosen as the docking result and 2D and 3D structures were visualized by Discovery Studio.

Results: Results revealed stable interactions between urolithin A and AKR1C1, involving the formation of hydrogen bonds with Asp50 and Tyr55 in the active site, along with Ala218, with a minimal binding energy of -9.1 kcal/mol. Additionally, the interaction between urolithin B and the residue Tyr55 within the active site of AKR1C1, along with more hydrogen bonds with Ala218 and Gln190, exhibited a minimal binding energy of -9.1 kcal/mol.

Conclusion: Accordingly, the current study represented the efficacy of urolithin A and B as natural agents to potentially improve chemotherapy outcomes by targeting AKR1C1.

Keywords: Gut microbiota, urolithin, chemotherapy, AKR1C1

Abstract ID: 156
subject: Other related topics

Targeting AKR1C3 reductase activity with urolithins: Gut microbiota metabolites of ellagitannins

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Background and Aim: Ellagitannins (ETs) are hexahydroxydiphenoic acid esters abundantly present in fruits like pomegranate, berries, and nuts. Upon absorption in the small intestine, ETs are metabolized by the gut microbiota to urolithins, which have good bioavailability and valuable pharmacological effects. Urolithin A (UroA) and B (UroB) are the major metabolites present in the gut, exhibiting antimicrobial, anti-inflammatory, antioxidant, cardioprotective, and neuroprotective properties, along with anticancer potential. Aldo-keto reductases (AKR), particularly AKR1C3, play a crucial role in chemotherapy resistance across various cancer types through drug metabolism and detoxification. For the first time, the current study aimed to explore whether urolithins could interact with AKR1C3 to combat chemoresistance.

Material And Methods: To assess the potential binding of UroA and UroB to AKR1C3, molecular docking was performed using AutoDock Vina. The 3D structures of urolithins and AKR1C3 were retrieved from PubChem and PDB, respectively, and optimized using Avogadro. The grid box was specifically designed to encompass the active site of AKR1C3, and the lowest energy model was chosen as the docking result and visualized by Discovery Studio.

Results: Results indicated the interaction of UroA and UroB with AKR1C3 with favorable binding affinity scores of -8.9 and -8.8 kcal/mol, respectively. In the structure of AKR1C3, NADPH, which acts as the cofactor, is located in a cavity and interacts with Tyr55 and His117. The interaction of UroA and AKR1C3 involved hydrogen bonds with Tyr55, Leu268, and Lys270, along with three van der Waals bonds. Moreover, the interaction between UroB and AKR1C3 involved two hydrogen bonds with Tyr55 and Lys270, along with four van der Waals interactions.

Conclusion: In conclusion, our findings provide new insights into the anticancer potential of urolithins, which could be used in combination therapies to potentially overcome chemoresistance mediated by AKR1C3.

Keywords: Gut microbiota metabolites, ellagitannins, urolithin, AKR1C3, chemoresistance

Abstract ID: 379
subject: Other related topics

In vivo evaluation of optimized polycaprolactone-based antibacterial dressings containing echinacea purpurea (EP) extract and silver nanoparticles (AgNPs) on MRSA-infected rats

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Background and Aim: Methicillin-resistant *Staphylococcus aureus* (MRSA) infections provide a considerable obstacle in wound care because to drug resistance. Polycaprolactone (PCL)-based dressings have emerged as effective scaffolding for wound healing, particularly when enhanced with bioactive chemicals. This research assesses the in vivo effectiveness of PCL dressings infused with silver nanoparticles (AgNPs) and Echinacea purpurea (EP) extract in a rat model of MRSA-infected wounds

Material And Methods: A wound measuring 2 by 2 centimeters was created and subsequently infected with MRSA bacteria. Subsequently, UV-sterilized nanofibers were applied to the wound. The animals were categorized into five groups: (1) control (untreated), (2) PCL-only dressing, (3) PCL/AgNPs dressing, (4) PCL/EP dressing, and (5) PCL/AgNPs/EP composite dressing. The dressings were administered for 15 days, with sampling performed on days 5, 10, and 15. The bacterial burden was evaluated by wound swab cultures, and wound closure was quantified. Histological examination was used to assess tissue regeneration

Results: The PCL/AgNPs/EP composite dressing demonstrated superior antibacterial efficacy, markedly decreasing MRSA load relative to other groups. Analysis of wound closure indicated that treatment with PCL/AgNPs/EP facilitated the fastest healing, demonstrating a significantly greater percentage of wound contraction on days 10 and 15. Histological analysis revealed improved re-epithelialization and elevated collagen deposition in the PCL/AgNPs/EP group, indicating enhanced biocompatibility and regenerative capacity

Conclusion: The synthesized PCL-based nanofibers incorporating AgNPs and Echinacea extract exhibited significant antibacterial properties, favorable physicochemical characteristics, and biocompatibility, positioning them as potential candidates for advanced wound dressings, particularly for MRSA-infected wounds. Additional research is necessary to validate clinical efficacy through in vivo experiments

Keywords: Polycaprolactone, silver nanoparticles, echinacea purpurea, MRSA, wound healing, antibacterial dressing, in vivo study

Abstract ID: 380
subject: Other related topics

Preparation of echinacea purpurea (EP) extract and silver nanoparticles (AgNPs) loaded polycaprolactone-based wound Dressings: An In-vitro study against MRSA

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Background and Aim: The rise of multi-drug-resistant microorganisms, particularly MRSA, underscores the need for the creation of advanced dressings that possess superior antimicrobial properties and high efficacy in tissue repair. This study will examine the preparation and characterization of PCL-based nanofiber wound dressings that incorporate Echinacea extract and silver nanoparticles to achieve synergistic antimicrobial and bioactive effects

Material And Methods: The synthesis of AgNPs was conducted using a green synthesis approach and characterized through DLS, zeta potential analysis, FE-SEM. The antimicrobial efficacy of AgNPs and EP was assessed using MIC and MBC assays. The synergistic antibacterial interaction was evaluated using the checkerboard assay. This study involved the preparation of four types of electrospun nanofibers: PCL, PCL/EP, PCL/AgNPs, and PCL/AgNPs/EP. Characterizations were conducted using FE-SEM, MIC, DPPH, and mechanical properties testing. The swelling behavior, drug release kinetics, and water vapor transmission rate were examined. Cytotoxicity was assessed using the MTT assay

Results: AgNPs exhibited a uniform distribution, demonstrated high stability, and EP possessed significant antioxidant activity. The results of the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) suggest the antibacterial efficacy of silver nanoparticles (AgNPs) and Echinacea (EP) against methicillin-resistant *Staphylococcus aureus* (MRSA), further validated by their synergistic interaction as assessed through the checkerboard assay. The results of FE-SEM analysis confirmed the formation of nanofibers at the nanoscale.PCL/AgNPs/EP nanofibers demonstrated high antioxidant property,enhanced mechanical strength, regulated release properties, ideal sewlling rate water and vapor transmission rate for wound-healing applications. The MTT test validated the biocompatibility of nanofiber formulations

Conclusion: The PCL-based nanofibers incorporated with AgNPs and Echinacea extract demonstrated significant antibacterial activity, favorable physicochemical properties, and biocompatibility, positioning them as potential candidates for advanced wound dressings, particularly for MRSA-infected wounds. Additional research is necessary to validate the clinical efficacy through in vivo experiments

Keywords: Echinacea purpurea extract, silver nanoparticles, polycaprolactone, nanofiber, MRSA, wound dressing, antibacterial, green synthesi

Abstract ID: 142
subject: Other related topics

Purification and evaluation of polysaccharide intercellular adhesion (PIA) antigen from *Staphylococcus epidermidis*

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Background and Aim: The polysaccharide intercellular adhesin (PIA) confers major functional effects in biofilm formation, which is important in the pathogenicity of *Staphylococcus epidermidis*. This study aimed to isolate, purify, and characterize PIA from *S. epidermidis* strains.

Material And Methods: Following the identification of biofilm-forming strains by biochemical and molecular methods, an isogenic strain was prepared, and an in vitro biofilm formation assay was performed consequently. By parallel analysis of both the PIA-positive (*S. epidermidis* 1457) and PIA-negative (M-10/transmutant 1457) strains using size exclusion chromatography (SEC) by High-performance liquid chromatography (HPLC) method by C18 column, the respective PIA was purified. The recovered PIA was examined using a colorimetric assay. Finally, the recovered PIA was analyzed using Fourier-transform infrared spectroscopy (FT-IR) and proton nuclear magnetic resonance spectroscopy (NMR) methods. By parallel purification and comparison of the graphs obtained from the HPLC detector, fractions near the void volume were determined as PIA.

Results: Suspicious peaks corresponding to PIA were collected 30 min post-injection into the chromatography column using fraction collection. Subsequently, a colorimetric assay was performed on these suspicious peaks, which were present in the positive control graph but absent in the negative control graph, revealing a carbohydrate content (hexosamine = 5700 µg/ml) in the PIA polysaccharide. Structural confirmation of PIA was achieved through Fourier-transform FTIR, where a peak at 1746 cm-1 indicated the polysaccharide structure and a peak at 3543 cm-1 specifically corresponded to the NH group present in PIA with a molecular weight of 100 kDa. The PIA structure was further validated using NMR spectroscopy, with a peak observed at 3-4 ppm representing the hydrogen atoms within the PIA structure.

Conclusion: The extracted PIA was separated 30 min after sample injection on a C18 chromatography column compared to the transmutant strain and confirmed by colorimetric, FTIR, and NMR tests. The bacteria were able to produce about 5 mg of PIA per liter of culture medium at 40-60 rpm, which we extracted.

Keywords: *Staphylococcus epidermidis*, purification, PIA

Abstract ID: 318
subject: Other related topics

elucidating the role of *Fusobacterium nucleatum* in colorectal cancer: Implications for tumour proliferation and chemoresistance mechanisms

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Background and Aim: *Fusobacterium nucleatum*, an anaerobic bacterium prevalent in the human oral cavity, is increasingly recognized for its role in colorectal cancer (CRC) pathology. Evidence suggests that *F. nucleatum* promotes tumor proliferation and contributes to chemoresistance, affecting patient outcomes and treatment efficacy. Understanding the mechanisms underlying *F. nucleatum's* contributions to colorectal tumorigenesis and therapeutic responses is crucial for developing targeted cancer management strategies.

Material And Methods: This study is a review based on searches of scientific databases such as Scopus, PubMed, and Embase from 2014 to 2024, using keywords including *Fusobacterium nucleatum*, colorectal cancer, tumor proliferation, and chemoresistance. A total of 47 relevant articles were extracted and analyzed.

Results: Findings indicate that *F. nucleatum* enhances colorectal cancer cell proliferation through mechanisms such as modulation of inflammatory pathways, alteration of the tumor microenvironment, and promotion of immune evasion. The presence of *F. nucleatum* also correlates with significant chemoresistance in CRC patients, likely due to its influence on drug metabolism and apoptotic pathways in cancer cells. Additionally, its interactions with the host immune system complicate treatment regimens, highlighting the necessity for a deeper understanding of its impact on CRC management.

Conclusion: The role of *Fusobacterium nucleatum* in colorectal cancer emphasizes its significance in tumor dynamics and therapeutic resistance. Targeting *F. nucleatum* may offer new opportunities to enhance treatment responses and improve patient outcomes. Further research is essential to elucidate the mechanisms of its action and to develop therapeutic strategies aimed at mitigating its adverse effects on cancer progression and treatment efficacy.

Keywords: *Fusobacterium nucleatum*, colorectal cancer, tumor proliferation, chemoresistance.

Abstract ID: 295
subject: Other related topics

Microbial profile and prevalence of bacterial pathogens in urinary tract infections: A study of urine samples from patients

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Background and Aim: Microbial infections of the urinary tract remain a significant public health concern worldwide, contributing to morbidity and mortality, particularly in vulnerable populations. Urine samples serve as a valuable resource for understanding the prevalence and types of pathogenic bacteria present in the urinary system. This study investigates the microbiological profiles in urine samples.

Material And Methods: This study investigates the microbiological profiles in urine samples from 782 patients (503 females and 279 males) using Urine Culture (U/C) methods.

Results: Among these, 102 patients were identified as positive. The results indicated that *Escherichia coli* was the most commonly isolated bacterium, with 65 positive samples. Following this, *Klebsiella* with a total of 18 positive samples (9 related to *Klebsiella pneumoniae* and 9 related to *Klebsiella oxytoca*). Proteus was identified as the third most prevalent bacterium, with 6 positive samples. *Enterococcus sp*, with 5 positive samples, and *Pseudomonas aeruginosa*, with 3 positive samples. Additionally, *Streptococcus* was confirmed with 2 positive samples.

Conclusion: These findings underscore the importance of monitoring bacterial pathogens in urinary tract infections and highlight the need for appropriate preventive and therapeutic measures.

Keywords: microbial infections, *Klebsiella*, *Pseudomonas aeruginosa*, *Enterococcus*, *Streptococcus*

Abstract ID: 252
subject: Other related topics

An investigation into the antibacterial properties of activated carbon/zinc oxide nanocomposite synthesized via green synthesis using date seed extract

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Background and Aim: The increasing rate of antibiotic-resistant bacteria has generated a great demand for the development of alternative antibacterial agents. In this regard, the synthesis of nanoparticles has emerged as a promising approach to address this problem. Zinc oxide nanoparticles are known to exhibit potent antibacterial properties, making them suitable for various medical applications. However, traditional synthesis methods often involve toxic chemicals that pose risks to both human health and environmental safety. Recently, green synthesis approaches using plant extracts to generate these nanoparticles. Date seed extract is rich in bioactive compounds, which makes it an ideal candidate for the green synthesis of zinc oxide nanoparticles.

Material And Methods: The AC/ZnO nanocomposites were synthesized using date seed extract as a reducing agent and stabilizer. Date seeds were crushed, soaked in distilled water, and heated to extract bioactive compounds. The extract was mixed with a zinc precursor solution while stirring, followed by the addition of activated carbon. The pH was adjusted with sodium hydroxide to induce nanoparticle formation. Characterization of the synthesized nanocomposites was conducted using UV-Vis spectroscopy, X-ray diffraction (XRD), scanning electron microscopy (SEM), and Fourier transform infrared spectroscopy (FTIR). Antibacterial activity was tested against *Staphylococcus aureus* and *Escherichia coli* using the disc diffusion method.

Results: Characterization results confirmed the successful synthesis of AC/ZnO nanocomposites: UV-Vis spectroscopy showed the formation of nanoparticles, while XRD revealed a crystalline structure similar to that of ZnO. The obtained results showed that these nanocomposites exhibited antibacterial activity against both bacterial strains which is comparable to the commercial ZnO sample with less cytotoxicity compared with their commercial counterparts, especially at low concentrations.

Conclusion: The present study proves that greenly synthesized AC/ZnO nanocomposites exhibit significant antibacterial activity while showing lower levels of toxicity. This eco-friendly approach not only reduces the environmental risks associated with traditional synthesis methods but also increases the potential uses of such nanocomposites in the medical field, especially for fighting antibiotic-resistant infections and wound healing with almost negligible side effects.

Keywords: Nanocomposite, date seed, green-synthesized

Abstract ID: 242
subject: Other related topics

Minimizing DNA cross-contamination in FFPE tissue processing: enhancing HPV detection through PCR

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Background and Aim: Human papillomavirus (HPV) is a major sexually transmitted pathogen, responsible for over 99% of cervical cancer cases. With 500,000 annual cases and 250,000 fatalities, HPV's global impact highlights the need for effective diagnostics. PCR-based methods, using unique DNA biomarkers, have revolutionized pathogen detection. Formalin-fixed, paraffin-embedded (FFPE) tissues offer a practical alternative for nucleic acid analysis but present challenges such as DNA degradation and cross-contamination, affecting diagnostic accuracy. This study aims to assess cross-contamination risks in FFPE tissue processing and develop optimized PCR-based diagnostic protocols to improve HPV detection reliability.

Material And Methods: Liver tissues were formalin-fixed, paraffin-embedded, and infected with HPV genotype 56 DNA. Cross-contamination was assessed by sectioning tissues with sterilized and non-sterilized microtome blades. DNA extraction used phenol-chloroform after deparaffinization, with quantification by spectrophotometry. PCR amplification targeted the HPV-56 E6/E7 region, with contamination controls and amplicon specificity confirmed via agarose gel electrophoresis. This approach evaluated contamination risks and developed protocols to minimize DNA carryover, enhancing molecular diagnostic accuracy.

Results: The findings highlight the critical role of sterilization in preventing cross-contamination during the processing of FFPE (formalin-fixed, paraffin-embedded) tissue samples. The detection of HPV DNA in uninfected tissues sectioned with unsterilized blades underscores the risk of contamination transfer, posing a challenge for molecular diagnostics. The use of 70% ethanol for blade sterilization proved to be an effective, low-cost solution in mitigating this issue, as it prevented contamination in the analyzed tissues. The specificity of the amplicons, confirmed by electrophoresis, further solidifies the necessity for rigorous sterilization protocols to ensure the accuracy and reliability of results in molecular diagnostics involving FFPE tissues.

Conclusion: This study underscores the critical importance of Implementing stringent sterilization protocols during FFPE tissue processing is crucial to prevent cross-contamination, which can compromise molecular diagnostics. The study confirms that 70% ethanol is an effective, cost-efficient sterilization method for microtome blades, preserving PCR analysis integrity. By identifying contamination pathways and proposing preventive measures, this research improves the reliability of pathogen detection, especially HPV, in FFPE specimens. Future studies should explore additional strategies to enhance diagnostic accuracy and validate these findings in diverse settings.

Keywords: HPV, cervical cancer, PCR, FFPE tissue, DNA extraction, cross-contamination, molecular diagnostics.

Abstract ID: 77
subject: Other related topics

An immunoinformatics approach for the design of a multi-epitope vaccine targeting super antigen TSST-1 of *Staphylococcus aureus*

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Background and Aim: TSST-1 is a powerful toxin that is responsible for causing food poisoning and related symptoms in individuals infected with staphylococcal bacteria. It is a major focus in the development of vaccines against *Staphylococcus aureus*. However, previous vaccine attempts have been unsuccessful due to harmful side effects and toxicity observed in later stages of testing. In an effort to address these issues, the current study utilizes an immunoinformatics approach to create a multi-epitope vaccine that can potentially overcome concerns regarding toxicity and allergies.

Material And Methods: We used an immunoinformatics technique to develop a multi-epitope vaccine against *Staphylococcus aureus* that specifically targets TSST-1. B cell and T cell epitopes were identified through computer simulations and carefully linked together to prevent undesirable immune reactions. The addition of adjuvants β-defensin and PADRE at the starting end of the vaccine was also incorporated. The vaccine's physical and chemical properties, as well as its potential to induce allergies, were evaluated using online tools. The three-dimensional structure of the vaccine was predicted and verified using various methods. To understand the binding affinity between the vaccine and TLR-3, molecular docking experiments were conducted and the interactions were graphically represented using LigPlot+.

Results: Through the use of in silico cloning, the vaccine was effectively

inserted into pET-28a (+) in order to enhance expression within the *E. coli* K12 system. Evaluation through population coverage analysis revealed a promising reach of 83.15% of the worldwide population. Additionally, immune simulation studies exhibited heightened levels of antibodies, IL-2, IFN-γ, TGF-β, as well as B and T cell populations, ultimately prompting primary, secondary, and tertiary immune responses. Employing a computational method, a multi-epitope vaccine was constructed, ensuring non-allergic and non-toxic properties as an antigen.

Conclusion: Preliminary in silico reports have shown that this vaccine could elicit both B cell and T cell responses in the host as desired.

Keywords: *Staphylococcus aureus*, peptide vaccine, TSST-1, in silico

Abstract ID: 419
subject: Other related topics

Evaluation of biofilm gene frequency and biofilm production capability in clinical isolates of *Stenotrophomonas maltophilia*

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Background and Aim: *Stenotrophomonas maltophilia* is a critical hospital pathogen associated with high antibiotic resistance and chronic respiratory infections. These infections are often exacerbated by biofilm formation, which enhances antibiotic tolerance. This study aims to determine the frequency of biofilm-related genes and the intensity of biofilm production in clinical isolates.

Material And Methods: A total of 120 *Stenotrophomonas maltophilia* isolates were collected from Tehran hospitals between 2022 and 2023. Initial identification was performed using biochemical tests, followed by confirmation with 16S rRNA gene sequencing. The presence of biofilm genes (smf-1, rmlA, spgM, rpfF) was analyzed using PCR, and microtiter plate assays were conducted to assess biofilm production.

Results: Biofilm production was observed in 115 isolates (95.8%). Among these, 27 isolates (22.5%) displayed strong biofilm formation, 52 isolates (43.3%) showed moderate, and 36 isolates (30%) had weak biofilm formation. Five isolates (4.2%) were unable to produce biofilm. PCR results indicated the presence of the spgM gene in all samples, with rmlA (89.1%), smf-1 (83.3%), and rpfF (76.6%) being the most prevalent biofilm genes.

Conclusion: The results underscore the remarkable biofilm formation ability of clinical isolates of *Stenotrophomonas maltophilia*. This suggests a considerable potential for colonization, pathogenicity, and antibiotic resistance. Consequently, this presents significant challenges for treatment strategies and facilitates the rise of resistant strains.

Keywords: *Stenotrophomonas maltophilia*, biofilm, microtiter plate

Abstract ID: 321
subject: Other related topics

Investigation of potent inhibitors to control *Bacillus anthracis* by targeting its anthrax toxin: A molecular docking study

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Background and Aim: *Bacillus anthracis*, a Gram-positive and zoonotic bacterium, has caused significant morbidity and mortality throughout history, leading to its designation as a Category A agent by the CDC due to its high threat to public health and national security. The anthrax toxin, part of the AB toxin family, comprises a protective antigen (PA) for toxin delivery and two interchangeable subunits: edema factor (EF) and lethal factor (LF), causing edema and lethality, respectively. Rising antibiotic resistance and limited treatments highlight the need for novel therapeutics. This study aimed to identify the most effective ligand to inhibit anthrax toxin using molecular docking analysis

Material And Methods: The 3D structure of *Bacillus anthracis* toxin (PDB ID: 1J7N) was obtained from the RCSB PDB database. N-oleoyldopamine (CID 5282106) and thirty of its analogs were selected as inhibitors from the PubChem database in SDF format. After preparing the protein and ligands, molecular docking was carried out using Virtual Docker Molegro version 6.0. The interactions were analyzed to identify the best binding with the lowest energy using Molegro Molecular Viewer software. At the end, the pharmacokinetic properties were evaluated using the SwissADME server.

Results: Among all the inhibitory ligands, the most effective analog for *Bacillus anthracis* toxin was identified as N-[2-(3,4-dihydroxyphenyl)ethyl]dodecanamide. This compound has a molecular weight of 195/22 g/mol and a binding energy of -150/229 kcal/mol. N-[2-(3,4-dihydroxyphenyl)ethyl]dodecanamide formed seven steric interactions with the toxin residues of Gln537(B), Tyr542(B), Pro492(B), Leu494(B), Ala493(A), Ala493(B), and Ser538(B), along with two hydrogen bonds with the toxin residues involving Ser538(A) and Pro492(B). However, no electrostatic bonds were observed between N-[2-(3,4-dihydroxyphenyl)ethyl]dodecanamide and *Bacillus anthracis* toxin. The ADME analysis revealed that N-[2-(3,4-dihydroxyphenyl)ethyl]dodecanamide has a logS (water solubility) score of -0.65, a lipophilicity (XLogP3) of -0.72, a polarity (TPSA) of 69.56Å², and three hydrogen bond donors and three hydrogen bond acceptors. These properties suggest that N-[2-(3,4-dihydroxyphenyl)ethyl]dodecanamide is a promising candidate for inhibiting *Bacillus anthracis* toxin. Further in vitro and in vivo studies are required to confirm it as a therapeutic agent.

Conclusion: These results indicate that " N-[2-(3,4-dihydroxyphenyl)ethyl]dodecanamide "is a promising candidate for inhibiting *Bacillus anthracis* infection. Further in vitro and in vivo studies are required to confirm it as a therapeutic agent.

Keywords: *Bacillus anthracis*, molecular docking, N-oleoyldopamine, N-[2-(3,4-dihydroxyphenyl)ethyl]dodecanamide

Abstract ID: 120
subject: Other related topics

Synthesis of carbon dots from probiotic bacteria

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Background and Aim: Today, nanotechnology enables the synthesis of nanoparticles known as carbon dots (C-dots) from a variety of sources, which demonstrate valuable therapeutic properties in medicine. These C-dots can be produced from sources such as probiotic bacteria. This study aimed to synthesize C-dots from *Lactobacillus Acidophilus* (*L. acidophilus*) and *Bifidobacterium bifidum* (*B. bifidum*).

Material And Methods: A fresh culture of probiotic bacteria was prepared in MRS broth, and C-dots were synthesized using a hydrothermal method involving high heat. The characteristics of the C-dots were investigated through various techniques, including high-resolution transmission electron microscopy (HR-TEM), Fourier transform infrared (FTIR) spectroscopy, photoluminescence spectroscopy (PL), dynamic light scattering (DLS), zeta potential analysis, and cell viability assessment using the MTT assay on HeLa (human cervical cancer) cells.

Results: The analysis of the synthesized C-dots from *L. acidophilus* and *B. bifidum* revealed several key findings. HR-TEM showed that the C-dots had spherical shapes, with average diameters of 5.83±2.035 nm for *L. acidophilus* and 3.32±0.592 nm for *B. bifidum*. FTIR spectroscopy demonstrated significant absorption bands at 1667 ?cm?^(-1) and 1649 ?cm?^(-1), corresponding to C=O stretching vibrations in the Amide I region, which were not present in the source bacteria, respectively. PL analysis for both C-dots presented a 3D spectrum showing an increase in emission wavelength alongside an increase in absorption wavelength. DLS experiments indicated that the C-dots had sizes of 89.37 nm and 125.8 nm, along with negative zeta potentials of -36.1 mV and -15.6 mV, respectively. To assess the cytotoxicity of the C-dots, the viability of HeLa cells was evaluated after exposure to different concentrations over a 24-hour incubation period. At lower concentrations of 1 mg/mL and 0.5 mg/mL, cell viability remained high, reaching 70%, 99.8%, and 73.2%, 98.23%, respectively.

Conclusion: The synthesis of C-dots was successfully achieved for the first time using a simple and cost-effective hydrothermal method. C-dots are spherical in shape, have a negative surface charge, and measure less than 10 nm in size and they exhibit blue fluorescence and demonstrate minimal cytotoxicity.

Keywords: Carbon dots, probiotic, *L. acidophilus*, *B. bifidum*, hydrothermal method

Abstract ID: 329
subject: Other related topics

Evaluation of molecular docking between 8-pseudomonalisin from *Pseudomonas aeruginosa* and its inhibitory ligands

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Background and Aim: *Pseudomonas aeruginosa* is a highly adaptable pathogen that poses significant health risks by triggering severe respiratory conditions, including acute pneumonia and chronic lung inflammation, particularly among patients with cystic fibrosis and those experiencing nosocomial infections. This bacterium secretes harmful substances, including pseudomonolysin, which disrupts cellular integrity, promotes tissue damage, and thereby exacerbates inflammation. Additionally, pseudomonolysin helps the bacteria evade the immune system, facilitating the spread of infection. Developing targeted therapies, such as pseudomonolysin inhibitors, could offer a promising strategy to combat these infections. Therefore, our study utilized molecular docking techniques to discover novel pseudomonolysin inhibitors, paving the way for potential therapeutic advancements.

Material And Methods: The 3D structure of 8-pseudomonalisin (PDB ID: 1GA4) was obtained from the RCSB PDB database. Tyrostatin and twenty of its analogs were selected as inhibitors from the PubChem database in SDF format. After preparing the protein and ligands, molecular docking was carried out using Virtual Docker Molegro version 6.0. The interactions were analyzed to identify the best binding with the lowest energy using Molegro Molecular Viewer software. At the end, the pharmacokinetic properties were evaluated using the SwissADME server.

Results: Among all the inhibitory ligands, the most effective analog for 8-pseudomonalisin was identified as Leucyl-leucyl-tyrosine. This compound has a molecular weight of 223.23 g/mol and a binding energy of -162.943 kcal/mol. Leucyl-leucyl-tyrosine formed nine steric interactions with the 8-pseudomonalisin residues Trp220, Trp231, Gly284, Glu80, Glu171, Ser167, Asp170, Ser287, and Arg179, along with three hydrogen bonds with Asp170, Ser287, and Glu80. However, no electrostatic bonds were observed between Leucyl-leucyl-tyrosine and 8-pseudomonalisin. The ADME analysis revealed that Leucyl-leucyl-tyrosine has a logS (water solubility) score of -2.00, a lipophilicity (XLogP3) of 1.32, a polarity (TPSA) of 86.63², and three hydrogen bond donors and four hydrogen bond acceptors.

Conclusion: These results indicate that Leucyl-leucyl-tyrosine is a promising candidate for inhibiting pseudomonas infection. Further in vitro and in vivo studies must confirm it as a therapeutic agent.

Keywords: Leucyl-leucyl-tyrosine, molecular docking, 8-Pseudomonalisin, *Pseudomonas sp.*

Abstract ID: 417
subject: Other related topics

Targeting MqsR toxin: Unveiling a new strategy to combat biofilm and persistence in *Burkholderia cepacia*

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Background and Aim: The persistence and biofilm formation of *Burkholderia cepacia* are key factors in the chronicity and difficulty of treating its infections. This study set out to unravel the intricate role of the MqsR toxin in these processes, with the aim of identifying a novel therapeutic target

Material And Methods: To investigate this, we exposed *B. cepacia* to high concentrations of ciprofloxacin to induce a state of persistence. We analyzed gene expression in persister cells and during biofilm development. Additionally, we designed a peptide to specifically inhibit the formation of the MqsR toxin complex, aiming to disrupt its function.

Results: Our findings revealed that high doses of ciprofloxacin successfully induced persistence in *B. cepacia*. There was a marked increase in the expression of the MqsR toxin during both biofilm formation and persistence phases. Detailed structural and protein-protein interaction analysis of the MqsR/MqsA system indicated that an inhibitory peptide could potentially dismantle this complex, preventing its formation and function.

Conclusion: These compelling results suggest that the MqsR toxin is not just a passive player but a critical orchestrator of persistence and biofilm formation in *B. cepacia*. Targeting this toxin with an inhibitory peptide could pave the way for innovative treatments, revolutionizing our approach to combatting chronic and resistant infections caused by this pathogen. The MqsR toxin thus stands out as a promising beacon of hope in the fight against *B. cepacia* infections

Keywords: *B. cepacia*; biofilm; MqsR/MqsA system; 3D structure; docking; inhibitory peptide

Abstract ID: 334
subject: Other related topics

Computational design and screening of autolysin inhibitors for *Streptococcus pneumoniae*

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Background and Aim: Pneumococcal autolysin is an enzyme essential bacterial autolysis which releases pneumolysin and contributes to pneumococcal infections like otitis media, pneumonia, and meningitis. Recent research aims to combat infections caused by multi-drug resistant *Streptococcus pneumoniae* by targeting key genes or proteins. Therefore, this study focuses on identifying the most effective inhibitor for pneumococcal autolysin via molecular docking analysis.

Material And Methods: The 3D structure of autolysin (PDB ID: 2BML) was obtained from the RCSB PDB database. Three autolysin inhibitor ligands included 2,2':6',2"-Terpyridine Platinum (Ii), Capric dimethyl amine oxide, and D-Levofloxacin, and a total of 20 analogs for each ligand were retrieved from the PubChem database in SDF format. After preparation of protein and ligands, molecular docking was performed using Virtual Docker Molegro. The best interaction with the lowest binding energy was analyzed using Molegro Molecular Viewer software. Finally, pharmacokinetic properties such as distribution, absorption, metabolism and excretion of the ligand were investigated using SwissADME server.

Results: Among all the inhibitory ligands, the best ligand was N-methyl-N-octyloctan-1-amine oxide (PubChemCID 10967623) with a molecular weight of 271.48 g/mol and the most negative ΔGbind (-110/137 kcal/mol). This ligand formed 1 hydrogen bond with the Steroid Delta-isomerase residues Tyr249(A) and 3 steric interactions involving Ala277(A) and Tyr249(A) and Trp249(A). Moreover, the ADME results indicated that this ligand had a water solubility score of (LogS) -4.77, 1 hydrogen bond acceptors, 0 hydrogen bond donors, a lipophilicity score of (LOGP) 3.76, and a polarity score (TPSA) of 29.43.

Conclusion: Consequently, compared with other ligands, N-methyl-N-octyloctan-1-amine oxide (PubChemCID 10967623) may be used as an important candidate for targeting inhibition of *Streptococcus pneumoniae* Autolysin protein after further in vitro and in vivo analysis.

Keywords: Molecular docking , autolysin , *Streptococcus pneumoniae*.

Abstract ID: 337
subject: Other related topics

Prevalence and Molecular Detection of vly and pho genes and Antibiotic Resistance Pattern of *Gardnerella vaginalis* in adult Women in Yazd, Iran

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Background and Aim: Bacterial vaginosis represents the predominant cause of vaginal discharge among women of reproductive age. This study aimed to assess the prevalence of Bacterial vaginosis across various age groups and to employ molecular techniques for the detection of *Gardnerella vaginalis* in patients diagnosed with bacterial vaginosis.

Material And Methods: A total of 69 vaginal samples were collected from patients seeking medical care at the clinic. The researchers utilized polymerase chain reaction (PCR) to specifically identify the 16S rRNA, vaginolysin (vly), and phospholipase (pho) genes of *Gardnerella vaginalis*, the primary causative agent of BV. Samples were selected to investigate the susceptibly patterns of the following 6 antimicrobial agents from different antimicrobial classes. Metronidazole (5µg), Co-trimoxazole (25µg), Amikacin (30µg), Clindamycin (2 µg), Ciprofloxacin (5µg), and Gentamicin (10µg) discs (Padtan Teb, Iran). The antibiotic susceptibility patterns of *G. vaginalis* isolates were determined by the Kirby-Bauer method, and the results were interpreted according to CLSI guidelines.

Results: To analyze the correlation between the presence of the vly and pho genes, the Pearson Chi-square test was conducted using SPSS software, with a significance threshold set at a p-value of ≤0.05. The findings revealed that 42.6% of the participants were affected by Bacterial vaginosis, with *G. vaginalis* detected in the same percentage of women diagnosed with the condition. The prevalence rates for the vly and pho genes in *G. vaginalis* associated with Bacterial vaginosis were found to be 37.5% and 32.7%, respectively. Furthermore, the prevalence rates for the vly and pho genes in *G. vaginalis* associated with Bacterial vaginosis were determined to be 37.5% and 32.7%, respectively.

Conclusion: Importantly, the research findings highlighted a statistically significant relationship between the presence of the virulence genes and the Bacterial vaginosis status of the microorganism. This suggests that the molecular detection of specific genes in *G. vaginalis* could serve as a valuable tool for the diagnosis and management of bacterial vaginosis in clinical settings.

Keywords: *Gardnerella vaginalis*, Virulence factor, Vaginolysin, Vaginitis

Abstract ID: 34
subject: Other related topics

The impact of *Listeria monocytogenes* on apoptotic gene expression and embryonic mortality: A step towards embryonic microbiology

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Background and Aim: Embryonic microbiology is an emerging field that explores the effects of pathogens on the processes of embryonic growth and development. *Listeria monocytogenes*, a significant pathogenic bacterium, can invade host cells and alter molecular pathways, disrupting embryonic development. This study investigates the effect of *L. monocytogenes* on the expression of apoptotic genes Bax and Bcl2 in the chicken embryo chorioallantoic membrane (CAM) model. The goal of this research is to combine microbiology and embryology knowledge to better understand the molecular mechanisms of pathogen-induced embryonic mortality.

Material And Methods: Fourteen fertilized chicken eggs were randomly divided into two groups: Experimental group: CAMs were inoculated with *L. monocytogenes* at 1 0 6 10 6 CFU/mL on embryonic day 9. Control group: CAMs were treated with phosphate-buffered saline (PBS). The eggs were incubated at 37.7°C with 60% humidity for 72 hours. After incubation, CAM samples were collected for RNA extraction and cDNA synthesis. The expression of apoptotic genes Bax and Bcl2 was measured using Real-time PCR. Data were analyzed to interpret the relationship between infection, apoptotic regulation, and embryonic mortality.

Results: In the infected group, a significant increase in the expression of the pro-apoptotic gene Bax and a marked decrease in the expression of the anti-apoptotic gene Bcl2 were observed ($p < 0.05$). These changes indicate the activation of apoptotic pathways, leading to cell death in infected embryos.

Conclusion: This study demonstrates that *Listeria monocytogenes* can alter apoptotic gene expression, leading to increased embryonic mortality in the CAM model. The findings highlight the importance of embryonic microbiology in understanding the interactions between microbial infections and embryonic development. These insights could provide a foundation for new strategies to manage infections that affect embryonic growth.

Keywords: *Listeria monocytogenes*, apoptosis, chorioallantoic membrane (CAM), embryonic microbiology

Abstract ID: 301
subject: Other related topics

Illustration of inflammatory mechanisms of *Bacteroides fragilis* and its contribution to colorectal carcinogenesis

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Background and Aim: Bacteroides fragilis, an anaerobic bacterium in the gut microbiota, plays a critical role in maintaining microbial balance within the gastrointestinal tract. However, the enterotoxigenic strain of *Bacteroides fragilis* through secretion of its specific toxin, *Bacteroides fragilis* toxin, can promote the development and progression of colorectal cancer (CRC). The aim of this study was exploring the inflammatory molecular mechanisms of *Bacteroides fragilis* and its contribution to colorectal carcinogenesis.

Material And Methods: The inflammatory mechanisms of *Bacteroides fragilis* and its contribution to colorectal carcinogenesis were investigated in in vitro cultured human CRC cell lines, animal models and CRC patients.

Results: *Bacteroides fragilis* toxin disrupted the intestinal barrier by degrading E-cadherin, leading to cellular structural alterations, enhanced inflammation, and facilitated tumorigenesis. Furthermore, this toxin enhanced the cyclooxygenase-2 activity and production of prostaglandin E2, which drived chronic inflammation, cell proliferation, and cancer cell migration. Additionally, *Bacteroides fragilis* toxin activated STAT3 signaling pathways, promoted IL-6 production, which facilitated tumor cell survival and expansion. *Bacteroides fragilis* toxin also increased the induction of regulatory T cells and decreased interleukin-2 levels, resulting in elevated IL-17 production. This inflammatory shift further enhanced tumor cell growth and persistence. Moreover, *Bacteroides fragilis* toxin showed direct effects on the genome, including DNA damage and genetic alterations, which play a pivotal role in tumorigenesis.

Conclusion: These results showed that enterotoxigenic strain of *Bacteroides fragilis* simultaneously suppresses host antitumor immunity and creates a pro-inflammatory microenvironment conducive to tumor growth through various mechanisms including activation of STAT3 pathway, increased production of cyclooxygenase-2 enzyme and prostaglandin E2, as well as induction of tumor-promoting cytokines and regulatory T cells. These findings highlight the necessity for further investigations of molecular pathways involved in bacterial-induced colorectal carcinogenesis to advance therapeutic modalities of CRC.

Keywords: *Bacteroides fragilis*, colorectal cancer, chronic inflammation, cyclooxygenase-2, STAT3, cytokines, regulatory T cells.

Abstract ID: 297
subject: Other related topics

Anticancer peptides: Development, mechanisms, and challenges in targeted cancer therapy

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Background and Aim: A systematic review of relevant publications from 2013 to 2024 was conducted using reliable databases such as PubMed, Scopus, and Web of Science to explore recent trends and innovations in anticancer peptides (ACPs) and their clinical applications. Cancer remains one of the leading causes of death globally, and traditional treatment strategies like chemotherapy and radiotherapy often face significant challenges, including severe side effects, limited specificity, and the emergence of drug resistance. Anticancer peptides (ACPs), derived from antimicrobial peptides (AMPs), offer a promising alternative due to their selective cytotoxicity, reduced toxicity, and lower potential for resistance. This review delves into their development, mechanisms of action, structural diversity, and the challenges associated with clinical implementation.

Material And Methods: A comprehensive review of literature published between 2013 and 2022 was conducted to gather information on the development and characteristics of ACPs. Studies on the structure-function relationship of ACPs, their interactions with cancer cells, and their efficacy in preclinical and clinical settings were analyzed.

Results: The mechanisms of ACP action involve disrupting cancer cell membranes via electrostatic interactions, inducing apoptosis by mitochondrial damage, and inhibiting tumor angiogenesis. Peptides such as Magainin II, Aurein, and Gomesin exhibit significant cytotoxicity against cancers like lung, breast, and prostate, while showing minimal toxicity to normal cells. Despite these advantages, ACPs face challenges such as instability in physiological environments and incomplete selectivity, occasionally leading to off-target effects.

Conclusion: ACPs represent a groundbreaking approach to cancer therapy, addressing the shortcomings of traditional treatments. Their ability to selectively kill cancer cells, combined with reduced toxicity and low resistance, underscores their potential as future cancer treatments. Further research is essential to optimize their design, improve stability, and expand clinical applications. Emerging technologies like computational design and nanotechnology hold promise for overcoming current limitations, paving the way for more effective anticancer peptide therapies.

Keywords: Anticancer peptides (ACPs), mechanisms of action , cancer therapy, selective cytotoxicity , drug resistance

Abstract ID: 114
subject: Other related topics

A comparative study on the synergistic effects of thymol/ceftazidime against *Escherichia coli* and *Acinetobacter baumannii*

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Background and Aim: This study aims to compare the synergistic antimicrobial effects of thymol/ceftazidime on *Escherichia coli* and *Acinetobacter baumannii.*

Material And Methods: Antimicrobial effects of thymol/ceftazidime were performed first individually and then combined on *E. coli* ATCC 25922 and *A. baumannii* ATCC 19906 by the MIC-MBC method. Therefore, the antimicrobial effects of the compounds that had a synergistic impact were performed on clinical strains using the MIC-MBC method. The identification of chemical bonds, functional groups, and molecular interactions of the mentioned compound was investigated using an FT-IR device. Checkered method, biofilm inhibition on *E. coli* ATCC 25922 and *A. baumannii* ATCC 19906, and cytotoxicity investigation on red blood cells (RBCs) by hemolysis and human skin fibroblast cells (Ffk) by MTT method were performed. Finally, the results of the tests were compared between the two bacteria.

Results: The results of this study showed that the antimicrobial effects of the thymol/ceftazidime (16/4 µg/ml) were on *E. coli* better than on *A. baumannii* (512/128 µg/ml) in both clinical and ATCC strains. In the examination with the FT-IR device, it had bonds of OH carbohydrates proteins, polyphenols, C=O Amide I band, C-O-C polysaccharide, C-N amide III band, but one band named C=C conjugated, C≡C in compound showed the connection between thymol with ceftazidime. The biofilm inhibition effects of thymol/ceftazidime on *E. coli* ATCC 25922 (75.51%) were better on *A. baumannii* ATCC 19906 (23.41%). The cytotoxicity of synergistic compounds on RBCs and human Ffk cells was not different and was lower than that of Triton X-100.

Conclusion: Considering the antibiotic resistance of ceftazidime in the treatment of diseases caused by *E. coli* and *A. baumannii*, thymol/ceftazidime showed better antimicrobial and anti-biofilm effects in *E. coli* than *A. baumannii* in this study. After further studies, this compound can be used as a new drug in patients.

Keywords: *Escherichia coli*, *Acinetobacter baumannii*, thymol, ceftazidime, synergistic

Abstract ID: 115
subject: Other related topics

Comparative investigation of synergistic effects of thymol/cefotaxime on *Escherichia coli* and *Klebsiella pneumoniae*

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Background and Aim: The purpose of this study is to compare the synergistic antimicrobial effects of thymol/cefotaxime on *Escherichia coli* and *Klebsiella pneumoniae*.

Material And Methods: Antimicrobial effects of thymol/cefotaxime were performed first individually and then combined on *E. coli* ATCC 25922 and *K. pneumoniae* ATCC 100031 by the MIC-MBC method. Therefore, the antimicrobial effects of the compounds that had a synergistic impact were performed on clinical strains using the MIC-MBC method. The identification of chemical bonds, functional groups, and molecular interactions of the mentioned compound was investigated using an FT-IR device. Checkered method, biofilm inhibition on *E. coli* ATCC 25922 and *K. pneumoniae* ATCC 100031, and cytotoxicity investigation on red blood cells (RBCs) by hemolysis and human skin fibroblast cells (Ffk) by MTT method were performed. Finally, the results of the tests were compared between the two bacteria.

Results: The results of this study showed that the antimicrobial effects of the thymol/cefotaxime (4/2 µg/ml) were on *K. pneumoniae* better than on *E. coli* (128/16 µg/ml) in both clinical and ATCC strains. In the examination with the FT-IR device, had bonds of OH carbohydrates proteins, polyphenols, C=O Amide I band, C-O-C polysaccharide, and C-N amide III band, but one band named C=C conjugated, C≡C in compound showed the connection between thymol with cefotaxime. The biofilm inhibition effects of thymol/cefotaxime on *K. pneumoniae* ATCC 100031 (46.36%) were better on *E. coli* ATCC 25922 (39.28%). Cytotoxicity of the synergistic compound on RBCs and human Ffk cells was not different and was lower than that of Triton X-100.

Conclusion: Considering the antibiotic resistance of cefotaxime in the treatment of diseases caused by *E. coli* and *K. pneumoniae*, thymol/cefotaxime showed better antimicrobial and anti-biofilm effects in *K. pneumoniae* than *E. coli* in this study. After further studies, this compound can be used as a new drug in patients.

Keywords: *Escherichia coli*, *Klebsiella pneumoniae*, thymol, cefotaxime, synergistic

Abstract ID: 113
subject: Other related topics

A comparative study on the synergistic effects of thymol/ceftazidime against *Escherichia coli* and *Klebsiella pneumoniae*

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Background and Aim: This study compares the synergistic antimicrobial effects of thymol/ceftazidime on *Escherichia coli* and *Klebsiella pneumoniae*.

Material And Methods: Antimicrobial effects of thymol/ceftazidime were performed first individually and then combined on *E. coli* ATCC 25922 and *K. pneumoniae* ATCC 100031 by the MIC-MBC method. Therefore, the antimicrobial effects of the compounds that had a synergistic impact were performed on clinical strains using the MIC-MBC method. The identification of chemical bonds, functional groups, and molecular interactions of the mentioned compound was investigated using an FT-IR device. Checkered method, biofilm inhibition on *E. coli* ATCC 25922 and *K. pneumoniae* ATCC 100031, and cytotoxicity investigation on red blood cells (RBCs) by hemolysis and human skin fibroblast cells (Ffk) by MTT method were performed. Finally, the results of the tests were compared between the two bacteria.

Results: This study showed that the antimicrobial effects of the thymol/ceftazidime (4/2 µg/ml) were on *K. pneumoniae* better than on *E. coli* (16/4 µg/ml) in both clinical and ATCC strains. In the examination with the FT-IR device, had bonds of OH carbohydrates proteins, polyphenols, C=O Amide I band, C-O-C polysaccharide, and C-N amide III band, but one band named C=C conjugated, C≡C in compound showed the connection between thymol with ceftazidime. The biofilm inhibition effects of thymol/ceftazidime on *E. coli* ATCC 25922 (75.51%) were better on *K. pneumoniae* ATCC 100031 (58.44%). The cytotoxicity of synergistic compounds on RBCs and human Ffk cells was not different and was lower than that of Triton X-100.

Conclusion: Considering the antibiotic resistance of ceftazidime in the treatment of diseases caused by *E. coli* and *K. pneumoniae*, thymol/ceftazidime showed better antimicrobial and anti-biofilm effects in *E. coli* than in *K. pneumoniae* in this study. After further studies, this compound can be used as a new drug in patients.

Keywords: *Escherichia coli*, *K. pneumoniae*, thymol, ceftazidime, synergistic

Abstract ID: 116
subject: Other related topics

Comparative investigation of synergistic effects of thymol/cefotaxime on *Escherichia coli* and *Acinetobacter baumannii*

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Background and Aim: The purpose of this study is to compare the synergistic antimicrobial effects of thymol/cefotaxime on *Escherichia coli* and *Acinetobacter baumannii.*

Material And Methods: Antimicrobial effects of thymol/cefotaxime were performed first individually and then combined on *E. coli* ATCC 25922 and *A. baumannii* ATCC 19906 by the MIC-MBC method. Therefore, the antimicrobial effects of the compounds that had a synergistic impact were performed on clinical strains using the MIC-MBC method. The identification of chemical bonds, functional groups, and molecular interactions of the mentioned compound was investigated using an FT-IR device. Checkered method, biofilm inhibition on *E. coli* ATCC 25922 and *A. baumannii* ATCC 19906, and cytotoxicity investigation on red blood cells (RBCs) by hemolysis and human skin fibroblast cells (Ffk) by MTT method were performed. Finally, the results of the tests were compared between the two bacteria.

Results: The results of this study showed that the antimicrobial effects of the thymol/cefotaxime (128/16 µg/ml) were on *E. coli* better than on *A. baumannii* (512/512 µg/ml) in both clinical and ATCC strains. In the examination with the FT-IR device, had bonds of OH carbohydrates proteins, polyphenols, C=O Amide I band, C-O-C polysaccharide, and C-N amide III band, but one band named C=C conjugated, C≡C in compound showed the connection between thymol with cefotaxime. The biofilm inhibition effects of thymol/cefotaxime on *E. coli* ATCC 25922 and *A. baumannii* ATCC 19906 were (39.28%). Cytotoxicity of synergistic compound on RBCs and human Ffk cells was not different and was lower than that of Triton X-100.

Conclusion: Considering the antibiotic resistance of cefotaxime in the treatment of diseases caused by *E. coli* and *A. baumannii*, thymol/cefotaxime showed better antimicrobial effects in *E. coli* than in *A. baumannii* in this study. After further studies, this compound can be used as a new drug in patients.

Keywords: *Escherichia coli*, *Acinetobacter baumannii*, thymol, cefotaxime, synergistic

Abstract ID: 26
subject: Other related topics

Comparison of bacterial infections in abdominal surgery in dogs and humans: Risk factors and preventive strategies

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Background and Aim: Bacterial infections during abdominal surgeries pose significant risks to both dogs and humans, leading to prolonged recovery periods, increased healthcare costs, and even mortality. The aim of this review is to compare the incidence, risk factors, and preventive strategies of bacterial infections in abdominal surgeries between these two species, thereby identifying commonalities and differences that may inform improved clinical practices and outcomes.

Material And Methods: This literature review involved a systematic search of scientific databases including PubMed, Google Scholar, and Veterinary Information Network. Key search terms included "bacterial infections," "abdominal surgery," "dogs," "humans," "risk factors," and "preventive strategies." Studies were selected based on their relevance, quality, and publication date, prioritizing those published within the last ten years to ensure current data.

Results: In both dogs and humans, common bacterial pathogens identified include *Escherichia coli*, *Staphylococcus aureus*, and *Enterococcus species*. Risk factors such as prolonged surgery duration, contaminated surgical environment, and compromised immune systems were prevalent in both species. However, specific risk factors, such as the prevalence of multi-drug resistant bacteria, were more significant in human cases due to higher hospital-acquired infection rates. Preventive strategies like preoperative antibiotics, strict aseptic techniques, and postoperative wound care were effective across both species. However, the use of prophylactic antibiotics was more rigorously standardized and monitored in human medicine compared to veterinary practices.

Conclusion: The comparative analysis reveals that while there are similarities in the types of bacteria and general risk factors, human abdominal surgeries face greater challenges related to antibiotic resistance and hospital-acquired infections. Enhanced preventive strategies, particularly in veterinary practices, could benefit from adopting some of the stringent protocols used in human medicine. Further interdisciplinary studies are needed to develop universally applicable guidelines to reduce the risk of bacterial infections in abdominal surgeries for both dogs and humans.

Keywords: Surgical site infections, antibiotic prophylaxis, comparative medicine

Abstract ID: 344
subject: Other related topics

Investigation of the relationship between serum vitamin D levels and the presence of *Mycobacterium avium* subspecies paratuberculosis in patients with Hashimoto's thyroiditis

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Background and Aim: One of the most common autoimmune disease affecting the thyroid gland is Hashimoto's thyroiditis. Due to the genetic and environmental factors, individuals with genetic susceptibility exposed to environmental factors, including bacteria, activate immune responses that play a role in the development of the disease. _*Mycobacterium avium*_ subspecies _paratuberculosis_ (MAP) has been suggested to play a role in triggering Hashimoto's disease in recent years. Additionally, many studies have reported the role of normal levels of vitamin D in reducing mycobacterial infections and thyroid autoantibodies. This study aimed to investigate the relationship between vitamin D and concurrent MAP infection in Hashimoto's patients.

Material And Methods: In this case-control study, 60 blood samples were collected from two groups: patients with Hashimoto's thyroiditis and control individuals. The presence of MAP was examined using Nested-PCR and ELISA methods, and vitamin D levels were assessed using ELISA. Statistical analysis of the data was conducted.

Results: In the group of Hashimoto's patients who tested positive for MAP, 40% had a vitamin D deficiency, 57.1% had insufficiency, and 2.9% had sufficient vitamin D levels. In contrast, in the MAP-negative group, 6.7% of patients had a deficiency, 54.7% had insufficient levels, and 38.7% had adequate levels of vitamin D, which was statistically significant. Furthermore, vitamin D levels were significantly lower in the Hashimoto's group compared to the control group.

Conclusion: in addition to the relationship between *Mycobacterium avium* subspecies paratuberculosis infection and Hashimoto's disease, these findings suggest that vitamin D deficiency is not only a risk factor for Hashimoto's disease but may also be associated with the presence of Mycobacterium avium subspecies paratuberculosis in the patients with Hashimoto's thyroiditis.

Keywords: Hashimoto's thyroiditis, *Mycobacterium avium* subspecies paratuberculosis, vitamin D

Abstract ID: 368
subject: including the role of probiotics in health and disease

The role of probiotics in reducing prostate-specific antigen (PSA)

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Background and Aim: Prostate-specific antigen (PSA) is a protein produced by the prostate gland, and elevated PSA levels can indicate conditions such as benign prostatic hyperplasia, inflammation, or prostate cancer. Probiotics, particularly beneficial bacteria like *Lactobacillus* and *Bifidobacterium*, are well-known for their positive effects on overall health and reducing inflammation. This study investigates the potential role of probiotics in lowering PSA levels and improving prostate health.

Material And Methods: A study was conducted on men with elevated PSA levels and prostate-related symptoms. Participants were divided into two groups: a probiotic group and a control group. The probiotics used included *Lactobacillus rhamnosus* and *Bifidobacterium longum*. Participants consumed probiotics or placebo for 12 weeks. PSA levels, systemic inflammation markers (such as CRP), and urinary symptoms were assessed before and after the intervention.

Results: Results showed a significant reduction in PSA levels in the probiotic group compared to the control group. Additionally, systemic inflammation markers decreased, and urinary symptoms improved. Probiotics appeared to positively influence prostate health by modulating the gut microbiome and reducing the production of inflammatory substances.

Conclusion: Probiotic consumption may help lower PSA levels and alleviate symptoms associated with prostate disorders. This effect is likely due to reduced inflammation and improved gut microbiome balance. Further studies are needed to confirm these findings and clarify the precise mechanisms of probiotic action.

Keywords: Prostate-specific antigen, probiotics, *Lactobacillus rhamnosus*, *Bifidobacterium longum*

Abstract ID: 395
subject: including the role of probiotics in health and disease

The role of cosmetic probiotics in preventing skin wrinkles: Effects on skin microbiota and barrier function

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Background and Aim: Skin aging, often marked by the appearance of wrinkles, results from intrinsic factors (e.g., collagen degradation) and extrinsic factors (e.g., oxidative stress and UV damage). Recent evidence suggests that skin microbiota plays a vital role in maintaining skin health and youthfulness. This study investigates the effects of cosmetic probiotics on preventing skin wrinkles. To evaluate the impact of cosmetic probiotics on reducing oxidative stress, enhancing skin barrier function, and improving skin elasticity to prevent wrinkle formation.

Material And Methods: In this clinical study, a group of 30 participants applied probiotic-enriched creams containing strains such as *Lactobacillus Acidophilus* and *Bifidobacterium* breve for 12 weeks. Changes in skin elasticity, hydration, wrinkle depth, and inflammatory markers were assessed using skin analysis devices and laboratory methods.

Results: The results showed a significant increase in skin elasticity (+25%), improvement in skin hydration (+30%), and a reduction in wrinkle depth (-20%). Additionally, levels of inflammatory markers (IL-6 and TNF-α) significantly decreased.

Conclusion: Cosmetic probiotics, by modulating skin microbiota, enhancing the skin barrier, and reducing oxidative stress, can effectively prevent wrinkle formation. These findings suggest that probiotic-based products could serve as a novel approach in skincare.

Keywords: Cosmetic probiotics, skin wrinkles, skin microbiota

Abstract ID: 364
subject: including the role of probiotics in health and disease

The relationship between oral microbiome and dental caries

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Background and Aim: Dental caries is one of the most common oral diseases, particularly prevalent in urban populations. It is primarily caused by the activity of microorganisms in the mouth, which produce acids that demineralize tooth enamel. The oral microbiome, which includes a variety of bacteria, fungi, and viruses, plays a critical role in oral health. Alterations in the composition of the oral microbiome may contribute to an increased risk of dental caries. This study aims to investigate the relationship between changes in the oral microbiome and dental caries.

Material And Methods: In this study, saliva samples were collected from both healthy individuals and those with dental caries. Advanced techniques such as next-generation sequencing (NGS) were used to identify the oral microbiome composition. The data were analyzed to identify differences in microbial diversity and richness between the groups. Specific bacterial species associated with an increased risk of dental caries were also identified.

Results: The results showed that individuals with dental caries had a significantly lower microbial diversity in their oral microbiome compared to healthy individuals. Specific bacteria such as *Streptococcus mutans* and *Lactobacillus* were found to be significantly more prevalent in caries-affected individuals. These bacteria are associated with acid production and enamel degradation. In contrast, species such as *Streptococcus salivarius* and *Prevotella* were more abundant in healthy individuals, providing a protective effect against dental caries.

Conclusion: This study suggests that changes in the composition of the oral microbiome may serve as a risk factor for dental caries. Identifying specific bacteria associated with caries could help in designing novel preventive and therapeutic strategies. Further studies are recommended to better understand the underlying mechanisms of this association.

Keywords: Oral microbiome, dental caries, *Streptococcus mutans*, *Lactobacillus*, next-generation sequencing

Abstract ID: 407
subject: including the role of probiotics in health and disease

Effect of *Lactobacillus Acidophilus* probiotic in cosmeceutical products on reducing inflammation in vitiligo disease

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Background and Aim: Vitiligo is an autoimmune skin condition characterized by the loss of melanocytes, leading to white patches on the skin. Oxidative stress and inflammation play significant roles in the progression of the disease. Probiotics, especially *Lactobacillus Acidophilus*, are gaining attention for their anti-inflammatory properties and immune-modulating effects, making them promising in improving skin diseases. To evaluate the effect of *Lactobacillus Acidophilus*-based cosmeceutical products in reducing inflammation and improving symptoms of vitiligo.

Material And Methods: Cosmeceutical products containing *Lactobacillus Acidophilus* were applied topically to patients with vitiligo. The parameters assessed included a reduction in inflammatory markers, improvement in pigmentation, and skin tolerance.

Results: The use of *Lactobacillus Acidophilus*-containing products significantly reduced inflammatory markers (such as IL-6 and TNF-?). Improvement in pigmentation was observed in affected areas. High product tolerance with no side effects reported.

Conclusion: *Lactobacillus Acidophilus*-based cosmeceuticals can be an effective, non-invasive adjunct therapy in managing vitiligo. These products help reduce inflammation and strengthen the skin's defense barrier, offering significant benefits to patients.

Keywords: *Lactobacillus Acidophilus*, probiotics, vitiligo, inflammation, cosmeceuticals.

Abstract ID: 351
subject: including the role of probiotics in health and disease

Probiotic supplementation of *Lactobacillus* and *Bifidobacterium* in the prevention and improvement of human diseases: Scientific evaluation and their impact on cancer treatment

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Background and Aim: Probiotics, particularly *Lactobacillus* and *Bifidobacterium* species, have garnered attention for their potential health benefits, including their roles in preventing and improving various human diseases. This study aims to evaluate their efficacy in cancer treatment and overall health promotion through a systematic review of existing literature

Material And Methods: A comprehensive literature search was conducted across multiple biomedical databases, including PubMed, Scopus, and Cochrane Library, focusing on clinical trials and intervention studies from 2000 to 2023. Inclusion criteria encompassed studies that assessed the effects of *Lactobacillus* and *Bifidobacterium* supplementation on cancer incidence, progression, treatment response, and overall health outcomes. Data were extracted and analyzed using meta-analytical methods to summarize findings

Results: The analysis revealed that probiotic supplementation significantly improved immune responses and quality of life in cancer patients undergoing treatment. Notably, *Lactobacillus* and *Bifidobacterium* were associated with reduced side effects of chemotherapy and radiotherapy, enhanced gut microbiota balance, and improved nutritional status. Several studies indicated a potential reduction in tumor markers, suggesting a role in anticancer activity.

Conclusion: Probiotic supplementation with *Lactobacillus* and *Bifidobacterium* shows promise in the prevention and management of various diseases, particularly in enhancing cancer treatment outcomes. These findings underscore the importance of incorporating probiotics into health strategies, warranting further clinical investigation to establish optimal strains, dosages, and treatment protocols

Keywords: Probiotics, *Lactobacillus*, *Bifidobacterium*, cancer treatment, immune response, gut microbiota

Abstract ID: 410
subject: including the role of probiotics in health and disease

The relationship between oral microbiome and stomach cancer

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Background and Aim: Stomach cancer is a major cause of cancer-related deaths worldwide. While factors like *Helicobacter pylori* infection, diet, and genetics are well-known contributors, recent research suggests the oral microbiome may also influence gastric cancer development. This study explores the role of oral bacterial composition in gastric carcinogenesis, focusing on inflammation and immune responses.

Material And Methods: Saliva and oral swab samples were collected from stomach cancer patients and healthy controls. Using 16S rRNA sequencing, bacterial diversity and species were analyzed. Some groups received probiotics or antibiotics to modify the oral microbiota, and their effects on gastric cancer were assessed. Tumor progression, *H. pylori* levels, and inflammation-related gene markers (e.g., IL-6, TNF-α) were evaluated through histological and molecular methods.

Results: Cancer patients exhibited oral dysbiosis, marked by an increase in pathogenic bacteria like *Fusobacterium* and *Porphyromonas* and a decrease in protective species like *Lactobacillus*. Oral dysbiosis correlated with higher *H. pylori* levels in the stomach and increased inflammation, contributing to mucosal damage and tumor development. Modifying the oral microbiome with probiotics or antibiotics reduced gastric inflammation and slowed cancer progression in animal models.

Conclusion: Oral microbiome dysbiosis plays a significant role in stomach cancer by promoting inflammation and immune dysfunction. Restoring oral microbial balance may offer a potential strategy for preventing or managing gastric cancer, though further clinical studies are needed.

Keywords: Oral microbiome , stomach cancer

Abstract ID: 176
subject: emerging and re-emerging diseases

Utilization of the virulent strain *Clostridium novyi-NT* in cancer therapy: Potentials, challenges, and the future of novel treatments

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Background and Aim: The use of oncolytic bacteria represents a novel approach in cancer therapy, with *Clostridium novyi-NT* emerging as a leading candidate due to its ability to selectively target and lyse malignant tumor cells. This virulent strain thrives in the anaerobic environments of solid tumors, proliferating within necrotic tissues while inducing considerable immune responses against cancer. *C. novyi-NT* not only reduces tumor size in preclinical models but also enhances the efficacy of traditional therapies through systemic immune activation. The aim of this article is to explore the potentials, challenges, and future prospects of utilizing *Clostridium novyi-NT* in cancer treatment.

Material And Methods: This study conducts a review based on searches in scientific databases, including Scopus, PubMed, and Embase, from 2016 to 2024, using keywords such as *Clostridium novyi-NT*, Cancer Therapy, and Virulent. A total of 67 relevant articles were reviewed and analyzed.

Results: Findings highlight that *C. novyi-NT* effectively targets solid tumors, generating necrotic areas and improving immune responses. Research indicates that this bacterium can reduce tumor size and increase survival rates in animal cancer models, positively affecting cancer cells. However, significant challenges remain, including managing side effects, avoiding unwanted immune reactions, and determining optimal dosing strategies to enhance therapeutic outcomes.

Conclusion: *C. novyi-NT* shows promise as an immunotherapeutic option for cancer, necessitating further investigation. Thorough assessments of side effects and efficacy in human subjects are crucial for progressing this therapy into clinical application. Moreover, developing combination strategies that synergize *C. novyi-NT* with existing therapies could reshape the future landscape of cancer treatments.

Keywords: *Clostridium novyi-NT*, cancer therapy, virulent.

Abstract ID: 177
subject: emerging and re-emerging diseases

The role of *Mycobacterium bovis* (BCG) vaccine in enhancing immune response and tumor suppression: A systematic review on therapeutic applications in various cancers

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Background and Aim: The BCG (Bacillus Calmette-Guérin) vaccine, initially created for tuberculosis prevention, has emerged as a promising immunotherapeutic agent in treating various malignancies, particularly bladder cancer. BCG activates both innate and adaptive immune systems—engaging macrophages, dendritic cells, and T lymphocytes—to suppress tumor growth. By inducing localized inflammation within tumors, BCG enhances immune cell infiltration and cytokine production, fostering an environment conducive to antitumor activity. While its effectiveness for superficial bladder cancer is established, its applications in other cancers like melanoma, prostate cancer, and non-small cell lung cancer remain under investigation. Although some studies show promising outcomes, challenges such as dosing, administration routes, and patient selection persist. This systematic review aims to evaluate evidence regarding *Mycobacterium bovis* BCG's role in enhancing immune responses and suppressing tumors across different cancers. It compiles data from preclinical and clinical trials to assess BCG's efficacy, examine antitumor mechanisms, and identify barriers for broader oncology implementation.

Material And Methods: This study synthesizes findings from searches in databases including Scopus, PubMed, and Embase from 2014 to 2024 using keywords like *Mycobacterium bovis*, BCG vaccine, and bladder cancer, extracting and analyzing 57 relevant articles.

Results: Findings demonstrate that BCG increases the activity of immune cells, especially T lymphocytes and macrophages, contributing to tumor suppression and improved outcomes in bladder cancer and potentially other cancers. BCG also induces a beneficial inflammatory response, enhancing the immune system's capacity to combat tumors. These mechanisms may inform new therapeutic strategies in cancer treatment.

Conclusion: This review highlights the effectiveness of *M. bovis* (BCG) in enhancing immune responses and tumor suppression, indicating its potential as a safe and effective cancer treatment. While beneficial for bladder cancer, BCG may also yield positive effects in other malignancies. Future research should focus on elucidating immune mechanisms and developing comprehensive protocols to optimize BCG's therapeutic applications.

Keywords: *Mycobacterium bovis*, BCG vaccine, bladder cancer, immune response

Abstract ID: 61
subject: emerging and re-emerging diseases

Emerging *Mycobacterium tuberculosis* lineages: Challenges and implications for public health: A systematic review

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Background and Aim: *Mycobacterium tuberculosis* (*Mtb*) remains a leading cause of global morbidity and mortality, complicating public health efforts due to the emergence of new strains. Recent discoveries of novel *Mycobacterium tuberculosis* complex (MTBC) lineages pose challenges to current diagnostic and therapeutic strategies. This review provides an in-depth exploration of the most recent emerging species of Mtb, highlighting their genetic characteristics, epidemiological significance, and implications for public health.

Material And Methods: A comprehensive literature systematic review was conducted using databases such as PubMed, Scopus, and Web of Science to identify recent publications on emerging Mtb species from 2018 to 2023. Relevant studies were selected based on their focus on genetic analysis, clinical outcomes, and geographical distribution of novel strains. Information was synthesized to present a coherent overview of these emerging species' impact on Mtb epidemiology and management.

Results: Recent findings have identified several novel Mtb lineages, including *Mycobacterium tuberculosis* var. canettii and newly categorized strains from Africa and Southeast Asia. Genetic analyses revealed distinct mutations associated with drug resistance, including mutations not previously linked to treatment failure. Epidemiological data indicate a significant prevalence of these emerging strains in specific regions, underscoring their potential to disrupt established treatment protocols and challenge existing vaccine efficacy.

Conclusion: The emergence of new *Mycobacterium tuberculosis* species highlights the need for tailored public health responses and updated clinical guidelines. Continued monitoring and research into the genetic diversity of Mtb are critical to understanding transmission dynamics and developing effective interventions. This review reinforces the importance of global cooperation in surveillance and the urgent need for innovative approaches to combat these emerging threats to tuberculosis control efforts.

Keywords: *Mycobacterium tuberculosis*, emerging strains, genetic diversity, drug resistance, epidemiology, public health strategies, surveillance, tuberculosis control

Abstract ID: 216
subject: emerging and re-emerging diseases

A systematic review on reverse-zoonosis: Global impact and changes in transmission patterns

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Background and Aim: Pathogens are transmitted from people to animals through reverse zoonosis, also known as zooanthroponosis. Despite the considerable threats to both animal and public health, this phenomenon is far less studied than zoonotic illnesses. Reverse zoonotic incidents have increased due to increased human-animal interactions brought on by urbanization, globalization, and environmental changes. This review looks at global trends of reverse zoonosis, with an emphasis on bacterial infections, risk factors, and prevention efforts

Material And Methods: Articles published between 2000 and 2022 were used in a systematic review. Keywords like "human-to-animal transmission," "zooanthroponosis," and "reverse zoonosis" were used to search databases like ISI Web of Science and PubMed. 91 pertinent research articles were discovered following an initial screening of 2,509 papers. The study focused on the rates at which diseases brought on by bacteria, viruses, parasites, fungus, and protozoa spread

Results: The data indicates that bacterial infections, such as *Salmonella* species, *Mycobacterium TB*, and methicillin-resistant *Staphylococcus aureus* (MRSA), are among the most often reported agents of reverse zoonosis. There have been reports of TB transmission from humans to goats, elephants, and cattle in Ethiopia, India, and Nigeria. In Taiwan, the US, and Germany, MRSA was discovered in livestock, including dairy cows and pigs. Dogs and horses throughout Europe have been found to harbor *Escherichia coli*, especially those that produce extended-spectrum beta-lactamase (ESBL). Antimicrobial resistance brought on by inappropriate antibiotic usage, habitat loss from urbanization and deforestation, and wildlife commerce were important risk factors. Disease transmission was aided by intensive farming methods and intimate human-animal contact in both domestic and wild environments. Notable geographical hotspots included the United States, India, and Hong Kong, with documented cases spanning Asia, North America, and Europe.

Conclusion: The findings demonstrate the urgent need for robust surveillance systems to monitor the transmission of viruses from humans to animals. It takes interdisciplinary partnership among public health, veterinary medicine, and environmental studies to address the causes of reverse zoonosis. Targeted efforts are needed to lessen the risks connected to this phenomenon, such as reducing antibiotic use, enhancing animal husbandry biosecurity, and stopping habitat deterioration. Public awareness campaigns and research on human-animal relations can also assist prevent future outbreaks and protect global health

Keywords: public health, emergent diseases, bacterial infections, reverse zoonosis, and antibiotic resistance.

Abstract ID: 359
subject: emerging and re-emerging diseases

Prevalence of *Mycobacterium abscessus* bacteria in the lungs of patients with cystic fibrosis in the world based on a meta-analysis study

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Background and Aim: In recent years, infections caused by *Mycobacterium abscessus* (MABS) have emerged as significant pathogens in patients with cystic fibrosis (CF). The prevalence of this microorganism in the lungs of CF patients can lead to serious clinical complications and adversely affect their quality of life. This study aims to examine the global prevalence of MABS in CF patients through a meta-analysis, providing valuable insights into risk factors and infection patterns. Ultimately, this research seeks to enhance our understanding and management of MABS-related infections in this vulnerable population.

Material And Methods: For this meta-analysis, relevant articles on the prevalence of *Mycobacterium abscessus* (MABS) in the lungs of patients with cystic fibrosis (CF) were searched in databases including PubMed, Google Scholar, Scopus, and Web of Science. The search was conducted up to January 2024 using appropriate keywords. Selected articles were based on inclusion criteria that encompassed study design, sample size, and precise reporting of MABS prevalence. For data analysis, statistical tests such as Analysis of Variance (ANOVA), random-effects modeling, and hypothesis testing were utilized. Additionally, heterogeneity was assessed using the I^2 test, and sensitivity analysis was performed to evaluate the impact of any specific study on the final results.

Results: In this meta-analysis, we reviewed a total of 17 articles across the four databases regarding the prevalence of *Mycobacterium abscessus* (MABS) in patients with cystic fibrosis. Our findings indicated an overall prevalence rate of 8.21%, with a 95% confidence interval (CI) ranging from 3% to 19%. These results underscore the significance of MABS infections in the cystic fibrosis population and highlight the necessity for ongoing surveillance and effective management strategies.

Conclusion: In conclusion, this meta-analysis highlights the significant presence of *Mycobacterium abscessus* (MABS) in patients with cystic fibrosis. The findings emphasize the need for increased awareness of MABS as a crucial pathogen that can lead to serious clinical complications. Continuous monitoring and early detection strategies are essential for effective management of these infections. Additionally, future research should explore the underlying mechanisms of infection and the development of targeted therapies to reduce the impact of MABS on the health of cystic fibrosis patients.

Keywords: *Mycobacterium abscessus*,prevalence,cystic fibrosis

Abstract ID: 128
subject: emerging and re-emerging diseases

Borrelia theileri infections in Rhipicephalus annulatus ticks from the North of Iran

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Background and Aim: Ticks are vectors for *Borrelia* species that can cause diseases in humans and animals. Mazandaran, a fertile region in northern Iran, hosts at least 26 hard tick species. Ticks serve as vectors and reservoirs for various pathogens, such as viruses, bacteria, and protozoa, which can cause diseases in humans, livestock, and wild animals. Mazandaran Province is a fertile green land in the Caspian Sea littoral of Iran. The prime pastures and forests for livestock grazing make this area home to various tick species. This study investigated Borrelia infection in hard ticks from forest areas of this province and compared their identity with Borrelia species available in the GenBank database.

Material And Methods: Ticks were collected by hand from mammalian hosts, including sheep, goats, cows, and dogs, or by dragging and flagging practices. The specimens were grouped into 231 pools or individuals according to developmental stage, gender, and species. Following DNA extraction, Borrelia was detected by amplifying a 136-bp sequence of the 16S rRNA gene using a real-time PCR (qPCR). The qPCR-positive samples were further analyzed by amplification and sequencing the *flaB* and *glpQ* genes, followed by BLAST and phylogenetic analysis.

Results: The qPCR detected Borrelia in 27 tick samples from Rhipicephalus annulatus, Ixodes ricinus, and Haemaphysalis punctata. The *flaB* gene was amplified from eight Rh. annulatus and one Ix. ricinus tick samples. Additionally, *glpQ* was amplified from six specimens, all belonging to Rh. annulatus. The flaB sequences from Rh. annulatus ticks had variations and exhibited the highest identity (98.1%-100%) with *Borrelia theileri* and related undefined isolates from other geographical areas. The *glpQ* sequences matched the most (98.2%) with the only available sequence from *B. theileri* KAT in Mali. Also, phylogenetic analysis based on *flaB* and *glpQ* genes clustered our sequences with *B. theileri* and closely related undefined isolates.

Conclusion: The highest identity of generated *flaB* and *glpQ* sequences with *B. theileri* and their clustering within well-supported clades with this species and closely related isolates from different geographical origins corroborated the occurrence of *B. theileri* in the North of Iran.

Keywords: Rhipicephalus annulatus, *Borrelia theileri*, hard ticks, Phylogenetic analysis, Mazandaran, Iran

Abstract ID: 129
subject: emerging and re-emerging diseases

Molecular diversity and antibiotic resistance patterns of *Brucella* strains using molecular genotyping in Khomein, Iran

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Background and Aim: Brucellosis is a persistent zoonotic disease posing significant public health and economic challenges in various regions, including Khomein, Iran. Understanding the molecular diversity and antibiotic resistance patterns of Brucella isolates is crucial for effective disease management and control. This study aimed to investigate the molecular characteristics and antibiotic resistance profiles of *Brucella* strains isolated from human and animal samples in Khomein using advanced molecular genotyping techniques

Material And Methods: A total of 200 samples were collected from suspected human cases (n=100) and livestock (n=100) in Khomein. Clinical samples included blood, milk, and lymph node aspirates, while animal samples comprised milk and tissue samples from infected livestock. Following collection, samples were processed and cultured on Brucella Agar supplemented with 5% sheep blood under appropriate incubation conditions. A total of 58 Brucella isolates (29%) were successfully cultured, with 35 isolates originating from human samples and 23 from livestock. Molecular identification was performed using 16S rRNA gene sequencing and multiplex PCR targeting specific Brucella genes. Additionally, variable number tandem repeat (VNTR) analysis was conducted for molecular genotyping to assess genetic diversity among the isolates. Antibiotic susceptibility testing was carried out using the disk diffusion method according to CLSI (M24-A2) guidelines, employing a panel of commonly used antibiotics

Results: Of the 58 Brucella isolates, molecular identification revealed the predominance of *Brucella melitensis* (74.1%, n=43), followed by Brucella abortus (20.7%, n=12), and other Brucella species (5.2%, n=3). VNTR analysis identified 15 distinct genotypic profiles, indicating significant genetic diversity and suggesting multiple transmission pathways between human and animal populations. Antibiotic susceptibility testing demonstrated that 17.2% of isolates were resistant to tetracycline, 12.1% exhibited resistance to rifampin, while no resistance was observed for streptomycin and doxycycline. Furthermore, 10 isolates (17.2%) were classified as multidrug-resistant (MDR), showing resistance to three or more antibiotic classes tested

Conclusion: The identification of MDR Brucella strains underscores the urgent need for continuous surveillance, stringent antibiotic stewardship, and the implementation of targeted control measures to mitigate the spread of resistant infections. Molecular genotyping proved to be an effective tool in elucidating the epidemiological links and enhancing our understanding of Brucella population structure in this region

Keywords: Brucella, zoonotic disease, Molecular identification

Abstract ID: 119
subject: emerging and re-emerging diseases

Epidemiology of *Francisella tularensis* in the countries of the WHO eastern

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Background and Aim: *Francisella tularensis*, the bacterium that causes tularemia, has been a persistent and wide-spread pathogen in various regions of the world for centuries. *F. tularensis* can affect humans and various domestic and wild animals. The current study aimed to determine the epidemiological status of tularemia in countries of the WHO Eastern Mediterranean Region (EMRO) through a systematic review and meta-analysis.

Material And Methods: All included studies were identified through a systematic search of online databases, including Scopus, PubMed, Web of Science, and EMBASE, through July 26, 2022, using key-words and suitable combinations. We focused on cross-sectional studies investigating the prevalence of *F. tularensis*. The weighted pooled prevalence was calculated using a random effects model.

Results: A total of 206 studies were identified, of which 20 were finally included in the analysis. The human seroprevalence of tularemia in WHO-EMRO countries was 6.2% (95% CI, 4.2 9.2). In the subgroup analysis, anti *F. tularensis* antibodies were found in 6.92% and 5.5% of the high-risk individuals and Iran, respectively. The pooled prevalence of *F. tularensis* in environmental samples (water and soil) from the WHO-EMRO countries was 5.8% (9.4% by PCR and 0.5% by culture). In addition, 2.5% (95% CI, 0.2 0.22.7) of ticks in WHO-EMRO countries were positive for *F. tularensis*. The pooled prevalence of *F. tularensis* in rodents is2.0% (1.1% by PCR and 3.7% by serology). In addition, 0.6% of domestic ruminants (0.4%by PCR and 2.4% by serology) were positive for *F. tularensis* in WHO-EMRO countries.

Conclusion: According to the results of the present study, tularemia is an endemic but neglected disease in the WHO-EMRO region. However, most studies on tularemia are limited to a few countries in this region. Studies on tularemia in human populations, reservoirs, and vectors have been conducted in all countries in the WHO-EMRO region to obtain more detailed information about the epidemiology of tularemia in these regions.

Keywords: *Francisella tularensis*, tularemia, eastern mediterranean region (EMRO)

Abstract ID: 118
subject: emerging and re-emerging diseases

Recombinant GroEL protein from *Francisella tularensis*: A promising candidate for enhanced tularemia diagnosis

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Background and Aim: Tularemia, caused by the zoonotic pathogen *Francisella tularensis*, presents with diverse clinical manifestations, making accurate diagnosis challenging. Existing diagnostic methods are hindered by low sensitivity, biosafety concerns, and limited applicability in low-resource settings. Antigen FTT1696 (GroEL) of *F. tularensis* was selected for its significant immunological properties and diagnostic potential. This study aims to evaluate the conservation of GroEL gene among different *F. tularensis* and then express the recombinant protein in expression prokaryotic system.

Material And Methods: The gene encoding *GroEL* was analyzed across all *F. tularensis* strains in the GenBank database (https://www.ncbi.nlm.nih.gov/gene). Cloning and expression of the *GroEL* gene from *F. tularensis* subsp. holarctica LVS NCTC 10857 strain was done in pET28a-*E. coli* BL21 (DE3) expression system. Then, the recombinant expressed protein was evaluated by SDS-PAGE and confirmed using western blot. Then, the recombinant protein GroEL was purified using Nickel column under denaturation condition.

Results: The results revealed minimal genetic variation (less than 0.5%), indicating a high degree of conservation of *GroEL* gene across different *F. tularensis* strains. The physicochemical properties of *GroEL* gene including molecular weight (57428.73 Da), number of amino acids (544), theoretical pI (4.96), instability index (23.39, Stable), estimated half-life, aliphatic index (94.01), and grand average of hydropathicity (GRAVY) were evaluated using the Expasy ProtParam online tool (https://web.expasy.org/protparam/). The results of the SDS-PAGE analysis showed the presence of a 60 KD protein band that was confirmed by western blot. The protein was purified with high purity and concentration on the Nickel resin.

Conclusion: Due to the potential of *F. tularensis* strains in pathogenesis, finding diagnostic protocols could enhance early and accurate detection, particularly in endemic areas or settings with limited access to advanced diagnostic tools. The findings of this study identified the high conservation of *GroEL* gene among different *F. tularensis* strains and showed the potential of this candidate as a promising serological biomarker for diagnosing tularemia. In addition, the high purity and quantity of the purified *GroEL* could be useful for diagnostic purposes. Further studies are recommended to validate the efficacy of the purified protein to be used as a potential target for diagnostic purposes.

Keywords: *Francisella tularensis*,*GroEL* ,cloning, expression

Abstract ID: 135
subject: rational antibiotic prescription and resistance mechanisms

Investigation of antibiotic resistance byeExtended-spectrum β-lactamase in uropathogenic *E.coli*

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Background and Aim: Gram-negative *Escherichia coli*, belonging to the *Enterobacter*iaceae family, as one of the main factors causing urinary tract infections, respiratory tract infections, digestive tract infections, and hospital infections, has been associated with the emergence and spread of new resistant strains. As part of the normal flora of the intestine, this bacterium colonizes the digestive system of humans and mammals a few hours after birth, and with this action, it plays an important role in the physiology of the digestive system. Considering the increasing resistance to some antibiotics and the wide changes in the effective spectrum of drugs and preventing the increase of drug-resistant cases, it seems very necessary to carry out drug sensitivity tests. Finally, the prevalence of beta-lactam resistance is a useful marker for investigating resistance genes and can be useful in ecological studies. Therefore, it is important to use molecular methods to fully identify these enzymes. Beta-lactamase enzymes SHV, TEM, CTX-M are among the enzymes located on transposable elements. ESBLs are beta-lactamases that hydrolyze penicillins and broad-spectrum cephalosporins. The purpose of this research is to investigate the antibiotic resistance of ESBL-producing uropathogenic *Escherichia coli* isolates and the frequency of TEM genes, SHV, CTX-M, and their antibiotic sensitivity pattern.

Material And Methods: 100 *Escherichia coli* isolates were isolated from urine samples and the antibiotic sensitivity of the strains was determined by Disk Diffusion method and the presence of SHV, TEM, and CTX-M genes was measured by PCR using specific primers.

Results: The amount of antibiotic resistance of the isolated strains to ceftazidime (16%), ceftriaxone (27%) and cefotaxime (27%) antibiotics was obtained. The abundance of genes was obtained in 32 ESBL-producing samples, (25%) SHV, (59.4%) CTX-M, (50%) TEM.

Conclusion: The interpretation of the experiments shows that the production of ESBL beta-lactamase enzymes in the studied strains by PCR showed an average frequency of 45% of the studied genes, and to prevent the spread of ESBL-producing *Escherichia coli* strains, careful medical care and correct use are required. And timely use of appropriate antibiotics.

Keywords: SHV; TEM; CTX-M; *Escherichia coli*

Abstract ID: 374
subject: rational antibiotic prescription and resistance mechanisms

The use of bacteriophages for treating bacterial throat infections

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Background and Aim: Bacterial throat infections, particularly those caused by Group A *Streptococcus*, are common medical issues. The rising antibiotic resistance of these bacteria has highlighted the need for alternative treatments, such as bacteriophages. Bacteriophages are viruses that specifically target and destroy bacterial pathogens.

Material And Methods: In this study, specific bacteriophages targeting Streptococcal strains were isolated and tested under laboratory conditions (in vitro) and animal models (in vivo). The effectiveness of the phages was evaluated through bacterial load reduction and clinical improvement in infection symptoms. Additionally, the stability of the phages in the throat environment and their impact on the natural microbiome of the area were assessed.

Results: Phages significantly reduced Streptococcal bacterial loads in vitro. In animal models, phage treatment improved throat infection symptoms and reduced inflammation. The phages had minimal effects on the beneficial bacteria in the throat, indicating high safety levels for this method.

Conclusion: Bacteriophages have great potential for treating throat infections, especially those resistant to antibiotics. Further research is needed to optimize production, safety, and efficacy of this therapeutic method.

Keywords: Bacteriophage, bacterial throat infection, bacteriophage therapy

Abstract ID: 268
subject: rational antibiotic prescription and resistance mechanisms

Carcasses of slaughtered goats in Kerman: A potential reservoir of β-lactam-resistant *Escherichia coli* and a public health challenge

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Background and Aim: Extended-spectrum β-lactamase (ESBL)-producing *Escherichia coli* is one of the significant food-borne pathogens transmissible from food products of animal origin to humans. The aim of this study was to investigate the phenotypic and genotypic resistance of *E. coli* isolates obtained from goat carcasses in Kerman abattoir against β-lactam antibiotics.

Material And Methods: In this study, 150 goat carcasses were examined at the Kerman slaughterhouse over a one-year period in 2023. From each carcass, two swab samples were collected, one from the internal surface and one from the external surface, resulting in a total of 300 swabs. After culturing the swabs and isolating *E. coli*, the resistance of the isolates to cefotaxime and ceftazidime was determined using the disk diffusion method, and the genes *blaTEM, blaSHV, blaCTX-M*, and *blaOXA* were detected using PCR.

Results: Overall, 190 of 300 the swabs (63.33%) were positive for *E. coli*, resulting in 190 isolates. Among these, 45.27% were resistant to cefotaxime, and 26.32% were resistant to ceftazidime. The frequencies of *the blaTEM, blaCTX-M, blaSHV*, and *blaOXA* genes were 8.94%, 7.89%, 2.1%, and 2.1%, respectively.

Conclusion: As a result, this study identifies goat carcasses as a potential reservoir of β-lactam-resistant *E. coli*, posing a significant public health challenge in the studied region.

Keywords: β-lactam, antibiotic resistance, *Escherichia coli*, goat carcasses

Abstract ID: 101
subject: rational antibiotic prescription and resistance mechanisms

Investigation of the level of resistance to colistin, fosfomycin and azithromycin in clinical isolates of *Shigella* that produce carbapenemase and ESBL

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Background and Aim: *Shigella* is recognised as one of the primary causes of diarrhoea worldwide. The ai of the current study was to examine the prevalence of resistant genes and their ability to form biofilms.

Material And Methods: Fifty samples of various Shigella species were collected from patients admitted to Milad Hospital, Tehran, Iran. The samples underwent an antibiotic susceptibility test (antibiogram), an extended spectrum beta-lactamase (ESBL) phenotypic test, a carbapenemase enzyme detection test, and a biofilm formation ability test. Additionally, the presence of mcr-1, mcr-2, fosA3, and mphA resistance genes was tested after extracting bacterial DNA.

Results: Out of the 50 isolated samples, 22 (44%) were female and 28 (56%) were male. The antibiogram test results showed the highest resistance to trimethoprim-sulfamethoxazole (92%) and tetracycline (90%) antibiotics. All isolates produced carbapenemase enzymes, of which 50% also produced ESBL enzymes. In the biofilm formation assay, 94% of isolates had weak biofilm formation ability and 6% had moderate biofilm formation. The PCR results indicate that 28% of the samples tested positive for the azithromycin resistance gene (*mphA*). None of the isolates were found to contain the mcr-1, mcr-2, or *fosA3* genes.

Conclusion: Understanding the antibiotic resistance profile and the presence of resistance associated genes, can enhance our understanding of the local epidemics which can be extremely helpful in treatment of such infections. Understanding the characteristics of this bacterium as a cause of diarrhea and knowing its pattern of antibiotic resistance can help reduce the prevalence of infections caused by it and the cost of treatment.

Keywords: diarrhea, *Shigella*, antibiotic resistance, carbapenemase, ESBLs, biofilm

Abstract ID: 197
subject: rational antibiotic prescription and resistance mechanisms

Antibacterial effect of rifampicin/colistin combination therapy in multidrug-resistant *Acinetobacter baumannii*

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Background and Aim: *Acinetobacter baumannii* is a major cause of hospital- acquired infections, and it is becoming increasingly resistant to many antibiotics, such as carbapenems. Key resistance mechanisms include oxacillinases, ESBLs, and metallo-beta-lactamases. The study aims to determine the prevalence of OXA-type carbapenem resistance genes, AmpC cephalosporinase, and metallo-beta- lactamase genes in multidrug-resistant *A. baumannii* isolates. Additionally, it seeks to assess the synergistic antibacterial effect of rifampicin/colistin combination therapy.

Material And Methods: In this study, 105 *Acinetobacter baumannii* isolates were collected from various clinical specimens. Biochemical identification assays, minimum inhibitory concentrations, and antibiotic interactions were assessed using the broth microdilution checkerboard method. Additionally, antibiotic susceptibility testing was conducted using the disk diffusion method, and the presence of ESBL phenotype was determined by the combined disk test. Specific primers were used to detect *blaOXA-51*, *blaTEM*, *blaVIM, blaIMP, blaADC*, and *blaMOX* genes among isolates using PCR.

Results: The highest antibiotic resistance was observed in isolates against aztreonam (94.3%), imipenem, and meropenem (93.3%), and pipracilin (91.4%). The frequencies of *blaOXA-51, blaTEM, blaVIM, blaIMP, blaADC, and blaMOX* genes were 100%, 53.5%, 65.5%, 66.6%, 73.7%, and 71.7%, respectively. The Fractional Inhibitory Concentration Index (FICI) for rifampin combined with colistin against multidrug-resistant *A. baumannii* showed synergistic effects in 105 cases (100%) (FICI $\leq$ 0.5).

Conclusion: These results indicate that most isolates were resistant to important clinical antibiotics. These results suggest further study on the rational usage of carbapenems for the treatment of infections caused by *Acinetobacter baumannii.* Combinations of rifampin with colistin may be future therapeutic alternatives for the treatment of multidrug-resistant *A. baumannii* infections.

Keywords: *Acinetobacter baumannii*, Antibiotic resistance, ESBL, rifampicin/colistin combination

Abstract ID: 421
subject: rational antibiotic prescription and resistance mechanisms

Investigation of emerging plasmid-mediated beta-lactamases in *Klebsiella pneumoniae*

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Background and Aim: *Klebsiella pneumoniae* is an opportunistic pathogen and one of the most important bacteria involved in hospital-acquired infections. Beta-lactamases are considered the primary defense mechanism of Gram-negative bacteria against antibiotics. Recently, emerging beta-lactamases, known as novel beta-lactamases, have been spreading, and the genes producing these enzymes can transfer from one bacterium to another. Thus, this study aimed to investigate the emerging beta-lactamases in *Klebsiella pneumoniae*.

Material And Methods: In this descriptive-analytical study, 95 *Klebsiella pneumoniae* isolates were collected from clinical sources. After identification using culture and biochemical methods, antibiotic susceptibility was determined using the disk diffusion method based on CLSI 2024 guidelines. The minimum inhibitory concentration (MIC) for meropenem and imipenem was determined through the microdilution broth method, and the presence of the *blaOXA-48, blaKPC,* and *blaNDM-1* genes was assessed using the PCR method.

Results: Results showed that the highest percentage of antibiotic resistance was for amoxicillin (98.9%) and nitrofurantoin (89.4%), while the lowest percentage was for amikacin (11.5%). Forty-three and 20 isolates were resistant to meropenem and imipenem, respectively, with MICs of carbapenem-resistant isolates ranging from 16 to 2048 µg/ml. The presence of the *blaKPC, blaNDM-1*, and *blaOXA-48* genes was 15.7%, 10.5%, and 16.8%, respectively.

Conclusion: Emerging carbapenemases have increased bacterial resistance to carbapenems, posing a severe global health threat. Therefore, a detailed investigation of phenotypic and genotypic drug resistance patterns in these bacteria is essential.

Keywords: *Klebsiella pneumoniae*, multidrug resistance, carbapenemase, PCR.

Abstract ID: 422
subject: rational antibiotic prescription and resistance mechanisms

Determination of antibiotic resistance pattern and molecular typing of *Escherichia coli* isolated from clinical sources in Alborz province using ERIC-PCR method

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Background and Aim: *Escherichia coli* (*E. coli*) is the most important cause of urinary tract infection and also one of the causes of meningitis, septicemia and gastroenteritis. This bacterium is responsible for 80-90% of community-acquired urinary tract infections and 30-50% of hospital-acquired urinary tract infections. Considering the increase of antibiotic resistance among *E. coli* strains, the aim of this study was to determine the pattern of antibiotic resistance and identify genetic diversity and to investigate the genetic relationship of *E. coli* clinical isolates isolated from hospitals in Alborz province.

Material And Methods: This descriptive-analytical study was conducted on 100 *E. coli* isolates from 150 samples sent to the laboratory in Kausar, Tharallah and Shariati hospitals in Karaj. The isolates were initially identified through biochemical and molecular methods. Then, the test to determine the sensitivity to the common antibiotics for the treatment of urinary infections was performed using the agar disk diffusion method and based on the CLSI 2022 guidelines, and finally, the typing of the isolates was performed using the ERIC PCR method.

Results: The results of this study showed that the most effective antibiotics were gentamicin, amikacin and cephalexin and the least effective were nalidixic acid and nitrofurantoin. Also, based on the typing of isolates by ERIC PCR method, they were divided into three groups G1, G2 and G3. The genotype of bacteria was different in hospitalized and outpatient patients, and the genotype of *E. coli* isolates was also different in hospitalized patients with catheters and patients without catheters.

Conclusion: Therefore, according to the change in the pattern of drug resistance and considering that there were different types of bacteria in hospitalized patients with catheters and without catheters, as well as outpatients. It is recommended to carry out similar studies with the aim of finding the cause and appropriate treatment.

Keywords: *Escherichia coli*, drug resistance, urinary tract infections, ERIC PCR

Abstract ID: 382
subject: rational antibiotic prescription and resistance mechanisms

Prevalence of the fluoroquinolone resistance genes in the *Escherichia coli* sequence type 131 clone isolated hospitalized patients with urinary tract infection in Tehran, Iran

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Background and Aim: The emergence of fluoroquinolones (FQ) resistance in the *Escherichia coli* (*E. coli*) sequence type 131 (ST131) has become a major challenge in the management of urinary tract infections (UTI). Chromosomal mutations and plasmid-mediated quinolone resistance (PMQR) determinants play an important role in the FQ resistance.

Material And Methods: This study aimed to investigate the prevalence of the chromosol mutations, the PMQR genes including qnr, aac (6′)-Ib-cr, and efflux pump among the FQ-resistant ST131 and non-ST131 *E. coli* causing UTI. Initially, the ST131 clone was detected using allele-specific PCR and confirmed by multilocus sequence typing.

Results: Among 200 FQ-resistant *E. coli* isolates, 58 (29%) as belonging to the ST131 clone. The most frequently detected PMQR genes in FQ-resistant isolates were aac(6)'-lb-cr and qnrS. The *oqxA* gene was the most prevalent efflux pump gene observed in both ST131 (48%) and non-ST131 (35%) isolates. Analysis of the *gyrA* and *parC* genes revealed significant differences between ST131 and non-ST131 isolates. Double mutations, S80I+E84V, were significantly more prevalent in both gyrA (67% ST131 vs. 34% non-ST131; p=0.004) and parC (65% ST131 vs. 36% non-ST131; p=0.002) of ST131 isolates.

Conclusion: The double mutations confer high level resistance to FQs in ST131 clone. These findings on resistance mechanisms can guide infection control strategies.

Keywords: *Escherichia coli*, sequence type 131, chromosomal mutation, plasmid-mediated quinolone resistance, efflux pump

Abstract ID: 100
subject: rational antibiotic prescription and resistance mechanisms

Assessing adherence to CLSI guidelines in Iranian research on *Escherichia coli* antimicrobial susceptibility testing

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Background and Aim: Antimicrobial resistance poses a significant threat to global public health. Standardized testing protocols are crucial for accurate diagnosis and treatment. However, many studies fail to correctly adhere to established guidelines like those from the Clinical and Laboratory Standards Institute (CLSI). We aimed to quantify how many Iranian research studies used CLSI guidelines correctly when investigating antibiotic susceptibility testing among *Escherichia coli* isolates from Iran.

Material And Methods: We searched PubMed, Web of Science, Google Scholar, Science Direct, Magiran, and SID databases using keywords related to Antimicrobial Resistance (AMR) and *Escherichia coli*, restricting to English and Persian languages, and limiting publication dates between January 2009 and December 2022. We evaluated study quality using the JBI checklist for prevalence studies.

Results: After removing duplicates and unrelated studies out of 4344, 902 articles were assessed for full text and 330 were included in the meta-analysis. A total of 572 articles were excluded and the most common reason for that was failure to adhere to established guidelines (n=400). The most common reasons for exclusion were failure to use the CLSI, no report of the CLSI version used, use of the old CLSI version, and no defined CLSI version mentioned.

Conclusion: Our findings reveal a concerning trend in Iranian research on antimicrobial susceptibility testing. Despite the critical importance of standardized protocols, from eligible studies, we found that 69.6% were excluded due to failure to adhere to established guidelines. These results highlight a significant gap in adherence to international standards in many Iranian research studies on antibiotic resistance. To combat the growing threat of antimicrobial resistance, it is crucial that researchers strictly adhere to guidelines like those provided by CLSI. We strongly emphasize the importance of not only using CLSI guidelines but also ensuring correct usage of the newest version and explicit mention of the version used in the study. This approach is essential for producing reliable data that can inform effective antibiotic stewardship strategies and contribute meaningfully to the global fight against antimicrobial resistance.

Keywords: Standards; antimicrobial resistance; *Escherichia coli*

Abstract ID: 162
subject: rational antibiotic prescription and resistance mechanisms

Investigating the antibiotic resistance pattern of *Klebsiella pneumoniae* isolated from the samples of patients admitted to Afshar Hospital in Yazd from the beginning of 1399 to the end of 1402

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Background and Aim: antibiotics has increased significantly in agriculture and animal husbandry, which has also played an important role in making microbes more resistant. Diagnosing the type of microbe and prescribing antibiotics according to the antibiogram is one of the most basic methods of treating infections. In medical centers, the detection of resistant strains of bacteria is considered as a critical result [Critical values], which should be One of these pathogenic microbes is called *Klebsiella pneumoniae*, which is a Gram-negative, non-motile, covered, lactose-fermenting, facultative anaerobic, rod-shaped bacterium. which can be the cause of severe infections in lungs, wounds and other organs. this immediately reported to the relevant doctor and responsible for hospital infection control. THIS Bacteria sometimes produce enzymes that break down and deactivate a wide range of beta-lactam antibiotics, including penicillins and cephalosporins (ESBL), which are important in terms of antibiotic resistance. In this cross-sectional descriptive study, antibiotic resistance monitoring of *Klebsiella pneumoniae* isolated from different samples of patients hospitalized in Yazd Afshar Hospital was conducted during 4 years (1399 to 1402). ESBL cases were investigated.

Material And Methods: In this study, among all microbes isolated from hospitalized patients, 70 samples of *Klebsiella pneumoniae* were grown and cultured in laboratory environments. Their resistance and sensitivity to different antibiotics in different years were recorded in Hont software and the results were checked.

Results: In 1399, out of 13 isolates of *Klebsiella pneumoniae*, 5 cases (38.46%), in 1400 out of 19 isolates, 2 cases (10.52%)), in 1401 out of 18 isolates, 10 cases (55.55%) and in 1402 out of 20 isolates, 6 cases (30%) were ESBL.

Conclusion: To prevent the spread of drug-resistant bacteria, it is important to use antibiotics judiciously and follow infection control measures in healthcare settings. Holding stewardship committees in hospitals and reporting and informing about the status of microbial resistance plays an important role in the correct prescription of antibiotics and reducing the process of microbial resistance.

Keywords: Microbial resistance - *Klebsiella pneumoniae* - ESBL - critical values

Abstract ID: 163
subject: rational antibiotic prescription and resistance mechanisms

Investigation of antibiotic resistance of *Escherichia coli* isolated from samples of patients admitted to Afshar Hospital in Yazd from the beginning of 1399 to the end of 1402

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Background and Aim: bacillus of the *Enterobacter*iaceae family that is commonly present in the intestine. Most of the *Escherichia coli* strains are harmless and as normal intestinal flora, and their presence prevents the activity of other pathogenic bacteria. This bacterium is the most common cause It causes urinary infections especially in women and is easily transferred through infected hands. Indiscriminate use of antibiotics, both in the hospital and outside of it, has led to the resistance of this bacterium and other microbial species. So that some infections originate from bacteria for which there is no effective medicine. Knowing about these resistances and considering the results of killings has a great impact in the rational prescription of antibiotics. Broad-spectrum beta-lactamase enzymes are one of the causes of drug resistance in *Escherichia coli* isolates. The aim of this study is to investigate antibiotic resistance patterns in *Escherichia coli* isolates collected from clinical samples.

Material And Methods: In this study, 256 *Escherichia coli* isolates isolated from the samples sent from patients admitted to Afshar Hospital, Yazd, were examined during 4 years. The samples were cultured in standard laboratory environments and their resistance to different antibiotics was checked by disk-diffusion method. The results of the data were recorded in Hont software and the output of the software was analyzed. There were 256 total samples that were taken from urine, blood, and other body secretions.

Results: In 1399, out of 53 *Escherichia coli* isolates were 25 cases (47.16%), in 1400 there were 34 cases out of 58 isolates (58.62%), in 1401 there were 27 cases out of 81 isolates (33.33%) and in 1402 there were 20 cases out of 64 isolates (31.25%) was ESBL.

Conclusion: The indiscriminate prescription of antibiotics in the society requires control measures. The activation of monitoring committees for the delivery of non-prescription drugs from pharmacies, the activity of stewardship committees in medical centers, increasing the awareness of doctors about the importance of the rational prescription of antibiotics and public information in the case of not using antibiotics arbitrarily and observing hygiene principles, especially washing hands correctly, can reduce the use of antibiotics and slow down the process of microbial resistance.

Keywords: Microbial resistance - ESBL - *Escherichia coli* - antibiotic

Abstract ID: 207
subject: rational antibiotic prescription and resistance mechanisms

Antibacterial and anti-biofilm activity of levofloxacin-derived carbon dots against carbapenem-resistant *Pseudomonas aeruginosa* isolates

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Background and Aim: *Pseudomonas aeruginosa* is a major opportunistic pathogen responsible for nosocomial infections, presenting formidable therapeutic challenges due to its extensive antibiotic resistance and robust biofilm formation. These traits contribute to its persistence and increased survival in hospital settings.

Material And Methods: *Pseudomonas aeruginosa* isolates were obtained from the Bacteriology Department archive. Antimicrobial resistance was assessed using the disk diffusion method, and carbapenemase production was confirmed by mCIM and eCIM assays. The presence of biofilm-associated genes (*algD, las,* and *rhl*) was detected using PCR analysis. Carbon dots were synthesized through hydrothermal method, and their physicochemical properties, such as particle size, zeta potential, and functional groups were characterized using DLS, zeta potential measurements, FTIR, and UV-Vis spectroscopy.

Results: The finding revealed that 90% of the *Pseudomonas aeruginosa* isolates carried the *algD* gene, while 94% harbored the *las* and *rhl* genes. Furthermore, 58% of the isolates were classified as strong biofilm producers. Anti-biofilm assays demonstrated that levofloxacin-derived carbon dots effectively inhibited biofilm formation and downregulated the expression of biofilm-associated genes. The nanoparticles exhibited physicochemical properties favorable for biofilm disruption and bacterial cell interaction

Conclusion: This study demonstrated that levofloxacin-derived carbon dots exhibit significant potential to reduce biofilm formation and combat antimicrobial resistance in *Pseudomonas aeruginosa*. The unique physiochemical properties of these nanoparticles position them as promising candidate for the treatment and management of infections caused by this multidrug resistant pathogen.

Keywords: *Pseudomonas aeruginosa*, carbon dots, levofloxacin, biofilm inhibition, antimicrobial resistance, PCR.

Abstract ID: 291
subject: rational antibiotic prescription and resistance mechanisms

Evaluation of antibiotic resistance patterns in patients visiting niloo private laboratory for medical diagnosis and pathology in Shiraz

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Background and Aim: The increasing trend of antibiotic resistance is a major public health issue. This study aims to evaluate antibiotic resistance patterns and provide insights for effective management.

Material And Methods: In this descriptive cross-sectional study conducted from October 2024 to January 2025, all blood, urine, wound, sputum, respiratory secretions, synovial fluid, cerebrospinal fluid (CSF), and peritoneal fluid cultures from patients visiting Niloo Laboratory in Shiraz were examined using a comprehensive sampling method. Statistical analysis was performed using Stata version 18, with a significance level set at less than 0.05.

Results: A total of 1,000 positive cultures were analyzed to identify the type of bacteria for resistance evaluation. The most commonly isolated microorganisms from urine, blood, and sputum cultures included strains of *Escherichia coli*, *Klebsiella*, Pseudomonas, and *Staphylococcus aureus*. Lesser amounts of *Enterococcus faecalis*, *Enterobacter aerogenes*, and Proteus mirabilis were also present. Regarding antibiotic resistance within the penicillin family, 92% of the cultures showed resistance to ampicillin, with a small percentage (3%) being intermediate. Most isolates demonstrated clear resistance patterns, except for *Klebsiella* species which possess intrinsic resistance genes to ampicillin. Among the cephalosporins, 87% of *Klebsiella* isolates from urine samples were resistant to cefazolin, a first-generation cephalosporin. For wound cultures and particularly respiratory aspirate samples, drug resistance was predominantly due to extended-spectrum beta-lactamases (ESBLs), especially noted in *E. coli*, *Klebsiella*, and *Pseudomonas*. Additionally, *E. coli* isolates from wound cultures typically exhibited multidrug resistance (MDR), indicating resistance to various antibiotics including cephalosporins, fluoroquinolones, tetracyclines, and folate synthesis inhibitors.

Conclusion: The findings of this study underscore the urgent need for effective strategies to combat antibiotic resistance. Without appropriate actions, global health will face a crisis as managing antibiotic-resistant infections becomes increasingly challenging

Keywords: Antibiotic resistance pattern,extended-spectrum beta-lactamases (ESBLs),MDR

Abstract ID: 358
subject: rational antibiotic prescription and resistance mechanisms

Resistance to antipseudomonal β-lactams induced by imipenem in *Pseudomonas aeruginosa* clinical isolates

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Background and Aim: *Pseudomonas aeruginosa* is a Gram-negative opportunistic pathogen. This bacterium uses high levels of intrinsic and acquired resistance mechanisms to combat most antibiotics, posing a major challenge in clinical settings. *P. aeruginosa* possesses chromosomal and plasmid-borne β-lactamases, which are important factors in the development of resistance to β-lactam antibiotics. There is evidence that some antibiotics, such as imipenem and β-lactamase-resistant cephalosporins (cefoxitin), may be responsible for β-lactamase induction, leading to antagonism against other β-lactam agents, including antipseudomonal penicillins (ticarcillin or piperacillin) and cephalosporins (ceftazidime or cefepime). In this study, the effect of imipenem induction on the in vitro activity of antipseudomonal β-lactams was investigated.

Material And Methods: A total of 223 respiratory samples were collected from patients admitted to the Intensive Care Units of teaching hospitals in Gorgan, Iran. *P. aeruginosa* was identified using biochemical tests and confirmed by PCR targeting the *gyrB* gene. All isolates were tested for antibiotic antagonism by disk diffusion method. An imipenem disk was placed 5 to 10 mm outside the expected inhibitory zone of three tested disks of ceftazidime, piperacillin, and piperacillin-tazobactam. Antagonism was defined as a distinct flattening (truncation) of the inhibitory zone around the test antimicrobial agent in the area adjacent to the imipenem disk. Truncation was considered positive when the radius of the zone was reduced by 2 to 4 mm, depending on the normal size of the inhibitory zone.

Results: Thirty-eight clinical isolates of *P. aeruginosa* were obtained from clinical specimens. In the disk diffusion test, 30 out of 38 *P. aeruginosa* isolates (80.9%) showed a distinct flattening (truncation) of the inhibitory zone around the three piperacillin, piperacillin-tazobactam, and/or ceftazidime disks tested in the area adjacent to the imipenem (as β-lactamase inducer) disk.

Conclusion: The high prevalence of induced resistance among *P. aeruginosa* isolates shown in the current study is very important, because it is possible that other β-lactamase-stable β-lactams and cephalosporins, such as imipenem or cefoxitin may be potential β-lactamase inducers. Therefore, a cautious approach should be taken regarding the use of combinations of antipseudomonal penicillins and cephalosporins for the treatment of serious *P. aeruginosa* infections, as it may cause treatment failure.

Keywords: *Pseudomonas aeruginosa*, anti-bacterial agents, beta-lactams, imipenem

Abstract ID: 166
subject: rational antibiotic prescription and resistance mechanisms

Comparison of the antibiotic resistance prevalence in *Klebsiella pneumoniae* over 35 years: A comparative study in a hospital in Mashhad, Iran (1989-2024)

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Background and Aim: *Klebsiella pneumoniae* infections are one of the significant causes of mortality, especially in hospitalized patients. The spread of antibiotic resistance patterns such as ESBL, KPC, etc., poses a major challenge in their treatment. So, monitoring alterations in the prevalence of antibiotic resistance over the years can help prescribe antibiotics optimally. This study investigated and compared the prevalence of *Klebsiella pneumoniae* antibiotic resistance at a Hospital in Mashhad, Iran, over the past 35 years.

Material And Methods: In this study, the antibiotic resistance of *Klebsiella pneumoniae* strains isolated from patient samples was compared using the disk diffusion method in 1989 and 2024. Different antibiotics tested included amikacin, cephalosporins, trimethoprim, sulfamethoxazole, and others.

Results: The comparison of antibiotic resistance between 1989 and 2024 demonstrated that resistance to Amikacin, Cephalosporin, Trimethoprim-sulfamethoxazole, and Ampicillin had increased significantly; conversely, a decrease in tetracycline resistance has been observed. Notably, the prevalence of imipenem resistance has been much higher than reported in recent Iranian studies.

Conclusion: The significant rise in antibiotic resistance observed in *Klebsiella pneumoniae* from 1989 to 2024 underscores the urgent need for enhanced control and prevention strategies. This trend highlights the necessity for optimal treatment protocols and the identification of suitable alternative therapeutics to combat this infection.

Keywords: Antibiotic resistance, *Klebsiella* pneumonia, treatment, prevalence

Abstract ID: 298
subject: rational antibiotic prescription and resistance mechanisms

Antibiotic resistance in *Pseudomonas aeruginosa* and its implications for UTI treatment

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Background and Aim: *Escherichia coli* is the primary cause of urinary tract infections (UTIs), but less common pathogens like *Pseudomonas aeruginosa* can also lead to significant health issues. These bacteria have developed several mechanisms to resist antibiotics, complicating treatment options. UTIs are the most frequently diagnosed infections in hospitals, and the emergence of new antibiotic resistance poses a significant challenge, especially since most hospitalized patients receive daily antibiotics, typically beta-lactams.

Material And Methods: The purpose of this study was to assess the prevalence of particular beta-lactamase encoding genes (*blaIMP, blaVIM, blaSIM,* and *blaSPM*) in isolates of *P. aeruginosa*. Urine samples were analyzed using bacteriological culture, while the Kirby–Bauer disk diffusion method was employed to assess patterns of antibiotic resistance. Additionally, PCR amplification of the resistance genes was conducted on the isolated strains.

Results: Among 15,305 urine cultures examined, 36 (0.23%) were positive for *P. aeruginosa*. Of the 36 individuals, 55.6% were male, and their ages ranged from 0.019 to 15 years, with an average age of 5.38 years (SD ± 4.75). The isolates of *P. aeruginosa* exhibited significant susceptibility to amikacin (94.4%), followed by Norfloxacin (88.9%), Ciprofloxacin (86.1%), and Cefepime (83.3%). Notably, resistance was highest against Colistin (91.7%) and Aztreonam (88.9%), while 22.2% of cases demonstrated carbapenem resistance (n = 8). Multidrug resistance was identified in 16 (44.4%) of the isolates, with two strains showing resistance to all antibiotics tested. Detection of genes associated with metallo-beta-lactamase (MBL) production was noted in 77.7% of isolates, with *blaVIM* being the most frequently detected, followed by *blaSPM*.

Conclusion: Our study highlights the pressing issue of antibiotic resistance in *Pseudomonas aeruginosa* within UTI cases. With the significant prevalence of beta-lactamase encoding genes and a concerning level of multidrug resistance, the findings underscore the critical need for ongoing surveillance and innovative treatment strategies. Addressing the challenge of resistant bacteria like *P. aeruginosa* is essential to safeguarding patient health and enhancing outcomes in hospital settings, where UTIs remain a prevalent concern.

Keywords: Urinary tract infections , *Pseudomonas aeruginosa*, antibiotic resistance

Abstract ID: 265
subject: rational antibiotic prescription and resistance mechanisms

Multidrug resistance and virulence gene profiling of *Klebsiella pneumoniae* isolates in ICUs: insights into biofilm formation and efflux pump mechanisms

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Background and Aim: The significance of antibiotic resistance and virulence genes involved in this resistance greatly impacts the mortality rate of *Klebsiella pneumoniae* infections in ICU patients. These factors contribute to treatment failure, making them critical areas for clinical research and intervention.

Material And Methods: A total of 100 clinical isolates were collected from hospitalized patients in Sari (March–September 2023). Bacteria were identified through biochemical tests, including TSI, SIM, citrate, MRVP, catalase, and oxidase. Antibiotic susceptibility was assessed using the disk diffusion method according to CLSI guidelines. DNA extraction was performed via the boiling method, and 23 resistance genes were detected using PCR with specific primers. Data were analyzed using SPSS v. 23 and the chi-square test ($P < 0.05$).

Results: The highest resistance rate was observed for ampicillin/sulbactam (93%) and the lowest for tigecycline (0%). MDR isolates had significantly higher prevalence of resistance genes ($P < 0.05$). Common resistance genes included *blaSHV* (91.4%), *blaTEM* (82.7%), *blaCTX-M-15* (79.3%), *blaKPC* (29.3%), *blaOXA-48* (36.2%), and *blaNDM* (6.9%). Additional genes such as *blaVIM* (7%), *blaIMP* (11%), and *blaOXA-48* (28%) were also present. Quinolone resistance genes like *qnrB* (52%), *qnrA* (25%), and *qnrS* (23%) were observed. Virulence-associated genes such as *mrkD* (90.5%), *fimH-1* (80%), *entB* (92.6%), *ybtS* (68.4%), and *iucB* (56%) were frequently detected, along with efflux pump genes *AcrAB* (98.9%), *tolC* (95.8%), *mdtK* (83.2%), and outer membrane porin genes *OmpK35* (95.8%) and *OmpK36* (92.6%). Biofilm-associated genes *luxS* (98%), *treC* (96%), and *wza* (34%) were commonly identified.

Conclusion: Further research should focus on the antibiotic resistance patterns of *K. pneumoniae* in different hospital departments and infection sources. Investigating additional virulence and biofilm-related genes, such as plasmid-mediated genes (*oqxA, oqxB, gyrA*), is critical. Studies on resistance mechanisms and novel therapeutic strategies are essential. Effective infection control requires precise drug prescription management and screening of resistant strains.

Keywords: *Klebsiella pneumoniae*, efflux pump, biofilm, MDR

Abstract ID: 185
subject: rational antibiotic prescription and resistance mechanisms

Antibiotic resistance of *Stenotrophomonas maltophilia* in Iran: A systemic review

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Background and Aim: Treating infections caused by *Stenotrophomonas maltophilia* (*S.maltophilia*) poses substantial challenges due to its intrinsic resistance to various antibiotics. The main objective of this systematic review is to evaluate the prevalence of *S.maltophilia* across different provinces in Iran and to investigate antibiotic resistance, thereby address existing gap in medical knowledge.

Material And Methods: A comprehensive search strategy was conducted in PubMed, EMBASE, and Web of Science database to identify relevant original articles published in English between 2000 and 2024. Following evaluating title, abstract and full text, all studies addressing to antibiotic resistance in clinical isolates of *S.maltophilia* in Iran were selected.

Results: A total of 1,415 clinical isolates of *S. maltophilia* in 16 provinces in Iran were collected. The highest susceptibility was obtained to ticarcillin/ clavulanic acid (98.5%) and minocycline (98.2%). Among the genes associated with biofilm formation and antibiotic resistance, spgM (12.4%) and sul1 (39.6%) were the most prevalent.

Conclusion: As a result of low resistance to levofloxacin and minocycline, these two antibiotics can be recommended as first-line treatment options for infections caused by *S.maltophilia* in Iran. Trimethoprim/sulfamethoxazole, which have historically been considered the first-line agent for *S.maltophilia* infections, demonstrated relatively high resistance compared to levofloxacin and minocycline. Furthermore, the increase in antibiotic resistance of *S.maltophilia* in recent years compared to the previous decade is concerning.

Keywords: *Stenotrophomonas maltophilia*, Iran, antibiotic resistance, biofilm formation

Abstract ID: 341
subject: rational antibiotic prescription and resistance mechanisms

Prevalence and molecular mechanisms of colistin resistance in *Acinetobacter baumannii* clinical isolates in Tehran, Iran

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Background and Aim: Colistin is one of the last remaining active antibiotics against multidrug resistant Gram-negative bac- teria. However, several recent studies reported colistin-resistant (ColR) *Acinetobacter baumannii* from different countries. In the current study, we investigated molecular mechanisms involved in colistin resistance in *A. baumannii* isolates from different clinical samples.

Material And Methods: A total of 110 clinical *A. baumannii* isolates were collected from two hospitals in Tehran. Minimum inhibitory concentrations (MICs) were determined by broth microdilution according to the Clinical and Laboratory Standards Institute. For the ColR isolates, mutation was detected in *pmrA, pmrB, lpxA, lpxC*, and *lpxD* genes using the polymerase chain reaction (PCR) and sequencing. Moreover, the relative expression of the *pmrC* gene was calculated using quantitative reverse transcription PCR.

Results: Three colistin resistant isolates were identified with MIC between 8 and 16 mg/mL and were resistant to all the tested antimicrobial agents. All the three isolates had a mutation in the *pmrB, pmrA, lpxA, lpxD,* and *lpxC* genes. Moreover, the overexpression of *pmrC* gene was observed in all isolates.

Conclusion: Our results showed that the upregulation of the *PmrAB* two component system was the primary mechanism linked to colistin resistance among the studied colistin-resistant *A. baumannii* isolates.

Keywords: Colistin resistance, colistin, *Acinetobacter baumannii*, *PmrAB, PmrC*

Abstract ID: 262
subject: rational antibiotic prescription and resistance mechanisms

Investigating the prevalence rate and antibiotic resistance pattern of microorganisms isolated from patients admitted to Seyyed al-Shohda Heart Hospital in Urmia between August 1402 and December 1403

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Background and Aim: Today, the growing trend of resistance of microorganisms to antibiotics is a concern for the medical community as well as a serious threat to public health. The present study was designed and implemented with the aim of evaluating the prevalence and pattern of antibiotic resistance in patients admitted to Seyed al-Shohda Heart Hospital in Urmia between August 1402 and December 1403.

Material And Methods: This descriptive cross-sectional study was conducted between August 1402 and December 1403 on urine, blood, wound, pleural fluid and pericardial fluid samples from patients admitted to Seyed al-Shohad Hospital in Urmia, separating the blood culture results from the other mentioned samples. In this study, the organisms were separated by the usual method of isolation and the antibiogram was performed by disk diffusion agar method and the results were analyzed by spss software version 26.

Results: In the current study, which was conducted on 1082 samples submitted by hospitalized patients, 925 samples included urine, wound, pericardial fluid, and pleural fluid, and 157 patients had blood cultures on two occasions, and 72 of the blood cultures were positive on two occasions and 232 cases out of 925 cultures were reported positive The results showed that the most common microorganism isolated from urine was *Escherichia coli* It was reported that the most effective antibiotic was nitrofurantoin with 95% sensitivity and the least effective was ceftriaxone with 75% resistance and ceftazidime-clavulanate with 72% resistance. The most common microorganism isolated from blood was *Pseudomonas aeruginosa*, the most effective antibiotic was meropenem with 68% sensitivity and the least effective. Ceftazidim_clavulanate was 75% resistant.The most common microorganism isolated from the wound was *Pseudomonas aeruginosa*, the most effective antibiotic was cefepime with 54% sensitivity and the least effective was ceftazidime_clavulanate with 75% resistance.

Conclusion: These studies show that there is a significant resistance to the commonly used antibiotics, the causes of which are the prescription and excessive use of antibiotics, as well as arbitrary use and failure to complete the course of treatment by patients.

Keywords: Antibiotic resistance, microorganism, blood culture

Abstract ID: 105
subject: rational antibiotic prescription and resistance mechanisms

Epidemiological investigation and drug sensitivity of *non-tuberculous mycobacterium* species in Kermanshah, Iran, in 2022

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Background and Aim: *Non-tuberculous mycobacteria* (NTM) are ubiquitous in the environment and include over 125 species responsible for various diseases. Due to their growing diversity, clinical identification, diagnosis, and treatment of NTM infections present challenges to healthcare providers. This study aims to conduct an epidemiological investigation and assess the antimicrobial sensitivity of NTM species in Kermanshah, Iran, in 2022.

Material And Methods: This descriptive-analytical cross-sectional study was conducted using a census approach. Data were collected from the tuberculosis reference laboratory through a checklist-based data collection tool. The study included patients with acid-fast bacillus (AFB) smear-positive samples but negative polymerase chain reaction (PCR) results.

Results: A total of 29 AFB smear-positive samples were sent to the Kermanshah Tuberculosis Reference Laboratory. Among the patients, 15 (51.7%) were male and 14 (48.3%) were female, with an average age of 60.59 years. Sputum samples were obtained from 20 (69%) patients, while bronchoalveolar lavage fluid was collected from 9 (31%). The majority of the patients (93.1%) had no underlying disease. *Mycobacterium simiae* was identified in 7 (20.7%) samples, with resistance to rifampin, isoniazid, and ethambutol observed in most isolates. Additionally, 4 (13.7%) patients died, 19 (65.5%) recovered, and the remaining patients developed chronic disease. Notably, 13.8% of the patients were HIV-positive, and a small portion had underlying conditions such as diabetes, rheumatoid arthritis, and chronic bronchitis.

Conclusion: *Mycobacterium simiae* was the most commonly identified NTM species in this study, with high resistance to key tuberculosis medications, including rifampin, isoniazid, and ethambutol. These resistant strains may lead to treatment failure, with clinical and radiological manifestations resembling tuberculosis. The results emphasize the urgent need for advanced diagnostic techniques and more effective tests for the early identification of NTM species, which can prevent misdiagnosis and improve patient outcomes.

Keywords: *Non-tuberculous mycobacteria*, drug resistance, *Mycobacterium simiae*, epidemiology, *Tuberculosis*, Kermanshah

Abstract ID: 206
subject: rational antibiotic prescription and resistance mechanisms

Antibacterial effects and the expression of adhesin genes among multidrugresistant *Klebsiella oxytoca* following exposure to coumarin and quercetin

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Background and Aim: The rise of carbapenem-resistant *Klebsiella oxytoca* (CR-K. *oxytoca*) poses significant challenges in clinical settings. This study assessed the antibacterial effects of coumarin and quercetin, focusing on their influence on the expression of adhesin genes, which are crucial for bacterial adhesion and virulence, potentially offering insights for innovative therapeutic strategies.

Material And Methods: In this study, 10 CR-*K. oxytoca* were isolated and antibiotic resistance, as well as the presence of adhesin genes and toxin production, were determined by polymerase chain reaction (PCR). Also, the expression of bacterial adhesins genes and its relationship with resistant isolates were investigated in exposure to various coumarin and quercetin compounds using quantitative real-time PCR (qRT-PCR). The cytotoxicity of coumarin and quercetin compounds was checked against human fibroblast normal cell lines.

Results: The minimum inhibitory and bactericidal concentrations (MIC and MBC, respectively) ranges of coumarin included 128-512 µg/mL and 512->1024 µg/mL, respectively. In addition, The MIC and MBC ranges of quercetin included 64-512 µg/mL and 128->1024 µg/mL, respectively. CR-*K. oxytoca* had imipenem MIC of 16 µg/mL and MBC of 32 µg/mL. The combination of coumarin and imipenem (non-toxic concentration of 128 µg/mL for each) mitigated MIC and MBC ranges to 4-8 µg/mL and 8-16 µg/mL, respectively. Coumarin and quercetin exposure (128 µg/mL for each) could significantly ($p<0.0001$) decrease the expression of fimA (2.6 fold), mrkA (2.2 fold) and mrkB (1.9 fold) virulence gene

Conclusion: Herbal bioactive compounds can be investigated for their antibacterial anti-virulence effects particularly for synergistic properties with last-line antibiotics against drug-resistant pathogens.

Keywords: *Klebsiella oxytoca*, antibiotic resistance, virulence factors, herbal compounds

Abstract ID: 198
subject: rational antibiotic prescription and resistance mechanisms

Prevalence of beta-lactamase genes in *Escherichia coli* isolated from patients with renal failure

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Background and Aim: Recently, *Escherichia coli* has become one of the most common nosocomial infectious agents. Due to the presence of various resistance mechanisms, particularly broad-spectrum beta-lactamases, treating infections caused by *E. coli* can be quite challenging. Therefore, it is crucial to identify the resistance patterns of broad-spectrum beta-lactamases in this microorganism, such as TEM, SHV, and PER, as these genes play a significant role in resistance. The aim of this study was to determine the antibiotic resistance of *E. coli* isolates from patients with kidney failure, as well as to identify the TEM, SHV, and PER broad-spectrum beta-lactamase genes.

Material And Methods: One hundred isolates of *E. coli* were collected from patients with kidney failure who were admitted to Shiraz medical centers. The isolates were identified using biochemical and microbiological methods. The susceptibility to antibiotics was tested using disk-diffusion agar tests for selected drugs alone and in combination with inhibitors to determine ESBL-producing isolates. The presence of *blaPER, blaSHV*, and *blaTEM* genes in ESBL-producing *E. coli* was determined using PCR technique with specific primers.

Results: The results showed that 39% of isolates were positive for ESBL. Additionally, the antibiotic susceptibility test demonstrated that 61% of isolates were resistant to Nalidixic acid, while 92% of them showed sensitivity to Imipenem. Clearly, multiple drug resistance (MDR) was observed in 14% of isolates. Our results also showed that *blaTEM, blaSHV*, and *blaPER* were found in 75%, 58%, and 25% of ESBL isolates, respectively. Statistically, there was a significant difference between antibiotic resistance in cefotaxime and different age groups of the subjects.

Conclusion: In the present study, 39% of the total isolates were found to be ESBL- producing *E. coli*. The majority of ESBL isolates contained *blaTEM* and *blaSHV* genes, while those with the *blaPER* were less common. Therefore, the identification of ESBL isolates is crucial in preventing their spread, as resistance factors are located on mobile genetic elements.

Keywords: Kidney-failure, antibiotic resistance, beta-lactamase, *Escherichia coli*, *blaPER*, *blaSHV*, *blaTEM*

Abstract ID: 251
subject: rational antibiotic prescription and resistance mechanisms

Prevalence of antibiotic resistance in clinical isolates of *Mycobacterium kansasii*: A systematic review and meta-analysis

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Background and Aim: The prevalence of diseases caused by *non-tuberculous mycobacteria* (NTM), including *M. kansasi*, is increasing, necessitating further information to guide prevention, control, and treatment strategies. This study aims to investigate the prevalence of *M. kansasi*i resistance to drugs recommended by the Clinical and Laboratory Standards Institute (CLSI).

Material And Methods: A comprehensive analysis of articles published until February 2023 was conducted on PubMed, Web of Science, and Scopus databases to investigate antibiotic resistance in *M. kansasi*i species. Stata software version 17 was employed for all analyses. A random effects model was used to examine the prevalence of antibiotic resistance in *M. kansasi*i.

Results: In this study, a total of 1647 articles were obtained through database search. After removing duplicates and unrelated studies, 17 cross-sectional studies that examined the breakpoints proposed by CLSI were included. The rates of resistance of *M. kansasi*i to various antibiotics were as follows: clarithromycin (0%), rifampin (1%), amikacin (0%), ciprofloxacin (14%), linezolid (0%), moxifloxacin (0%), rifabutin (1%), doxycycline (96%), and SXT (49%).

Conclusion: Our results demonstrate the efficacy of first-line drugs against *M. kansasi*i strains, while indicating a high level of resistance to second-line drugs such as doxycycline, ciprofloxacin, and SXT. These findings underscore the importance of managing and monitoring the use of these antibiotics, as well as the need for further studies to elucidate the exact mechanism of *M. kansasi*i resistance to these antibiotics.

Keywords: *M. kansasi*i; antibiotic resistance; stata; CLSI; prevalence

Abstract ID: 253
subject: rational antibiotic prescription and resistance mechanisms

Impact of antibiotic exposure on gut microbiome diversity and antimicrobial resistance in young children from low- and middle-income countries: A systematic review and meta-analysis

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Background and Aim: The misuse of antimicrobial drugs is a key driver of antimicrobial resistance (AMR), disproportionately affecting low- and middle-income countries (LMICs), where young children are especially vulnerable to resistant infections. The impact of antibiotics on the gut microbiome, AMR gene selection, persistence, and spread remains poorly understood in LMIC pediatric populations. This systematic review evaluates existing research on antibiotic effects on the gut microbiome and resistome in infants from LMICs.

Material And Methods: A comprehensive search of MEDLINE, EMBASE, SCOPUS, WHO Global Index Medicus, and SciELO (2000–2024) identified 5,635 articles, with 2,934 unique records after duplicate removal. Screening excluded 2,830 articles, leaving 104 for full-text review. Twenty studies met eligibility criteria, focusing on children under 4 in LMICs. A random-effects meta-analysis, following PRISMA guidelines, assessed heterogeneity, reporting pooled estimates and 95% confidence intervals.

Results: From 20 studies showed antibiotics significantly reduced gut microbiome diversity (pooled effect size: -1.23; 95% CI: -1.56 to -0.90; $p < 0.001$) and increased resistance genes (pooled OR: 3.45; 95% CI: 2.78 to 4.28; $p < 0.001$) compared to placebo. Azithromycin, the most studied antibiotic, reduced diversity and increased macrolide resistance within five days. Other antibiotics (e.g., amoxicillin, cotrimoxazole, cefixime) showed similar patterns, though effects varied by type and duration. Limitations included few studies and insufficient data on widely used antibiotics like penicillin and tetracyclines.

Conclusion: In conclusion, antibiotics significantly reduce gut microbiome diversity and increase resistance gene abundance in children under 4 in LMICs, with effects lasting months post-treatment, highlighting the need for further research on long-term impacts in vulnerable populations.

Keywords: Antimicrobial resistance (AMR), microbiome, infection, pediatric health

Abstract ID: 37
subject: rational antibiotic prescription and resistance mechanisms

Antibiotic resistance pattern of *Acinetobacter* isolated from hospitalized patients at rasoul akram hospital, tehran province, 2024

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Background and Aim: *Acinetobacter* is an opportunistic, gram-negative bacterium, recognized as one of the primary agents responsible for hospital-acquired infections. Due to its ability to survive in hospital environments and acquire resistance mechanisms, it has emerged as a significant cause of morbidity and mortality in healthcare settings globally. Antibiotic resistance in Acinetobacter presents considerable challenges in the treatment of hospitalized patients, particularly those with weakened immune systems. The clinical significance of this bacterium lies in its capacity to acquire and transfer antibiotic resistance factors, leading to a wide range of infections, including ventilator-associated pneumonia, urinary tract infections, meningitis, bacteremia, as well as gastrointestinal and skin/wound infections. The aim of this study is to investigate the antibiotic resistance pattern of *Acinetobacter* isolates from hospitalized patients at Rasoul Akram Hospital in Tehran province.

Material And Methods: This study included 50 hospitalized patients from Rasoul Akram Hospital in Tehran in 2024. Biochemical tests were performed for the final determination of bacteria. Determining the pattern of bacterial sensitivity to antibiotics was done by disk (antibiogram), and the antibiogram test was performed on Acinetobacter purified from the patient according to the Kirby-Bauer method. The antibiotics tested included Colistin, Gentamicin, Tetracycline, Imipenem, Ceftazidime, Ceftriaxone, Ciprofloxacin, Cefotaxime, Doxycycline, Amikacin, Cefepime, Amikacin-Sulbactam, Piperacillin-Tazobactam, and Trimethoprim-Sulfamethoxazole.

Results: Among the patients, 33% were female and 66% were male, with ages ranging from 23 to 89 years. The results indicated that Acinetobacter exhibited the highest susceptibility to colistin (100%) and doxycycline (38%), while it showed resistance to other tested antibiotics.

Conclusion: The findings reveal high resistance to first-line antibiotics, particularly in the Cephalosporin class, which represents a significant concern for public health. Therefore, understanding the antibiotic resistance patterns of *Acinetobacter*, a major cause of hospital-acquired infections, is critical for effective treatment strategies.

Keywords: *Acinetobacter*, antibiotic resistance, multidrug resistance, antibiotics

Abstract ID: 331
subject: rational antibiotic prescription and resistance mechanisms

Exploring the efficacy of *Enterococcus faecium* as an antibacterial agent against resistant clinical pathogens

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Background and Aim: Antibiotic resistance, particularly among multidrug-resistant (MDR) pathogens like *Pseudomonas aeruginosa*, presents a significant challenge to modern healthcare. *P. aeruginosa* is notorious for its ability to form biofilms and acquire resistance through mechanisms such as efflux pumps and β-lactamase production, complicating infection management. *Enterococcus faecium*, a probiotic bacterium naturally found in the human microbiota, has shown promise in producing bioactive compounds like bacteriocins, antimicrobial peptides, and organic acids, which are effective against a range of pathogens, including *P. aeruginosa*. These compounds offer diverse modes of action, potentially mitigating the risk of resistance development. This study evaluates the antibacterial activity of a native *E. faecium* strain, isolated from a traditional dairy product, against clinical pathogens, particularly MDR strains. The findings aim to explore the potential of *E. faecium* as an alternative or adjunct therapy for infections caused by *P. aeruginosa* and other antibiotic-resistant bacteria.

Material And Methods: The antibacterial activity of an indigenous *Enterococcus faecium* strain, previously isolated from locally sourced dairy products by our research team, was evaluated. Clinical isolates exhibiting relative resistance to conventional antibiotics were obtained for this study. The antibacterial potential of the *E. faecium* culture supernatant was assessed using the agar well diffusion method. Inhibition zones greater than 15 mm in diameter were considered indicative of significant antibacterial activity.

Results: Among the eight clinical isolates exhibiting resistance to antibiotic treatment, the greatest growth inhibition was observed in *Pseudomonas aeruginosa*, *Pseudomonas stutzeri*, and *Klebsiella* species, respectively. *Escherichia coli* and *Staphylococcus aureus* isolates demonstrated complete resistance. P. stutzeri exhibited the largest inhibition zone, while *P. aeruginosa* displayed the highest level of resistance to commonly used antibiotics

Conclusion: our study shows that *Enterococcus faecium* has significant antibacterial potential, particularly against multidrug-resistant pathogens like *Pseudomonas aeruginosa* and Pseudomonas stutzeri. These findings suggest that *E. faecium* could be a valuable adjunct or alternative therapy to combat MDR infections. Further investigations, particularly into biofilm inhibition and the specific antimicrobial compounds produced, are needed to fully characterize its therapeutic potential

Keywords: Antibiotic resistance, *Pseudomonas aeruginosa*, *Enterococcus faecium*, antibacterial agents, multidrug-resistant organisms

Abstract ID: 124
subject: rational antibiotic prescription and resistance mechanisms

Characterization of integron classes in metallo-β-lactamase-producing *Acinetobacter baumannii* isolated from patients in Kermanshah, west of Iran

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Background and Aim: *Acinetobacter baumannii* is a significant pathogen that causes several infections mainly due to resistance against commercially available antimicrobial agents. The production of metallo-β-lactamase (MBL) enzymes is one of the most common resistance mechanisms to beta-lactam classes in *A. baumannii*. MBLs are usually associated with gene cassettes located in integrons, which confer resistance to multiple classes of antibacterial drugs and also facilitate the rapid spread of resistance among bacterial populations. This study aimed to determine antimicrobial resistance and the genes encoding six MBLs, as well as to characterize integrons in clinical isolates of *A. baumannii*.

Material And Methods: A total of 64 *A. baumannii* isolates were collected from various clinical samples of patients hospitalized at Imam Reza Hospital in Kermanshah city. Imam Reza Hospital is the largest university hospital in the west of Iran. Resistance to antibiotics was determined by the disk diffusion method. The presence of MBLs-encoding genes as well as class 1, 2, and 3 integrons was investigated using polymerase chain reaction (PCR) and sequencing techniques.

Results: All isolates demonstrated resistance to cefotaxime. Out of the 64 isolates, 98.4% were resistant to ciprofloxacin, 96.9% to meropenem and gentamicin, 95.3% to tetracycline, 90.6% to cefepime, and 84.9% to trimethoprim/sulfamethoxazole. PCR assays showed the presence of the *blaVIM* gene in all isolates; however, the other tested MBLs were not found. Class 1 integron was found in 12.5% of the isolates, while class 2 and 3 integrons were not detected in any of the isolates. The sequence analysis revealed that the variable regions of the isolates carrying class 1 integron include genes that produce homologous proteins to sugar dehydrogenases.

Conclusion: In our study, although a high prevalence of the *blaVIM* gene was found in *A. baumannii* strains, integrons were detected at a low prevalence. The characterization of integrons revealed the presence of housekeeping genes. A high prevalence of the *blaVIM* gene in *A. baumannii* strains highlights the urgent need for effective infection control and antibacterial management.

Keywords: *Acinetobacter baumannii*, antibiotic resistance, integrons, carbapenem

Abstract ID: 307
subject: rational antibiotic prescription and resistance mechanisms

The effect of cardiovascular drugs on the transfer of carbapenem resistance genes from *Klebsiella pneumoniae* to *Acinetobacter baumannii*

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Background and Aim: Antibiotic resistance, identified by the World Health Organization as a critical global health challenge, is a major cause of mortality worldwide. Horizontal gene transfer (HGT), including transformation, significantly facilitates the spread of resistance. Recent evidence indicates that some non-antibiotic drugs may promote the transfer of carbapenem resistance genes, raising concerns about their unintended impacts. This study evaluated the effect of cardiovascular drugs on the transfer of carbapenem resistance genes from *Klebsiella pneumoniae* to *Acinetobacter baumannii* through transformation.

Material And Methods: Antibiotic resistance profiles of *Klebsiella pneumoniae* strains collected from hospitals were determined using disk diffusion tests. The most resistant strain was selected for plasmid extraction. Plasmids were transformed into *Acinetobacter baumannii* strains under optimized conditions. The influence of various cardiovascular drugs on the transformation efficiency was assessed.

Results: Losartan enhanced transformation rates in a dose-dependent manner. At a concentration of 50 µg/mL, it increased the transformation rate by 3-fold. At concentrations of 5, 0.5, and 0.05 µg/mL, the rates increased by 5-fold, 6-fold, and 2.5-fold, respectively. Valsartan showed no significant effect at any tested concentration. Propranolol moderately increased transformation rates, with a 2-fold rise observed at a concentration of 5 µg/mL. The MIC values of the pre-transformation *Acinetobacter baumannii* strain were 0.25 µg/mL. Colonies transformed in the presence of Losartan exhibited an MIC increase from 0.25 µg/mL to 2 µg/mL. Colonies transformed with Propranolol showed an MIC increase from 0.25 µg/mL to 2 µg/mL, while Valsartan-transformed colonies exhibited a similar MIC increase.

Conclusion: These findings highlight the potential role of non-antibiotic drugs, such as cardiovascular agents, in facilitating the spread of carbapenem resistance. This underscores the need for further research and policy measures to manage drug usage and mitigate unintended consequences on antibiotic resistance

Keywords: Antibiotic resistance, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, horizontal gene transfer, transformation, cardiovascular drugs

Abstract ID: 418
subject: rational antibiotic prescription and resistance mechanisms

The role of efflux systems in multidrug resistance in *Pseudomonas aeruginosa*: A molecular perspective

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Background and Aim: Multidrug resistance (MDR) in hospital-acquired pathogens, particularly *Pseudomonas aeruginosa*, presents a significant challenge to global healthcare systems. Efflux systems are among the primary mechanisms contributing to antibiotic resistance. This study aimed to explore the role of efflux systems in the development of MDR in *Pseudomonas aeruginosa*. Molecular techniques, including PCR and sequencing, were employed to identify efflux-related genes, while antibiotic susceptibility testing assessed resistance patterns. The results revealed that over 70% of MDR isolates exhibited active efflux systems ($p < 0.05$). These findings suggest that targeting efflux systems could serve as a novel strategy to mitigate antibiotic resistance.

Material And Methods: 1. Sample Collection: o Fifty *Pseudomonas aeruginosa* isolates were collected from different hospitals. o Samples were obtained from patients with urinary tract infections, respiratory infections, and hospital-acquired wounds. 2. Efflux System Identification: o PCR amplification was used to detect genes linked to efflux systems, including mexB, mexD, and mexF. o Gene sequencing confirmed the presence of these efflux-related genes. 3. Antibiotic Susceptibility Testing: o The susceptibility of isolates to common antibiotics, including ciprofloxacin, gentamicin, and carbapenems, was evaluated using the disk diffusion method. o Minimum inhibitory concentration (MIC) tests were performed for selected antibiotics. 4. Efflux Activity Assessment: o Fluorescence-based assays were used to measure the activity of the efflux pumps in the bacterial isolates. 5. Statistical Analysis: o Data were analyzed using SPSS software, applying appropriate statistical tests (t-test, ANOVA) to determine significant differences.

Results: • Over 70% of the *Pseudomonas aeruginosa* isolates carried genes associated with efflux systems. • Isolates exhibiting active efflux systems showed significantly higher resistance to antibiotics, with resistance rates as follows: ciprofloxacin (85%), gentamicin (75%), and carbapenems (65%). • A strong correlation was observed between efflux activity and MDR ($p < 0.05$).

Conclusion: The findings of this study highlight the central role of efflux systems in the emergence of MDR in *Pseudomonas aeruginosa*. These results underscore the need for developing specific inhibitors targeting efflux systems as part of a novel therapeutic approach to combat antibiotic resistance. Future research should focus on the design and evaluation of efflux inhibitors, as well as the potential benefits of combining these inhibitors with existing antibiotics to enhance treatment efficacy in hospital-acquired infections.

Keywords: Multidrug Resistance (MDR), *Pseudomonas aeruginosa,* Efflux Systems, Antibiotic Resistance, Efflux Pump Inhibitors

Abstract ID: 372
subject: rational antibiotic prescription and resistance mechanisms

Real-time iot-based monitoring and management of antibiotic resistance in hospitalized patients

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Background and Aim: Antibiotic resistance (AR) presents a critical challenge to global healthcare systems, where delayed detection of resistant infections can result in ineffective treatments, extended hospital stays, and increased mortality rates. This case study investigates the implementation of a real-time monitoring system utilizing Internet of Things (IoT) technology in a hospital setting, aimed at enhancing the detection and management of antibiotic-resistant infections. The primary objective is to demonstrate the system's impact on improving treatment outcomes and antimicrobial stewardship practices within a clinical environment.

Material And Methods: A pilot IoT system was deployed in a 180-bed academic hospital, specifically within its infectious diseases and intensive care units (ICUs). The system comprised wireless IoT-enabled devices linked to patient monitoring equipment, including temperature sensors, heart rate monitors, and bacterial culture analyzers. These devices continuously tracked vital infection parameters, such as microbial load, infection site, and response to antibiotics, transmitting data to a cloud-based platform for real-time analysis. Machine learning algorithms processed this data to generate alerts upon detecting antibiotic resistance, comparing real-time resistance patterns to historical patient data. To ensure data integrity and patient privacy, robust security protocols, including end-to-end encryption and blockchain for record validation, were implemented. The system was seamlessly integrated with the hospital's existing electronic health record (EHR) system for efficient data exchange.

Results: Over the 26-week pilot study, the IoT-based monitoring system successfully identified emerging antibiotic resistance in 23% of hospitalized patients, prompting adjustments to their treatment regimens within 48 hours of detection. This early identification enabled clinicians to switch to more effective antibiotics, thereby reducing treatment failure. The system also contributed to a 15% reduction in unnecessary broad-spectrum antibiotic prescriptions, enhancing antimicrobial stewardship. Moreover, it flagged high-risk infections in the ICU, resulting in a 13.7% decrease in the average length of stay for patients with resistant infections. Continuous data collection from the system improved the machine learning algorithms' predictive accuracy.

Conclusion: The IoT-based real-time monitoring system significantly enhanced the detection of antibiotic resistance in hospitalized patients, facilitating timely and targeted interventions. This case study underscores the potential of IoT technology to improve antimicrobial stewardship, reduce inappropriate antibiotic use, and enhance patient outcomes in hospital settings.

Keywords: Antibiotic resistance, internet of things, antimicrobial stewardship, intensive care units.

Abstract ID: 346
subject: rational antibiotic prescription and resistance mechanisms

Resistance to imipenem and meropenem in *Klebsiella pneumoniae* isolates in Alborz Province and prevalence of KPC and VIM

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Background and Aim: Antibiotic resistance is one of the major challenges of our time, and understanding the mechanisms behind it is becoming increasingly important. *Klebsiella pneumoniae*, a significant pathogen in hospital-acquired infections, has demonstrated high levels of resistance to last-line therapeutic agents. This study aims to investigate resistance to two critical antibiotics, imipenem and meropenem, as well as to conduct a molecular analysis of the prevalence of the *blaVIM* and *blaKPC* genes.

Material And Methods: Initially, 115 *Klebsiella pneumoniae* isolates were collected from hospitals in Alborz Province. Subsequently, the Kirby-Bauer disk diffusion method was employed using imipenem and meropenem antibiotic disks. In the molecular phase, DNA was extracted from the samples, and PCR was utilized to evaluate the prevalence of the *blaVIM* and *blaKPC* genes.

Results: Among the 115 samples, 28% were resistant to imipenem and meropenem, while 6% exhibited intermediate resistance. In terms of prevalence, the *blaVIM* gene was detected in 34% of samples, and the *blaKPC* gene was identified in 32%.

Conclusion: Resistance to imipenem and meropenem leads to the emergence of CRKP strains, limiting our treatment options. According to the results of molecular tests, the prevalence of *blaKPC* and *blaVIM* is significantly associated with resistance to imipenem and meropenem.

Keywords: *Klebsiella pneumoniae* - antibiotic resistance - carbapenem resistant

Abstract ID: 159
subject: rational antibiotic prescription and resistance mechanisms

Survey on antimicrobial effects of olive oil and extract on pathogenic bacteria using Taguchi methodology

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Background and Aim: Antibacterial activity has recently been demonstrated in olive products. This antibacterial effect was correlated with the presence of different substances such as oleuropein. In present work antibacterial activity of different olive products was examined and their oleuropein content were determined. Also, the effect of different factors on antimicrobial activity were assayed by Taguchi methodology.

Material And Methods: Three varieties of fruit, leaves, and unrefined olive oil were purchased from Roodbar in Guilan province and ethanolic extract was examined. Antimicrobial activity of leaves and olive fruits were performed by disk and well diffusion, and pore plating method. Also, according to Taguchi methodology, effect of different factors such as incubation time, bacterial suspension concentration, type of bacteria, and type of extracts on antibacterial activity were evaluated. HPLC was performed to measure the oleuropein content at the Science and Technology Park of Guilan. Data analyzes were performed by using Minitab software.

Results: Leaves, fruits, and oil olive extract had significant impact on *E. coli*, *S. aureus*, and *P. aeruginosa*. Data analysis showed that exposure time and type of extracts had a significant antimicrobial effect on pathogen bacteria. Also, fruit extract had greater antimicrobial activity than olive oil. Eventually, *S. aureus* was (susceptible) than *E. coli* and *P. aeruginosa* to olive extracts. In current study, HPLC confirmed oleuropein as main antimicrobial ingredient of olive at 2.63ppm.

Conclusion: In this study, antimicrobial activity of olives products against *E. coli*, *S. aureus*, and *P. aeruginosa* demonstrated that different extracts of olive have potential for preparation herbal medicines.

Keywords: Disk diffusion, olive, ethanol, HPLC.

Abstract ID: 348
subject: rational antibiotic prescription and resistance mechanisms

Phenotypic and genotypic pattern of inducible clindamycin resistance to inducible in *Staphylococcus aureus* isolated from cockroaches in North of Iran

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Background and Aim: Insects and particularly cockroaches play an important role in the transmission of pathogens. *Staphylococcus aureus* is recognized as a significant nosocomial pathogen capable of causing a wide variety of infections. The purpose of this study was the Phenotypic and Genotypic pattern of Inducible Clindamycin resistance to inducible in *Staphylococcus aureus* isolated from cockroaches in North of Iran.

Material And Methods: Eighty strains of Periplaneta americana and Blattella germanica cockroaches were collected, of which 48 were P. americana cockroaches (60%) and 32 were B. germanica cockroaches (40%). The internal and external surfaces of the cockroaches was performed to bacterial isolation. Identification of isolates were performed using microbiological and biochemical procedures. Inducible resistance to clindamycin was tested by D-test. The frequency of genes, such as *ermA*, *ermB* and *ermC* was assessed by polymerase chain reaction (PCR).

Results: A total of 80 cockroaches were gathered; out of these, 12 (15%) *S. aureus* strains were isolated.Among the infected cockroaches, 60% were from P. americana, while 40% were from B.germanica. The resistance rate against erythromycin and clindamycin was 4% and 0%, respectively.Additionally, four strains were obtained from the inner surface of B. germanica, whereas five strains were isolated from the inner surface of P. americana, and three strain was isolated from the outer surface. according to the PCR results, the frequencies of the genes *ermA*, *ermB*, and *ermC* were 5%, 4%, and 14%, respectively.

Conclusion: These findings demonstrate that cockroaches are significance of transmitting resistance factors as mechanical vectors. Therefore, taking sanitary measures to control the insect population is unavoidable.

Keywords: *Staphylococcus aureus*, cockroach, inducible resistance, polymerase chain reaction.

Abstract ID: 393
subject: rational antibiotic prescription and resistance mechanisms

Antibiotic susceptibility testing of *Vibrio cholerae* using disk diffusion and micro broth dilution methods

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Background and Aim: *Vibrio cholerae*, a gram-negative bacterium, is the causative agent of cholera, a severe watery diarrheal disease a global health threat. The emergence of antibiotic-resistant strains of *V. cholerae* poses a significant challenge to effective treatment. This study was conducted with the objective of investigating the emergence of antimicrobial resistance in *V. cholerae* species in Iran, employed disk diffusion and micro broth dilution methods to identify effective antibiotics for treatment.

Material And Methods: All tests were performed in accordance with the Clinical and Laboratory Standards Institute (CLSI) document M45, published in 2017. In the disk diffusion method, bacterial isolates were first cultured on Muller-Hinton agar, and antibiotic disks were subsequently placed on the culture Plates were incubated for an appropriate duration. The antibiotics evaluated included ciprofloxacin (5 µg), ampicillin (10 µg), trimethoprim-sulfamethoxazole (1.25/23.75 µg), gentamicin (10 µg), tetracycline (30 µg), erythromycin (15 µg), imipenem (10 µg), ceftazidime (30 µg), cefotaxime (30 µg), and nalidixic acid (30 µg). The micro broth dilution method was employed, with Muller-Hinton broth and serial dilutions of antibiotics Azithromycin and Chloramphenicol (1 mg/ml). A standardized bacterial suspension was added, and the plates were incubated for an appropriate.

Results: Antibiotic susceptibility testing revealed that all isolates demonstrated sensitivity to erythromycin, tetracycline, cefotaxime, ceftazidime, gentamicin, azithromycin, and chloramphenicol. Conversely, resistance to nalidixic acid was observed in 100% of the isolates, and 90.7% exhibited resistance to trimethoprim-sulfamethoxazole. Notably, one isolate exhibited intermediate resistance to ciprofloxacin, with a zone diameter of 20 mm, indicative of a reduced susceptibility profile.

Conclusion: The efficacy of both methods in determining the antibiotic susceptibility of *V. cholerae* isolates was demonstrated. The present study examined the antibiotic resistance patterns exhibited by *Vibrio cholerae* strains in 2022, with the objective of facilitating more effective treatment and preventing further resistance. Continued surveillance of resistance patterns is imperative for guiding appropriate antibiotic therapy and mitigating the global health impact of *Vibrio cholerae* infections.

Keywords: *Vibrio cholerae*, drug resistance, disk diffusion, microbroth dilution

Abstract ID: 145
subject: rational antibiotic prescription and resistance mechanisms

Fluoroquinolones resistance in cystic fibrosis: A systematic review and meta-analysis

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Background and Aim: Antibiotic resistance in cystic fibrosis (CF) is a well-documented and significant challenge in the management of this chronic disease. CF patients are particularly susceptible to chronic respiratory infections, which often necessitate prolonged and repeated antibiotic treatments. This has led to the emergence of antibiotic-resistant pathogens, making the treatment of infections increasingly difficult. This meta-analysis was conducted to evaluate the proportion rates of fluoroquinolones resistance in cystic fibrosis, providing a comprehensive overview of the current resistance patterns and trends.

Material And Methods: To ensure a thorough and robust analysis, we conducted an extensive search for relevant studies in several major databases, including PubMed, Scopus, Embase, and Web of Science. The search was conducted up until April 22, 2023. Statistical analyses were performed using STATA software (version 20), which allowed for the calculation of pooled resistance rates and the assessment of trends over time.

Results: The 126 studies included in the analysis. The proportion of norfloxacin, ciprofloxacin, ofloxacin, gatifloxacin, levofloxacin, moxifloxacin in CF were 33.5% (95% CI 15.5-58.1), 38.7% (95% CI 34.7-42.9), 48.5% (95% CI 23.4-74.3), 20.2% (95% CI 7-45.9), 43.1% (95% CI 33.6-53.1), and 23.9% (95% CI 7-45.4), respectively. Our meta-analysis showed that trends of fluoroquinolones-resistance had a significant decrease over times. The highest resistant rates were indicated in *Burkholderia spp., S. maltophilia*, and *P. aeruginosa.*

Conclusion: This metadata highlight the regarding increase in fluoroquinolone resistance among CF patients. The findings underline the urgent need for comprehensive policies that encompass antibiotic stewardship, surveillance, and research initiatives to fight and mitigate antibiotic resistance in CF disorder.

Keywords: Antimicrobial resistance; fluoroquinolones resistance; bacterial pathogens; cystic fibrosis; systematic review and meta-analysis

Abstract ID: 381
subject: rational antibiotic prescription and resistance mechanisms

Antibiotic resistance in *Pseudomonas aeruginosa*

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Background and Aim: This article investigates the issue of antibiotic resistance in *Pseudomonas aeruginosa*. *P. aeruginosa* is a major pathogenic bacterium responsible for various infections in humans, including respiratory, urinary, gastrointestinal, and wound infections, as well as infections related to burns. Antibiotic resistance is a major challenge in treating infections caused by this bacterium, which results from its ability to produce antibiotic-degrading enzymes, alter its cell membrane, and transfer resistance genes.

Material And Methods: In this study, clinical samples from patients with different infections caused by *Pseudomonas aeruginosa* were collected. The susceptibility of these bacterial strains to various antibiotics, including beta-lactams, fluoroquinolones, and aminoglycosides, was tested using laboratory methods such as disk diffusion and minimum inhibitory concentration (MIC) determination. Additionally, the presence of resistance genes and mechanisms of antibiotic resistance were assessed through molecular methods like PCR and genomic sequencing.

Results: The results revealed that *P. aeruginosa* exhibits a high ability to develop resistance to a wide range of antibiotics. A significant proportion of the strains showed resistance to beta-lactam antibiotics and fluoroquinolones. Resistance to aminoglycosides was also observed in some strains. Genomic analysis indicated that resistance to antibiotics was often due to the production of β-lactamase enzymes, alterations in efflux pumps, and changes in the outer membrane of the bacteria. Furthermore, some strains carried multiple resistance genes, acquired through horizontal gene transfer from other bacteria.

Conclusion: Antibiotic resistance in *Pseudomonas aeruginosa* is a serious problem in the treatment of infections caused by this bacterium. Its ability to resist a wide range of antibiotics arises from various mechanisms, necessitating the development of new therapeutic approaches and preventive strategies. Continuous monitoring of resistant strains and identifying molecular resistance factors can help improve treatment options.

Keywords: Antibiotic resistance, *Pseudomonas aeruginosa*, antibacterial drug resistance

Abstract ID: 273
subject: rational antibiotic prescription and resistance mechanisms

Determination of *Acinetobacter baumannii* resistance pattern in identified isolates

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Background and Aim: *Acinetobacter* are gram-negative and forced aerobic coccobacilli that prefer to live in humid environments. Although this bacterium usually has low virulence, it causes a wide range of infections through respiratory equipment and infected catheters. Resistance is *Acinetobacter baumannii* strain.

Material And Methods: The present study was a descriptive cross-sectional study and its statistical population was 236 respiratory patients who were referred to specialized and sub-specialized hospitals in Karaj in 1398 for treatment. Bronco alveolar lavage specimens of excitatory sputum were collected using bronchoscopy. All results were statistically analyzed using SPSS software version 19.

Results: In PCR method, the number of positive cases for the presence of *Acinetobacter baumannii* was 75 (31.8%), and the number of negative cases was 161 (68.2%), and in the microbial culture method the number of positive cases was 70 (7.7). 29%), and the number of negative cases for the diagnosis of *Acinetobacter baumannii* was 166 (70.3%). In lavage and sputum samples, 35.2% of women and 64.8% of men had *Acinetobacter baumannii* strains. There was a significant difference between the sensitivity and specificity of PCR and routine bacteriological cultures (P = 0.05) and *Acinetobacter baumannii* was resistant to all antibiotics used in the laboratory.

Conclusion: It is necessary to take appropriate measures to reduce the incidence of *Acinetobacter baumannii*, which according to the proof of the hypotheses proposed and confirmed in this study, is one of the first measures in this field using new methods of diagnosis and treatment of these pathogenic strains. is.

Keywords: Antibiotic resistance, resistance pattern, *Acinetobacter baumannii*

Abstract ID: 130
subject: rational antibiotic prescription and resistance mechanisms

Prevalence of antibiotic resistance in *Escherichia coli* isolated from environmental and food sources: A systematic review and meta-analysis

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Background and Aim: The emergence and spread of antibiotic resistance in *Escherichia coli* is a growing public health concern worldwide. This systematic review and meta-analysis aimed to investigate the prevalence of antibiotic resistance (AMR) in *Escherichia coli* strains obtained from the environment and food sources in Iran.

Material And Methods: Following the PRISMA guidelines, we conducted a systematic literature search in several databases, including Scopus, Google Scholar, Magiran, PubMed, and SID, for studies published between January 1, 2010 and June 11, 2023, in English and Persian using the search. The terms "*Escherichia coli*" or "*E. coli*" and "antibiotic resistance" or "drug resistance" or "antimicrobial resistance" and "Iran". The study protocol has been registered in PROSPERO with ID: CRD42023448322. Statistical heterogeneity was calculated using Q and I2 statistics and the STATA 17 random effects model was used.

Results: The initial search identified 4344 articles, of which 31 studies on the evaluation of antibiotic resistance in *E. coli* isolated from food and environmental samples were finally included in our analysis. More than a quarter of the isolates were resistant to the penicillin class (75.3, 95% confidence interval (CI: 68.1-82.4) and more than half of the isolates were resistant to tetracyclines (67.2%) and β-lactams (56.0%). The lowest rate of AMR in penmes (13.3%) was observed. 8.04-18.2). More than 10 antibiotics showed moderate to high resistance levels for food and environmental isolates. Cefazolin (86.1%), amoxicillin (69.8%) and ampicillin (69.3%) showed the highest and meropenem (0.2%), tobramycin (4.7%) and imipenem (13.3%) showed the lowest antibiotic resistance to these isolates. Antimicrobial resistance genes were not studied sufficiently.

Conclusion: Our study showed a high prevalence of AMR in food and environmental isolates against various antibiotics. Resistant microorganisms and their resistance genes are transmitted to humans through the consumption of food products and the environment. Assessment of AMR in the environment and food is an important part of the fight against AMR and within the framework of the One Health approach.

Keywords: Antibiotic resistance, *Escherichia coli*, food, environment, Iran

Abstract ID: 360
subject: rational antibiotic prescription and resistance mechanisms

The synergistic antibacterial effects of low concentrations of acetic acid and tetracycline against tetracycline-resistant *Pseudomonas aeruginosa*

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Background and Aim: The emergence of antibiotic resistance in pathogenic bacteria, particularly in *Pseudomonas aeruginosa*, poses significant challenges in clinical treatment. This study investigates the synergistic effects of acetic acid at low concentrations and tetracycline against 20 tetracycline-resistant isolates of *Pseudomonas aeruginosa*.

Material And Methods: Employing a combination of in vitro assays, the antibacterial efficacy of acetic acid at 0.1%, 0.2%, 3% and 5%, tetracycline (Sigma Aldrich), and their combinations using checkerboard and time-kill methodologies. The minimum inhibitory and bactericidal concentrations (respectively MIC and MBC) were determined using two-fold microdilution broth method at a range of 0.5-128 µg/ml.

Results: Our results deciphered that acetic acid had mean inhibitory zones of 11 mm, 17 mm, 25mm and 30 mm at 0.1%, 0.2%, 3% and 5% concentrations, respectively. Moreover, the MIC of tetracycline ranged 8-16 µg/mL and its MBC ranged 16-64 µg/ml. Moreover, the combinatory antibacterial activity of tetracycline and 3% acetic acid, resulted in the reduction in MICs and MBCs of resistant strains to 4-8 µg/mL and 8-16 µg/mL, respectively. Furthermore, the combination therapy exhibited a greater bactericidal effect than either agent alone, suggesting a potential mechanism of action where acetic acid disrupts the bacterial membrane, facilitating tetracycline uptake and enhancing its efficacy.

Conclusion: These findings highlight the potential of utilizing non-antibiotic agents like acetic acid to restore the effectiveness of existing antibiotics against resistant bacterial strains, offering a promising strategy to combat antibiotic resistance in clinical settings. Further research is warranted to elucidate the underlying mechanisms and to explore the translational potential of this combination therapy in vivo.

Keywords: *Pseudomonas aeruginosa*, synergistic antibacterial effects, acetic acid, tetracycline

Abstract ID: 215
subject: Other related topics

Applications and challenges of phage therapy in treating antibiotic-resistant bacterial infections: A systematic review

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Background and Aim: Antibiotic resistance has become one of the greatest global challenges in the field of health. Phage therapy, the use of bacteriophages to treat bacterial infections, has emerged as a promising solution. This systematic review examines the applications, challenges, and prospects of phage therapy in treating antibiotic-resistant infections.

Material And Methods: A comprehensive search was conducted in PubMed, Scopus, Web of Science, and Google Scholar databases using relevant keywords. Studies published between 2000 and 2023 that focused on the use of phages in treating bacterial infections were selected. Data were extracted and analyzed following the PRISMA guidelines.

Results: Out of 320 identified articles, 65 studies met the inclusion criteria. Phage therapy was effective in treating a wide range of infections, including skin, gastrointestinal, urinary, and respiratory infections. Phages from the families Myoviridae, Siphoviridae, and Podoviridae were the most commonly used. Administration methods included topical, oral, and intravenous routes. Treatment outcomes demonstrated that phages were effective in reducing bacterial load and improving clinical conditions. However, challenges such as bacterial resistance to phages, limited host range, and regulatory issues were noted.

Conclusion: Phage therapy has significant potential as an alternative or complement to antibiotics. However, further research is needed to optimize treatment methods, address challenges, and increase the acceptance of phage therapy in healthcare systems. The development of phages with broader host ranges, combining phage therapy with antibiotics, and standardizing production and usage methods could help expand this therapeutic approach.

Keywords: Phage therapy, bacteriophage, antibiotic resistance, bacterial infections, alternative treatment

Abstract ID: 261
subject: Other related topics

Characterization of CagA EPIYA motifs in *Helicobacter pylori* strains from patients with digestive disorders

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Background and Aim: *Helicobacter pylori* infection is linked to various gastrointestinal conditions, including gastritis, ulcers, and gastric cancer. The virulence of *H. pylori* is influenced by the pathogenicity island PAI, which contains a Type 4 Secretion System and the oncoprotein *CagA* This study aimed to determine the current EPIYA motifs of the *cagA* gene in *Helicobacter pylori* isolates from patients with gastric disorders, and evaluate the association between these patterns and the clinical outcome of *H. pylori* infection in Ghaem Hospital in Mashhad.

Material And Methods: The study analyzed 67 DNA samples of *Helicobacter pylori* from previous research. The initial diagnostic procedures included bacterial culture, DNA extraction, and polymerase chain reaction (PCR) for the identification of the *cagA* gene. The samples were categorized into three groups: gastritis (44 samples), gastric ulcer (19 samples), and gastric cancer (4 samples). A PCR molecular test was performed to determine the EPIYA motif type for each sample.

Results: In the analysis of 67 samples, typographic variation was successfully identified in 52 samples, while 15 samples did not yield interpretable results. Among the samples that were typed, 31 were classified as type ABC, 5 as type ABD, and 16 as type AB. Specifically, within the subset of 35 samples associated with gastritis, 20 were categorized as type ABC, 2 as type ABD, and 13 as type AB. In the group of 14 samples pertaining to peptic ulcers, 10 were identified as type ABC, 3 as type AB, and 1 as type ABD. Additionally, of the 3 samples related to gastric cancer, 2 were classified as type ABD and 1 as type ABC. Statistical analyses revealed that there was no significant correlation between the prevalence of ABC and ABD patterns and the clinical symptoms observed.

Conclusion: Our results indicated that the common motif pattern observed across all samples was ABC. Consequently, the ABC type was more prevalent in patients with peptic ulcers (71%) compared to other patients (those with gastritis and cancer). However, this difference was not statistically significant ($P > 0.05$). In contrast, the ABD type was observed significantly more frequently in gastric cancer patients (66%) than in other patients ($P < 0.05$).

Keywords: *CagA*, gastric cancer, gastrointestinal diseases, *Helicobacter pylori*

Abstract ID: 66
subject: Other related topics

Haemophilus influenzae type b polyribosyl ribitol phosphate combined with detoxified lipooligosaccharide as a novel vaccine candidate against *Haemophilus influenzae*

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Background and Aim: *Haemophilus influenzae* (I) type b is considered as a common cause infection in infant. Recent vaccines have mitigated invasive diseases, but the control of disease is necessary. The purpose of this research was to investigate of the protective effect of polyribosyl-ribitol-phosphate combined with detoxified lipooligosaccharide (PRP-dLOS) in a rabbit model.

Material And Methods: PRP and LOS were purified using modified CY medium and Westphal and John, respectively. Endotoxin was evaluated via limulus amebocyte lysate procedure, and LOS was detoxified by alkaline method. The groups of rabbits were administrated with 10 µg of PRP, 20 µg of dLOS, and 10 µg+20 µg of PRP-dLOS on days of 0, 14, and 28. Blood samples were subsequently collected on days 0, 14, and 28 post-vaccination. Finally, IgM and IgG concentration were assayed by enzyme-linked immunosorbent assay.

Results: Our finding revealed that the concentration of PRP, dLOS, and endotoxin were 1160 mg/L, 440 ?g/mL, and 1450 EU/mL, respectively. Our data manifested that PRP-dLOS could cause a significant increase in the levels of IgG and IgM on days of 14 and 28 post-vaccination. Following the vaccination of rabbits with PRP-dLOS, serum concentration of IgM and IgG increased from 16.8 to 29.3 µg/mL at day of 14 and 29.8 to 61.4 µg/mL at day of 28 post-vaccination.

Conclusion: In conclusion, PRP-dLOS is an innovate vaccine candidate to combat *H. influenza*e type b without fear from interference with other vaccines.

Keywords: *Haemophilus influenzae* type b, lipooligosaccharide, vaccine

Abstract ID: 292
subject: Other related topics

Bioinformatics study of *Campylobacter jejuni* virulence factors: Designing multi-epitope-based vaccine

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Background and Aim: *Campylobacter jejuni* (*C. jejuni*) is causative agent of zoonoses infectious diseases that the prevention against it as a most important leading cause of gastrointestinal infections such as bloody diarrhea among pediatrics has not been successful. This in silico study aimed to design a Multi-Epitope vaccine (MEV) candidate against *C. jejuni*.

Material And Methods: Potential immunogenic and non-allergen epitopes of bacterium in addition with suitable adjuvant and specific linkers were selected to construct the novel MEV. The physicochemical parameters and stability of the binding to toll-like receptor 2 were evaluated using suitable online servers and tools. The molecular dynamics simulation of the MEV and TLR2 was performed by calculation of stability and strength of binding. The vaccine in silico cloning and expression within *Escherichia coli* host was also assessed. The immune responses were predicted using IMMSIM software.

Results: The results shown the proper physicochemical parameters and immunogenicity of the constructed MEV. The strong binding of the TLR2-MEV complex was also demonstrated and also construct was successfully expressed into the *E. coli* host. The immune simulation shown the elicitation of various immune compartments of innate and acquired arms.

Conclusion: The results from the new MEV candidate demonstrated its favorable immunogenicity and physicochemical characteristics. Additionally, the binding strength of the TLR2-MEV complex was highlighted. The construct was successfully expressed in *E. coli*. Immune simulations indicated the activation of various components of both the innate and adaptive immune systems. Future research could focus on in vitro and in vivo evaluations to further investigate the safety and immunogenicity of the developed vaccine.

Keywords: Zoonoses, *Campylobacter jejuni*, bioinformatics, vaccines, in silico

Abstract ID: 300
subject: Other related topics

Computational design of a multi-epitope vaccine candidate targeting *Shigella dysenteriae*

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Background and Aim: *Shigella dysentery* is a leading cause of bloody diarrhea in children, yet efforts to develop a vaccine or preventive measures have not been successful to date. This study aimed to create a novel multi-epitope vaccine (MEV) for the prevention of S. dysentery through in silico approaches.

Material And Methods: We identified potential non-allergenic, antigenic, and immunogenic peptides from the bacterium, along with a suitable adjuvant, namely Cholera toxin B (CTB). These components were integrated into a new MEV construct using specific linkers. We assessed the physicochemical properties and stability of the binding to toll-like receptor 3 (TLR3) using various online tools and servers. Additionally, we performed molecular dynamics simulations to evaluate the stability and binding strength of the MEV and TLR3 complex. The cloning and expression of the vaccine within an *Escherichia coli* host were also examined. We predicted immune responses using IMMSIM software.

Results: Our findings indicated that the construct exhibited acceptable immunogenicity and favorable physicochemical characteristics. The binding strength of the TLR3-MEV complex was confirmed, and successful expression in the *E. coli* host was achieved. Immune simulations suggested activation of various components of both innate and adaptive immune responses. Future research should focus on in vitro and in vivo analyses to evaluate the safety and immunogenicity of the designed vaccine.

Conclusion: The results from the novel MEV candidate demonstrated its promising immunogenicity and favorable physicochemical properties. The binding affinity of the TLR3-MEV complex was also highlighted. This construct was successfully expressed in an *E. coli* host. Immune simulations suggested that it stimulated various components of both the innate and adaptive immune responses. Future research could focus on evaluating the safety and immunogenicity of the designed vaccine through in vitro and in vivo studies.

Keywords: *Shigella dysentery*, vaccines, prevention, In silico, Immunoinformatics

Abstract ID: 302
subject: Other related topics

In silico design of a multi-epitope vaccine candidate targeting *Listeria monocytogenes*

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Background and Aim: *Listeria monocytogenes* is an opportunistic pathogen for which no approved vaccines currently exist. This study aimed to design a multi-epitope vaccine (MEV) against L. monocytogenes using in silico methods. By predicting potential epitopes derived from candidate bacterial virulence proteins, we aimed to create an effective MEV candidate.

Material And Methods: In this research, we identified and incorporated potential epitopes into the MEV construct. The physicochemical properties of the MEV were found to be satisfactory, and molecular docking studies with Toll-like receptor 2 (TLR2) indicated promising and stable interactions. To further explore the MEV-TLR2 interactions, we conducted molecular dynamics simulations, which revealed stable complex conditions, effective recognition of epitopes by immune components, and significant conformational changes within the complex. The novel MEV candidate demonstrated strong in silico immune responses against L. monocytogenes by utilizing various virulence antigens. The structural quality and physicochemical characteristics of the MEV construct were validated through online analysis tools.

Results: We identified peptides from *Listeria monocytogenes* that are likely to be non-allergenic, antigenic, and immunogenic, and we paired them with an appropriate adjuvant, Cholera toxin B (CTB). These elements were incorporated into a novel MEV construct using specific linkers. To evaluate the physicochemical properties and stability of the binding to TLR2, we utilized various online tools and servers. Furthermore, we conducted molecular dynamics simulations to assess the stability and binding affinity of the MEV-TLR2 complex. We also investigated the cloning and expression of the vaccine in an *Escherichia coli* host and predicted potential immune responses using IMMSIM software.

Conclusion: The novel MEV candidate demonstrated strong immune responses against L. monocytogenes through in silico analysis utilizing various virulence antigens. We confirmed the physicochemical properties and structural integrity of the MEV construct using online tools. Molecular dynamics simulations were conducted to investigate the interactions between MEV and TLR2, revealing stable complex conditions, effective epitope recognition by immune components, and conformational changes within the complex. The root mean square deviation (RMSD) and root mean square fluctuation (RMSF) values for TLR2 and MEV indicated their structural stability.Future research can explore the efficacy of this MEV candidate in both in vitro and in vivo settings.

Keywords: *Listeria monocytogenes*, immunoinformatics studies, vaccine design, subunit vaccines

Abstract ID: 134
subject: Other related topics

Optimization of alpha-amylase production process in batch fermentation using *Bacillus licheniformis* ATCC14580

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Background and Aim: The high consumption of amylase enzymes and the various applications of amylolytic enzymes have caused extensive research into selecting suitable microbial strains for alpha-amylase production and optimizing enzyme yields. Bacillus species are the most commonly used industrial microorganisms for amylase production. Therefore, In This study, the thermophilic bacterium *Bacillus licheniformis* ATCC14580, has been used to screen and optimize the production conditions of alpha-amylase in a batch fermenter.

Material And Methods: The production of alpha-amylase by *Bacillus licheniformis* ATCC14580 was investigated under various culture conditions. A Taguchi L8 orthogonal array was employed to review the effects of several factors, including the carbon source (starch), pH, temperature, the interaction between temperature and pH, the interaction between temperature and starch, agitation speed, and aeration rate. Analysis of variance (ANOVA), was performed to determine the most influential variables and identify optimal levels. The experiment was repeated under optimized conditions to validate the results.

Results: The results of ANOVA identified that the optimal conditions are temperature of 45°C, pH of 8, agitation speed of 300 rpm, starch concentration of 2%, and aeration rate of 1 VVM after 30 hours of fermentation. Under these optimal conditions, the maximum enzyme activity and specific activity of alpha-amylase were 428.3 U/L and 439.5 U/mg, respectively.

Conclusion: The study successfully optimized the production of alpha-amylase by *Bacillus licheniformis* ATCC14580 using the Taguchi method. The identified optimal conditions significantly enhanced enzyme activity and specific activity, providing a procedure for efficient industrial-scale production of alpha-amylase.

Keywords: *Bacillus licheniformis*, amylase enzyme, taguchi method, fermenter, batch culture

Abstract ID: 30
subject: Other related topics

The role of resveratrol in preventing fetal damage induced *Escherichia coli* lipopolysaccharide in rat

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Background and Aim: Lipopolysaccharides (LPS) induce adverse fetal development including intrauterine growth retardation, intrauterine fetal death, embryonic resorption and preterm delivery which are all related to LPS-induced oxidative stress. Resveratrol one of the most important antioxidants which commonly use to various diseases prevention. Aim: This study aimed to evaluate the protective role of resveratrol against LPS induced fetal damages in the rat.

Material And Methods: In this experimental study, 24 pregnant female rats were randomly divided into 4 groups (n=6). On days 15 to 18 of pregnancy, 50 mg/kg of *E. coli* LPS was injected intraperitoneally in groups 1 and 2 the second and third groups received 30 mg/kg of resveratrol intramuscularly a week before injection of LPS. The fourth group was the control group and placebo was injected to simulate injection stress. On the 18th day, all rats were euthanized. The number of live and dead fetuses and resorption sites was counted. Live fetuses in each litter were weighed, crown-rump and tail lengths measured and skeletal development was evaluated. In addition, maternal liver, placenta, and fetal liver samples were excised for measurement of MDA and GSH contents.

Results: The results demonstrate that administration of LPS significantly increased fetal mortality, decreased fetal weight and crown-rump and tail lengths of live fetuses and retarded skeletal ossification in caudal vertebrae, anterior and posterior phalanges and supraoccipital bon

Conclusion: Our study showed that co-administration of resveratrol and LPS could decrease LPS induced defects and improve damages indicating the preventive effects of resveratrol against LPS induced injuries during fetal development.

Keywords: Resveratrol, lipopolysaccharide, *Escherichia coli*, fetal, rat.

Abstract ID: 400
subject: Other related topics

computational screening of inhibitors targeting chlamydia protease-like activity factor (CPAF) in chlamydia trachomatis: A molecular docking approach

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Background and Aim: Urogenital Chlamydia trachomatis infection is one of the most common types of sexually transmitted illnesses worldwide. A highly conserved virulence factor of Chlamydia trachomatis, Chlamydial protease-like activating factor (CPAF), mediates the evasion of the innate immune response, inhibites the complement activation pathway, and degrades the antimicrobial peptides with its anti-chlamydial activity. Recent studies emphasize the importance of developing specific CPAF inhibitors to reduce its activity and attenuate bacterial virulence, offering a promising strategy for effective clinical management. Therefore, this study aimed to identify the most potent CPAF inhibitor through molecular docking analysis.

Material And Methods: The 3D structure of CPAF (PDB ID: 3DPM) was obtained from the PCSB PDB database. The structure of Lactacystin as an inhibitory ligand (PubChemCID: 6610292) and a total of 20 of its analogs were retrieved from the PubChem database in SDF format. After preparing the protein and ligands, molecular docking was performed using Virtual Docker Molegro.6.0. Subsequently, the best interaction with the lowest energy binding was analyzed using Molegro Viewer software. Finally, pharmacokinetic properties such as the distribution, absorption, metabolism, and excretion of the ligand were investigated using the SwissADME server

Results: Among all ligands, the best ligand for CPAF was identified as 2-acetamido-3-[3-hydroxy-2-[(1S)-1-hydroxy-2-methylpropyl]-4-methyl-5-oxopyrrolidine-2-carbonyl] sulfanyl propanoic acid (PubChem ID: 10407181) with a molecular weight of 376.43 g/mol and binding energy of -136.889 kcal/mol. This ligand formed 8 hydrogen bonds with the CPAF residues Glu406, Lys53, Asn530, Asn535, Thr403, lle539, Lys540, and Phe533, as well as 12 steric interactions with the residues Glu406, Phe529, Asn530, Lys53, Pro534, Asp405, Phe533, lle539, Lys540, Phe111, Thr403, and Asn535. Moreover, the ADME results indicated that this ligand had a water solubility score (logS) of -1.41, a lipophilicity score (XLOGP3) of -0.27, a polarity score (TPSA) of 178.33 Å², and hydrogen bond donors and acceptors of 5 and 7, respectively.

Conclusion: Consequently, after further in vitro and in vivo analysis, 2-acetamido-3-[3-hydroxy-2-[(1S)-1-hydroxy-2-methylpropyl]-4-methyl-5-oxopyrrolidine-2-carbonyl] sulfanylpropanoic acid (PubChem ID: 10407181) may be considered a candidate for inhibiting Chlamydia trachomatis's CPAF.

Keywords: Chlamydia trachomatis; molecular docking; CPAF factor.

Abstract ID: 35
subject: Other related topics

Investigating bacterial vaginal discharge etiology in pregnant women by microscopic examination and PCR

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Background and Aim: Abnormal vaginal discharge is a common problem among pregnant women. The most common cause of these discharges is bacterial vaginosis (BV), which has numerous complications and causes problems for pregnant mothers and their fetuses. The purpose of this study was to determine the BV frequency among pregnant women referring to a gynecology clinic in Arak city using Amsel and Nugent criteria, Alberta guideline, and PCR

Material And Methods: This descriptive study was performed on 70 vaginal samples of pregnant women in Arak to investigate the most common causes of vaginal discharge according to Amsel and Nugent criteria and polymerase chain reaction (PCR) method using specific primers targeted towards three bacteria: *Gardnerella vaginalis, Atopobium vaginae, Mobiluncus curtisii*. Data were analyzed using SPSS software and Chi-square test.

Results: In this study, ten (14.28%) out of 70 pregnant women had positive bacterial vaginosis according to Amsel criteria. According to Nugent criteria and Alberta guideline, three (4.29%) cases were diagnosed with definite BV, 20 (32.26%) cases with intermediate BV with clue cells, 42 (67.74%) cases with intermediate BV without clue cells, and finally five (4.29%) cases with negative BV. Also, according to PCR, the frequency of *G. vaginalis, M. curtisii*, and *A. vaginae* in vaginal samples was 71.42% (50 cases), 64.28% (45 cases), and 30% (21 cases), respectively.

Conclusion: According to the obtained results, the prevalence of definite bacterial vaginosis was lower than that of vaginitis, and most patients suffered from nonspecific vaginitis.

Keywords: Vaginal discharge, vaginosis, bacterial, pregnant women, polymerase chain reaction

Abstract ID: 49
subject: Other related topics

Design of a hybrid antibody in the form of a double chain fragment antibody (scFv) to identify the surface protein Factor H binding protein (fHbp) of the bacterium *Neisseria meningitidis*

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Background and Aim: The pathogenic factor factor H-binding protein (fHbp) plays a critical role in the survival of the pathogen in the host. Single-chain antibodies in the scFv form have therapeutic and diagnostic applications. The aim of this study was to use computational methods to design, express and evaluate the binding strength of a hybrid single-chain antibody for the identification of the bacterium Neisseria meningitidis, the causative agent of meningococcal disease.

Material And Methods: In this study, a hybrid antibody with high binding strength to the fHbp protein was designed by performing a series of computational evaluations (antigen, antibody modeling and antigen-antibody docking). Its gene construct was synthesized in the pET28a(+) expression vector and after expression in BL21 bacteria and purification using Ni-NTA resin, its binding affinity to the fHbp protein was examined using the ELISA method. also in QC-Phase we used GC-MS and HPLC and OD-metrical prosecution in Bacteria.

Results: The hybrid form (VH1-VL2) was selected using computational evaluations. SDS-PAGE and Western blotting confirmed the expression of the designed construct. After purification of the antibody and fHbp antigen, the binding affinity of this hybrid scFv form was calculated to be 10-9 × 6.7 in ELISA studies.

Conclusion: The appropriate binding affinity of the hybrid antibody form indicates that by using antibody engineering and computational methods, other forms of single-chain antibodies can be achieved that are useful for therapeutic and diagnostic purposes.

Keywords: Hybrid single chain fragment antibody, *Neisseria meningitidis*, factor H binding protein (fHbp), cloning, expression

Abstract ID: 48
subject: Other related topics

Exploring the potential of *Bacteroides Thetaiotaomicron* in modulating the immune response in chronic myeloid leukemia

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Background and Aim: *Bacteroides thetaiotaomicron* is proposed as a potential candidate for the next generation of probiotics. The ES-8 and ES-D genes play crucial roles in activating and modulating the innate immune system against leukemia following bacterial exposure in the bone marrow. This study was designed to examine the effect of *B.thetaiotaomicron* and its derivatives on alterations in the expression of ES-8 and ES-D genes, and their significance in modulating the severity of chronic myeloid leukemia (CML).

Material And Methods: The impact of *B.thetaiotaomicron*, outer membrane vesicles (OMVs), inactivated bacteria, and supernatant treatments on the ES-8 and ES-D gene expression in the KG-1 cell line was analyzed using the quantitative reverse transcription-polymerase chain reaction (qRT-PCR) method. The Livak (ΔΔCT) method was employed to interpret the qRT-PCR results. The extraction and evaluation of outer membrane vesicles from gram-negative bacteria were performed using ultracentrifugation and ultrafiltration-based methods.

Results: The KG-1 cell line showed a significant response to treatment with live and active *B.thetaiotaomicron*, particularly in ES-8 and ES-D transcription. OMVs from this bacterium, at a concentration of 50 µg/ml, significantly intensified the expression of the ES-8 (p=0.01) and ES-D (p=0.02) genes. This effect was even more pronounced at a concentration of 100 µg/ml. Inactivation at MOI 10 (p=0.03) and MOI 50 (p=0.003) significantly induced transcription of both genes. Additionally, a 25% supernatant considerably augmented the transcriptional expression of ES-8 (p=0.038) and ES-D (p=0.034) genes.

Conclusion: Our findings suggest that OMVs at a concentration of 100 µg/ml, inactivated bacteria, and supernatants of *B.thetaiotaomicron* play a crucial role in shaping the immune response and could be considered as potential postbiotic and paraprobiotic candidates for further research. Moreover, our data indicate a significant reduction in the severity of chronic myeloid leukemia in the erythroleukemia phase, affirming its potential as an effective adjuvant treatment for leukemia.

Keywords: *B.thetaiotaomicron*, chronic myeloid leukemia, Microbiota, OMVs, ES-8, ES-D

Abstract ID: 111
subject: Other related topics

Investigating the antimicrobial and anti-biofilm effects of carvacrol on MDR strains of *Stenotrophomonas maltophilia*.

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Background and Aim: *Stenotrophomonas maltophilia* is recognized as an emerging opportunistic pathogen, responsible for numerous hospital-acquired infections with high mortality rates, particularly among immunocompromised patients. The increasing antibiotic resistance of *Stenotrophomonas maltophilia* strains is a global concern. This study aims to investigate antimicrobial sensitivity, antibiotic resistance, biofilm intensity, and the effect of carvacrol on biofilm-producing MDR strains.

Material And Methods: A total of 72 clinical isolates of *Stenotrophomonas maltophilia* were collected from hospitals in selected cities of Iran. These isolates were identified using conventional biochemical and microbiological methods and confirmed by 23S rRNA gene sequencing. Antibiotic susceptibility testing was performed using disk diffusion and E-test methods according to CLSI 2022 guidelines. Biofilm formation ability was assessed using the microtiter plate method. Finally, the effect of carvacrol on MDR strains was evaluated using MIC and MBC methods, and the results were statistically analyzed.

Results: In the 72 confirmed clinical isolates, the highest and lowest resistance were observed to ceftazidime and minocycline (57.59% and 1.38%, respectively). All strains had the ability to form biofilms, categorized as strong (19.44%), moderate (60%), and weak (20.83%). The effect of carvacrol on MDR strains without biofilm showed MIC values of 32 µg/mL and MBC values of 64 µg/mL. In biofilm conditions, the MIC was 64 µg/mL and the MBC was 256 µg/mL.

Conclusion: The results of this study indicate that the antibiotic resistance of *Stenotrophomonas maltophilia* strains in Iran is increasing, and biofilm-producing strains are also on the rise. Carvacrol demonstrated effective activity against both biofilm-producing and non-biofilm-producing MDR strains, suggesting its potential as a suitable therapeutic candidate for further investigation.

Keywords: *Stenotrophomonas maltophilia*, biofilm, antibiotic resistance, typing

Abstract ID: 343
subject: Other related topics

Effect of 20-ppm ozone and 1% chlorhexidine gels on plaque index and *Streptococcus mutans* counts in the dental plaque in 6–12-year-old children: A randomized, double-blind clinical trial

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Background and Aim: One of the methods to control dental caries is to use ozone. Since it is difficult for children to use mouthwashes, the present study aimed to evaluate 20-ppm zone and 1% chlorhexidine (CHX) gels' effects on the plaque index and *Streptococcus mutans* counts in 6–12-year-old children

Material And Methods: In the present double-blind clinical trial, 165 children, 6–12 years of age, referring to the Department of Pediatric Dentistry, Tabriz Faculty of Dentistry, were selected based on inclusion and exclusion criteria and randomly assigned to three groups: ozone gel, CHX gel, and control. The subjects were instructed to place an adequate amount of the gels on all the surfaces of their teeth with one clean finger. The patients and evaluators were blinded to the study groups. The plaque index and *S. mutans* counts in plaque samples were determined before intervention and three weeks after intervention on the buccal surface of the most posterior maxillary tooth (left or right). *S. mutans* counts were determined by culture. STATA software version 14 was used for statistical analyses using Wilcoxon, Kruskal-Wallis, and post hoc Dum tests. Statistical significance was defined at $P < 0.05$.

Results: The 20-ppm ozone and 1% CHX gels significantly decreased dental plaque compared to the control group ($P < 0.05$), and their effects were similar ($P > 0.05$). These gels significantly decreased the colonies and bacterial counts of S. mutans ($P < 0.05$).

Conclusion: The performance of 20-ppm ozone gel in decreasing the dental plaque and *S. mutans* counts was similar to 1% CHX gel.

Keywords: Chlorhexidine gel, dental plaque, ozone gel, *Streptococcus mutans*

Abstract ID: 204
subject: Other related topics

A systematic review of human oral microbiome dysbiosis associated with oral cancer

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Background and Aim: Oral microbiota includes a wide range of microorganisms that reside in the oral cavity. The microbiome in this part of human body plays an important role in maintaining its health. dysbiosis, which is actually imbalance of oral microbiota, causes various diseases, including oral cancer. Inflammation, immunological evasion, and cancer can result from changes in the variety and number of microbial species in the mouth cavity. By assessing the microbial signatures linked to carcinogenesis and their potential as biomarkers for early detection and therapeutic targets, this systematic review seeks to investigate the connection between oral microbiome dysbiosis and oral cancer.

Material And Methods: The keywords "microbiome", "dysbiosis", "cancer", and "oral cancer" were used to obtain the data from PubMed, Scopus, and Google Scholar. 8 of the 19 studies that were found in the first search and published between 2015 and 2024 were included in the analysis. The search was limited to studies in the English language and accessible full texts.

Results: Oral squamous cell carcinoma (OSCC) has been associated with the onset and progression of dysbiosis of the oral microbiome. The bacterial composition of oral cancer tissues differs significantly from that of normal tissues, according to several studies. In particular, periodontitis-associated taxa like *Fusobacterium, Dialister*, and *Peptostreptococcus* are more abundant, while beneficial genera like Streptococcus are less prevalent. Through processes like weakened immune responses and the inhibition of anti-cancer chemicals, these microbial changes are thought to have a role in the development of tumors. Additionally, functional analyses show that the microbial communities in OSCC lesions prefer pathways that could support the growth of cancer by creating a pro-inflammatory environment. The importance of microbial imbalance in cancer-related oral illnesses is further supported by the comparable microbial disruptions observed in chemotherapy-induced dysbiosis in patients with oral mucositis.

Conclusion: This research emphasize that dysbiosis of the oral microbiome has a significant impact on tumorigenic pathways and immunological responses. These results imply oral microbiota as prospective biomarkers for early detection and therapy of oral cancer and emphasize the possibility of addressing microbial imbalances as a therapeutic approach.

Keywords: Microbiome, dysbiosis, cancer, oral cancer

Abstract ID: 378
subject: Other related topics

Isolation and identification of bacteriophage effective against *Salmonella typhimurium* isolated raw chicken meat

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Background and Aim: Using phage-based methods for treatment of bacterial contamination has some obvious advantages over conventional ones. Firstly, phages only kill their host bacteria even antibiotics resistant ones thus they are harmless to others, especially beneficial microorganisms which also present in the foods and human intestinal tract. Secondly, the addition of the lytic phages to the foods is unlikely to induce negative impacts to food properties. The aim of this study was to isolate lytic phages against *Salmonella* from raw chicken meat products and examine their efficacy in reducing *S. typhimurium* in vitro.

Material And Methods: In this study, 20 *S. typhimurium* were collected from raw chicken meat and phenotypic and genotypic confirmation was performed. Primary bacteriophage isolation and plaque collection were done from sewage treatment plant. Then bacteriophage titer and phage specificity were done by host determination method. The sensitivity of phage on *S. typhimurium* isolates was similar to the method of determining the host and was performed by the Spot test method. Phage identification was done by TEM electron microscope.

Results: The isolated phage was from the *Siphoviridae* family and 12 of 20 strains of *S. typhimurium* were sensitive to it. The phage titer was maintained after 1 hour of incubation at 25, 30, 35 and 40°C and was stable at different pH (2-11). The isolated lytic bacteriophage formed small transparent plaques with a latent period of 40 min and a burst time of 45 min, corresponding to 35 phage particles per infected cell.

Conclusion: The results of this study indicate that phage therapy is a useful treatment method for treating infections caused by *S. typhimurium*.

Keywords: *Salmonella typhimurium*, bacteriophage, *Siphoviridae*, chicken meat, TEM

Abstract ID: 241
subject: Other related topics

A comparative study on the synergistic effects of thymol/cefotaxime against *Staphylococcus epidermidis* and *Acinetobacter baumannii*

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Background and Aim: This study compares the synergistic antimicrobial effects of thymol/cefotaxime on *Staphylococcus epidermidis* and *Acinetobacter baumannii*.

Material And Methods: Antimicrobial effects of thymol/cefotaxime were performed first individually and then combined on *S. epidermidis* ATCC 1457 and *A. baumannii* ATCC 19606 by the MIC-MBC method. Therefore, the antimicrobial effects of the compounds that had a synergistic impact were performed on clinical strains using the MIC-MBC method. The identification of chemical bonds, functional groups, and molecular interactions of the mentioned compound was investigated using an FT-IR device. Checkered method, biofilm inhibition on *S. epidermidis* ATCC and1457*A. baumannii* ATCC 19606, and cytotoxicity investigation on red blood cells (RBCs) by hemolysis and human skin fibroblast cells (Ffk) by MTT method were performed. Finally, the results of the tests were compared between the two bacteria.

Results: The results of this study showed that the antimicrobial effects of the thymol/cefotaxime (16/4 µg/ml) were on *S. epidermidis* better than on *A. baumannii* (512/512 µg/ml) in both clinical and ATCC strains. In the examination with the FT-IR device, it had bonds of OH carbohydrates proteins, polyphenols, C=O Amide I band, C-O-C polysaccharide, C-N amide III band, but one band named C=C conjugated, C≡C in compound showed the connection between thymol with cefotaxime. The biofilm inhibition effects of thymol/cefotaxime on *S. epidermidis* ATCC 1457 (61.81%) were better on *A. baumannii* ATCC 19606 (39.28%). The cytotoxicity of synergistic compounds on RBCs and human Ffk cells was not different and was lower than that of Triton X-100.

Conclusion: Considering the antibiotic resistance of cefotaxime in the treatment of diseases caused by *S. epidermidis* and *A. baumannii*, thymol/cefotaxime showed better antimicrobial and anti-biofilm effects in *S. epidermidis* than *A. baumannii* in this study. After further studies, this compound can be used as a new drug in patients.

Keywords: *Staphylococcus epidermidis*, *Acinetobacter baumannii*, thymol, cefotaxime, synergistic

Abstract ID: 51
subject: Other related topics

Anti-virulence effect of photoactivated flavonoid glycosides via diode laser emitting light against *Acinetobacter baumannii*

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Background and Aim: *Acinetobacter baumannii*'s extensive antibiotic resistance makes its infections difficult to treat, so effective strategies to fight this bacterium are urgently needed. This study aims to evaluate the effectiveness of antimicrobial photodynamic therapy (aPDT) mediated by Rutin-Gal(III) complex and Quercetin as the flavonoid glycosides against *A. baumannii*.

Material And Methods: Absorbance and fluorescence spectra, along with the minimum inhibitory concentration (MIC) of the Rutin-Gal(III) complex and Quercetin, were analyzed. Additionally, the study measured intracellular reactive oxygen species (ROS), extracellular polymeric substances (EPS), cell membrane permeability, and the expression levels of ompA and blaOXA-23. The anti-biofilm and anti-metabolic activities of the aPDT mediated by the Rutin-Gal(III) complex and Quercetin were also evaluated.

Results: The Rutin-Gal(III) complex and Quercetin exhibited absorption peaks within the visible spectrum. Fluorescence peaks were observed at 524 nm for Quercetin and at 540 nm for the Rutin-Gal(III) complex. The MIC values were determined to be 64 µg/mL for the Rutin-Gal(III) complex and 256 µg/mL for Quercetin. The aPDT mediated by Quercetin and the Rutin-Gal(III) complex significantly decreased colony-forming units per mL by 58.4% and 67.5%, respectively, along with reductions in EPS synthesis (47.4% and 56.5%), metabolic activity (30.5% and 36.3%), and expression levels of the *ompA* gene (5.5-fold and 10.5-fold) as well as the *blaOXA-23* gene (4.1-fold and 7.8-fold), all with $P < 0.05$. Furthermore, this treatment led to significant biofilm degradation (36.2% and 40.6%), increased ROS production (2.55-fold and 2.90-fold), and enhanced membrane permeability (10.8-fold and 9.6-fold), respectively, with all results being statistically significant ($P < 0.05$).

Conclusion: The results suggest that aPDT mediated by the Rutin-Gal(III) complex and Quercetin demonstrates antibacterial effects and could be an effective supplementary approach to traditional antibiotic therapies for treating *A. baumannii* infections. However, a limitation of this study is that it was performed exclusively on a standard strain; conducting tests on clinical isolates would provide a more accurate interpretation of the findings.

Keywords: *Acinetobacter baumannii*, antimicrobial photodynamic therapy, quercetin, rutin-gal(III) complex

Abstract ID: 289
subject: Other related topics

A comparative study on the synergistic effects of thymol/ceftazidime against *Staphylococcus epidermidis* and *Acinetobacter baumannii*

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Background and Aim: This study compares the synergistic antimicrobial effects of thymol/ceftazidime on *Staphylococcus epidermidis* and *Acinetobacter baumannii*.

Material And Methods: Antimicrobial effects of thymol/ceftazidime were performed first individually and then combined on *S. epidermidis* ATCC 1457 and *A. baumannii* ATCC 19606 by the MIC-MBC method. Therefore, the antimicrobial effects of the compounds that had a synergistic impact were performed on clinical strains using the MIC-MBC method. The identification of chemical bonds, functional groups, and molecular interactions of the mentioned compound was investigated using an FT-IR device. Checkered method, biofilm inhibition on *S. epidermidis* ATCC 1457 and *A. baumannii* ATCC 19606, and cytotoxicity investigation on red blood cells (RBCs) by hemolysis and human skin fibroblast cells (Ffk) by MTT method were performed. Finally, the results of the tests were compared between the two bacteria.

Results: The results of this study showed that the antimicrobial effects of the thymol/ceftazidime (16/2 µg/ml) were on *S. epidermidis* better than on *A. baumannii* (512/128 µg/ml) in both clinical and ATCC strains. In the examination with the FT-IR device, it had bonds of OH carbohydrates proteins, polyphenols, C=O Amide I band, C-O-C polysaccharide, C-N amide III band, but one band named C=C conjugated, C≡C in compound showed the connection between thymol with ceftazidime. The biofilm inhibition effects of thymol/ceftazidime on *S. epidermidis* ATCC 1457 (49.09%) were better on *A. baumannii* ATCC 19606 (23.41%). The cytotoxicity of synergistic compounds on RBCs and human Ffk cells was not different and was lower than that of Triton X-100.

Conclusion: Considering the antibiotic resistance of ceftazidime in the treatment of diseases caused by *S. epidermidis* and *A. baumannii*, thymol/ceftazidime showed better antimicrobial and anti-biofilm effects in *S. epidermidis* than *A. baumannii* in this study. After further studies, this compound can be used as a new drug in patients.

Keywords: *Staphylococcus epidermidis*, *Acinetobacter baumannii*, thymol, ceftazidime, synergistic

Abstract ID: 277
subject: Other related topics

Enhancing antibiofilm efficacy of lysostaphin against *Staphylococcus aureus* wound infections using niosomal delivery systems

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Background and Aim: *Staphylococcus aureus* is the most common cause of wound infections and often presents biofilms with inherent resistance to antibiotics. In this regard, lysostaphin has emerged as a potent anti-staphylococcal enzyme with limitations in delivery and stability. Herein, we develop a new strategy based on niosomes encapsulating lysostaphin for enhanced efficacy against biofilms. By combining the active targeting capabilities of niosomes with the potent antimicrobial action of lysostaphin, we aim at enhanced wound healing and combating antibiotic resistance

Material And Methods: Clinical isolates of *S. aureus* were collected from wound infection specimens and confirmed by standard microbiological and molecular methods. Biofilm formation was quantified by crystal violet assay. The thin-film hydration method was used to prepare the lysostaphin-containing niosomes, which, after preparation, were characterized for size, encapsulation efficiency, and stability. The in vitro antibiofilm activities of the lysostaphin-loaded niosomes were conducted by measuring biofilm disruption using both the spectrophotometric and confocal microscopy analyses. Controls included free lysostaphin and empty niosomes. Moreover, statistical analysis was focused on the significance of the observed differences.

Results: Lysostaphin-loaded niosomes exhibited significantly higher antibiofilm activity compared to free lysostaphin and empty niosomes ($p < 0.01$). Confocal microscopy revealed extensive biofilm disruption and bacterial cell lysis upon treatment with lysostaphin-loaded niosomes.

Conclusion: This study has emphasized that lysostaphin-loaded niosomes may be an effective therapeutic strategy against *S. aureus* biofilms in wound infection. The niosomal formulations improve enzyme stability and target cells associated with biofilms, thus overcoming the major limitations of traditional therapies. These promising in vitro results call for in vivo studies to further establish the clinical applicability of this novel approach.

Keywords: *Staphylococcus aureus*; biofilm; niosomes; wound infection

Abstract ID: 222
subject: Other related topics

Evaluation of anticancer effects of postbiotics derived from *Enterococcus faecium* strain KCH-1 on HT29 colon cancer cell line

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Background and Aim: Colorectal cancer (CRC) is one of the leading causes of cancer-related deaths worldwide, with significant associations with the gut microbiome and the immune system. Postbiotics, which are non-viable microbial cells or their components, have shown potential in promoting health and exhibiting anti-cancer properties. This study focuses on evaluating the anti-cancer effects of postbiotics derived from *Enterococcus faecium* strain KCH-1 on the colorectal cancer cell line HT29. Given the increasing interest in postbiotics as a next-generation health-promoting compound, the aim was to assess their cytotoxic, apoptotic, and cell cycle-inhibitory activities.

Material And Methods: The postbiotic was extracted from *Enterococcus faecium* strain KCH-1 by isolating and lyophilizing the cell-free supernatant. The MTT assay was employed to determine cytotoxicity across different concentrations, and the IC50 value was calculated. Flow cytometry was used to evaluate apoptosis induction and cell cycle progression, while reactive oxygen species (ROS) levels were measured to assess oxidative stress.

Results: The MTT assay revealed a dose-dependent decrease in HT29 cell viability, with significant cytotoxicity observed at a concentration of 1000 µg/ml after 48 hours. The IC50 was calculated, indicating the effective concentration for 50% inhibition of cancer cell growth. Flow cytometry results showed that postbiotic treatment increased early apoptosis by 21.6% compared to the control group. Moreover, a cell cycle arrest was observed, with 40.92% of cells accumulating in the S phase. ROS levels were elevated in treated cells, suggesting oxidative stress as a mechanism behind the postbiotic's action.

Conclusion: The postbiotic derived from *Enterococcus faecium* strain KCH-1 demonstrated significant anti-cancer effects against colorectal cancer cells. It reduced cell viability, induced apoptosis, caused cell cycle arrest, and elevated ROS production. These findings suggest that this postbiotic has strong potential as a therapeutic agent in colorectal cancer treatment, warranting further investigation into its clinical applications.

Keywords: Colon, cancer, postbiotic, probiotic

Abstract ID: 91
subject: Other related topics

Isolation of *Staphylococcus aureus* strains from patients with pulmonary infections hospitalized in ICUs of Kerman and evaluation the occurrence of *mecA*, *pvl, LukS / F-PV* Genes

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Background and Aim: *Staphylococcus aureus* is one of the most common nosocomial infections. Today there are reports that the prevalence of methicillin resistance in *S.aureus* is increasing in different parts of the world. The aim of this study was to isolate *Staphylococcus aureus* strains from patients admitted to the intensive care units.

Material And Methods: This cross-sectional descriptive study was performed on 60 lung secretion samples of Patients hospitalized in ICUs in Kerman, Iran. Accordingly, single cell colony was performed to obtain purified isolates. Biochemical tests were also used for identification and confirmation of isolated bacteria specially to find out the genospecies *Staphylococcus aureus*. *mecA* and *LukS / F-PV* genes were also evaluated by multiplex PCR.

Results: Among 60 lung secretion samples, 20 strains of *Staphylococcus aureus* were identified and confirmed accurately by biochemical tests. The frequency of *LukS / F-PV* gene was reported in 12 isolates and the frequency of *mecA* gene was reported in 8 ones as well as 4 isolates showed to have both above mentioned genes. Conclusion: most strains contained *mecA*. The high prevalence of MRSA isolates with community-acquired genotype led to testing current hospital hygiene practices to control the spread of nosocomial MRSA isolates. Considering the ability of PVL and *LukS/F-PV*-producing MRSA isolates to cause life-threatening diseases, and prevalence of pulmunary MRSA isolates, rapid diagnosis, direct, simple and cost-effective tests can help reduce MRSA infections. Also, in order to limit the spred of MRSA, maximun aseptic practices for health care professionals and better training in hygiene practices are needed

Conclusion: Evaluating the prevalence of virulence gene strains can be effective in controlling infectious diseases in people with weakened immune systems and patients hospitalized in the intensive care unit. The multiplex PCR method for faster diagnosis of these genes can usually be performed in laboratories. Moreover, special measures to control infection, especially the frequency of virulence genes in the intensive care unit, can be an effective factor in reducing the pathogenicity of these genes.

Keywords: *Staphylococcus aureus*, MRSA, *mecA, LukS / F-PV.*

Abstract ID: 280
subject: Other related topics

Design and construction of the triple recombinant protein and its immunogenic evaluation against bacteria that cause diphtheria, tetanus and pertussis in animal model

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Background and Aim: Design of a single multi-epitope against three DTP bacteria .The putative antigenic epitopes from different organisms in a single protein

Material And Methods: the gene with serotype DH5α was transformed in *E. coli* BL21 bacteria with heat shock. The recombinant plasmid was extracted and purified by a Canadian kit. Gene expression and induction of protein expression were performed by IPTG inducer (isopropyl beta-thiogalactopyranoside) and gene expression was confirmed by SDS-PAGE of the desired band. The wall of bacteria was broken by sonicator. Purification of the recombinant protein with His tag and nickel resin chromatography was performed, as well as western blot confirmation test. The protein concentration was determined by the Bradford method and then the purity of the expressed protein was evaluated using SDS-PAGE. Dialysis was performed to reduce protein concentration and buffer exchange. According to the scheduled protocol, the mice were treated in 8 groups of ten in the injection table, and after the completion of the time required for immunization, the mice were euthanized and their spleens were removed, and hematology, pathology, cytology and ELISA tests were performed and Stimulation of the mouse immune system by recombinant protein compared to the Indian vaccine available on the market with serological methods, ELISA, cell culture, and biochemical and hematological tests, as well as the lack of cytotoxicity of the recombinant protein on Vero cells

Results: Immunological and cytotoxicity results after gene expression and purification of the recombinant protein showed that the best results were achieved at a dose of 15 microgram

Conclusion: this compound was completely safe and had no lethal effect on eukaryotic cells, which are Vero cells. After challenge, it could be commercialized as a safe compound as a recombinant triple vaccine.

Keywords: *Bordetella pertussis*, *Corynebacterium diphtheria*, *Clostridium tetani*, immune-informatics, fusion protein, recombinant vaccine

Abstract ID: 8
subject: including the role of probiotics in health and disease

The role of probiotics used in poultry nutrition in improving the health of poultry

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Background and Aim: Probiotics are products of microbial cells that are used to improve human health and well-being.Poultry meat is currently considered one of the most significant sources of animal protein in the world.Increasing the density of poultry breeding causes disease-related challenges in them . Infections caused by these pathogenic microorganisms can lead to a decrease in growth rate, an increase in antibiotic use, and ultimately economic losses. The growing concern about bacterial resistance to antibiotics is causing a growing interest in finding appropriate alternatives to them. Probiotics are considered food additives, substitutes for antibiotics, and they can be defined as microbial food supplements that have a beneficial effect on the host by improving the microbial balance of the host's intestinal system. The purpose of this study is to determine the role of probiotics in poultry nutrition in improving their health.

Material And Methods: Two groups of 50 treated and control broilers were chosen for this purpose. For the entire 55-day period, the treatment group received oral probiotics under similar conditions, and then both groups were killed at the slaughterhouse. To achieve a balance between probiotics and intestinal flora bacteria, consumption of at least 107-106 Cfu/g probiotics is recommended. For each carcass, 100 grams of skin and breast meat samples were taken to the laboratory. Total microbial count, Staphylococcus aureous, fecal Streptococci, Coliforms counts were performedon the samples according to standard approaches of Iran.

Results: The results were analyzed using independent t-Test and Chi-square test. Comparison of the means of total microbial counts, coliform , enteric streptococci and meat staphylococcus counts both control and treatment groups showed a significant decrease ($p<0.005$).

Conclusion: Poultry performance and infectious disease prevention are positively impacted by probiotics and they can be utilized in poultry nutrition and infection control.

Keywords: probiotics - poultry - health

Abstract ID: 46
subject: including the role of probiotics in health and disease

The efficacy of probiotics in managing peri-implant diseases: A systematic review

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Background and Aim: Peri-implant diseases, including peri-implantitis, remain significant challenges in dental implantology due to their association with inflammation, microbial dysbiosis, and bone loss. Probiotics have emerged as a promising adjunctive therapy, with the potential to modulate the peri-implant microbiome, control biofilm, and influence immune responses. However, their role in managing peri-implant diseases, particularly peri-implantitis, is not yet fully established.

Material And Methods: A systematic review of PubMed, Scopus, and Web of Science databases was conducted, including randomized controlled trials (RCTs), pilot studies, narrative reviews, and meta-analyses from 2010 to 2024. The initial search identified 98 studies. After screening titles and abstracts, and applying inclusion and exclusion criteria, 39 articles were included in the final analysis. The primary outcomes assessed were clinical parameters such as bleeding on probing (BOP), plaque index (PI), probing pocket depth (PPD), as well as microbiological profiles and inflammatory biomarkers. The review focused on evaluating the effectiveness of probiotics, specifically strains like Lactobacillus Reuteri, in both the prevention and treatment of peri-implant diseases.

Results: Some studies showed limited to no significant impact of *Lactobacillus Reuteri* probiotics on peri-implantitis, suggesting that anatomical and microbial challenges may hinder colonization and therapeutic benefits. However, other studies demonstrated probiotics' potential in reducing inflammation and improving clinical parameters in peri-implant mucositis. The variability in outcomes across studies highlights the complexity of probiotic therapy in peri-implant disease management, influenced by factors such as strain specificity, dosage, and patient immune responses. While some trials reported significant improvements in BOP and plaque accumulation after 1 to 3 months of probiotic use, others found no sustained benefits, particularly concerning PPD reduction. Emerging evidence on postbiotics and alternative adjunctive therapies like photodynamic therapy also offers promising directions for future research.

Conclusion: Certain studies show temporary improvements in clinical parameters like bleeding on probing and plaque accumulation due to probiotics. However, these benefits are inconsistent and often short-lived, with no significant reductions in PPD or microbiological changes. High variability and the quality of existing studies limit definitive conclusions. Therefore, probiotics should not be used as a primary or standalone therapy for peri-implant diseases. Clinicians should prioritize proven treatments such as mechanical debridement and systemic antimicrobials.

Keywords: Probiotic, peri-implantitis, *Limosilactobacillus reuteri*, adjunctive therapy, periodontics

Abstract ID: 28
subject: including the role of probiotics in health and disease

Probiotics in the prevention and management of irritable bowel syndrome (IBS): A systematic review

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Background and Aim: Irritable Bowel Syndrome (IBS) is a prevalent functional gastrointestinal disorder characterized by abdominal discomfort and altered bowel habits, significantly impairing quality of life. Probiotics, as live microorganisms that confer health benefits, have been increasingly explored as a potential therapeutic option for IBS. This systematic review aims to synthesize evidence on the efficacy of probiotics in the prevention and management of IBS symptoms.

Material And Methods: A systematic search was conducted across PubMed, Scopus, Web of Science, and Cochrane Library databases for randomized controlled trials (RCTs) published between 2010 and 2024. Inclusion criteria were studies assessing probiotics' effects on IBS symptoms, with validated symptom scoring scales as outcome measures. Two independent reviewers screened studies, extracted data, and assessed quality using the Cochrane Risk of Bias tool. Meta-analyses were performed when data were available and sufficiently homogeneous.

Results: Out of 1,236 identified records, 34 studies involving 3,897 participants met the inclusion criteria. Probiotics demonstrated significant improvements in global IBS symptoms, including abdominal pain, bloating, and stool irregularity. Multi-strain probiotics were generally more effective than single-strain formulations, particularly those containing *Lactobacillus* and *Bifidobacterium* species. Duration of intervention (≥8 weeks) and dose (>10^9 CFU/day) were critical factors influencing efficacy. Heterogeneity in study design, probiotic strains, and dosing regimens was a limitation, although most studies reported favorable safety profiles.

Conclusion: Probiotics, particularly multi-strain formulations, appear to be a promising adjunctive therapy for IBS symptom management. However, variations in probiotic composition and study methodologies underscore the need for standardized protocols in future research to optimize clinical recommendations.

Keywords: Bloating, irritable bowel syndrome, microbiota, probiotics, quality of life.

Abstract ID: 71
subject: including the role of probiotics in health and disease

The therapeutic potential of probiotics and psychobiotics in managing psychiatric disorders: A systematic review

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Background and Aim: The relationship between the gut microbiome and mental health has drawn significant attention, with the gut-brain axis emerging as a key research area. Psychiatric disorders, such as major depressive disorder (MDD), anxiety disorders, and neurodegenerative diseases, have been linked to alterations in the gut microbiota. This systematic review aims to evaluate the clinical evidence on the use of probiotics, prebiotics, and synbiotics as therapeutic interventions for psychiatric disorders.

Material And Methods: This systematic review followed the Preferred Reporting Items for Systematic Reviews and Meta-Analysis (PRISMA) guidelines. A comprehensive search of multiple databases identified randomized controlled trials (RCTs) assessing the effects of probiotics, prebiotics, or synbiotics on patients with classified psychiatric disorders. The quality of the included trials was evaluated using the Jadad scale.

Results: The review included data from several studies showing the therapeutic benefits of probiotics in psychiatric disorders. Probiotics, particularly strains of *Lactobacillus* and *Bifidobacteria*, significantly reduced symptoms of MDD, as measured by the Hamilton Depression Rating Scale (HDRS) and the Montgomerysberg Depression Rating Scale (MADRS) .Probiotics also showed promise in other conditions: reducing rehospitalization in acute mania and potentially preventing autism spectrum disorders when administered early. However, results for schizophrenia were less promising, with no significant benefits observed .The use of probiotics as an adjuvant therapy with selective serotonin reuptake inhibitors (SSRIs) for MDD and generalized anxiety disorder (GAD) was more effective than SSRI treatment alone. All MDD and GAD studies found adjuvant probiotic or synbiotic treatment to be more efficacious than first-line treatment alone or with placebo.

Conclusion: The current evidence supports the therapeutic potential of probiotics in psychiatric disorders, particularly in MDD and to some extent in anxiety disorders. However, variability in treatment approaches and the need for more personalized and mechanistic studies are crucial. The lack of long-term follow-up data and inconsistencies in probiotic dosing and strains used highlight the need for further research to fully realize the benefits of psychobiotics in clinical practice.

Keywords: Gut-brain axis, psychobiotics, probiotics, major depressive disorder, anxiety disorders, microbiota modulation, neurodegenerative diseases

Abstract ID: 125
subject: including the role of probiotics in health and disease

Evaluating the impact of *Lactobacillus plantarum* culture supernatant in reducing the expression of *blaNDM* and *blaOxa48* genes in carbapenem-resistant, biofilm-forming *Escherichia coli* isolates.

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Background and Aim: Given the increasing prevalence of carbapenem resistance among *Escherichia coli* isolates, a leading cause of pediatric infections, the presence of carbapenemase genes poses a significant clinical challenge. This study aims to investigate the antibacterial and antibiofilm effects of *Lactobacillus plantarum* supernatant on carbapenem-resistant *E. coli*, specifically its ability to reduce the expression of *blaNDM* and *blaOxa48* genes in biofilm-forming isolates

Material And Methods: This study will use 100 archived *Escherichia coli* isolates from children's feces to assess antibiotic resistance using the disk diffusion method per 2024 CLSI standards. Carbapenemase-producing isolates will be identified via the modified Carbapenem Inactivation Method (mCIM). Supernatant from *Lactobacillus plantarum* will be prepared to evaluate its antibiofilm activity and the presence of *blaOXA48* and *blaNDM* genes in carbapenem-resistant isolates through PCR. Finally, gene expression will be analyzed using Reverse Transcription quantitative Real-Time PCR (RT-qPCR).

Results: In 100 *Escherichia coli* isolates obtained from pediatric fecal samples, antibiotic susceptibility profiles were determined using the disk diffusion method following the 2024 CLSI guidelines. Carbapenem resistance was confirmed in these isolates using both mCIM and eCIM methods. Biofilm formation was assessed in these pathogenic bacteria using a 96-well microtiter plate assay. The presence of *blaNDM* and *blaOxa48* genes was investigated in all isolates via PCR. Subsequently, the antibacterial activity of *Lactobacillus plantarum* supernatant against carbapenem-resistant *E. coli* was evaluated using the microtiter plate broth microdilution method to determine the minimum inhibitory concentration (MIC

Conclusion: Our hypothesis is that the supernatant from *Lactobacillus plantarum* culture reduces the expression of the genes *blaNDM* and *blaOXA-48* in selected biofilm-forming and carbapenem-resistant *Escherichia coli* isolates.

Keywords: *Escherichia coli*, carbapenem, supernatant, *Lactobacillus plantarum*

Abstract ID: 140
subject: including the role of probiotics in health and disease

Probiotics and multiple sclerosis: Investigating the impact on neuroinflammation and disease progression

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Background and Aim: Multiple sclerosis (MS) is a chronic autoimmune disease characterized by neuroinflammation and demyelination in the central nervous system, leading to significant disability and quality of life impairment. The global burden of MS has increased over the past decades, with approximately 1.8 million prevalent cases and 22,400 deaths reported in 2019. Probiotics, beneficial microorganisms, have been explored for their potential to modulate the gut-brain axis and influence neuroinflammatory processes. This review aims to investigate the role of probiotics in modulating neuroinflammation and disease progression in MS.

Material And Methods: A literature review was conducted using keywords such as "probiotics," "multiple sclerosis," and "neuroinflammation" across databases including PubMed and Scopus. Studies published from 2015 to 2024 were included to ensure the relevance and recency of findings.

Results: In a study, probiotics containing *Lactobacillus*, *Bifidobacterium*, and *Streptococcus* reduced the abundance of taxa associated with dysbiosis in MS, such as *Akkermansia* and *Blautia*, while increasing beneficial taxa like *Lactobacillus*. Probiotics also induced an anti-inflammatory immune response by decreasing inflammatory monocytes and altering dendritic cell markers. Another study using *Saccharomyces boulardii* probiotics showed improvements in inflammatory markers, oxidative stress indicators, pain, fatigue, and quality of life in MS patients. The probiotic group experienced significant reductions in pain intensity and fatigue severity compared to the placebo group. A systematic review indicated that probiotics may have beneficial effects on mental health, inflammation, and oxidative stress in MS. Probiotics improved disability scores, reduced depressive symptoms, and decreased inflammatory markers in very few studies. A clinical trial demonstrated that probiotic supplementation significantly reduced serum levels of inflammatory biomarkers such as CRP, TNF-α, and IFN-γ in MS patients. Additionally, probiotics increased anti-inflammatory factors like TGF-β and FOXP3. Studies suggest that combining probiotics with natural compounds can inhibit immune cell infiltration and reduce inflammation in MS. Specific probiotic strains like *Bifidobacterium* lactis and *Lactobacillus* species have been shown to decrease clinical symptoms and inflammatory cytokines while increasing anti-inflammatory cytokines.

Conclusion: Probiotics demonstrate potential in reducing neuroinflammation and improving outcomes in multiple sclerosis by modulating the gut-brain axis, decreasing inflammatory markers, and enhancing quality of life, suggesting a promising adjunctive therapy that warrants further clinical investigation.

Keywords: Probiotics, multiple sclerosis, neuroinflammation

Abstract ID: 196
subject: including the role of probiotics in health and disease

The effect of probiotics on colorectal cancer: A systematic review

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Background and Aim: Colorectal cancer (CRC) is a malignant condition that starts in the colon or rectum and is frequently caused by dietary, lifestyle, and genetic abnormalities. According to new findings, microbiome is crucial to the pathophysiology of colorectal cancer. Probiotics are indigestible food ingredients, usually dietary fibers, that specifically encourage the development and activity of gut microbiota. Probiotics promote immune function, gut health, and may help prevent diseases like colorectal cancer. This systematic review aims to evaluate the current data on the effects of probiotics in modulating gut microbiota and influencing colorectal cancer outcomes, providing insights into their therapeutic potential and mechanisms of action.

Material And Methods: The data were collected by searching PubMed, Scopus and Google Scholar search engine. The advanced searched keywords were: “probiotic”, “cancer” and “colorectal”. The search was limited to studies in the English language and accessible full texts that published from 2015 to 2024. Out of the 20 studies identified in the initial search, 12 were included.

Results: Probiotic supplementation has shown significant advantages in patients with colorectal cancer (CRC) across various studies. Probiotics have effectively alleviated gastrointestinal complications related to chemotherapy, such as diarrhea, and have helped restore the diversity and composition of gut microbiota by promoting beneficial groups like Bifidobacterium and Lactobacillus. They have also increased the production of short-chain fatty acids. Research trials indicated a decrease in pro-inflammatory cytokines, including TNF-α and IL-6, along with improved expression of tumor suppressor genes, which has contributed to enhanced survival rates. Bioengineered probiotics have shown promise for CRC detection and targeted therapy, while interventional probiotics have been effective in reducing mucosal pathogens like Fusobacterium. Furthermore, perioperative probiotics have lowered serum zonulin levels, thus enhancing intestinal permeability and decreasing the risk of postoperative infections in surgeries for colorectal liver metastasis.

Conclusion: Based on these findings, probiotics play a crucial role in enhancing outcomes for colorectal cancer by reducing inflammation, restoring gut microbiota balance, and diminishing side effects associated with treatment. Their ability to improve gut barrier integrity and affect tumor pathways underscores their promise as supplementary therapy in both the treatment and prevention of colorectal cancer.

Keywords: Probiotic, cancer, colorectal cancer

Abstract ID: 29
subject: including the role of probiotics in health and disease

Probiotic use in stress management and its effects on mental health: A systematic review

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Background and Aim: Chronic stress significantly impacts mental health, contributing to disorders such as anxiety and depression. Emerging evidence highlights the gut-brain axis as a crucial pathway linking the gastrointestinal microbiota with mental health. Probiotics, as modulators of gut microbiota, have garnered attention for their potential in stress management and mental health improvement. This systematic review aims to evaluate the efficacy of probiotics in mitigating stress and enhancing mental health outcomes.

Material And Methods: A comprehensive literature search was conducted in PubMed, Scopus, Web of Science, and Cochrane Library databases for randomized controlled trials (RCTs) published between 2010 and 2024. Studies assessing the effects of probiotics on stress and mental health outcomes, including cortisol levels, validated psychological scales, and biomarkers of inflammation, were included. Two independent reviewers screened studies, extracted data, and assessed methodological quality using the Cochrane Risk of Bias tool. Meta-analyses were performed where appropriate.

Results: A total of 29 RCTs involving 2,845 participants met the inclusion criteria. Probiotic supplementation, particularly strains of *Lactobacillus* and *Bifidobacterium*, was associated with significant reductions in perceived stress scores, cortisol levels, and symptoms of anxiety and depression. Multi-strain probiotics showed superior efficacy compared to single-strain formulations. Subgroup analyses revealed that longer intervention durations (≥8 weeks) and higher doses (>10^9 CFU/day) yielded greater improvements. While most studies reported favorable safety outcomes, heterogeneity in probiotic strains, doses, and outcome measures limited direct comparisons.

Conclusion: Probiotics offer a promising, adjunctive approach to stress management and mental health improvement, primarily through modulation of the gut-brain axis. Despite positive findings, further research with standardized methodologies and larger sample sizes is needed to establish optimal probiotic regimens and mechanisms of action.

Keywords: Anxiety, depression, gut-brain axis, mental health, probiotics, stress.

Abstract ID: 396
subject: including the role of probiotics in health and disease

The effect of different prebiotics on the microbial load of *Akkermansia Muciniphila* in the intestines of laboratory rats

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Background and Aim: *Akkermansia Muciniphila* is a new team introduced as a probiotic and has a control role in some metabolic diseases such as obesity, disease and intestinal disease. A decrease in the number of *A.muciniphila* in the intestine is related to metabolic diseases, and increasing the number of this bacteria in the intestine provides the possibility of recovery, for this reason, increasing the number of this bacteria in the intestine is suitable for strengthening the immune system. This study was conducted with the aim of investigating the effect of adding several types of prebiotics to the diet of mice on the microbial load in *A.muciniphila* in the intestine of mice.

Material And Methods: For this purpose, the test materials were fed to mice through gavage for 4 weeks, and the number of *A. muciniphila* at time zero and after 4 weeks in the feces of mice was checked by Real Time PCR method.

Results: Among the 5 tested prebiotics, metformin, breast milk and tryptophan had an increasing effect from 82.8-times to 37.5-times on the growth of *A. muciniphila* , but powdered milk and mucus not only did not show an increasing effect, but also reduced the number of bacteria by about 5-times. They gave. The increase or decrease of *A. muciniphila* in the presence of various prebiotics was not related to the weight and consistency of mice feces.

Conclusion: The use of prebiotic substances such as metformin and tryptophan has a significant effect on the growth of *A. muciniphila*, and it is suggested to investigate its effect on health and treatment of metabolic diseases in future studies.

Keywords: *Akkermansia Muciniphila*, probiotic, prebiotic, metformin, tryptophan, mucus, breast milk, milk powder

Abstract ID: 212
subject: including the role of probiotics in health and disease

ROS modulation by probiotic cell free supernatant in colorectal cancer

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Background and Aim: Reactive oxygen species (ROS) have a multifaceted role in cancer biology, particularly in colorectal cancer (CRC), which significantly contributes to global morbidity and mortality rates. For most cells, a lack of oxygen, referred to as hypoxia, is harmful. On the other hand, cancer cells can thrive in low-oxygen conditions leading to more resistance against treatments. Hence, high levels of ROS are considered as a promising strategy in cancer treatment. Research indicates that probiotics might increase the responsiveness of cancer cells to therapies by raising ROS levels. This study intends to investigate the impact of a probiotic cell-free supernatant (CFS) on oxidative stress, apoptosis, and tumor growth in both in vitro and in vivo models of CRC.

Material And Methods: Caco-2 cells were treated with a 10.13% CFS concentration of three probiotic bacteria (*Lactobacillus acidophilus* (ATCC: 4356), *Bifidobacterium bifidum* (ATCC: 29521), and *Lactobacillus rhamnosus* (ATCC: 7469). Then ROS levels were measured using ELISA. Simultaneously, 100 µL of the probiotic CFS was given to the CRC-induced BALB/c mice model for four weeks, after which tumor growth and systemic ROS levels were assessed by ROS Kit.

Results: In Caco2 cells the ROS level in the treated group increased 1.807-fold compared to the control group ($P<0.0001$). In mice, the consumption of CFS led to an increase in ROS level in comparison to the control group ($P<0.001$) and patient group ($P<0.001$).

Conclusion: These results indicate that this novel probiotic CFS might serve as an effective modulator of oxidative stress, aiding in the suppression of CRC cell growth by increasing ROS levels. This research offers strong support for the possible role of probiotics as supplementary treatment in CRC care and it can be effective in treating CRC, justifying additional exploration into their mechanisms and clinical relevance.

Keywords: Colorectal cancer, probiotics, oxidative stress, ROS, reactive oxygen species, CFS

Abstract ID: 390
subject: including the role of probiotics in health and disease

The effect of *Lactobacillus plantarum* probiotic on gene expression in *Pseudomonas aeruginosa*

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Background and Aim: This study investigates the effect of *Lactobacillus plantarum* probiotic on the gene expression of *Pseudomonas aeruginosa*. *P. aeruginosa* is a major pathogenic bacterium known for its production of various enzymes and its ability to develop antibiotic resistance. In contrast, *Lactobacillus plantarum* is a probiotic bacterium with antibacterial effects and immune-modulating properties. This study explores how *Lactobacillus plantarum* influences the expression of genes in *P. aeruginosa*, particularly genes related to toxin production and antibiotic resistance.

Material And Methods: In this study, various clinical strains of *Pseudomonas aeruginosa* were collected. These strains were treated with *Lactobacillus plantarum* for a specified duration. To evaluate the impact of the probiotic on gene expression, RT-PCR and real-time PCR techniques were used. Various genes were assessed, including those related to toxin production (such as exotoxin A and lasA) and antibiotic resistance (such as blaOXA and mexAB-oprM).

Results: The results of this study demonstrated that treatment with *Lactobacillus plantarum* significantly reduced the expression of genes related to toxin production in *Pseudomonas aeruginosa*. In particular, the expression of the exotoxin A gene, which plays a major role in tissue damage in the host, was significantly decreased in the probiotic-treated strains. Furthermore, *Lactobacillus plantarum* had a negative effect on the expression of antibiotic resistance genes, leading to a reduction in the expression levels of *mexAB-oprM* and *blaOXA*.

Conclusion: This study suggests that *Lactobacillus plantarum* probiotic can effectively influence the gene expression of *Pseudomonas aeruginosa*, particularly genes related to toxin production and antibiotic resistance. These results highlight the potential of probiotics in reducing the risk of infections caused by this bacterium and improving the efficacy of antibiotic treatments.

Keywords: *Lactobacillus plantarum* probiotic

Abstract ID: 248
subject: including the role of probiotics in health and disease

Effects of *Lactobacillus fermentum* FH5 and capecitabine on colon cancer management and related antioxidant enzymes expression in BALB/c models

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Background and Aim: Colon cancer is one of the most common and dangerous types of cancer that constantly threatens human life. Therefore, in this study, we investigated the preventive and therapeutic effects of *Lactobacillus fermentum* FH in comparison with Capecitabine (chemotherapy drug) in Balb/c mice, a clone cancer model.

Material And Methods: We used probiotics (*Lactobacillus fermentum* FH5) on subcutaneous implantation of tumors induced by CT-26 cells. Moreover, the effect of L. fermentum FH5 was compared with the capecitabine drug against CRC. L. fermentum FH5 was given to animals by gavage two weeks prior to tumor implantation and 4 weeks after CRC induction. Also, capecitabine was orally added through feeding tube at the last week of treatment procedure. Their anticancer effects were evaluated by tumor size measurement and antioxidant enzymes analysis.

Results: In the cancer groups treated with capecitabine, probiotic and the capecitabine + probiotic cancer group, the volume of tumors decreased significantly compared to the cancer control group, and the smallest average tumor size was observed in the probiotic combination group with capecitabine. In addition, the release of antioxidant enzymes SOD, CAT, TAC, GPx and GR was at the lowest level in the cancer group, while in the group treated with probiotics alone and the combination group (Probiotic and capecitabine), the release these enzymes increased significantly compared to the cancer group. Finally, we used Real-time PCR and a standard curve to compare the frequency of selected bacteria in different groups, and there were no statistically significant differences.

Conclusion: Long term oral consumption of probiotic *L.fermentum* FH5 as an adjuvant treatment for colon cancer may play an important role in reducing cancer severity, strengthening the immune system, and modulating inflammation.

Keywords: *Lactobacillus fermentum* FH5, capecitabine, colon cancer, animal model

Abstract ID: 7
subject: the application of artificial intelligence and novel techniques in the diagnosis of bacterial infections, nosocomial infections

Application of artificial intelligence in laboratory diagnostics

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Background and Aim: Artificial intelligence has revolutionized the diagnosis, identification, and management of infectious diseases in clinical laboratory diagnostics. Techniques based on artificial intelligence enable faster, more accurate, and more comprehensive analysis of diverse data sources related to the diagnosis of infectious diseases. Machine learning models can be trained on structured data such as patient symptoms, laboratory test results, and demographic information to aid in disease diagnosis and risk prediction. Deep learning algorithms can analyze unstructured data such as digital microscope images, mass spectra, and genomic sequences to automatically identify pathogens. This article reviews and analyzes the applications of artificial intelligence in laboratory diagnostics, exploring how AI can increase the accuracy and efficiency of laboratory diagnoses and ultimately lead to improved patient outcomes.

Material And Methods: The experimental method involves training AI models on large datasets and comparing their performance to human diagnostics. AI's application includes automated image analysis, pathogen detection, and identification of disease patterns

Results: that artificial intelligence (AI) significantly enhances laboratory diagnostics, particularly in detecting infectious diseases and other complex conditions like cancer and diabetes

Conclusion: the integration of artificial intelligence (AI) in laboratory diagnostics significantly enhances the accuracy and efficiency of disease detection and management. AI techniques facilitate rapid analysis of diverse data, allowing for improved identification of infectious diseases through machine learning and deep learning algorithm

Keywords: Artificial Intelligence (AI), Laboratory Diagnostics, Infectious Diseases, Machine Learning, Deep Learning

Abstract ID: 258
subject: the application of artificial intelligence and novel techniques in the diagnosis of bacterial infections, nosocomial infections

The role of artificial intelligence in transforming healthcare: From prevention to treatment of infectious diseases

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Background and Aim: Artificial Intelligence (AI) is redefining healthcare by offering advanced solutions in disease prevention, diagnostics, treatment, and patient care. This study aims to evaluate the transformative impact of AI in healthcare, with a focus on infectious disease management, improving diagnostic accuracy, and optimizing patient engagement and care delivery.

Material And Methods: A systematic search was conducted in PubMed, Google Scholar databases up to December 2024 using combinations of keywords such as "Artificial Intelligence," "Infectious Diseases," "Diagnostics," "Machine Learning," "Clinical Decision Support," and "Patient Engagement." Eligible studies focused on the applications of AI in infectious disease management, including diagnostic advancements, treatment optimization, and patient care. Exclusion criteria included non-English articles, case reports, editorials, and studies not directly related to AI in healthcare. Data were qualitatively analyzed and synthesized to provide insights into the transformative impact of AI on healthcare systems and infectious disease management.

Results: Artificial intelligence (AI) has revolutionized infectious disease management across prevention, diagnosis, treatment, and patient care. AI enables real-time outbreak detection, improves diagnostic accuracy (over 90% for some cancers and 85% for COVID-19), and predicts disease progression with 80-95% accuracy. AI optimizes personalized treatments, reduces errors, and accelerates drug and vaccine development. Additionally, AI enhances patient engagement, reduces administrative work by 30-50%, and increases healthcare efficiency. AI-powered telemedicine and predictive algorithms further improve global healthcare access and resource allocation, making AI central to modern healthcare innovation.

Conclusion: AI is emerging as a cornerstone of modern healthcare, augmenting human capabilities in diagnostics, treatment, and patient management. However, challenges such as data scarcity, ethical concerns, and integration barriers remain significant and require collaborative efforts among stakeholders to address them. The future of AI in healthcare lies in delivering equitable, efficient, and sustainable solutions to meet global health challenges.

Keywords: Artificial intelligence, disease management, diagnostics, infectious diseases, machine learning, clinical decision support, patient engagement, healthcare workforce

Abstract ID: 247
subject: Hospital-Acquired Infections

Molecular characterization of *Staphylococcus aureus* isolated from hospital-acquired infections in Ilam, Iran

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Background and Aim: This research study was undertaken to investigate antimicrobial resistance patterns and the prevalence of hospital-acquired infections (HAIs). The study focuses on common microorganisms responsible for HAIs and explores emerging challenges posed by antimicrobial drug-resistant isolates.

Material And Methods: A comprehensive analysis of 123 patients with HAIs, hospitalized in surgical department and intensive care unit (ICU) at Imam Khomeini Hospital, Ilam, Iran, was conducted over a six-month period. Pathogenic bacterial isolates, including methicillin-resistant *Staphylococcus aureus* (MRSA) and vancomycin-resistant *Staphylococcus aureus* (VRSA), were isolated and subjected to antibiotic susceptibility testing.

Results: The study findings revealed a significant prevalence of multidrug-resistant (MDR) isolates, of which 73.3% were MRSA. Notably, 6.7% of *S. aureus* isolates exhibited resistance to vancomycin, indicating the emergence of VRSA. Respiratory infections were identified as the most prevalent HAI, constituting 34.67% of cases, often arising from extended ICU stays and invasive surgical procedures. Furthermore, patients aged 60 and above, particularly those associated with MDR, exhibited higher vulnerability to HAI.

Conclusion: This research sheds light on the intricate interplay between drug resistance and HAI, highlighting the imperative role of rational antibiotic use and infection control in addressing this critical healthcare challenge

Keywords: Antimicrobial resistance; hospital-acquired infection; methicillin-resistant *Staphylococcus aureus*; multidrug-resistant organisms; vancomycin-resistant *Staphylococcus aureus*.

Abstract ID: 18
subject: Hospital-Acquired Infections

Detection of aph(3')-IIb and aadA1 in aminoglycoside-resistant *Enteroabacter Spp*. isolated from clinical samples, Mofid children hospital

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Background and Aim: Background: *Enterobacter spp*. is one of the important gram-negative bacteria in nosocomial infections. This pathogen can cause different infectious diseases like; urinary tract infections, septicemia, wound infection, etc. Aminoglycoside is one of the antibiotic choices for *Enterobacter* infections treatment. Hence, resistance to this antibiotic family can cause therapeutic problems. The aim of this study was, the detection of aph(3')-IIb and aadA1 genes in aminoglycoside-resistant *Enterobacter spp*.

Material And Methods: In this cross-sectional study, 66 aminoglycoside-resistant *Enterobacter spp*. were collected. Aminoglycoside resistance was confirmed by antibiogram according to CLSI. DNA extraction was done by Thermo extraction kit and conserved in -80 oC up to PCR assay. aph(3')-IIb and aadA1 genes were identified by specific primers and PCR.

Results: Results: The results of PCR and electrophoresis indicated that 6, and 13 strains carried aph(3')-IIb and aadA1, respectively.

Conclusion: Conclusion: Aminoglycoside resistance can be considerable for healthcare centers, especially the strains that include aadA1gene. Because aadA1 is located on class I integrin and can transfer to other bacteria and spread in the hospital.

Keywords: Key words: *Enterobacter Spp*., aph(3')-IIb and aadA1

Abstract ID: 81
subject: Hospital-Acquired Infections

Investigation of *Acinetobacter* isolates from a referral hospital in Iran for resistance to colistin antibiotic

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Background and Aim: *Acinetobacter* is one of the bacteria that plays an important role in nosocomial infections. In Iran, in case of resistance to carbapenems, colistin is considered as the last line of defense against this bacterium. In addition, due to the high resistance of this bacterium to various types of antibiotics, the prevalence of resistance in different wards in hospital is very essential.

Material And Methods: 117 isolates of Acinetobacter were collected and identified from different wards of referral Hospital in Iran. All isolates were then tested for resistance to colistin using the MIC (minimum inhibitory concentration) method. The results were then analyzed using SPSS 23.

Results: The results showed that of the 117 isolates isolated, 76 isolates were sensitive, and 41 isolates were resistant to the colistin antibiotic.

Conclusion: Many studies show that resistance to the antibiotic colistin is increasing due to overuse. It also costs the patient a lot due to the high price of this drug in Iran. Therefore, resistance of these bacteria can be prevented by regularly checking the resistance pattern and prescribing antibiotics correctly.

Keywords: Colistin, *Acinetobacter*, resistant

Abstract ID: 82
subject: Hospital-Acquired Infections

Evaluation of colistin resistance in *Klebsiella* isolates from wards of a referral hospital in Iran

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Background and Aim: Resistance to antibiotics due to inappropriate prescribing is increasing worldwid*E. coli*stin is a drug used as a last choice for *Klebsiella* isolates resistant to carbapenem drugs. The aim of this study was to investigate the prevalence of colistin resistance in different wards of a referral hospital in Iran

Material And Methods: 186 *Klebsiella* isolates from different wards of a referral hospital were isolated and identified. The MIC (minimum inhibitory concentration) test against colistin was performed for each isolate.

Results: Out of 186 isolates, 90 *Klebsiella* isolates were susceptible and 96 *Klebsiella* isolates were reported to be resistant to the antibiotic colistin.

Conclusion: Overuse of the antibiotic colistin has made more than half of isolates resistant to this antibiotic. Therefore, further resistance to this antibiotic can be prevented by prescribing it correctly and using other antibiotics instead.

Keywords: *Klebsiella*, resistant, colistin

Abstract ID: 231
subject: Hospital-Acquired Infections

Prevalence of *ureaplasma urealyticum* in infertile men comparison with control group

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Background and Aim: Infertility is one of the most important problems for every family. The aim of this study is to test the prevalance of *Ureaplasma urealyticum* in infertile men. The patients that arrive to infertility clinics (Royan Institute in Tehran) with the semen culture analysis request are asked to fill in a questionnaire about infertility smear collection.

Material And Methods: In this case control study presence of *Ureaplasma urealyticum* were analysed in tested men. In this study we have compared 40 infertile males with unexplained infertility and 40 normal men with male factor as a control case group. The semen samples were sent to micrbiology laboratory for culture and Isolation of bacteria. The information were analysed with SPSS software by frequency, chi-square & T-test Method.

Results: The average age in patients and control groups were 31.87±5.22 and 31.45±5.81 the value of *Ureaplasma urealyticum* cases were 11(27.5%) and in normal men were 4(10%) (P=0.045). then we have found statistically significant defrences in the *Ureaplasma urealyticum* frequency of the patients. We have not found statistically significant relations between premature ejaculation and infertility. We have not found statistically siqnificant relations between educational levels, ages, marriage age, Duration of infertility, testis pain, smoking and infertility.

Conclusion: We have shown a significantly *Ureaplasma urealyticum* infections increase in the infertile men. The similarities between this study and the results obtained by others are limited and it may be due to different cultural and normal values in various societies. Though statistically significant due to limited number of subjects, however the difference observed in the prevalance of infection between cases and controls indicates an association between *Ureaplasma urealyticum* infection and infertility. So, it is suggested to check up those patients with unexplained infertility, for genital microorganisms infections and if positive, to control the rate of infertility with a suitable and cost effective therapy.

Keywords: Infertility, men, *Ureaplasma urealyticum*, culture

Abstract ID: 232
subject: Hospital-Acquired Infections

Prevalence of *Ureaplasma urealyticum* in women for IVF program and comparison with control group

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Background and Aim: Infertility is one of the most important problems for every family specially for women. The aim of this study is to test the prevalence of *Ureaplasma urealyticum* in infertile women. The patients that arrive to infertility clinics (Royan Institute in Teliran) with the cervical smear culture analysis request are asked to fill in a questionnaire about infertility smear collection.

Material And Methods: In this case control study presence of *Ureaplasma urealyticum* were analysed in tested women who have been sent by gynecologists because of infertility. In this study we have compared 40 infertile females with unexplained infertility and 40 Normal pregnant women as a control case group. The samples were sent to microbiology laboratory. The information was analysed with SPSS software by frequency, chi-square, Mann-whitney & T-test Method.

Results: The average age in patients and control groups were 28.92±6.20 and 24.97±3.37. The value of *Ureaplasma urealyticum* In infertile cases were 12 (310%) and in Normal pregnants were 6(15%) ($\chi 2 = 2.58$) and (P=0.1), then we have not found statistically significant differences in the *Ureaplasma urealyticum* frequency of the patients, But we have found statistically significant relations between educational levels, the history of abdominal pains, the history of genital secretions and infections with *Ureaplasma urealyticum* causing infertility, also we have not found statistically significant relations between marriage age, history of genital infections, history of smoking and infection with *Ureaplasma urealyticum* infertility

Conclusion: We have shown a significantly *Ureaplasma urealyticum* infections increase in the infertile women. The similarities between this study and the results obtained by others are limited and it may be due to different cultural and normal values in various societies. Though statistically non-significant due to limited number of subjects. However, the difference observed in the prevalance infection between cases and controls indicates an association between *Ureaplasma urealyticum* infection and infertility. So, it is suggested to check up those patients with unexplained infertility for genital microorganisms infections and if positive, to control the rate of infertility with a suitable and cost effective therapy.

Keywords: Infertility, women, *Ureaplasma urealyticum*

Abstract ID: 233
subject: Hospital-Acquired Infections

Prevalence of *Mycoplasma hominis* and *Ureaplasma urealyticum* in infertile women comparison with their husbands

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Background and Aim: Infertility is one of the most important problems for every family specially for women. The aim of this study is to test the prevalence of *Mycoplasma hominis* and *Ureaplasma urealyticum* in infertile women and their husbands. The patients that arrive to infertility clinics (Avesina Institu in Tehran) with the cervical smear and their husbands with semen fluid culture analysis request are asked to fill in a quastionaire about infertility smear collection.

Material And Methods: In this Cross-Sectional Study presence of *Mycoplasma hominis* and *Ureaplasma urealyticum* were analysed in tested women who have been sent by gynecologists because of infertility. In this study we have compared 56 infertile women with their husbands. The samples were sent to microbiology laboratory The information was analysed with SPSS software by Frequency, Chi-Square, Mann-whitney and T-test methods.

Results: The age average in patients was 30.41 and their marriage age average was 22.96. Prevalence of *Mycoplasma hominis* in patients was 22(39.27%) and in their husbands was 11(19.64%). Prevalence of *Ureaplasma urealyticum* in patients was 33 (58.92%) and in their husbands 26(46.42%). We have not found statistically significant differences in the infections cause of infertility with age, marriage age, educational levels and infertility duration. But between women infertility and their husbands *Mycoplasma hominis* infection statistically significant differences was present, also there was correlation between women infertility and their infected husbands with two bacteria, but there wasn't correlation between patient and presence of *Ureaplasma urealyticum* infection in men.

Conclusion: we have shown a high prevalence of *Mycoplasma hominis* and *Ureaplasma urealyticum* infections in both infertile women and their husbands, but this prevalence in patients higher than their wives, that is because of normal semen fluid of men and being STDs infection is expected and show that treatment of mares is necessary, despite more studies to find the role of these infections in female infertility is needed.

Keywords: Infertility, women, *mycoplasma hominis*, *Ureaplasma urealyticum*

Abstract ID: 174
subject: Hospital-Acquired Infections

Antibacterial effects and the expression of adhesin genes among methicillin-resistant *Staphylococcus aureus* following exposure to carvacrol

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Background and Aim: Methicillin-resistant *Staphylococcus aureus* (MRSA) poses a significant public health challenge due to its resistance to conventional antibiotics and its ability to cause severe infections. This study aims to evaluate the antibacterial effects of carvacrol on MRSA strains, focusing on bacterial viability and the modulation of adhesin gene expression.

Material And Methods: MRSA clinical isolates were obtained from wound infections. Strains were confirmed as MRSA using standard methods, including susceptibility testing to methicillin and molecular detection of the *mecA* gene.Carvacrol (purity ≥ 98%) was purchased from Sigma Aldrich.The MIC of carvacrol against MRSA isolates was determined using the broth microdilution method in accordance with the Clinical and Laboratory Standards Institute (CLSI) guidelines. Bacterial suspensions were adjusted to 105^55 CFU/mL, and serial twofold dilutions of carvacrol (ranging from 0.125 to 256 µg/mL) were tested. The bactericidal activity of carvacrol was assessed using a time-kill assay. MRSA cultures were exposed to carvacrol at concentrations equivalent to 1×, 2×, and 4× MIC. Samples were taken at 0, 2, 4, 6, and 24 hours, serially diluted, and plated on TSA for colony-forming unit (CFU) enumeration. The results were expressed as log reduction in CFU/mL over time.Bacteria were exposed to sub-inhibitory concentrations of carvacrol (0.5× MIC) for 6 hours. Total RNA was extracted.Quantitative real-time PCR (qRT-PCR) was performed using SYBR Green Master Mix and primers specific to adhesin genes (*clfA, clfB, fnbA, fnbB, icaA*). The housekeeping gene (16S rRNA or gyrB) was used for normalization.

Results: The minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) of carvacrol were observed to range between 128 µg/mL and 256 µg/mL, in that order. In comparison to the control, carvacrol decreased the expression levels of *clfA, clfB, fnbA, fnbB, icaA* genes to 2.9, 2.6, 2 and 1.8 fold respectively.

Conclusion: This study highlights the potent antibacterial activity of carvacrol against methicillin-resistant *Staphylococcus aureus* (MRSA) and its ability to modulate the expression of key adhesin genes involved in bacterial adhesion and biofilm formation. The findings demonstrate that carvacrol not only effectively inhibits MRSA growth but also significantly downregulates the expression of genes such as *clfA, clfB, fnbA, fnbB,* and icaA.

Keywords: Methicillin-resistant,*Staphylococcus aureus*,carvacrol

Abstract ID: 9
subject: Hospital-Acquired Infections

Isolation of gram-positive bacteria from the blood of children infected with corona in the covid-19 pandemic in Mofid children's hospital by the BACTEC method

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Background and Aim: Sepsis is a complex disorder which is caused by invasion of an infectious pathogen to the bloodstream and is potentially fatal. The prevalence of multidrug resistance among bacteria has grown dangerously in recent years. With the recent pandemic of covid-19 children are in danger of a bacterial co-infection when they are suspected of a covid infection which could worsen prognosis. We have designed this research to study the prevalence of Gram positive bacteria in children suspected of covid-19

Material And Methods: blood samples were collected from children with clinical suspicion of covid in BACTEC bottles during 2 years and brought to the clinical lab of pediatric health institute. The bottles had been characterized by selective cultures and biochemical tests as standard routine after the device's alarm. Antimicrobial susceptibility test and MDR identification had done for the gram-positive strains based on CLSI 2021.

Results: 421 hospitalized children suspected of covid infection were studied, 60.5% of them were boys and 39.4% of them were girls. 51.87% of the patients were under 3 years old and 48.21% were older than 3years old. 100/421 patients were covid positive. The most common clinical presentation was in order: fever, shortness of breath, and cough. The most frequent isolated gram positive bacteria were: *s.epdimermidis* 16.6% (70). Most cases of covid were seen in patients with *s.epidermidis* bacteremia followed by klebsiella and pseudomonas.

Conclusion: Based on the results of this study, the most frequent gram positive strains were S.epidermidis. BSI with MDR could lead to treatment limitation, increasing the length of hospital stay, and death. Moreover, co-infection with covid-19 can lead to complications and worsen the prognosis. Therefore, much attention should be paid to proper isolation and timely diagnosis of Covid-19 cases.

Keywords: sepsis, COVID-19, bacteremia, GPB, hospital acquired infection, infection control

Abstract ID: 64
subject: water and foodborne infections

Epidemiological study of brucellosis prevalence and risk factors in populations of charavimaq, Hashtroud, and Tabriz

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Background and Aim: Brucellosis, a zoonotic disease attributed to Brucella species, poses a notable public health concern, particularly in regions with significant livestock populations. This study aims to assess the prevalence of brucellosis in three cities—Charavimaq, Hashtroud, and Tabriz—through serological testing, thereby informing local public health strategies and deepening the understanding of the disease's epidemiological landscape.

Material And Methods: In a descriptive cross-sectional study, we examined anti-Brucella antibodies in the blood serum of 3,732 individuals who presented at health centers in the aforementioned cities from the beginning of the Iranian year 1402 to mid-1403. Utilizing the Wright and 2ME assays, we established diagnostic criteria with Wright titers ≥1.80 and 2ME titers ≥1.40 for confirming brucellosis. The data collected was analyzed using SPSS 18 software, employing the Chi-square statistical method.

Results: Our analysis revealed that 179 participants (4.7%) met the Wright criteria, while 140 participants (78.2%) were positive according to the 2ME criteria. Notably, Charavimaq exhibited the highest prevalence (5.6%), in contrast to Tabriz, which recorded the lowest prevalence (4.1%). Statistical analysis indicated significant associations between brucellosis prevalence and both occupation and residential location ($p=0.020$ and $p=0.031$, respectively), while no significant correlation was observed with gender or age.

Conclusion: These findings suggest a substantial exposure risk among the study population, attributable to lifestyles involving close contact with domestic animals and the consumption of unpasteurized dairy products. In light of the occupational implications of brucellosis in the region, we recommend the implementation of vaccination programs, enhanced disease surveillance, monitoring of livestock slaughter practices, and widespread advocacy for the consumption of pasteurized dairy products to mitigate the risk of infection.

Keywords: Brucellosis, prevalence, risk factors

Abstract ID: 320
subject: water and foodborne infections

Frequency of dermatological manifestations in leptospirosis patients: A case study from Razi Hospital, Qaemshahr, 2017-2023

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Background and Aim: Leptospirosis is a zoonotic infection that can range from mild flu-like symptoms to severe complications such as jaundice, hemorrhage, kidney failure, and even death. Although less common, dermatological manifestations like macules, papules, urticaria, petechiae, and purpura can occur. This study aims to assess the prevalence of skin symptoms among hospitalized leptospirosis patients at Razi Hospital in Qaemshahr between 2017 and 2023.

Material And Methods: A cross-sectional study was conducted from 2017 to 2023, including patients diagnosed with leptospirosis confirmed by serological tests. Demographic and clinical data, including the onset and progression of dermatological signs, were collected and analyzed using SPSS (version 20). Statistical methods such as chi-square and Bonferroni post-hoc tests were employed to identify significant relationships.

Results: Among 800 patients (81.5% male, 18.5% female; mean age: 48.55 ± 16.23 years), jaundice was the most common dermatological symptom (62.76%, $P < 0.001$). Other skin manifestations, such as ecchymosis and petechiae, were more prevalent in females ($P = 0.013$), although no significant differences related to age were observed ($P = 0.054$). The results revealed a gender disparity, with jaundice and ecchymosis occurring more frequently in females.

Conclusion: While dermatological manifestations in leptospirosis are relatively rare, they are gender-dependent, with jaundice being the most common. Although males account for the majority of cases, females exhibit higher frequencies of certain skin symptoms. These findings highlight the importance of focused clinical attention to dermatological signs in leptospirosis management.

Keywords: Leptospirosis, dermatology, skin manifestations, jaundice, zoonotic diseases

Abstract ID: 103
subject: emerging and re-emerging diseases

Genotyping SARS-CoV-2 and assessing aerobic bacterial infections in patients admitted to Isfahan's educational hospitals

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Background and Aim: Abstract: In patients with viral respiratory tract infections white Sars-Cov-2, bacterial pathogens are considered important causes of complications and mortality rates. Sars-Cov-2 had several variants with different epidemiological manifestations. Therefore, it is necessary to determine Sars-Cov-2 variants and the presence of bacterial infection to reduce the effects of antibiotic abuse and prevent the development of variants of concern and antibiotic resistance.

Material And Methods: Endotracheal aspirate (ETA) samples were collected from 150 COVID-19 patients. Bacteria isolation was done by conventional and molecular confirmation methods. antibiotic sensitivity pattern of isolates determined according to the instructions of the Clinical and Laboratory Standards Institute. Then SARS-COV-2 variants were determined with DNA sequencing analysis of the spike region.

Results: In this study, from 150 patients, 53 patients (39.2%) had secondary bacterial respiratory infections. in these patients, *K. pneumoniae* 15 isolates (28.3%), *A. baumannii* 10 isolates (18.9%), P. aeruginosa 5 isolates (9.4%), *S. aureus* 5 isolates (9.4%), *E. coli* 8 isolates (15.1%), *Shigella spp*. 3 isolates (5.7%), *Burkholderia spp*. 2 isolates (3.8%), *Candida*, and fungal infections in 5 (9.4%) patients were detected. The antibiotic sensitivity pattern showed that *A .baumannii* and *K. pneumoniae* strains showed the highest resistance and *E. coli* and *S. aureus* isolates showed the highest sensitivity to the tested antibiotics. Sequencing of the S gene (Spike) showed that %30.2 isolates were alpha variants, 69.8% of isolates were Delta variants and all of the isolates were VOC.

Conclusion: Secondary bacterial respiratory infections and the antibiotic resistance of some bacterial strains, increase the mortality of COVID-19 patients, therefore it is necessary for strains to be examined in terms of antibiotic sensitivity for successful and definitive treatment and to be treated with effective antibiotics. On the other hand, different viral variants are different in terms of transmissibility, ability to escape from the immune system, severity of pathogenicity, hospital admission rate, and mortality rate. For this reason, it seems that if people are infected with COVID-19, the virus variant should also be determined. so that effective measures can be taken in line with successful treatment and preventing epidemics and the severity and extent of the disease.

Keywords: Sars-Cov-2, secondary infections, variant of concern variant (VOC)

Abstract ID: 375
subject: emerging and re-emerging diseases

Prevalence of microbial infections (parasitic, bacterial, fungal, and viral) among HIV/AIDS patients: A 20-year study in Mazandaran university of medical sciences' covered population (2001–2021)

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Background and Aim: Introduction: AIDS is a clinical syndrome caused by the human immunodeficiency virus (HIV), leading to immune deficiencies and increased susceptibility to infections. This study aimed to investigate the prevalence of microbial infections (parasitic, bacterial, fungal, and viral) in AIDS and HIV-positive patients in the population covered by Mazandaran University of Medical Sciences from 1380 to 1400.

Material And Methods: This descriptive study included all AIDS and HIV-positive patients registered in the disease management center of Mazandaran health department from 1380 to 1400. Data were obtained from health networks and analyzed using SPSS 23.

Results: A total of 466 AIDS patients were investigated, with 72.8% being male and an average age of 45.6 ± 11.6 years. Among 184 patients tested for Hepatitis C, 38% had positive results. Acute Hepatitis B cases accounted for 4.5%, while 25.3% had chronic Hepatitis B. One active measles case (0.2%) and 12 patients (2.5%) with positive rubella antibodies were identified. Only one case of syphilis (0.2%) was detected using VDRL and PRP tests. Additionally, 6% of patients had a history of tuberculosis, with 4.1% recovered, 3 deceased, and 1.2% in acute condition. No co-infection with parasitic or fungal diseases was observed.

Conclusion: The study concluded that Hepatitis C and chronic Hepatitis B are the most common infections in HIV-positive individuals, which require immediate preventive and therapeutic interventions. The absence of co-infections with parasitic and fungal diseases indicates no need for special preventive programs in this regard.

Keywords: AIDS, HIV, Hepatitis C, chronic Hepatitis B, microbial infections

Abstract ID: 313
subject: emerging and re-emerging diseases

Investigating the occurrence of COVID-19 among individuals with tuberculosis history in Mazandaran university of medical sciences during the initial and subsequent peaks of the pandemic

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Background and Aim: In December 2019, a cluster of pneumonia cases was reported in Wuhan, China, later identified as COVID-19 by the WHO. Evidence suggests that respiratory conditions like tuberculosis may contribute to the severity of COVID-19. Tuberculosis, similar to SARS-CoV-2, spreads through respiratory droplets and affects the lungs. Studies indicate that *Mycobacterium tuberculosis* infection can lead to rapid and severe pneumonia in COVID-19 patients. This study assesses the frequency of COVID-19 cases during the first and second peaks of the pandemic among individuals with a history of tuberculosis.

Material And Methods: This descriptive cross-sectional study focused on patients diagnosed with tuberculosis between 2015 and 2020. A total of 1532 patients were included, using a census sampling method. Data was collected between mid-May 2019 and November 2019, after the first and during and after the second peak of COVID-19. A checklist was used for demographic and clinical data related to COVID-19 symptoms, collected via telephone interviews and document reviews. The data were analyzed using SPSS V.16 and chi-square tests.

Results: The prevalence of confirmed and probable COVID-19 cases among patients with a tuberculosis history was 5.5% (85 individuals), and suspected, probable, and confirmed cases totaled 15.6% (239 individuals). No significant correlation was found between age, gender, place of residence, tuberculosis type, marital status, or chronic diseases and COVID-19 prevalence. However, conditions such as heart disease, lung disease, cancer, chemotherapy, high blood pressure, and neurological disorders were associated with the spread of COVID-19. The highest prevalence occurred in 2019 (38.5%).

Conclusion: The study highlights the importance of vaccinating tuberculosis patients against the flu and prioritizing smoking cessation. Further research on COVID-19 in tuberculosis patients is needed.

Keywords: COVID-19, tuberculosis, *Mycobacterium tuberculosis*, pandemic, respiratory diseases

Abstract ID: 23
subject: rational antibiotic prescription and resistance mechanisms

Detecting of the ESKAPE bacteria among different clinical specimens in Tabriz, Iran

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1. Detecting of the ESKAPE bacteria among different clinical specimens in Tabriz, Iran

Background and Aim: The ESKAPE pathogens (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter spp*.) are the leading cause of nosocomial infections throughout the world. Most of them are multidrug-resistant isolates and one of the global serious challenges in clinical practice. The aim of this study was the detection of Carbapenem-resistant *Enterobacter*iaceae, Multidrug-resistant Acinetobacter, ESBL-producing *Enterobacter*iaceae, Vancomycin-resistant *Enterococcus* (VRE), Multidrug-resistant *Pseudomonas* aeruginosa, Drug-resistant Shigella, Methicillin-resistant *Staphylococcus aureus* (MRSA), Drug-resistant *Streptococcus* because CDC put these organisms on urgent and serious levels.

Material And Methods: In this cross-sectional study, different clinical specimens that were referred to the laboratory of Mofid Children's hospital were included during on five months in this study. Conventional biochemical and microbiological methods were used for identification. Antibiotic susceptibility testing was done according to CLSI for which bacteria. A combination disc method by cephalosporin and clavulanic acid was used to detect ESBL production in *Enterobacter*iaceae spp.

Results: 657 isolates were collected during five months that 244 of them were ESKAPE antibiotic resistant (table1). Table1. Isolated antibiotic resistant ESKAPE Antibiotic resistant ESKAPE MDR *Pseudomonas* MDR *Acinetobacter* ESBL *E. coli* ESBL *Klebsiella* ESBL *Enterobacter* MRSA VRE *S. pneumoniae* No.(%) 23 (26%) 66 (69%) 38 (35%) 16 (18%) 13 (14%) 41 (46%) 46 (51%) 1 (100%) 41% of patients were female and 59% was male with age range between two up to 92 years old (fig 1). Fig1. Percentage of classified sex

Conclusion: Antibiotic-resistant ESKAPE bacteria are globally threatening pathogens according to a CDC report in 2013. Thus, the frequency percentage of them should be determined in each hospital. The frequency of MDR *Pseudomonas*, MRSA, and VRE is more than 50% and it can be considered in the nosocomial infection committee in each health care system

Keywords: ESKAPE, antibiotic resistant, Tabriz

Abstract ID: 138
subject: rational antibiotic prescription and resistance mechanisms

Antimicrobial resistance in *Vibrio cholerae* O1/O139 clinical isolates

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Background and Aim: In recent decades, enterotoxin-producing *Vibrio cholerae* has been known as the causative agent of cholera, a notorious disease that remains a huge public health menace throughout the world, especially in developing countries in Asia, Africa, and Latin America [1–5]. The bacterium can survive well and multiply for several years in the marine environment [6,7]. Thus, cholera is associated with the consumption of contaminated food and water with *V. cholera*, and contaminated water is a major source of severe cholera outbreaks

Material And Methods: We systematically searched for relevant articles in four international databases including PubMed, Scopus, Embase, and Web of Science (Until January 2020) by using the related keywords: ('*Vibrio cholerae*' OR '*V. cholera*e') AND ('Antibiotic resistance' OR 'Drug resistance' OR 'Antimicrobial resistance') in the Title/ Abstract/Keywords fields. No limitation was conducted while searching databases, but the inclusion of the study in our full analysis required at least the abstract to be available in English. The search strategy was designed and conducted by study investigators.

Results: The susceptibility to tetracycline was determined in 99 studies including 17,828 O1/O139 *V. cholera*e isolates; the WPR was 20% (95% CI 14–27%) with substantial heterogeneity (I2 = 99.01%) (Supplementary Data and Figure 2). The subgroup analysis that compared the data from 1980–2000 (WPR 7%; 95% CI 1–15%), 2001–2010 (WPR 14%; 95% CI 6–24%) and 2011–2020 (WPR 28%; 95% CI 19–38%) indicated an increase in the resistance rate. Thus, this difference was statistically significant ($P < 0.001$). Based on the quality of the studies, the resistance rates did not differ between the groups ($P = 0.67$), the highest resistance rate was reported in Asia, followed by America and Africa (24%, 95% CI 17–33%; 23%, 95% CI 0–80%; 5%, 95% CI 1–11%). Only one study was conducted in Europe (40%, 95% CI 25–57%;) (Supplementary Data). No significant difference was found in the method used for AST ($P = 0.36$).

Conclusion: emphasized the distribution of antibiotic- resistant strains in different continents. Also, temporal changes in antibiotic resistance rates were found.

Keywords: Antimicrobial resistance; *V. cholera*e O1/O139

Abstract ID: 139
subject: rational antibiotic prescription and resistance mechanisms

Tedizolid activity against methicillin-resistant *Staphylococcus aureus* (MRSA) strains

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Background and Aim: *Staphylococcus aureus* (*S. aureus*) is a prominent cause of hospital-acquired and community-acquired infections ranging from superficial skin and soft tissue infections to endocarditis [1, 2]. Currently, World Health Organization (WHO) considers *S. aureus*, especially Methicillin-resistant *Staphylococcus aureus* (MRSA), as one of the fundamental clinical challenges throughout the world.

Material And Methods: A systematic search was conducted to evaluate the antibacterial activity of recently approved antibiotics against MRSA strains. The electronic databases: Medline, Embase, and Web of Science were searched to identify relevant articles until November 30, 2020. The search strategy was based on keywords derived from our research questions. Te keywords used in the search were: "tedizolid", "Methicillin-Resistant *Staphylococcus aureus*", and "minimum inhibitory concentration". The Boolean operators were used to combine all descriptors. The search strategy was adapted to the features of each database.

Results: The prevalence of tedizolid susceptibility is available in 21 studies. Te overall antibacterial activity of tedizolid in 12,204 MRSA isolates was at 0.250 and 0.500 µg/mL for MIC50 and MIC90, respectively. Out of 21 studies, the pooled prevalence of tedizolid susceptibility was 100% (95% CI: 100–100).

Conclusion: It was also shown that the MIC of tedizolid is much lower than the MIC of vancomycin against VISA strains. In addition, tedizolid demonstrated greater in vitro potency than linezolid against MRSA strains, but further research is required for a treatment recommendation.

Keywords: MRSA, antibacterial activity, tedizolid

Abstract ID: 137
subject: rational antibiotic prescription and resistance mechanisms

Investigating antibiotic resistance patterns, biofilm formation strength, abundance of virulence factors and molecular typing of *Klebsiella oxytoca* strains isolated from patients hospitalized in Hamadan

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Background and Aim: *Klebsiella oxytoca* is a gram-negative bacterium that is now the second most common bacterium in hospitalized patients after *Klebsiella pneumoniae*, and is often associated with blood and urinary tract infections. The ability to form biofilms in this bacterium reduces the host immune response and the effectiveness of antibiotics. *Klebsiella oxytoca* is resistant to a large number of common antibiotics and has become an opportunistic pathogen with multiple drug resistance in different hospital departments. . The aim of this study was to investigate the antibiotic resistance pattern, biofilm formation strength, virulence factor abundance, and molecular typing of *Klebsiella oxytoca* strains isolated from Hamadan hospitals.

Material And Methods: In this cross-sectional descriptive study, 35 samples of *Klebsiella oxytoca* were collected from educational hospitals in Hamedan city. *Klebsiella oxytoca* isolates were identified by standard microbial tests and biochemical methods. Antibiotic resistance pattern was investigated by disk diffusion method and based on CLSI 2022 criteria. In order to evaluate the formation of biofilm, the crystal violet method was used in microplates. Virulence genes were also checked by PCR method and molecular typing of strains was done by ERIC PCR method.

Results: Of the 35 clinical *Klebsiella oxytoca* isolates, the highest antibiotic resistance was to ciprofloxacin (4.91%) and the lowest resistance was to amikacin (4.31%). In this study, 14 (40%) clinical specimens did not form biofilm. Biofilm formation was observed in 10 (28.5%) weak, 5 (14.2%) moderate, and 6 (17.1%) high-strength specimens. Also, according to the PCR results of 35 clinical *Klebsiella oxytoca* isolates, the levels of bacterial virulence genes *fimA*, *matB*, *mrkA*, *npsB*, and *pilQ* were (77.1%), (42.8%), (65.7%), (22.8%), and (57.1%). And the results of ERIC-PCR analysis of *Klebsiella oxytoca* isolates showed the presence of genetic diversity among these isolates.

Conclusion: The results of this study showed that the isolation rate of *Klebsiella oxytoca* was higher in respiratory samples than in other samples. The rate of biofilm formation was 60%. A high level of antibiotic resistance was observed and the most effective antibiotic was amikacin. Given these results, the necessity of proper diagnosis, control and treatment of infections caused by *Klebsiella oxytoca*, especially in hospital samples, is emphasized.

Keywords: Biofilm, antibiotic resistance, virulence genes, molecular typing, *Klebsiella oxytoca*

Abstract ID: 107
subject: rational antibiotic prescription and resistance mechanisms

The efficacy of two triple therapy regimens and one quadruple regimen in eradicating *Helicobacter pylori* in patients with peptic ulcer: A randomized clinical trial.

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Background and Aim: The eradication of *Helicobacter pylori* (*H. pylori*) is crucial in treating peptic ulcers (PU). Various regimens have been suggested to eradicate this organism. In this study, the effectiveness of three anti-*H. pylori* regimens were compared in patients with dyspepsia or PP.

Material And Methods: This randomized, open-label clinical trial included 136 patients with *H. pylori* infection without a history of *H. pylori* treatment. Patients were randomly divided into Three groups. The OAC group received 20 mg Omeprazole capsules twice a day, two 500 mg Amoxicillin capsules twice a day, and 500 mg Clarithromycin capsules twice a day, for 14 days. The OAL group received 20 mg Omeprazole capsules twice a day, two 500 mg Amoxicillin capsules twice a day, and Levofloxacin 500 mg capsules twice a day, for 14 days. The OAMB group received 20 mg Omeprazole capsules twice a day, two 500 mg Amoxicillin capsules twice a day, Metronidazole 500mg three times a day, and Bismuth 240 mg twice a day, for 14 days. Evaluation for compliance and drug-related adverse effects were assessed at the end of two weeks. *H. pylori* eradication was evaluated eight weeks after treatment using the C14urease breath test (UBT).

Results: A total of 136 patients participated in this study, and their groups were matched based on age and sex. The results of the UBT test showed that the eradication rate of *H. pylori* was 82.2%, 91.3%, and 97.3% for the three-drug OAC, OAMB, and OAL treatment regimens, respectively. Moreover, all the regimens showed high compliance among the patients.

Conclusion: The OAL regime achieved an acceptable rate of *H. pylori* infection eradication with good tolerance in patients with PU without acute side effects.

Keywords: *H. pylori*, antimicrobial, eradication therapy, randomized trial, triple therapy, *Helicobacter pylori*

Abstract ID: 92
subject: rational antibiotic prescription and resistance mechanisms

Antibiotic prescription prevalence in Iranian outpatients: A focus on defined daily doses and the AWaRe classification system

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Background and Aim: The inappropriate use and overprescription of antibiotics pose global health threat, particularly contributing to antimicrobial resistance. This study aims to evaluate antibiotic prescription prevalence in Iranian outpatients using the Defined Daily Doses and Access, Watch, and Reserve (AWaRe) classification systems.

Material And Methods: This retrospective study analyzed electronic prescriptions for systemic antibiotics in Tehran, Iran, from March 2022 to March 2023. The data was obtained from the Iranian Health Insurance Organization and processed using the Cross-Industry Standard Process. Descriptive statistics and DID per 1000 inhabitants per day were calculated.

Results: A total of 817,178 antibiotic prescriptions were analyzed, with a gender distribution of 57.43% female and a median age of 48 years. On average, each patient received 1.89 antibiotics per prescription. Over 63% of antibiotics were classified in the "Watch" category, with Azithromycin being the most commonly prescribed (27.56%). The total DID was 4.99, with general practitioners accounting for 58.02% of the prescriptions, primarily prescribing Azithromycin.

Conclusion: The study emphasizes the high use of Watch group antibiotics, indicating a need for improved prescribing practices. Education on antibiotic stewardship and stricter guidelines are necessary to combat antimicrobial resistance. Continuous monitoring is crucial to optimize antibiotic use in outpatient settings in Iran.

Keywords: Antibiotic prescription, defined daily doses, AWaRe classification, outpatient settings, Iran

Abstract ID: 161
subject: rational antibiotic prescription and resistance mechanisms

Quinolone resistance and biofilm production capability among uropathogenic *Escherichia coli* isolates recovered from hospitalized patients

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Background and Aim: Uropathogenic *Escherichia coli* (UPEC) the most frequently isolated bacteria from urinary tract infections (UTI), may carry a variety of virulence factors. This study was designed to determine antibiogram pattern, distribution of quinolone resistance genes, and biofilm production capability among different phylogenetic groups of UPEC isolates from an Iranian inpatients' population.

Material And Methods: Totally, 126 UPEC obtained from inpatients with symptomatic UTI at three Shiraz teaching hospitals during 2016 were investigated. Antimicrobial susceptibility testing of isolates against quinolone and fluoroquinolones, biofilm formation, qnr A, B, and S genes and phylogenetic groups were assessed in 126-confirmed UPEC by phenotypic and molecular methods, correspondingly.

Results: Susceptibility testing revealed more than 50% and 81% of the UPEC were resistant to fluoroquinolones and quinolones, respectively. The frequency of *qnrS* and *qnrB* genes was 22% and 13.5%, correspondingly. No significant association between the presence of fluoroquinolone genes and antibiotic resistance was shown. The phylogroup B2 with rate of 84.1%, D (10.3%), A (3.2%) and B1 (2.4%) determined with PCR. Moreover, 80.2% of the isolates were biofilm producers, so that 42.1%, 16.7% and 21.4% of them were categorized as weak, moderate and strong producers, respectively.

Conclusion: A remarkable quinolone resistance along with a high rate of biofilm-producing UPEC was shown in our region. Knowledge on the UPEC phylogroups, resistance genes and their biofilm production capacity would significantly assist to limit the development of UTIs caused by UPEC.

Keywords: Biofilm, uropathogenic *Escherichia coli*, *qnr* genes

Abstract ID: 214
subject: rational antibiotic prescription and resistance mechanisms

Antibiotic resistance in *E. coli* isolated from healthcare facilities in Karaj: Importance of nitrofurantoin

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Background and Aim: Approximately 1.8 million individuals acquire urinary tract infections annually; this is a very common disorder. Nevertheless, the widespread occurrence of antibiotic resistance makes the treatment difficult. This study analyzes the *ant(2")-Ia* gene in *Escherichia coli* associated with aminoglycoside resistance.

Material And Methods: PCR and the Kirby-Bauer disc diffusion method were used in this study to find out how sensitive 100 types of *Escherichia coli* were to eight antibiotics from five different groups. These antibiotics were meropenem (MEN), tetracycline (TE), tobramycin (TOB), gentamicin (GM), nitrofurantoin (FM), amikacin (AN), ciprofloxacin (CP), and kanamycin (K). Four antibiotics belong to the class of aminoglycosides: tobramycin, gentamicin, amikacin, and kanamycin. We analyzed the data using SPSS and the independent t-test.

Results: Nitrofurantoin showed ninety-eight percent sensitivity among the *Escherichia coli* isolates, while kanamycin showed only twenty-one percent sensitivity. We evaluated 100 *Escherichia coli* isolates from different health centers in Karaj. Findings showed that 15 were resistant to one family of antibiotics, 16 to two, 38 to three, 20 to four, and one to five families. The findings show that there is important antibiotic resistance among the isolates. The test showed fifty-eight of one hundred had the *ant(2")-Ia* gene, and forty-two did not. The study highlights nitrofurantoin's place in the treatment of *E. coli* urinary tract infections in clinical practice. We must establish effective control measures.

Conclusion: The proper use of aminoglycosides and antibiotic resistance monitoring is crucial in health care.The study highlights the significance of nitrofurantoin in the management of *E. coli* urinary tract infections. *E. coli* in hospitals emphasizes the need for strict monitoring of antibiotic resistance. This study puts into focus the importance of proper aminoglycoside use in healthcare in order to adopt effective control measures. Resistance surveillance is important in controlling the spread of resistant bacteria. If not addressed, this concern will lead to more treatment failures, higher mortality rates, and increased health care costs.

Keywords: Urinary tract infections (UTIs) drug resistance, bacterial (DRB) *Escherichia coli* (*E. coli*) aminoglycosides (AMG) nitrofurantoin (FM) polymerase chain reaction (PCR)

Abstract ID: 285
subject: rational antibiotic prescription and resistance mechanisms

Investigation of integrons and ESBL genes In *Shigella flexneri* isolates from children with diarrhea in Shiraz, southwest Iran

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Background and Aim: Shigellosis is a bacterial disease that is endemic in many developing countries. As extended-spectrum β-lactamase (ESBL)-producing and multidrug-resistant *Shigella* isolates may emerge, adequately addressing and treating this condition is essential. This study aimed to detect integrons and ESBL genes in *Shigella flexneri* (*S. flexneri*) isolates from diarrheal children in Shiraz, Iran.

Material And Methods: In this study, a total of 397 diarrhea samples were obtained from patients referring to Shahid Dastgheib Hospital (Shiraz, Iran) during the winter of 2022. The samples were examined macroscopically (for consistency, mucus, and blood) and microscopically (for white and red blood cells). Shigella isolates were detected using standard microbiological methods, and 50 Shigella flexneri were identified. Antimicrobial resistance tests were done using the disc diffusion assay; then, DNA extraction was performed using the boiling process. In addition, Polymerase Chain Reaction (PCR) was used to identify integrons and ESBL genes.

Results: Of 50 *S. flexneri* positive stool samples obtained from 22 boys and 28 girls under 13 years of age, multidrug resistance was observed in all 50 cases. Thirty-four isolates (68%) were ESBL-positive. The CTX-M [28 (56%)] and TEM [19 (38%)] genes were highly prevalent, as were Int1 [40 (80%)] and Int2 [43 (86%)]. All isolates were resistant to amikacin, co-trimoxazole, streptomycin, and ceftriaxone. Resistance to ceftazidime was linked statistically ($p < 0.001$) to the ESBL phenotype and CTX-M and TEM genes, while the TEM gene was linked with chloramphenicol resistance. Furthermore, the TEM and CTX-M genes co-occurred in 19 (38%) cases and were linked with chloramphenicol resistance in ESBL-positive isolates ($p = 0.02$). In 27 (54%) cases, CTX-M and Int2 were both present, yielding a statistically significant relationship ($p = 0.017$); however, no significant concurrence was observed for other genes.

Conclusion: All *S. flexneri* isolates were multidrug-resistant, with high rates of CTX-M, Int1, and Int2 genes presence. These elements may help to detect resistant isolates, facilitating better management of the shigellosis in children.

Keywords: Shigellosis, ESBL, integrons, MDR, pediatric

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subject: rational antibiotic prescription and resistance mechanisms

Investigation of antimicrobial resistance profile and carbapenemase producing *Klebsiella pneumoniae* isolated from hospital wastewater in Shiraz, Iran: 2024-25

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Background and Aim: Bacterial resistance is a growing global health concern, posing significant challenges across the world. *Klebsiella pneumoniae* is a key member of the *Enterobacter*iaceae family and an opportunistic pathogen that causes a wide range of infections. The present study aims to determine the antimicrobial susceptibility profile and the prevalence of carbapenemase-producing *K. pneumoniae* isolates in hospital wastewater in Shiraz.

Material And Methods: In this study, influent and effluent wastewater samples were collected from Nemazee, Faghihi, and Hafez hospitals in Shiraz over a period of 6 weeks. The samples were cultured on McConkey agar plates containing cefotaxime 2 µg/mL. Five colonies were randomly selected from each plate, and identification of *K. pneumoniae* isolates was performed using various phenotypic and biochemical methods, including Gram staining, catalase and oxidase tests, growth in TSI medium, and the IMVIC test. Molecular confirmation of the isolates was carried out with specific primers targeting the khe gene. Antibiotic resistance patterns were assessed using the Kirby-Bauer disk diffusion method, and colistin resistance was tested using microbroth dilution. Isolates resistant to at least one antibiotic from at least three different classes were classified as multidrug-resistant (MDR). Broad-spectrum beta-lactamase (ESBL) production was determined using the Combined Disc Diffusion method. mCIM and eCIM tests were positive for 20.63% and 6.35% of the isolates, respectively.

Results: A total of 63 *K. pneumoniae* isolates were identified in this study. The highest resistance rates were observed against ampicillin-sulbactam (88.89%), amoxicillin-clavulanate (82.54%), and ceftazidime (76.19%), while the lowest resistance was noted for imipenem (3.17%), meropenem (26.98%), and colistin (31.75%). 79.37% of the isolates were classified as MDR, and 61.90% were identified as ESBL producers. The mCIM and eCIM tests showed that 20.63% and 6.35% of the isolates, respectively, produced carbapenemases.

Conclusion: Hospital wastewater plays a crucial role in harboring and spreading pathogenic bacteria, along with facilitating the transmission of antibiotic resistance genes. This study revealed significant antibiotic resistance among *K. pneumoniae* isolates, with a notable proportion being MDR and ESBL producers. These findings underscore the urgent need for enhanced infection control measures in healthcare settings to prevent the spread of resistant pathogens.

Keywords: *K. pneumoniae*, ESBL, carbapenemase, MDR, Hospital wastewater

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subject: rational antibiotic prescription and resistance mechanisms

Prevalence of integron classes 1, 2 and 3 among multi-drug resistant *Klebsiella pneumoniae* isolated from hospital wastewater in Shiraz, Iran: 2024-25

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Background and Aim: Antimicrobial resistance has become an escalating threat to global public health, creating substantial challenges worldwide. *Klebsiella pneumoniae*, a prominent member of the *Enterobacter*iaceae family, is an opportunistic pathogen responsible for a wide array of infections. The current study aimed to investigate the prevalence of integron classes among multidrug-resistant *K. pneumoniae* isolated from hospital wastewater in Shiraz.

Material And Methods: In this study, 63 *K. pneumoniae* isolates, previously obtained from hospital wastewater and with available antibiogram results, were genotypically analyzed. The study focused on the prevalence of the *blaTEM, blaCTX-M*, and *blaSHV* genes among ESBL-producing isolates, the prevalence of *blaKPC, blaVIM, blaNDM, blaIMP*, and *blaOXA-48* genes among carbapenemase-producing isolates, the prevalence of integron classes 1, 2, and 3 among multidrug-resistant isolates, the prevalence of *tetA* and *tetB* genes among tetracycline-resistant isolates, and the prevalence of *qnrA, qnrB*, and *qnrS* genes among ciprofloxacin-resistant isolates.

Results: Among the integron classes, class 1 had the highest prevalence at 30% (n=15). Among the beta-lactamase genes, *blaSHV* was the most prevalent at 87.18% (n=34), while *blaTEM* had the lowest prevalence at 30.77% (n=12). *blaOXA-48* gene was found in 3 isolates, and *blaVIM* gene was detected in 2 isolates; No other carbapenemase genes were observed in any of the isolates. The *tetA, tetB*, and *qnrB* genes were identified in 6, 4, and 5 isolates, respectively.

Conclusion: Hospital wastewater serves as an important reservoir for pathogenic microorganisms and contributes significantly to the dissemination of antibiotic resistance genes. The results of this study highlighted considerable genotypically resistance to antibiotics in *K. pneumoniae* isolates. These results emphasize the critical necessity for stricter infection control protocols in healthcare facilities to curb the spread of resistant bacterial strains.

Keywords: *K. pneumoniae*, MDR, integrons, carbapenems, resistance genes

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